Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818920.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_SRR1818920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:18:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,035,484
Mapped reads	2,842,240 / 93.63%
Unmapped reads	193,244 / 6.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,016 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	927,545 / 30.56%
Duplication rate	27.29%
Clipped reads	2,855,608 / 94.07%

2.2. ACGT Content

Number/percentage of A's	74,025,173 / 28.13%
Number/percentage of C's	53,825,433 / 20.46%
Number/percentage of T's	77,272,386 / 29.37%
Number/percentage of G's	58,004,946 / 22.04%
Number/percentage of N's	4,093 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0851

Standard Deviation	1.0334

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

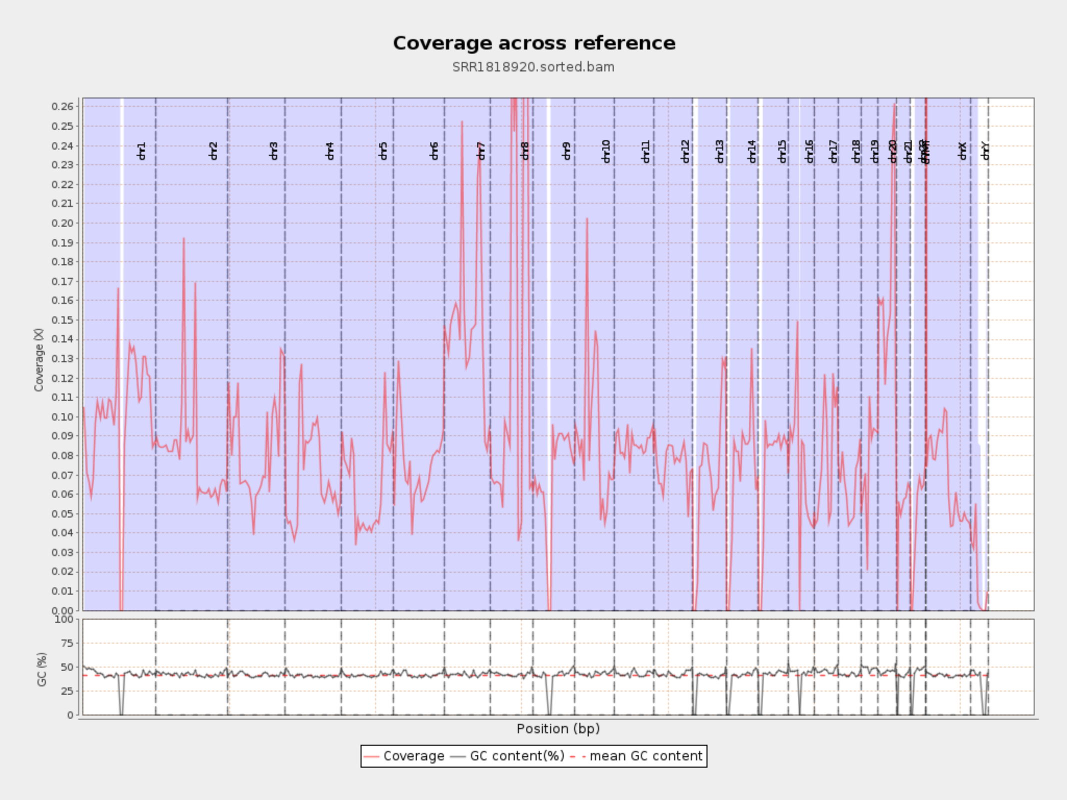
General error rate	0.65%
Mismatches	1,611,453
Insertions	41,920
Mapped reads with at least one insertion	1.42%
Deletions	89,185
Mapped reads with at least one deletion	3.06%
Homopolymer indels	41.09%

2.6. Chromosome stats

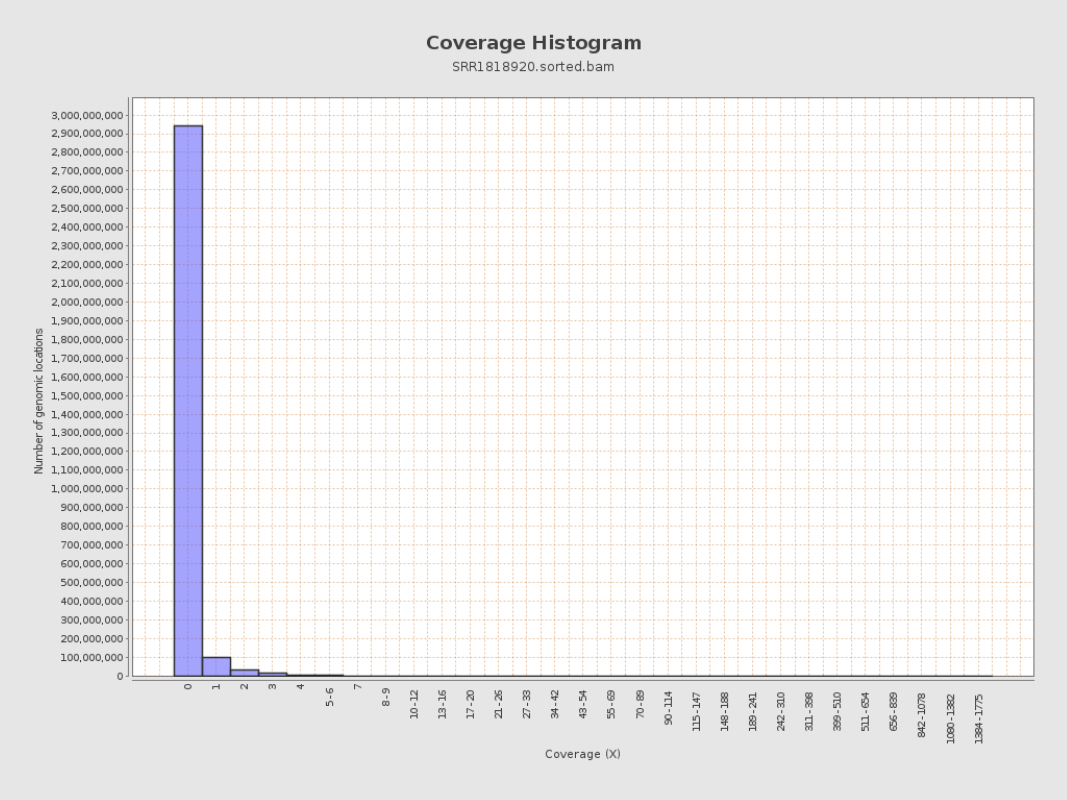
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24947872	0.1001	1.5237
chr2	243199373	19936235	0.082	1.6442
chr3	198022430	16586522	0.0838	0.4529
chr4	191154276	13430312	0.0703	0.5719
chr5	180915260	11677800	0.0645	0.4319
chr6	171115067	12878685	0.0753	0.4819
chr7	159138663	23806947	0.1496	2.2951

chr8	146364022	23037433	0.1574	0.8178
chr9	141213431	9695087	0.0687	0.8267
chr10	135534747	12224458	0.0902	1.3029
chr11	135006516	11569218	0.0857	0.5717
chr12	133851895	10179945	0.0761	0.4376
chr13	115169878	8064814	0.07	0.4062
chr14	107349540	7763029	0.0723	0.4686
chr15	102531392	7315973	0.0714	0.4129
chr16	90354753	6493631	0.0719	1.1415
chr17	81195210	6428802	0.0792	0.5984
chr18	78077248	5067712	0.0649	0.9163
chr19	59128983	4507220	0.0762	1.2326
chr20	63025520	10843111	0.172	0.7205
chr21	48129895	2526246	0.0525	0.4352
chr22	51304566	2334249	0.0455	0.3811
chrMT	16571	367744	22.192	13.6886
chrX	155270560	10651617	0.0686	0.4901
chrY	59373566	972567	0.0164	1.2826

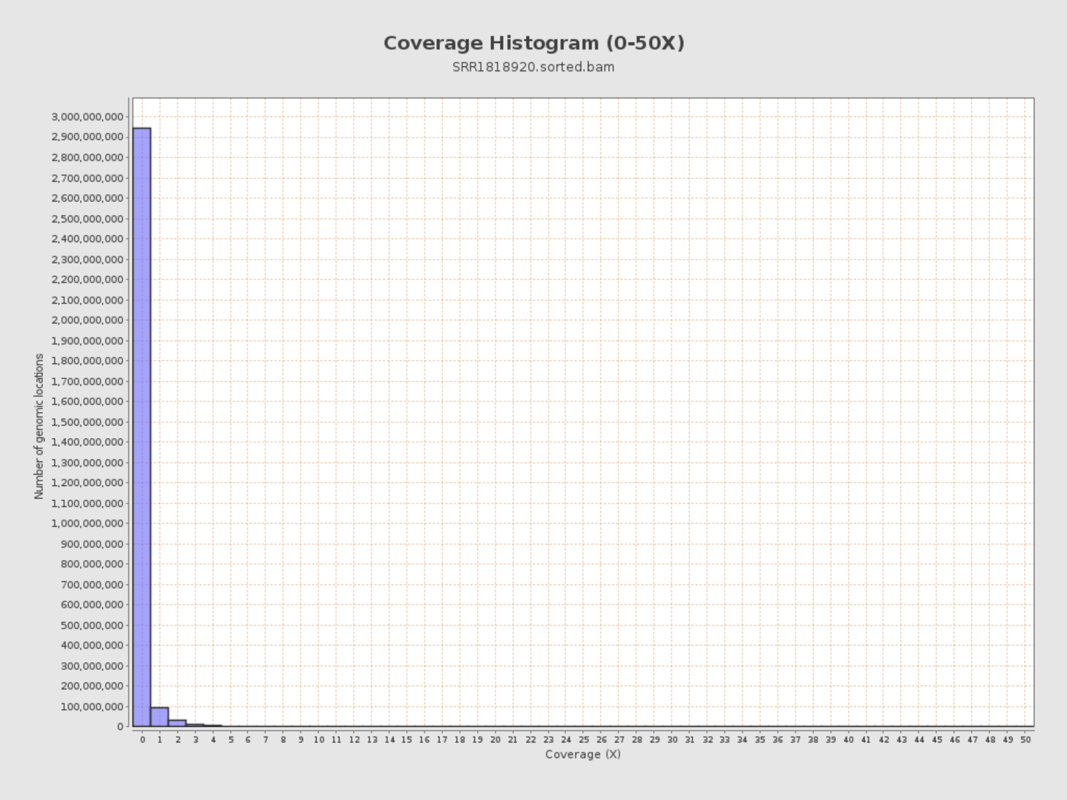
3. Results : Coverage across reference



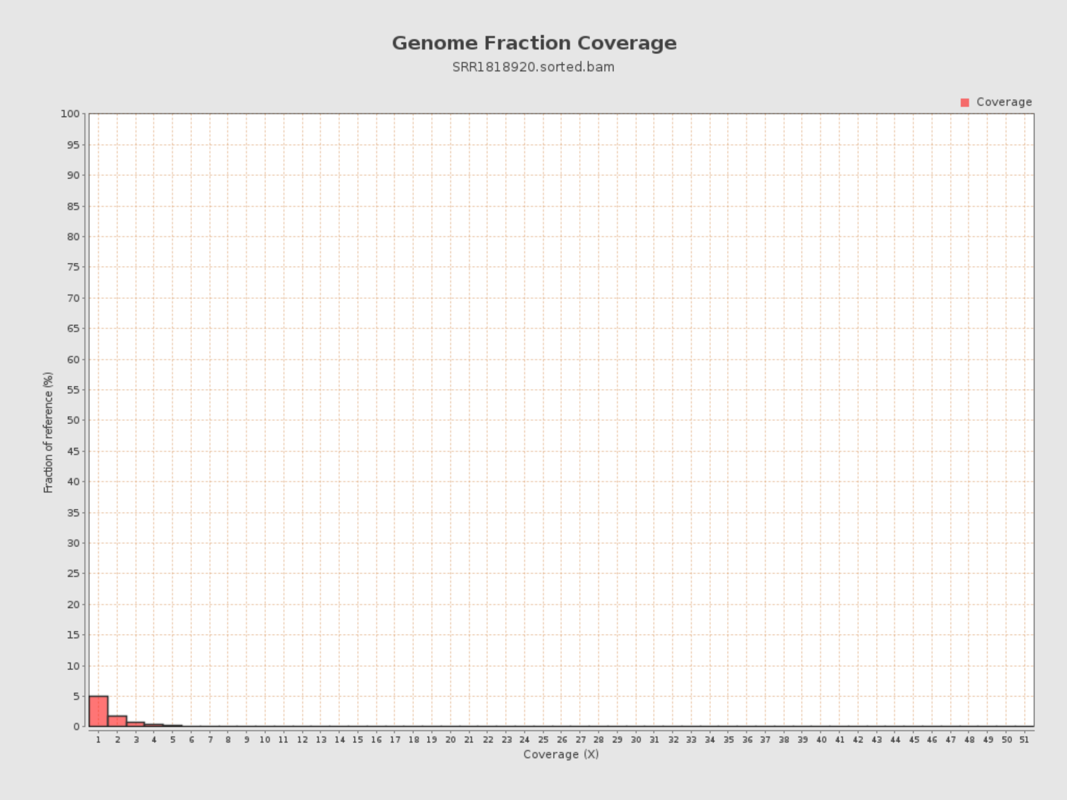
4. Results : Coverage Histogram



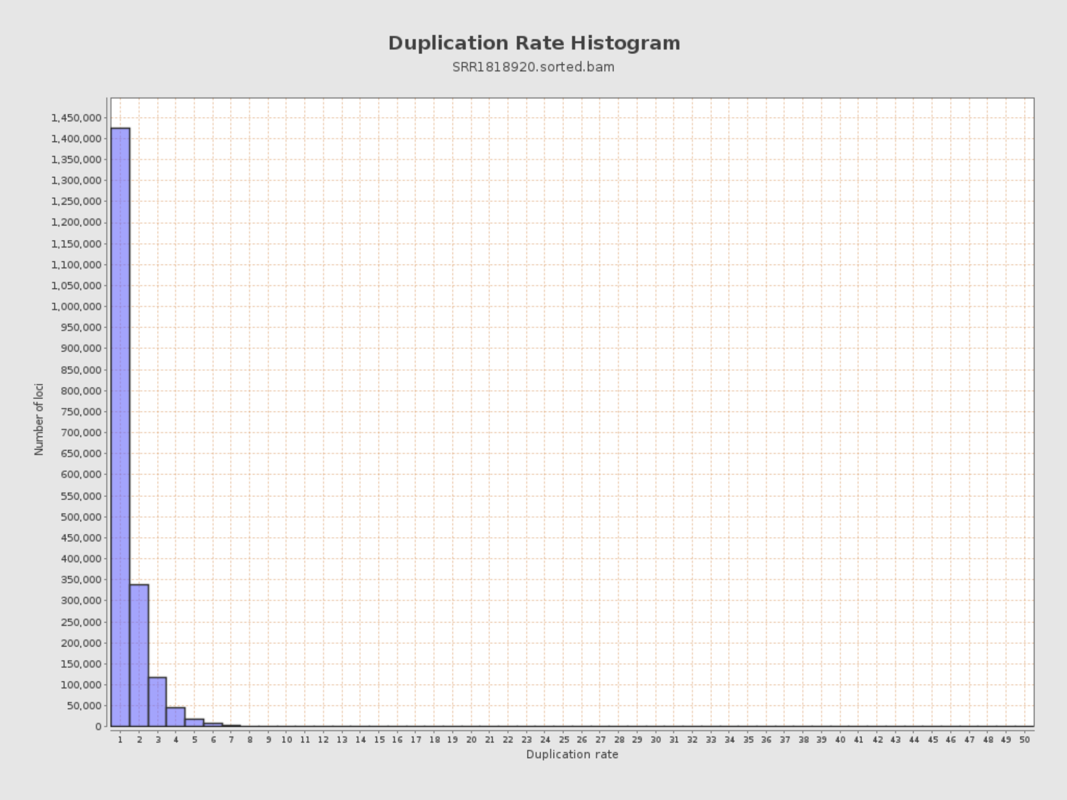
5. Results : Coverage Histogram (0-50X)



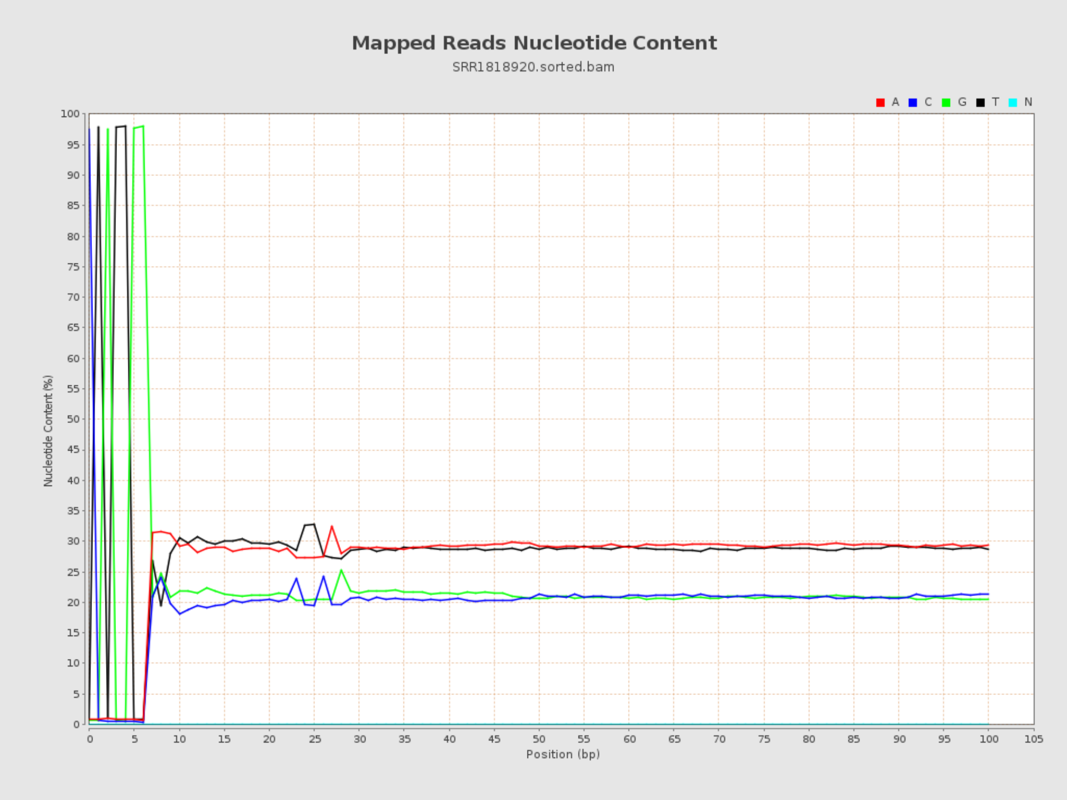
6. Results : Genome Fraction Coverage



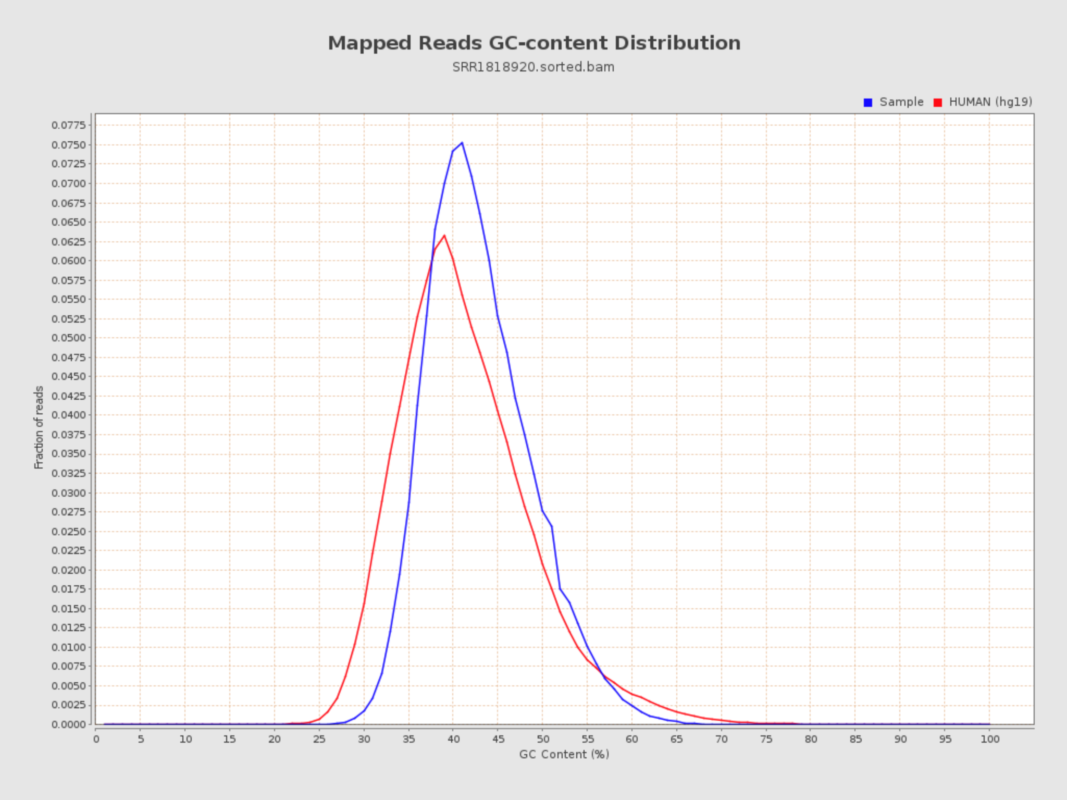
7. Results : Duplication Rate Histogram



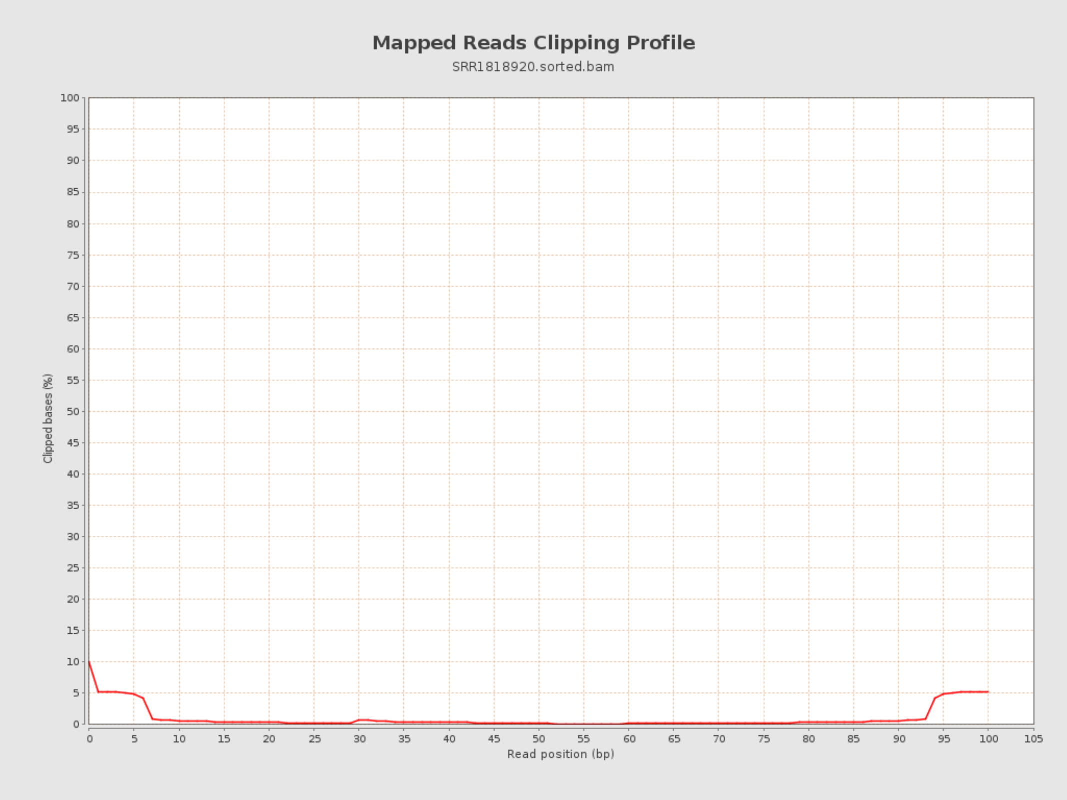
8. Results : Mapped Reads Nucleotide Content



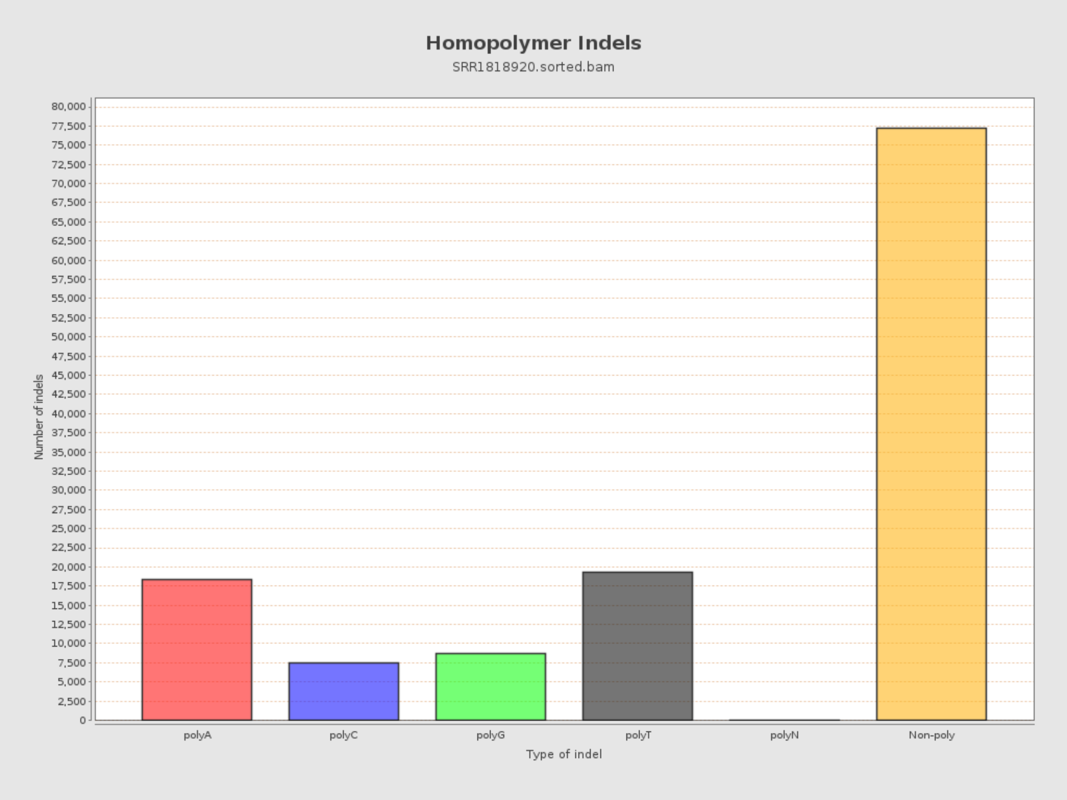
9. Results : Mapped Reads GC-content Distribution



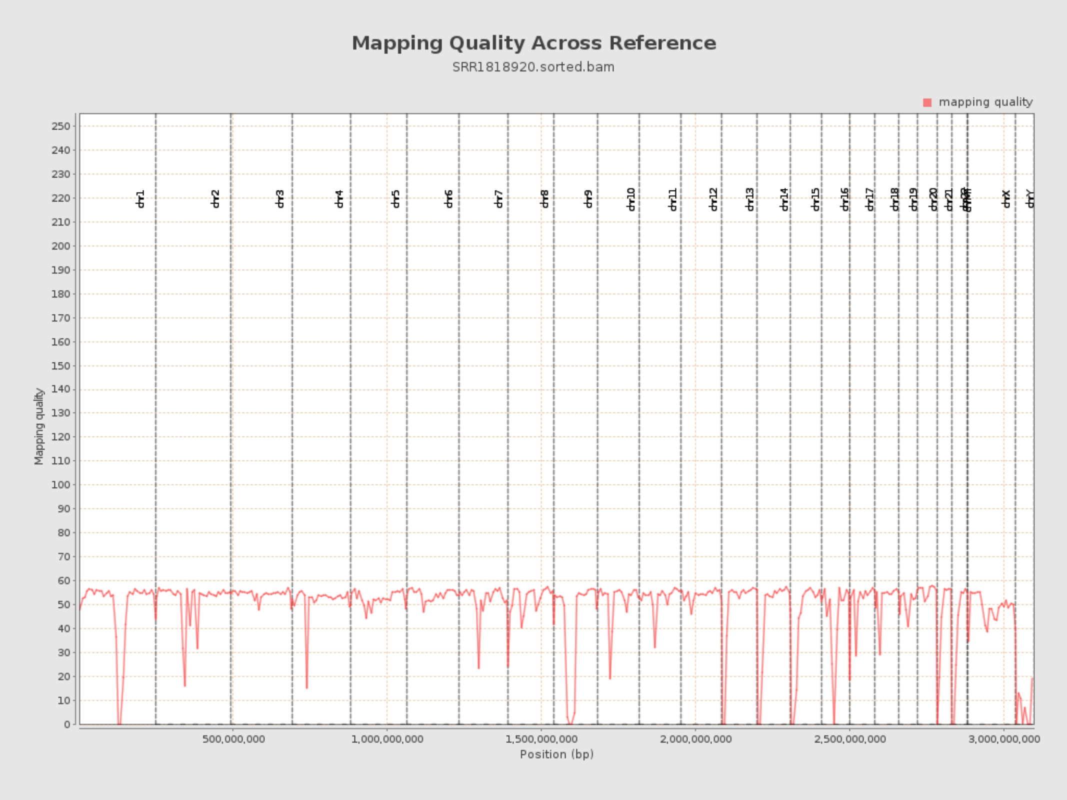
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram