Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:24:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819003.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_SRR1819003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819003.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:24:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,214,765
Mapped reads	1,191,761 / 98.11%
Unmapped reads	23,004 / 1.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,870 / 1.64%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	410,120 / 33.76%
Duplication rate	29.21%
Clipped reads	1,209,638 / 99.58%

2.2. ACGT Content

Number/percentage of A's	32,321,505 / 29.41%
Number/percentage of C's	23,674,770 / 21.54%
Number/percentage of T's	31,081,746 / 28.28%
Number/percentage of G's	22,825,455 / 20.77%
Number/percentage of N's	4,674 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.4844

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Mismatches and indels

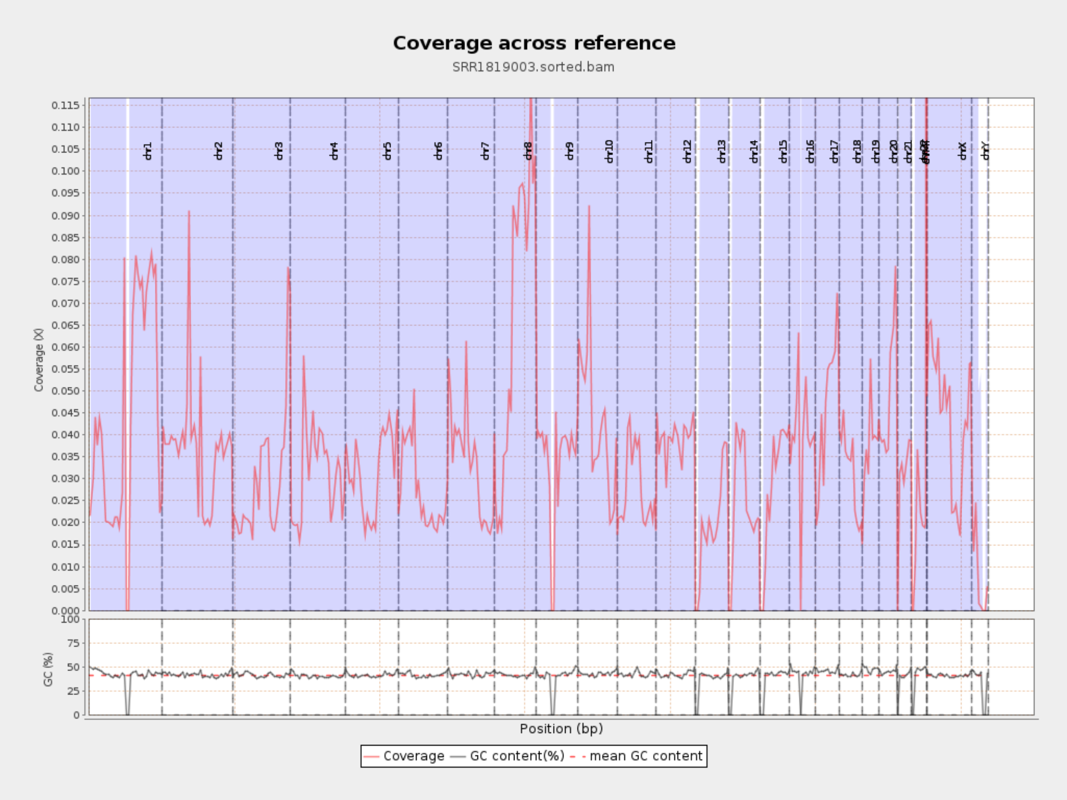
General error rate	0.7%
Mismatches	730,711
Insertions	15,522
Mapped reads with at least one insertion	1.26%
Deletions	35,894
Mapped reads with at least one deletion	2.95%
Homopolymer indels	42.67%

2.6. Chromosome stats

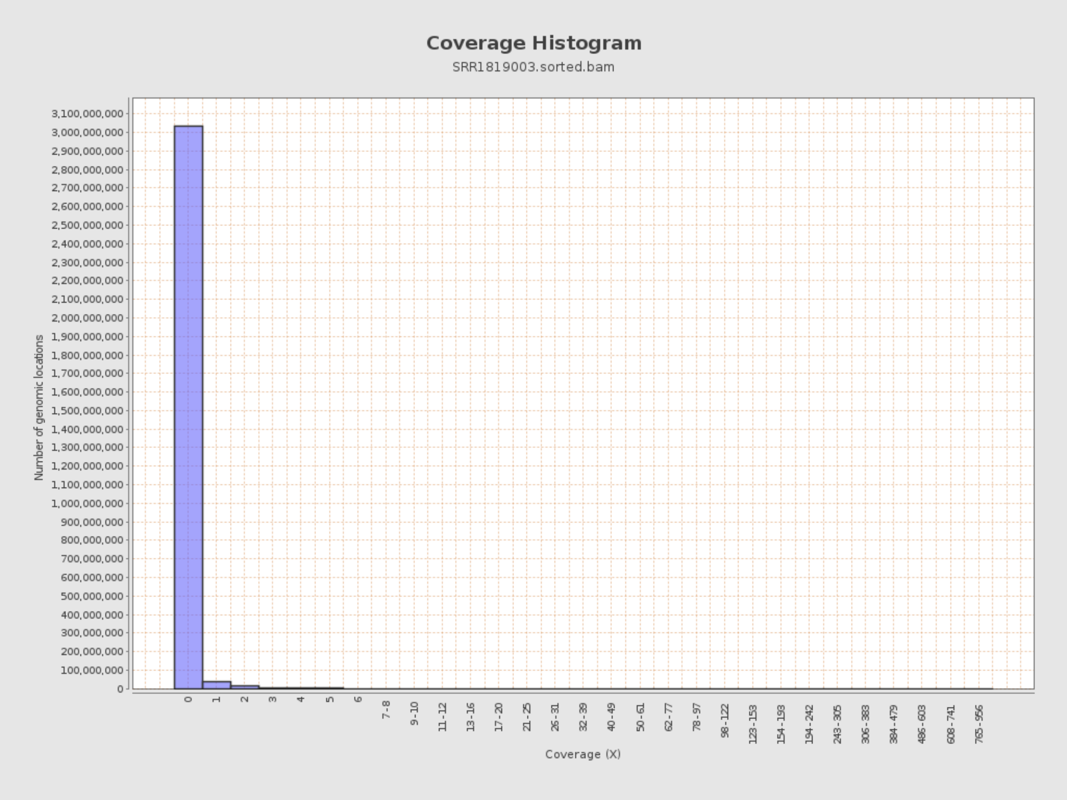
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11095058	0.0445	0.9254
chr2	243199373	9088394	0.0374	0.6563
chr3	198022430	5756555	0.0291	0.2676
chr4	191154276	5934946	0.031	0.325
chr5	180915260	5718549	0.0316	0.2885
chr6	171115067	4692281	0.0274	0.3187
chr7	159138663	5336256	0.0335	0.4999

chr8	146364022	9991474	0.0683	0.4499
chr9	141213431	4703435	0.0333	0.4194
chr10	135534747	5850646	0.0432	0.6068
chr11	135006516	3781408	0.028	0.3205
chr12	133851895	5228859	0.0391	0.3148
chr13	115169878	2284616	0.0198	0.2143
chr14	107349540	2634346	0.0245	0.2599
chr15	102531392	2877987	0.0281	0.2685
chr16	90354753	3556716	0.0394	0.5491
chr17	81195210	3846359	0.0474	0.3784
chr18	78077248	2483540	0.0318	0.4823
chr19	59128983	2247898	0.038	0.8121
chr20	63025520	3157067	0.0501	0.3717
chr21	48129895	1485228	0.0309	0.3033
chr22	51304566	879151	0.0171	0.2216
chrMT	16571	13879	0.8375	1.3893
chrX	155270560	6874678	0.0443	0.4024
chrY	59373566	455593	0.0077	0.466

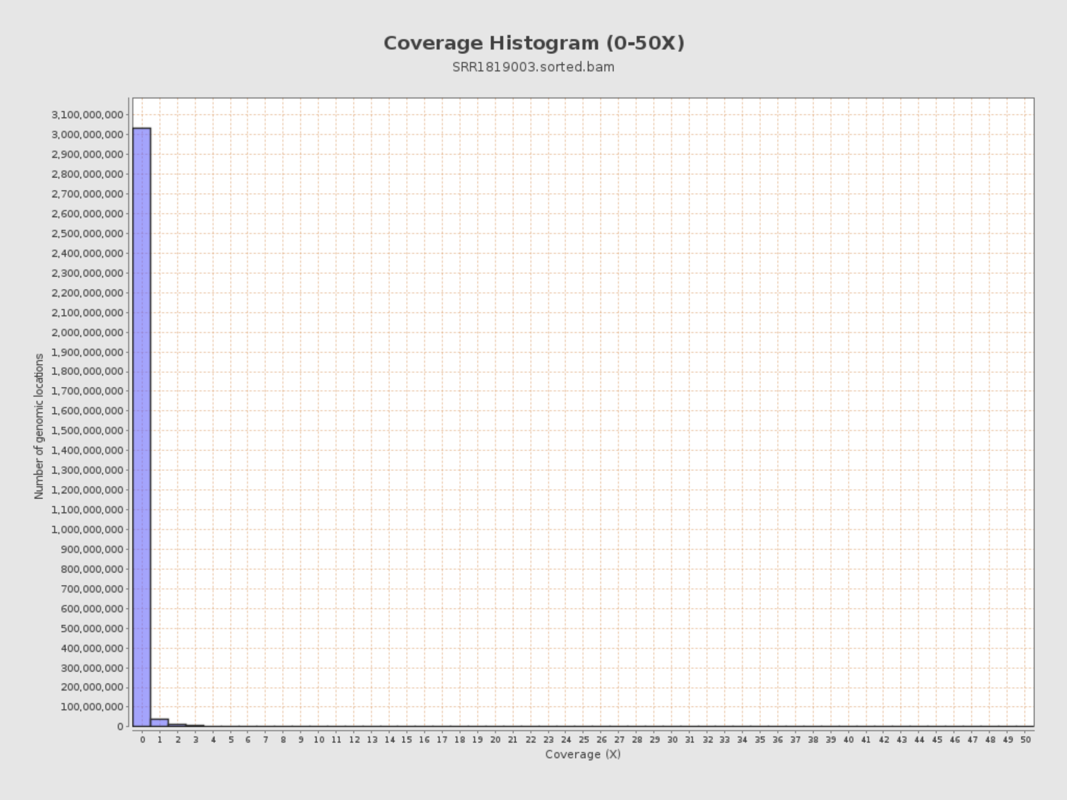
3. Results : Coverage across reference



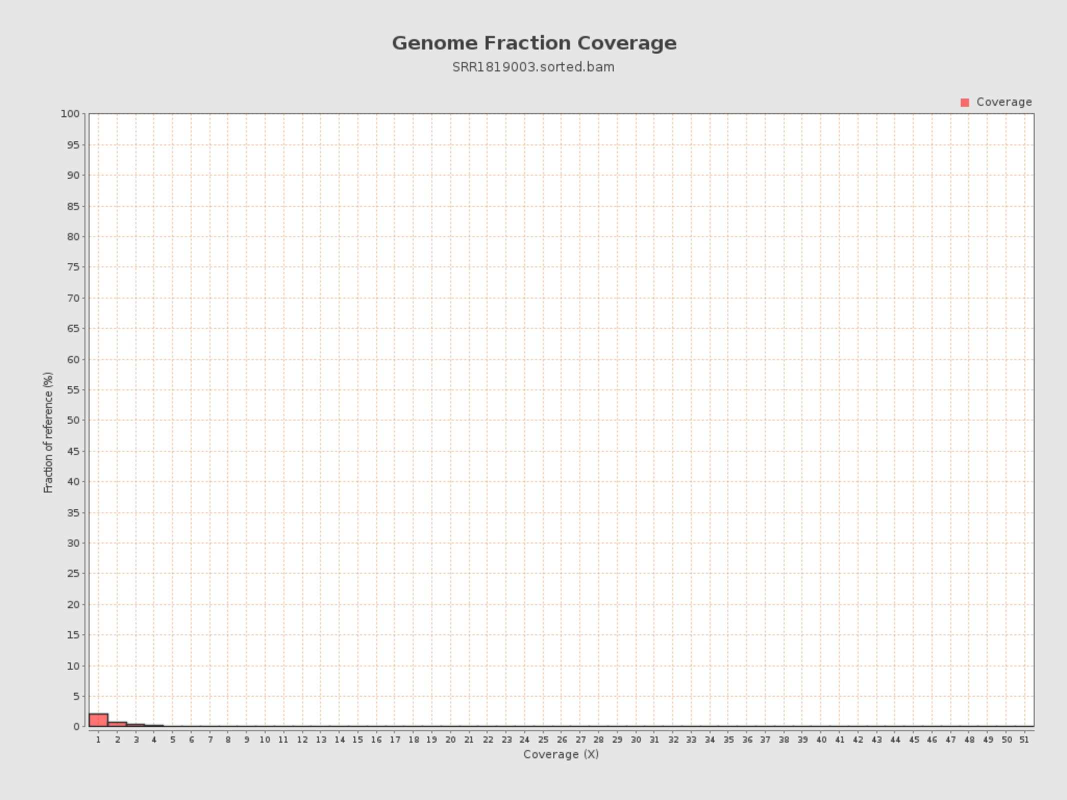
4. Results : Coverage Histogram



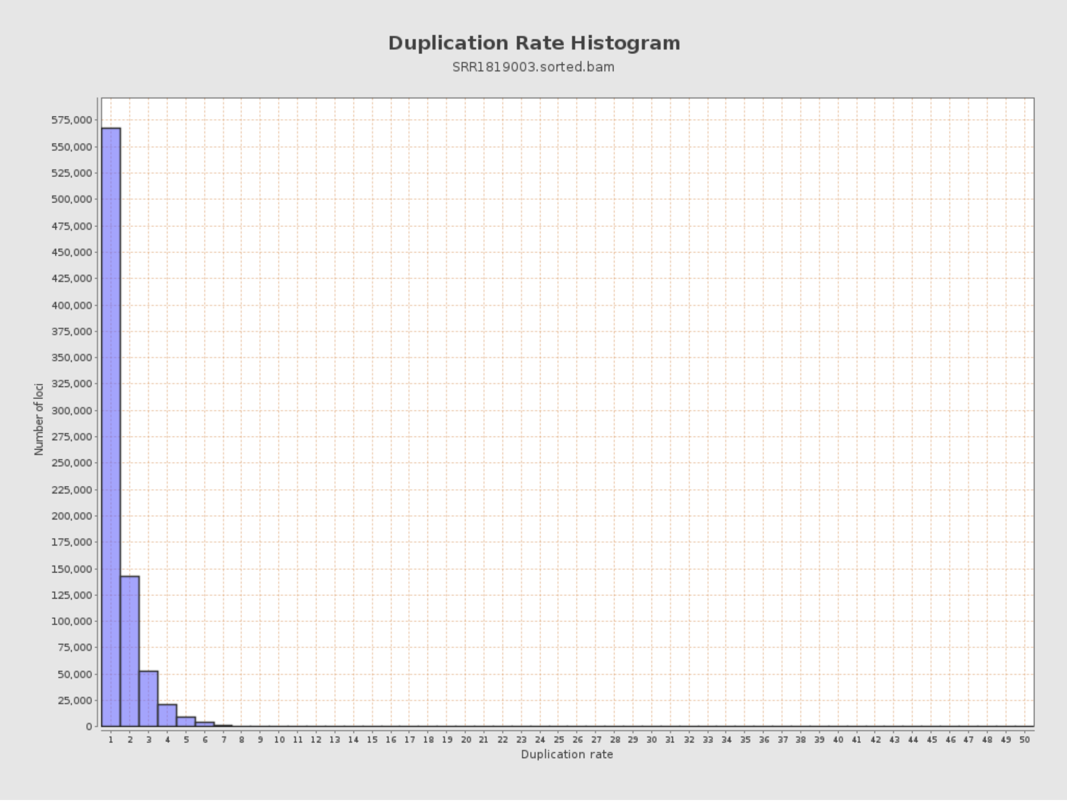
5. Results : Coverage Histogram (0-50X)



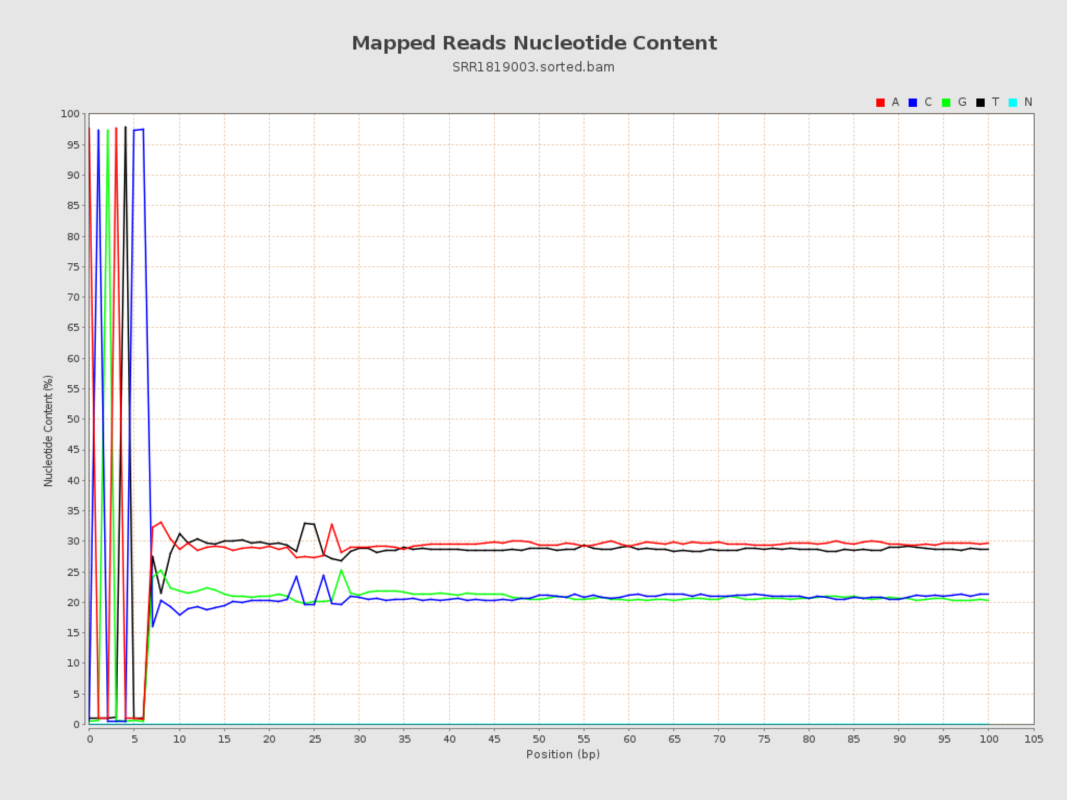
6. Results : Genome Fraction Coverage



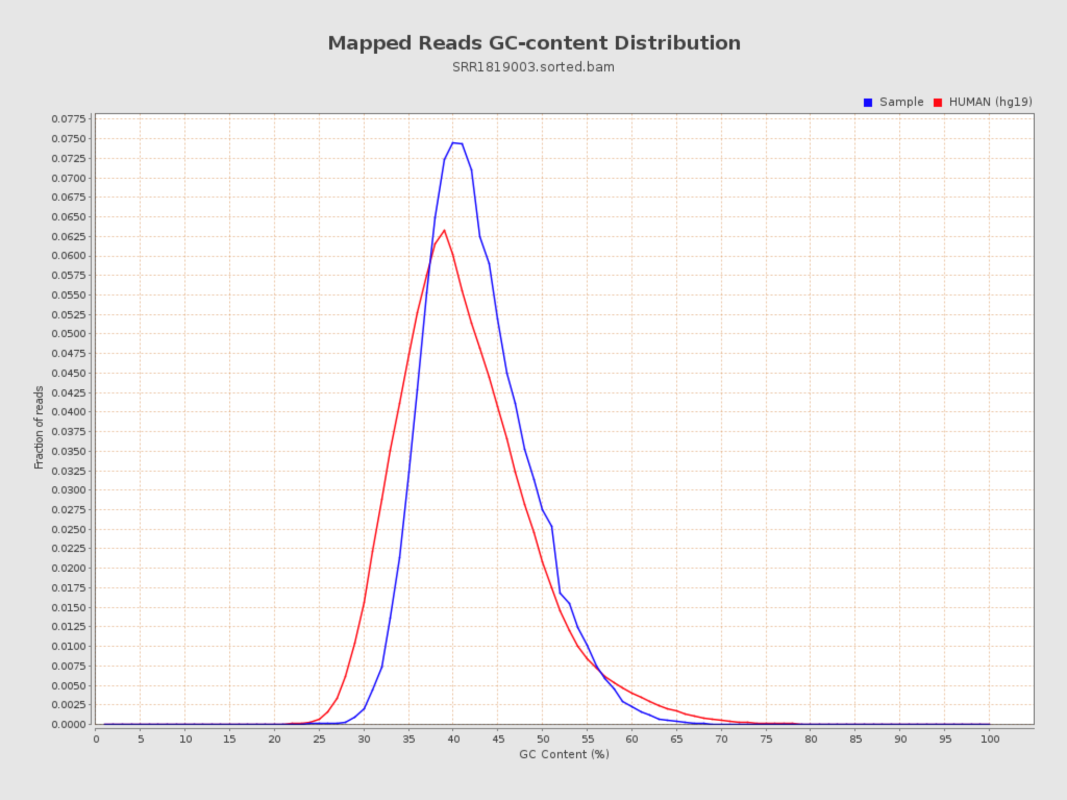
7. Results : Duplication Rate Histogram



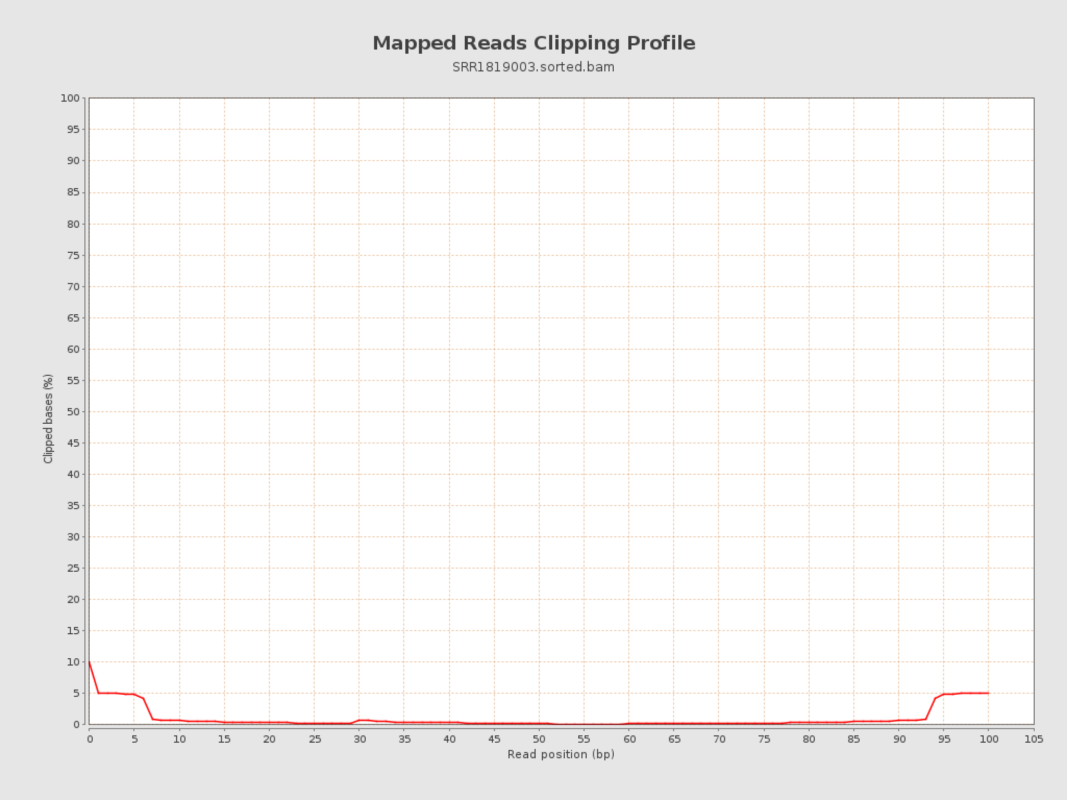
8. Results : Mapped Reads Nucleotide Content



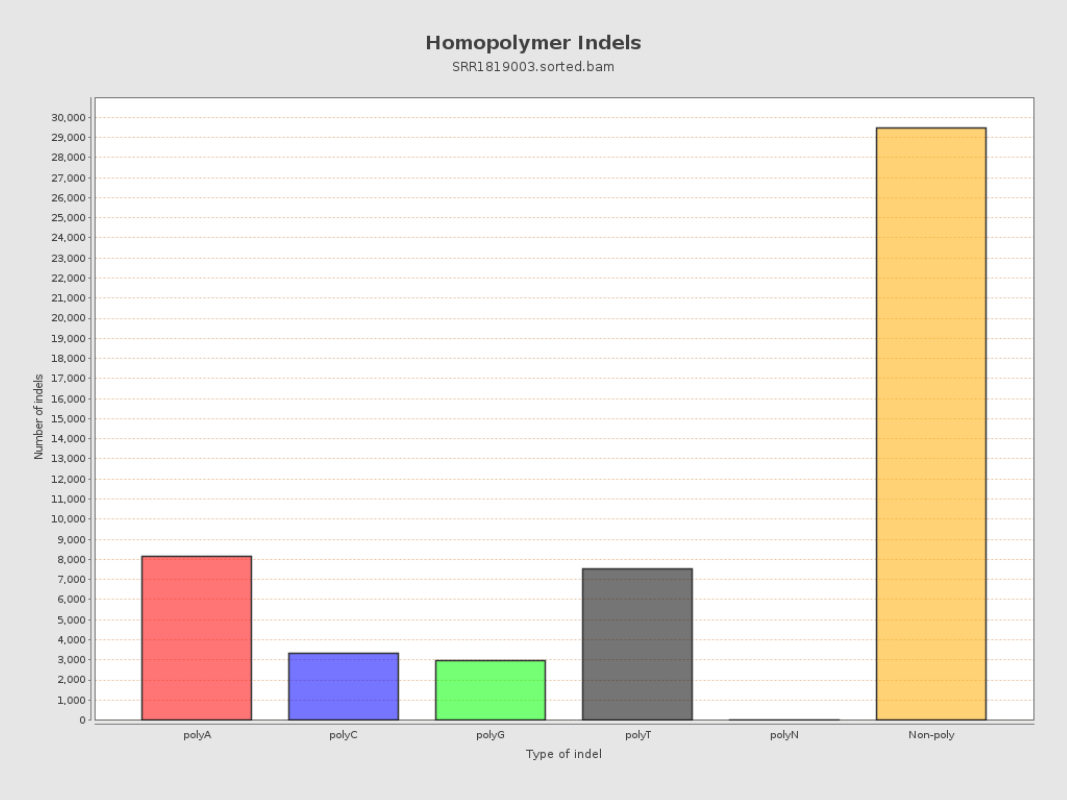
9. Results : Mapped Reads GC-content Distribution



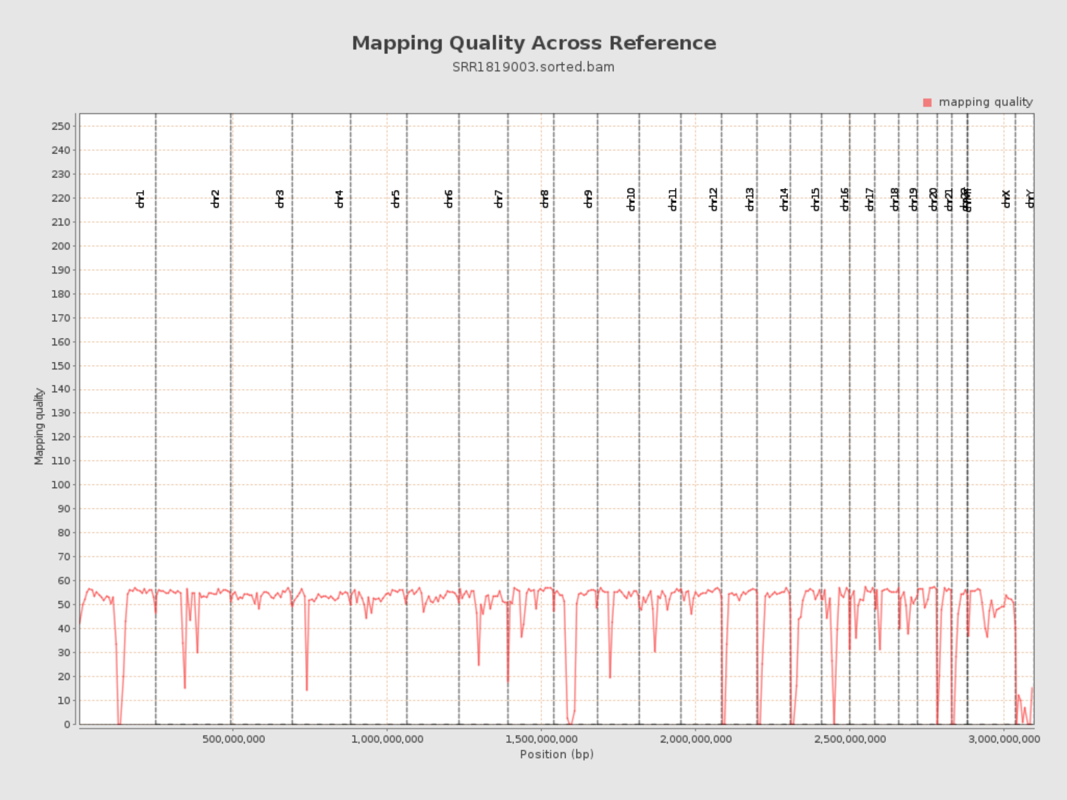
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram