Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:11:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818786.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_SRR1818786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:11:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,264,005
Mapped reads	2,201,494 / 97.24%
Unmapped reads	62,511 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,238 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,086,399 / 47.99%
Duplication rate	41.69%
Clipped reads	2,202,618 / 97.29%

2.2. ACGT Content

Number/percentage of A's	44,621,924 / 29.85%
Number/percentage of C's	31,597,285 / 21.14%
Number/percentage of T's	41,183,843 / 27.55%
Number/percentage of G's	32,061,318 / 21.45%
Number/percentage of N's	8,991 / 0.01%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.6043

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

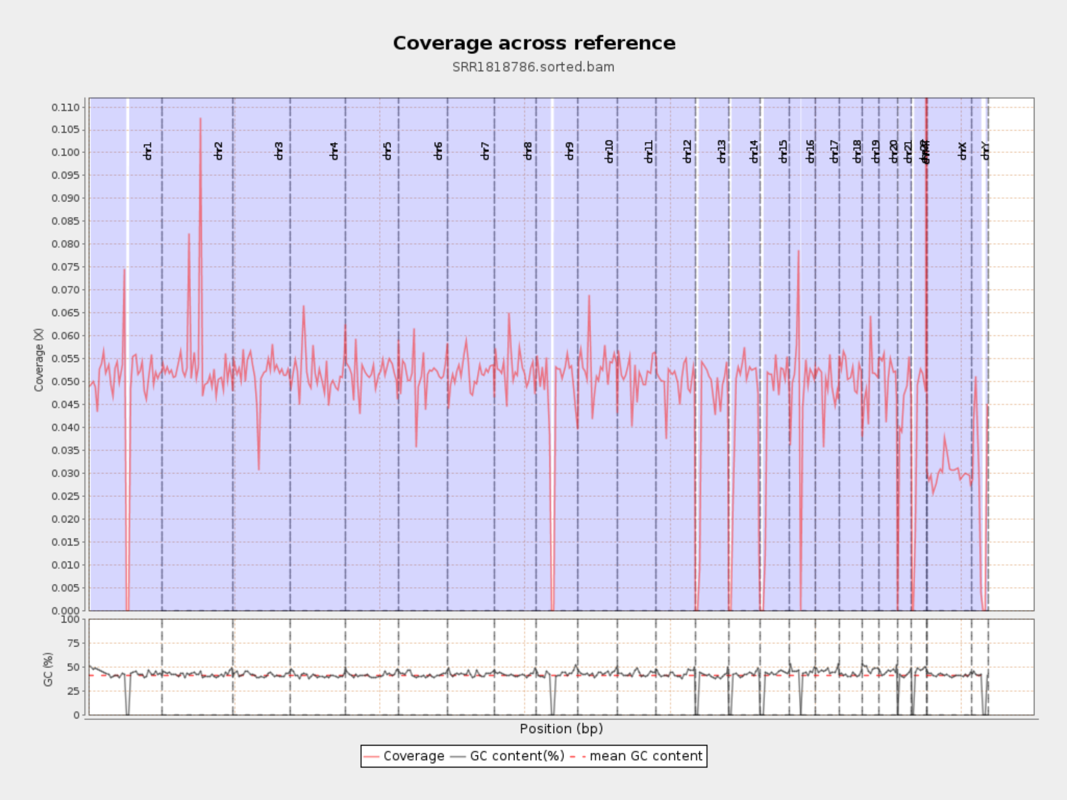
General error rate	0.54%
Mismatches	756,018
Insertions	21,788
Mapped reads with at least one insertion	0.98%
Deletions	38,655
Mapped reads with at least one deletion	1.74%
Homopolymer indels	40.74%

2.6. Chromosome stats

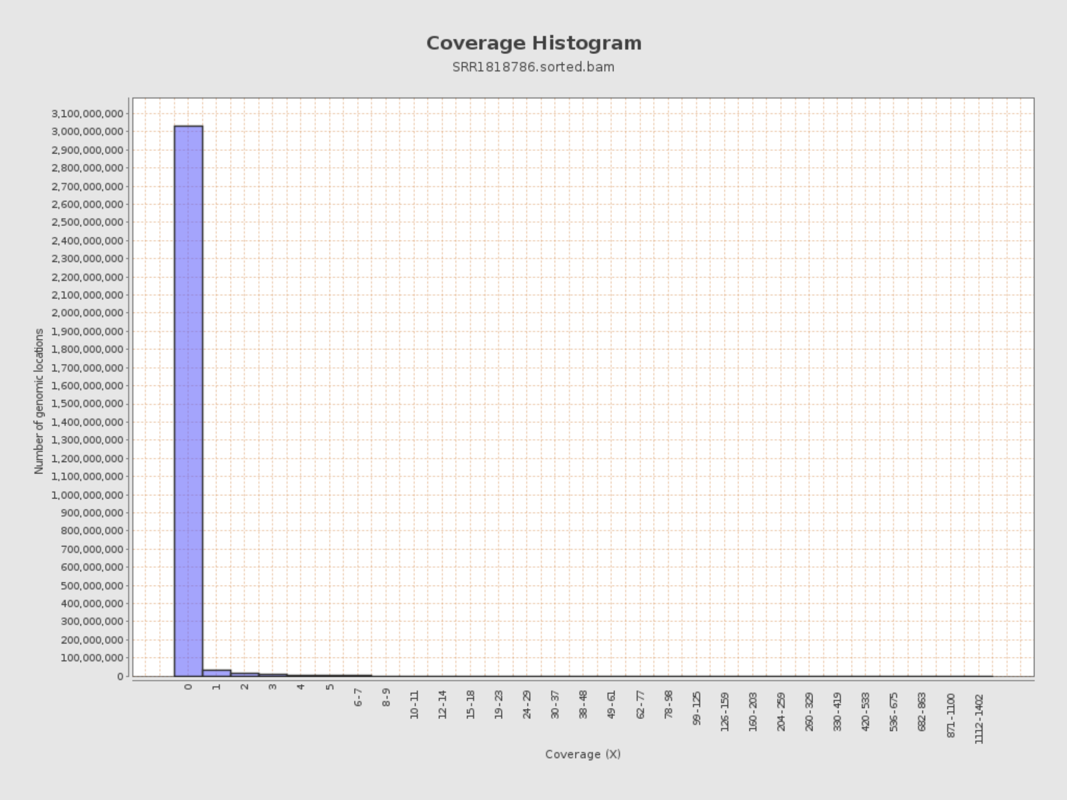
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12187290	0.0489	0.7692
chr2	243199373	13235810	0.0544	1.0323
chr3	198022430	10250913	0.0518	0.4419
chr4	191154276	9855363	0.0516	0.5146
chr5	180915260	9374252	0.0518	0.457
chr6	171115067	8820288	0.0515	0.5012
chr7	159138663	8239450	0.0518	0.5324

chr8	146364022	7740734	0.0529	0.5044
chr9	141213431	6406239	0.0454	0.4917
chr10	135534747	7211246	0.0532	0.6481
chr11	135006516	6942294	0.0514	0.5074
chr12	133851895	6720017	0.0502	0.4826
chr13	115169878	4812210	0.0418	0.3969
chr14	107349540	4654596	0.0434	0.4745
chr15	102531392	4246557	0.0414	0.3972
chr16	90354753	4390463	0.0486	0.7241
chr17	81195210	3958744	0.0488	0.46
chr18	78077248	4082861	0.0523	0.6519
chr19	59128983	2964529	0.0501	0.6722
chr20	63025520	3262683	0.0518	0.4742
chr21	48129895	2013668	0.0418	0.4241
chr22	51304566	1800921	0.0351	0.4027
chrMT	16571	175349	10.5817	12.047
chrX	155270560	4709436	0.0303	0.3824
chrY	59373566	1481219	0.0249	1.1116

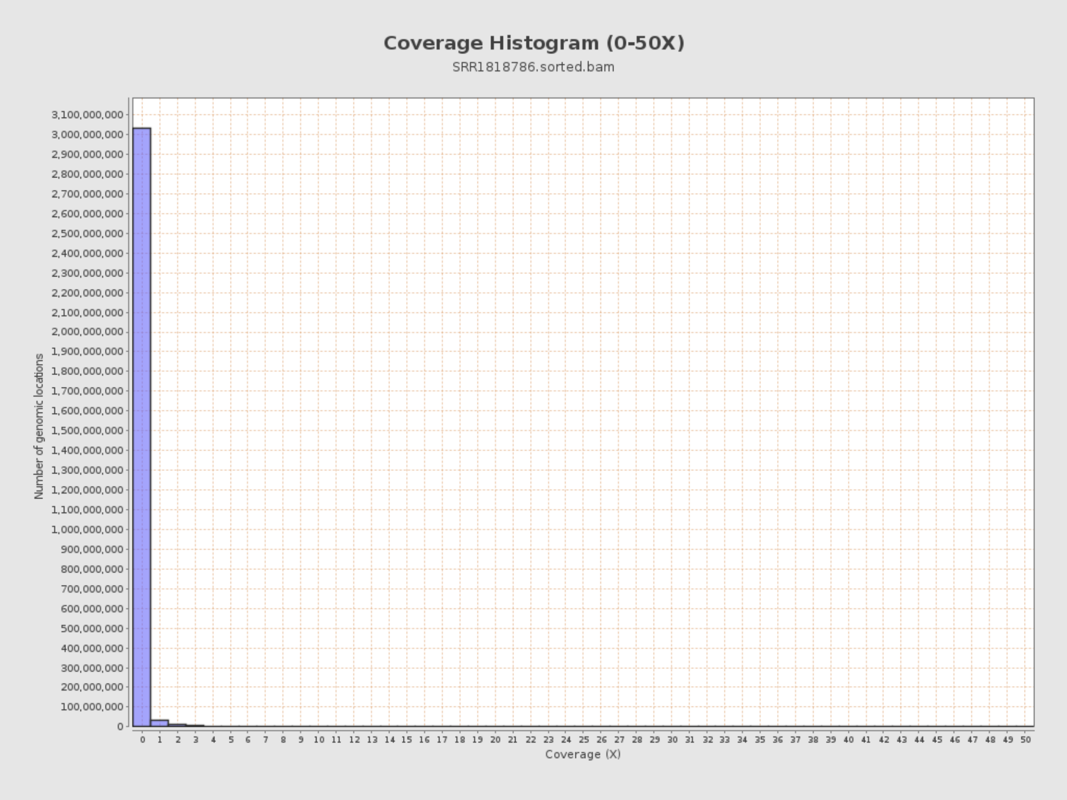
3. Results : Coverage across reference



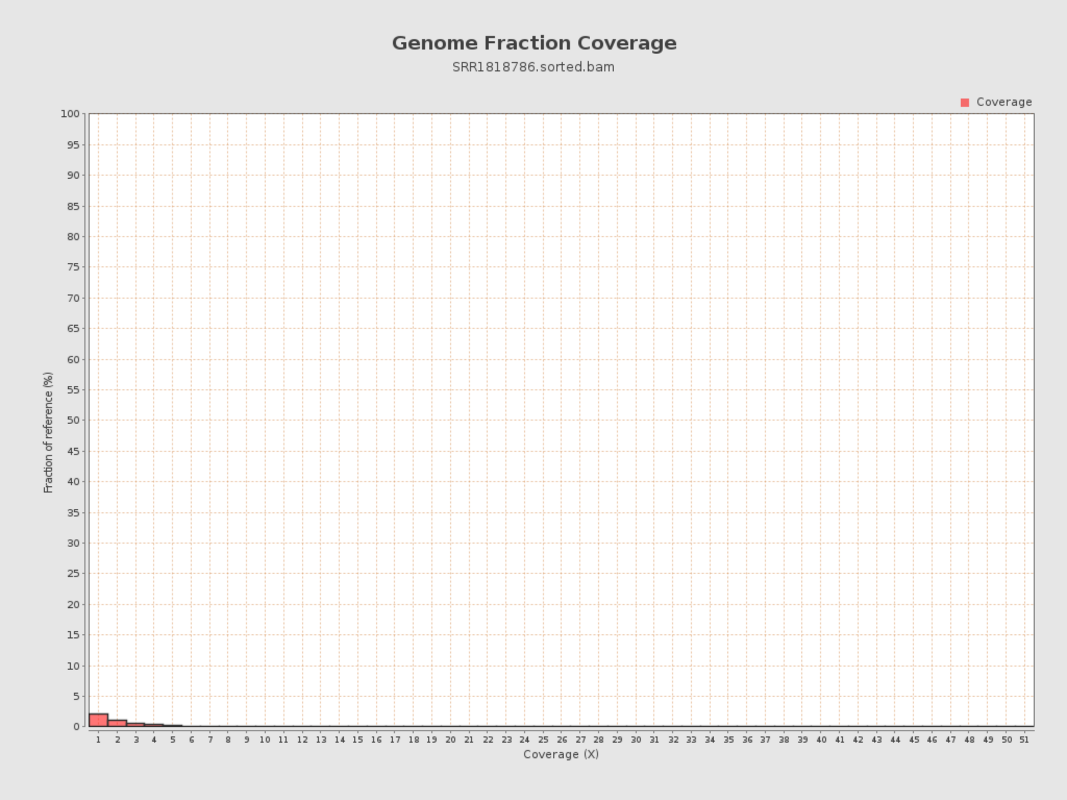
4. Results : Coverage Histogram



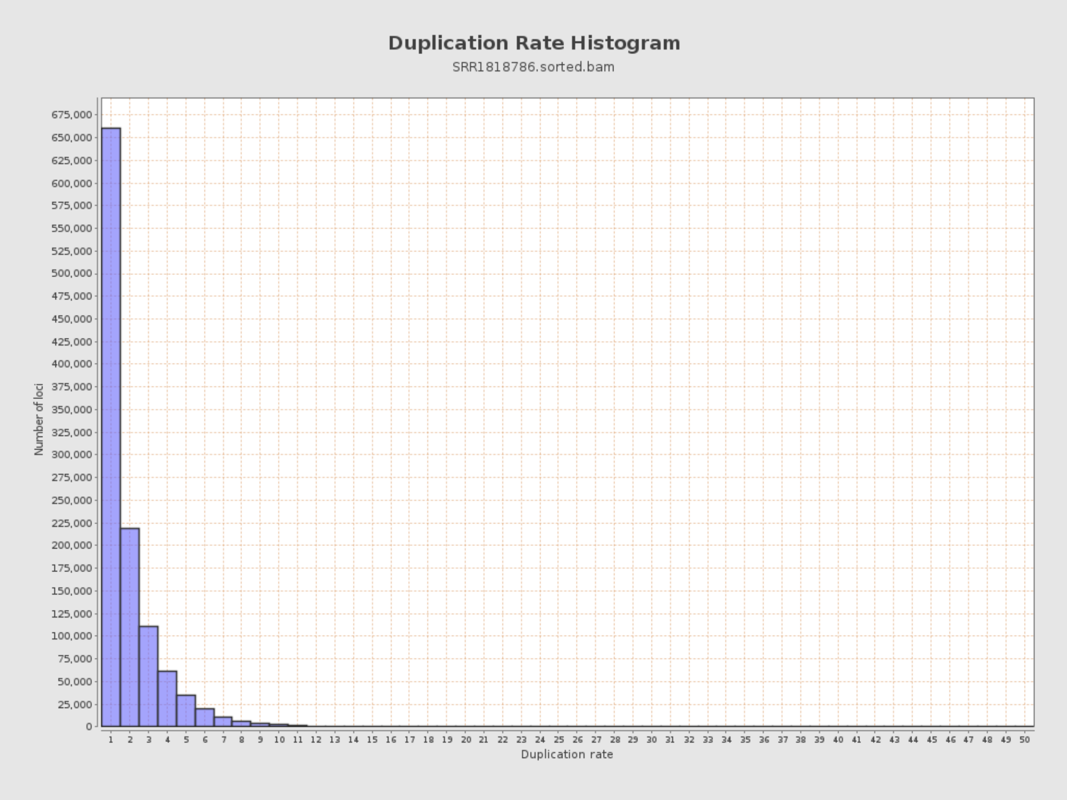
5. Results : Coverage Histogram (0-50X)



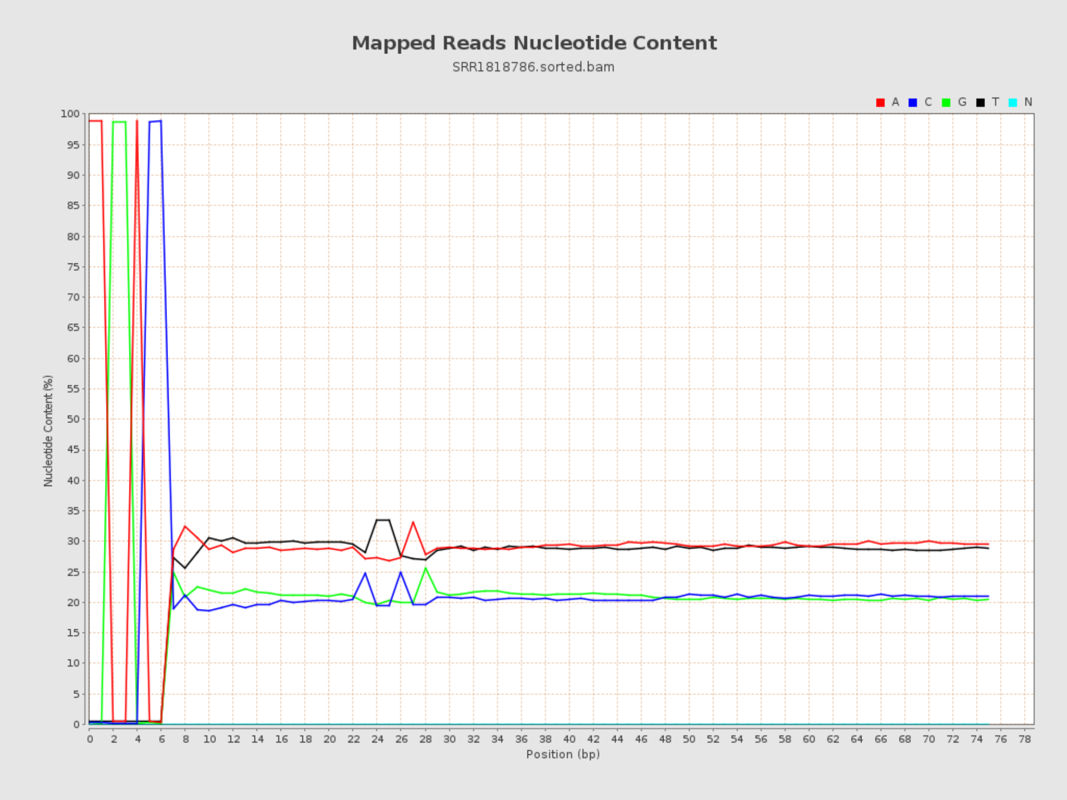
6. Results : Genome Fraction Coverage



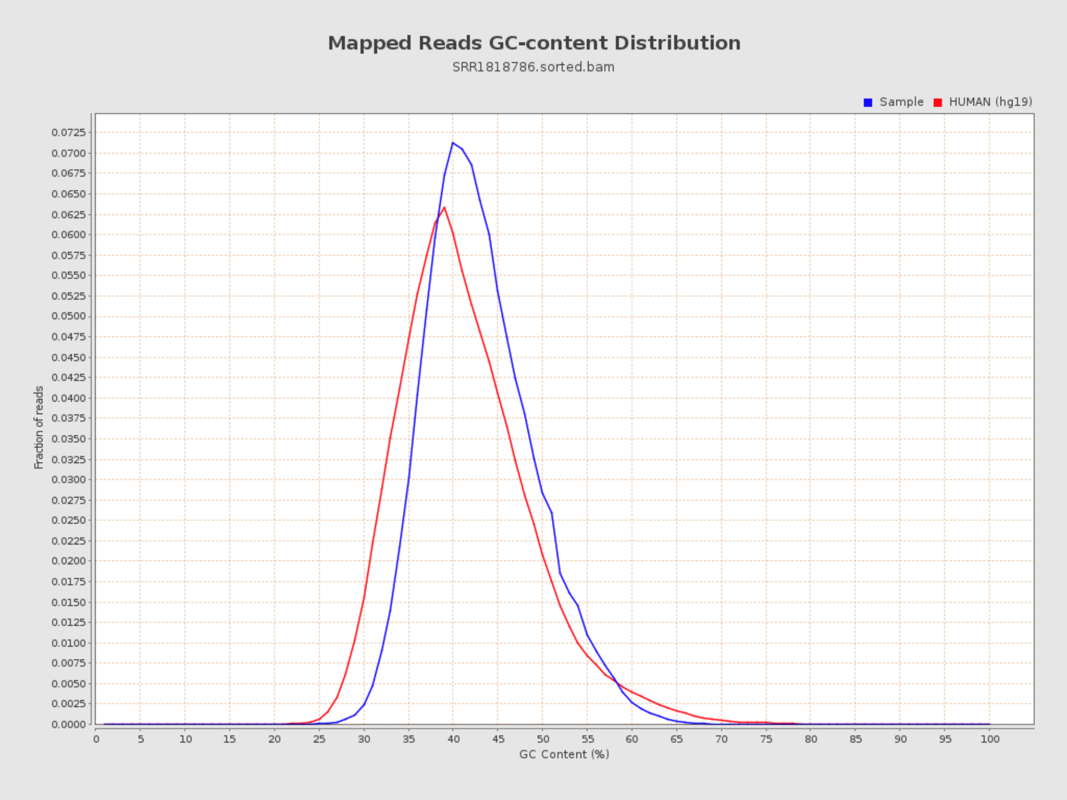
7. Results : Duplication Rate Histogram



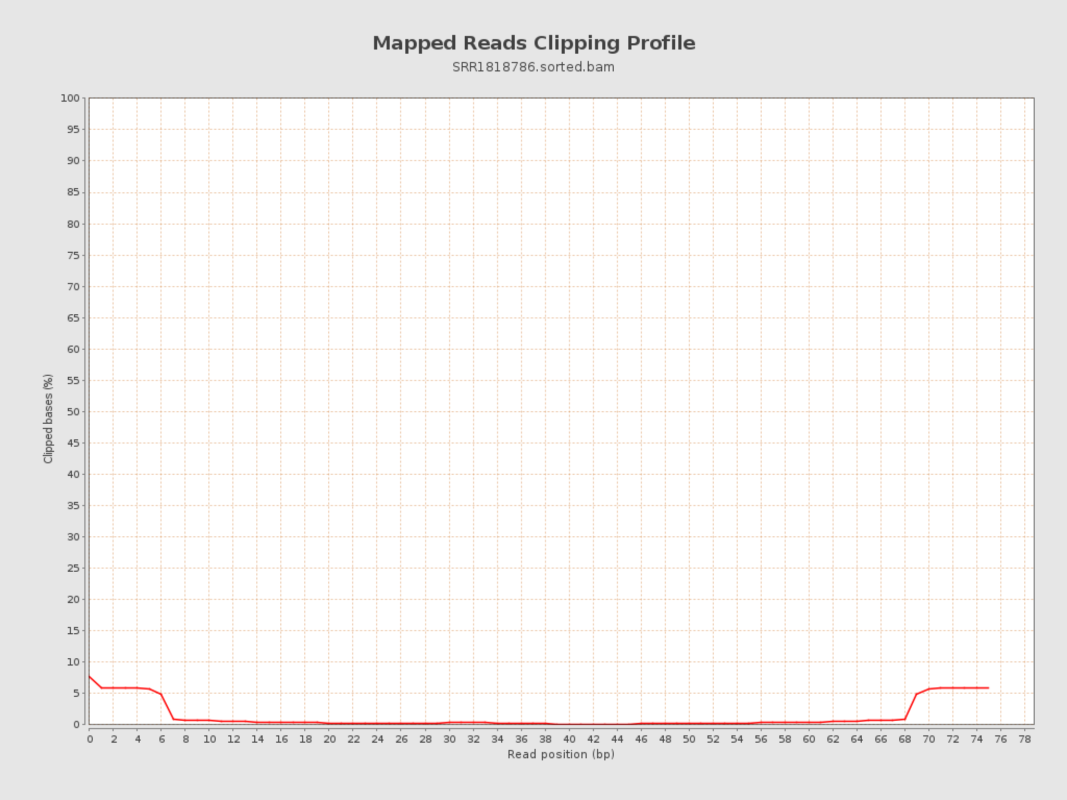
8. Results : Mapped Reads Nucleotide Content



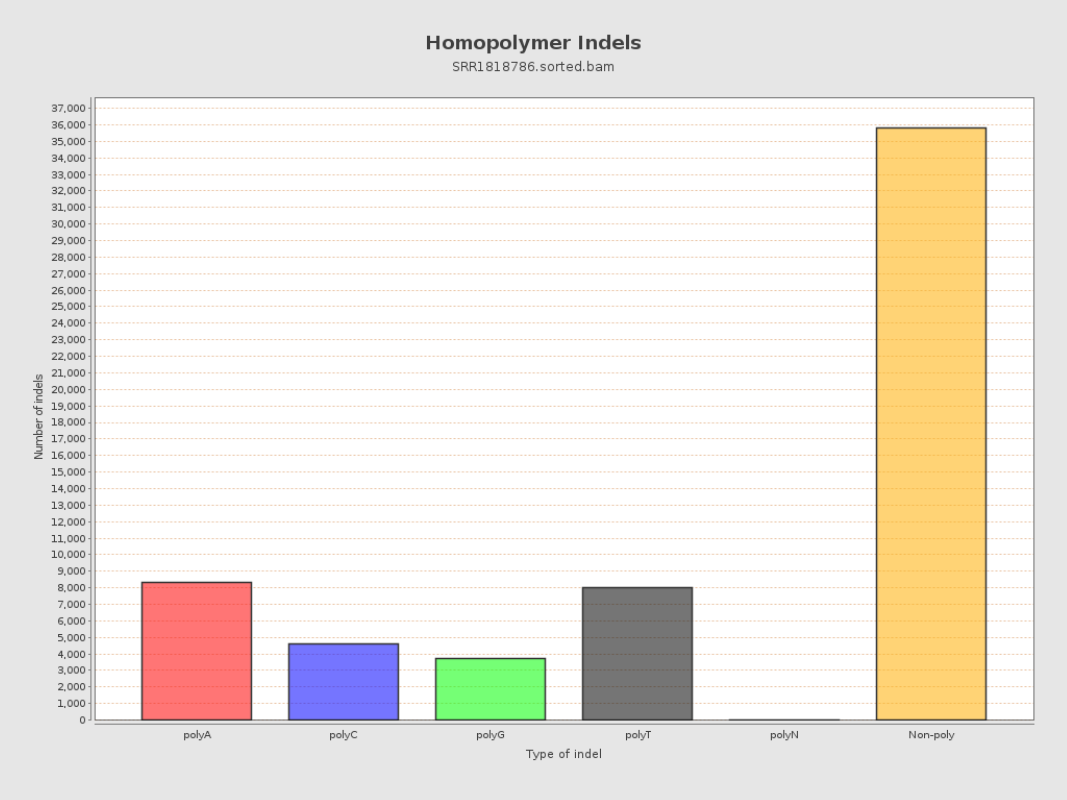
9. Results : Mapped Reads GC-content Distribution



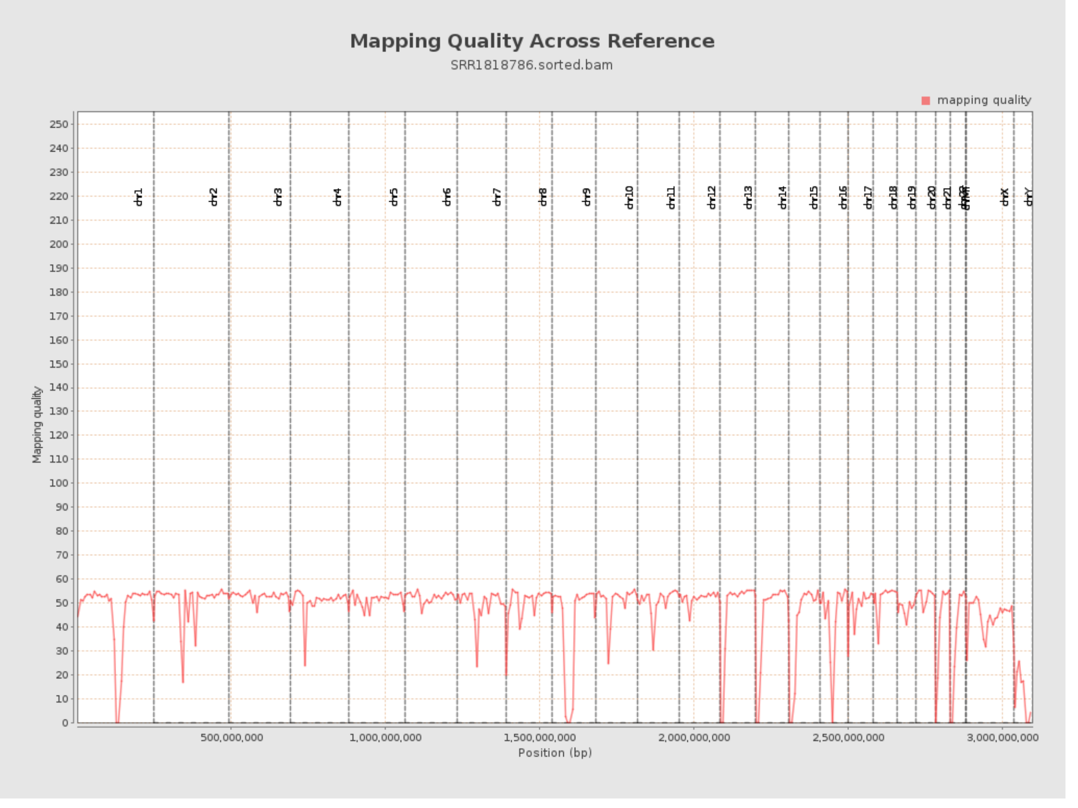
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram