Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:52:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818981.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_SRR1818981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818981.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:52:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,606,179
Mapped reads	2,472,499 / 94.87%
Unmapped reads	133,680 / 5.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,114 / 1.31%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	1,223,233 / 46.94%
Duplication rate	41.33%
Clipped reads	2,480,431 / 95.18%

2.2. ACGT Content

Number/percentage of A's	66,768,489 / 29.14%
Number/percentage of C's	46,830,210 / 20.44%
Number/percentage of T's	64,968,990 / 28.36%
Number/percentage of G's	50,547,678 / 22.06%
Number/percentage of N's	11,408 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0741

Standard Deviation	0.874

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

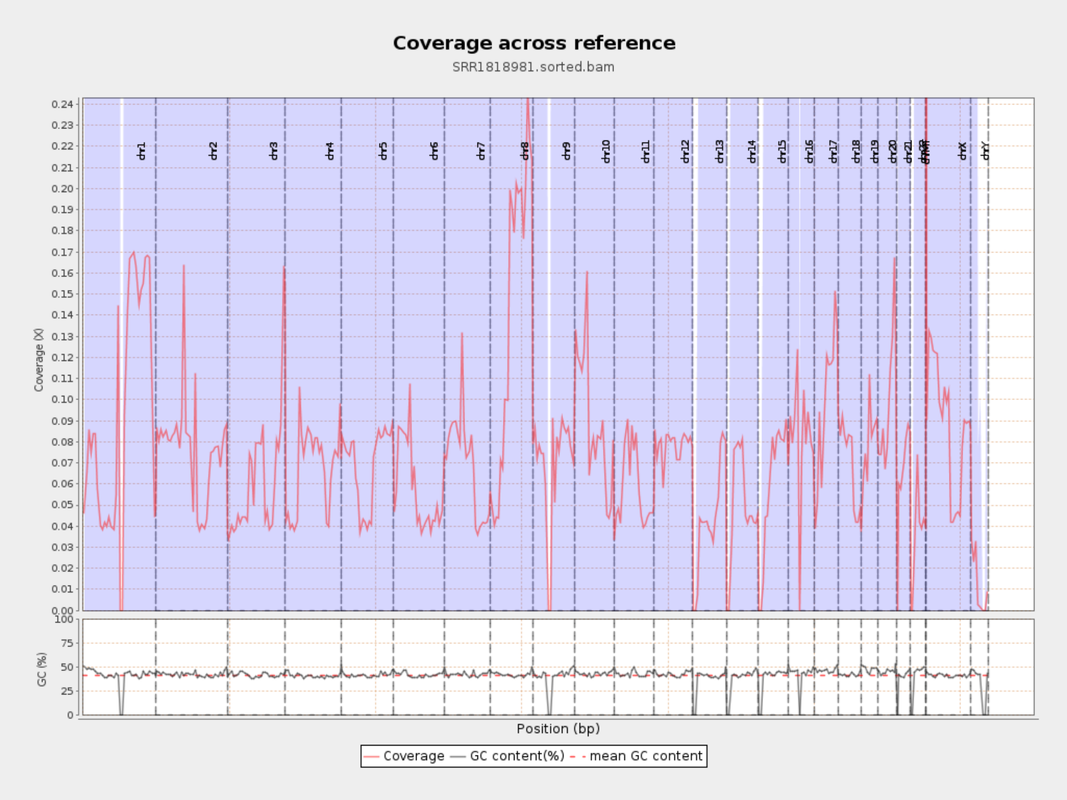
General error rate	0.65%
Mismatches	1,417,646
Insertions	36,464
Mapped reads with at least one insertion	1.43%
Deletions	72,075
Mapped reads with at least one deletion	2.85%
Homopolymer indels	41.76%

2.6. Chromosome stats

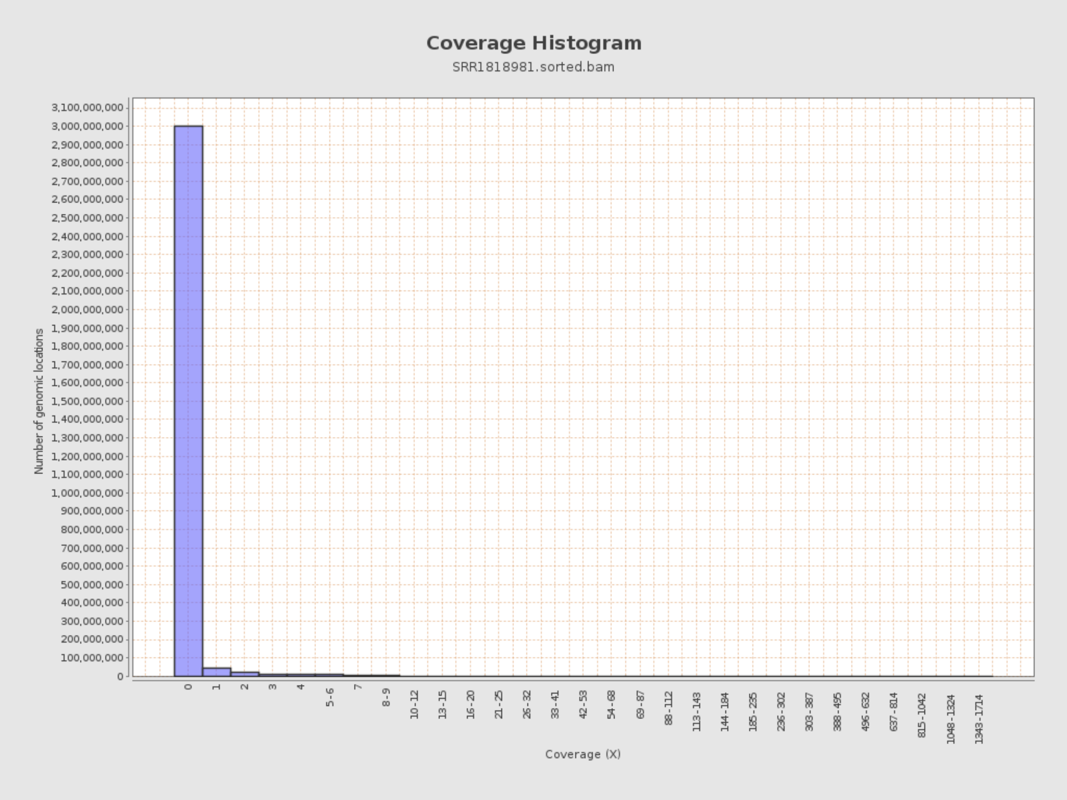
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23128757	0.0928	1.5681
chr2	243199373	18715145	0.077	1.1848
chr3	198022430	12166150	0.0614	0.4932
chr4	191154276	12887852	0.0674	0.5977
chr5	180915260	12463033	0.0689	0.5349
chr6	171115067	9871936	0.0577	0.5769
chr7	159138663	11041769	0.0694	1.0947

chr8	146364022	21092865	0.1441	0.8518
chr9	141213431	9789627	0.0693	0.7904
chr10	135534747	12032933	0.0888	1.0672
chr11	135006516	7824557	0.058	0.5592
chr12	133851895	10538619	0.0787	0.5721
chr13	115169878	5018704	0.0436	0.415
chr14	107349540	5367738	0.05	0.4771
chr15	102531392	5946448	0.058	0.4893
chr16	90354753	7250262	0.0802	0.9665
chr17	81195210	8006487	0.0986	0.7345
chr18	78077248	5463760	0.07	0.9501
chr19	59128983	4675063	0.0791	1.4958
chr20	63025520	6376368	0.1012	0.6825
chr21	48129895	3184404	0.0662	0.5607
chr22	51304566	1810178	0.0353	0.4141
chrMT	16571	36571	2.2069	3.2742
chrX	155270560	13862287	0.0893	0.6949
chrY	59373566	707239	0.0119	0.7059

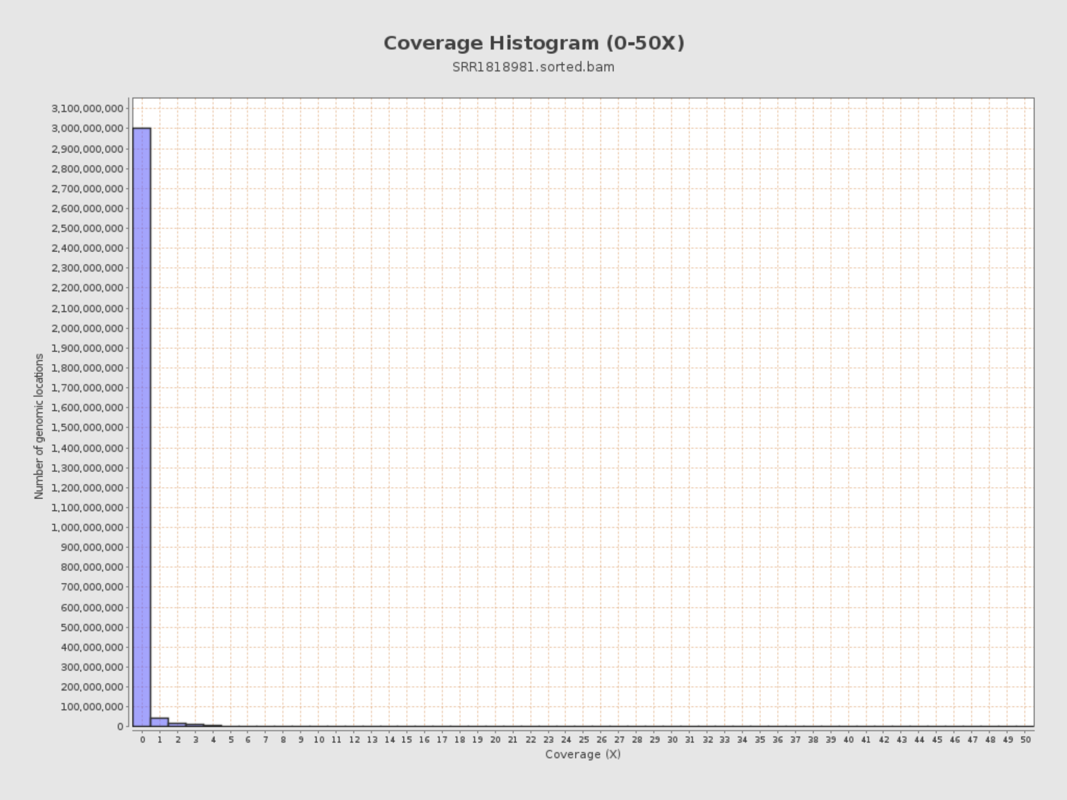
3. Results : Coverage across reference



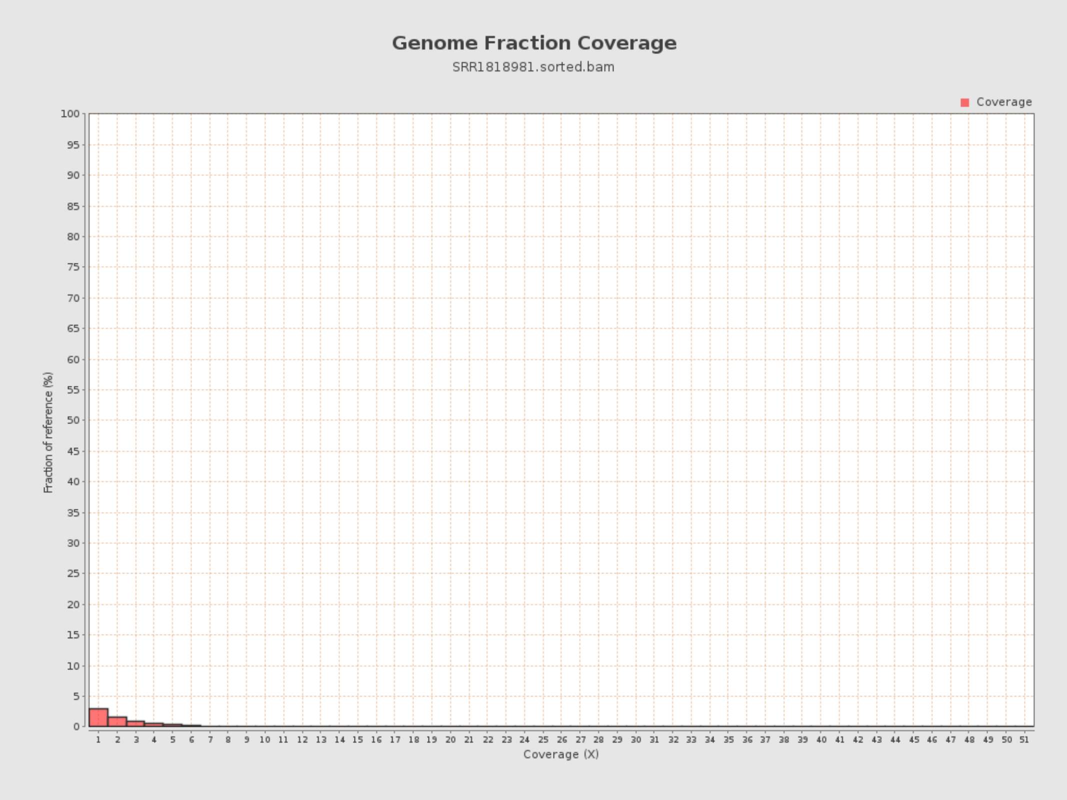
4. Results : Coverage Histogram



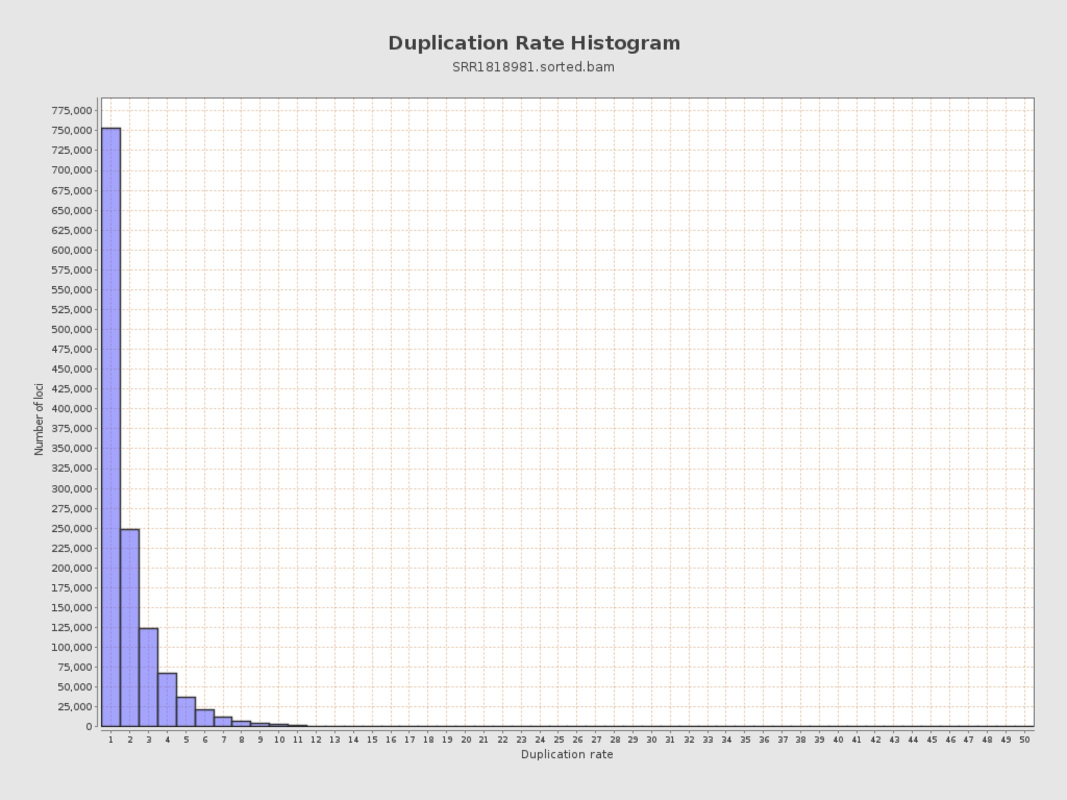
5. Results : Coverage Histogram (0-50X)



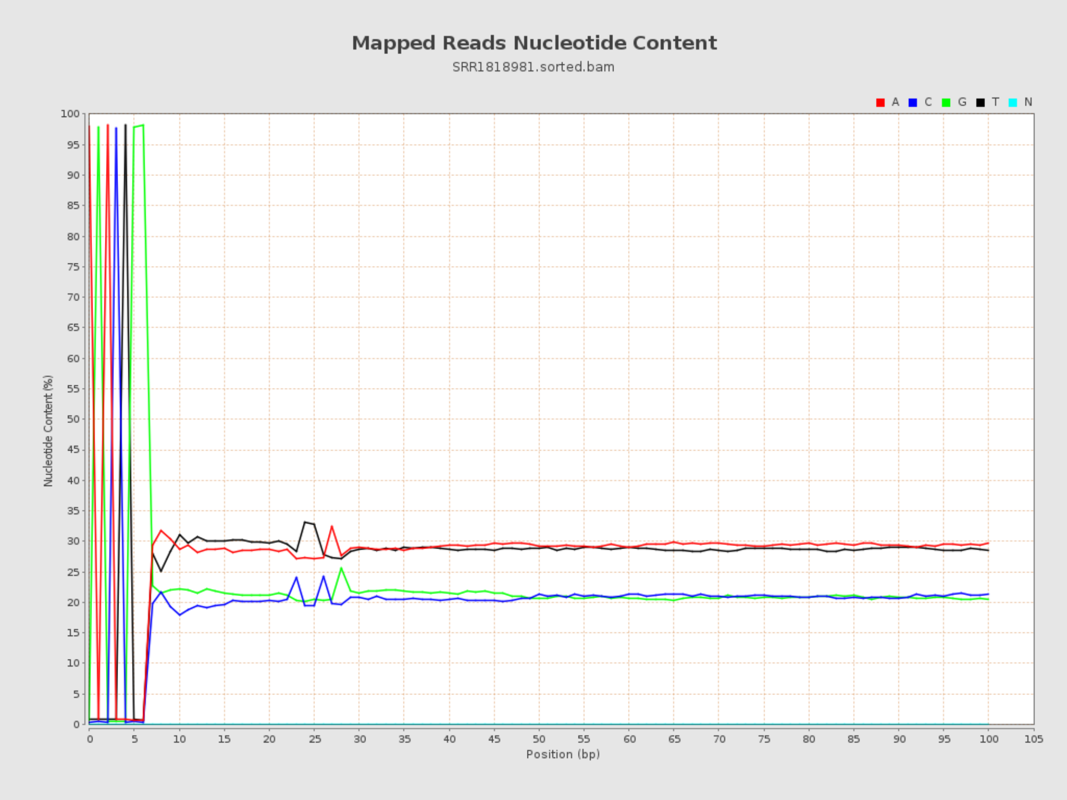
6. Results : Genome Fraction Coverage



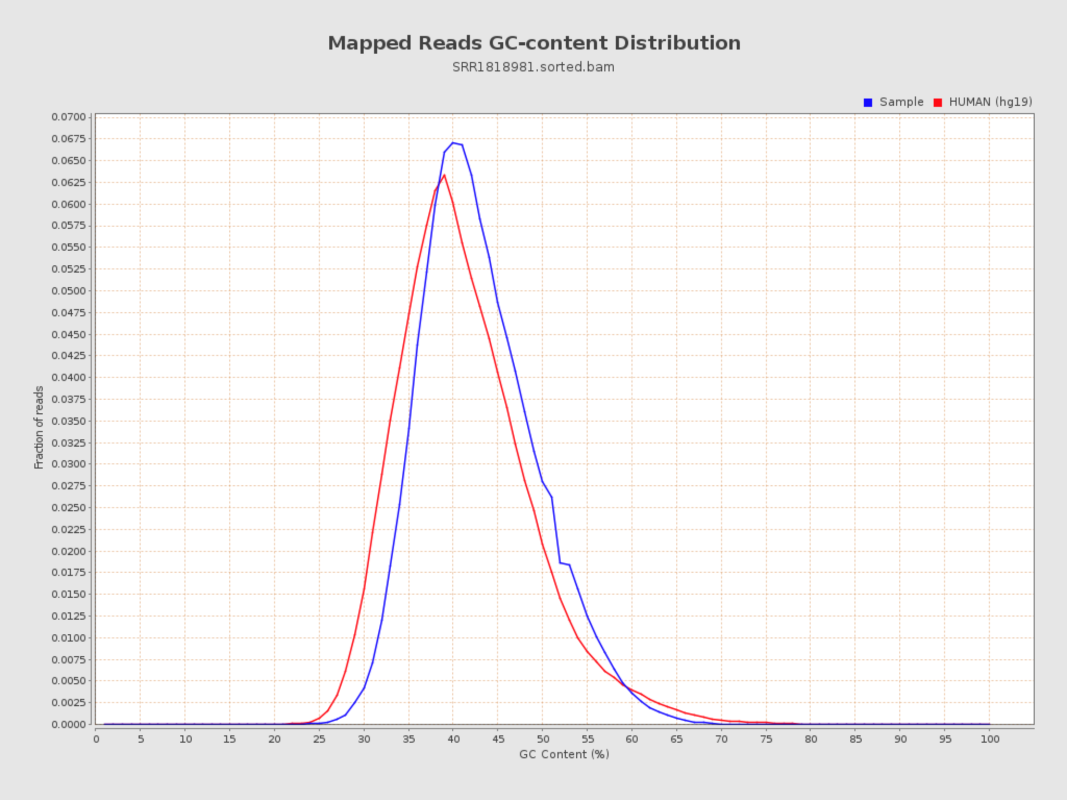
7. Results : Duplication Rate Histogram



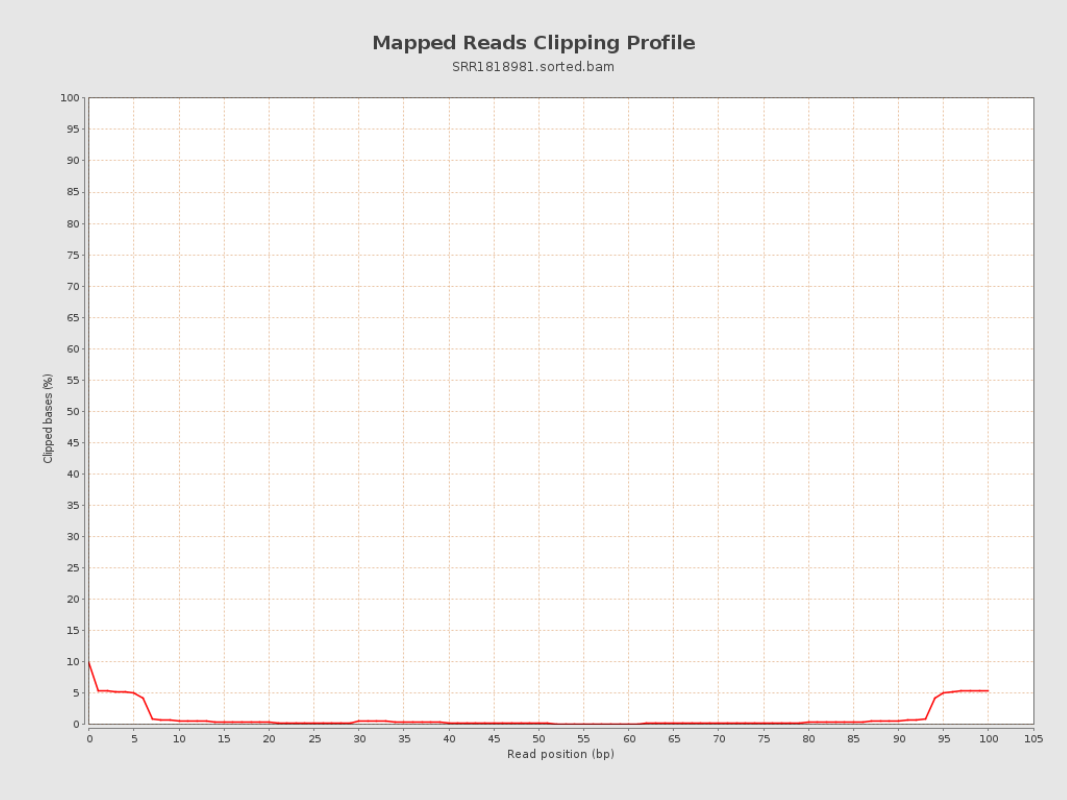
8. Results : Mapped Reads Nucleotide Content



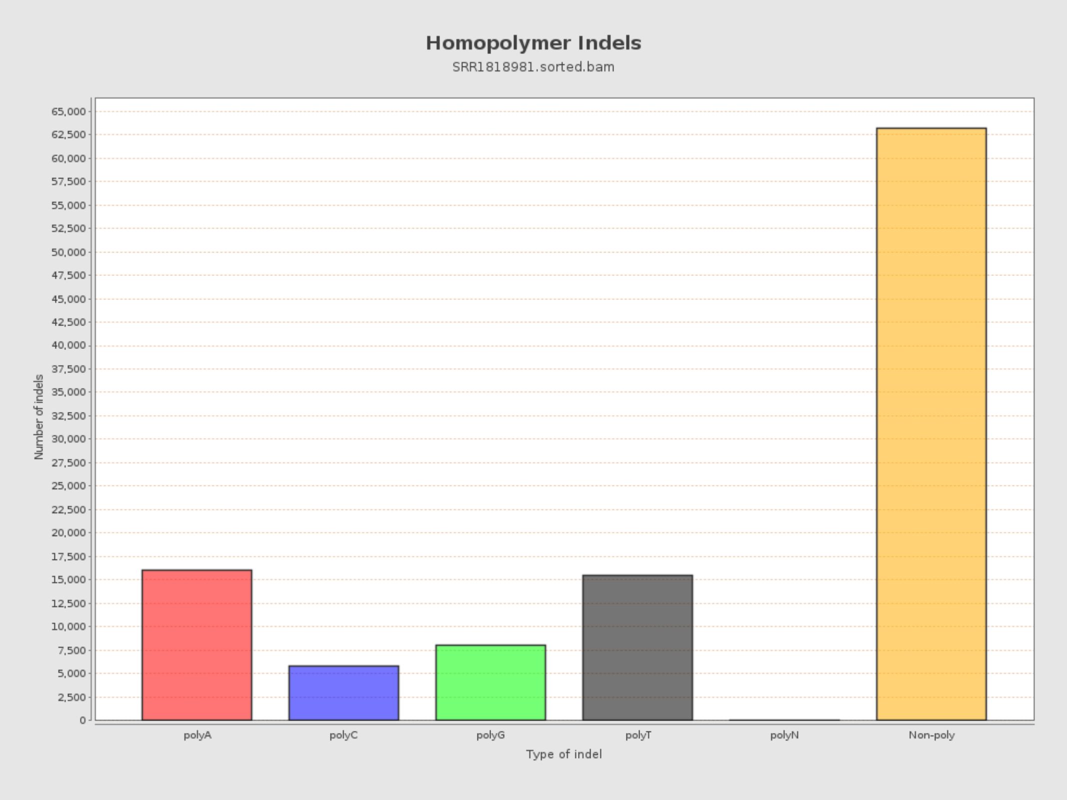
9. Results : Mapped Reads GC-content Distribution



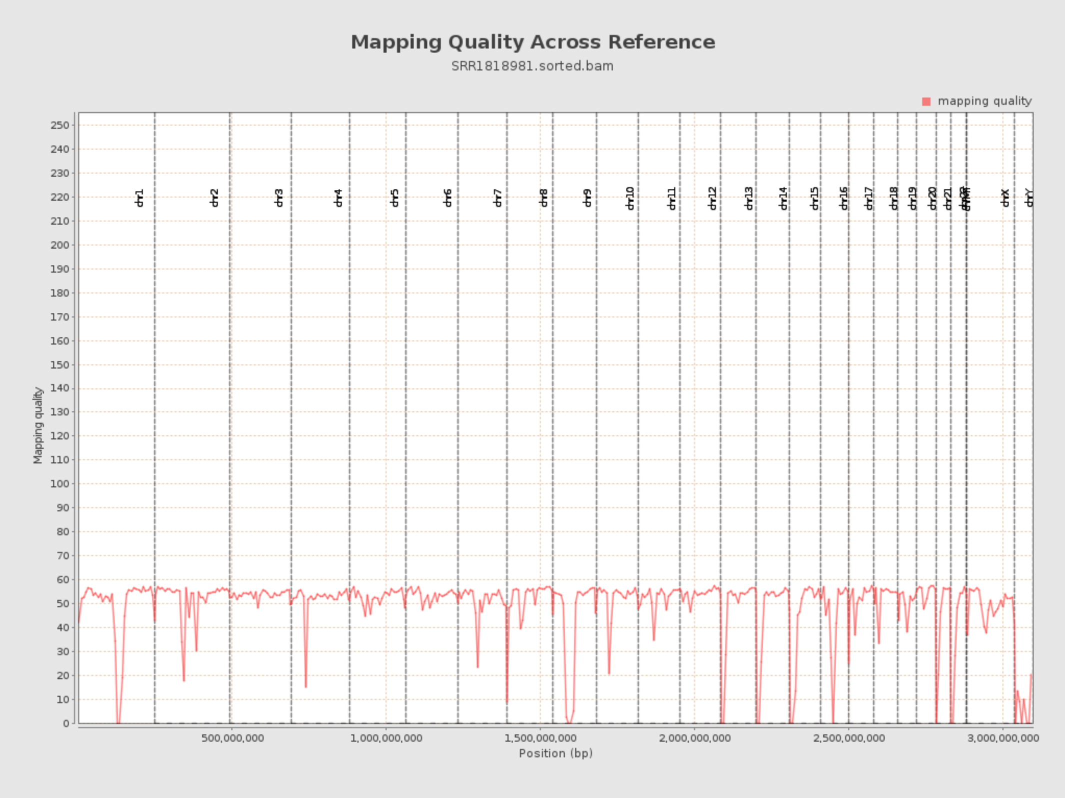
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram