Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:08:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818918.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_SRR1818918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:08:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,915,031
Mapped reads	1,891,743 / 98.78%
Unmapped reads	23,288 / 1.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,362 / 1.38%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	452,856 / 23.65%
Duplication rate	20.05%
Clipped reads	1,901,941 / 99.32%

2.2. ACGT Content

Number/percentage of A's	49,704,725 / 28.36%
Number/percentage of C's	37,087,898 / 21.16%
Number/percentage of T's	50,169,247 / 28.62%
Number/percentage of G's	38,302,909 / 21.85%
Number/percentage of N's	2,692 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.728

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Mismatches and indels

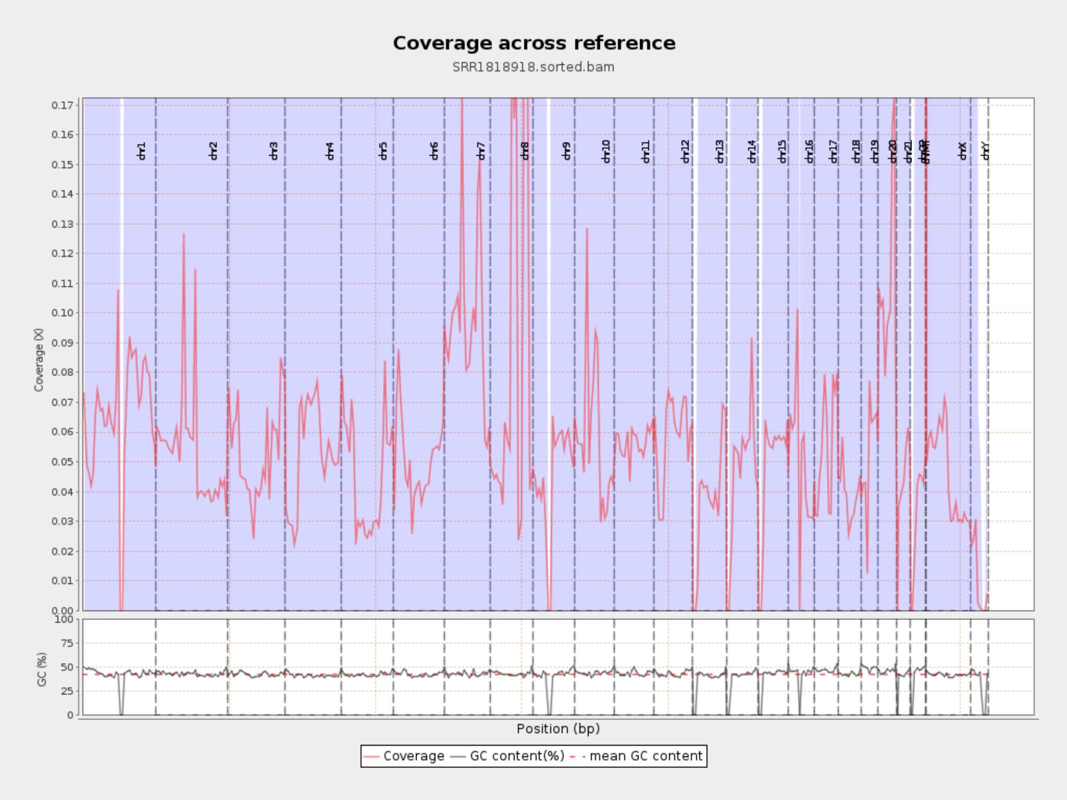
General error rate	0.64%
Mismatches	1,062,757
Insertions	25,492
Mapped reads with at least one insertion	1.3%
Deletions	58,391
Mapped reads with at least one deletion	3.01%
Homopolymer indels	39.87%

2.6. Chromosome stats

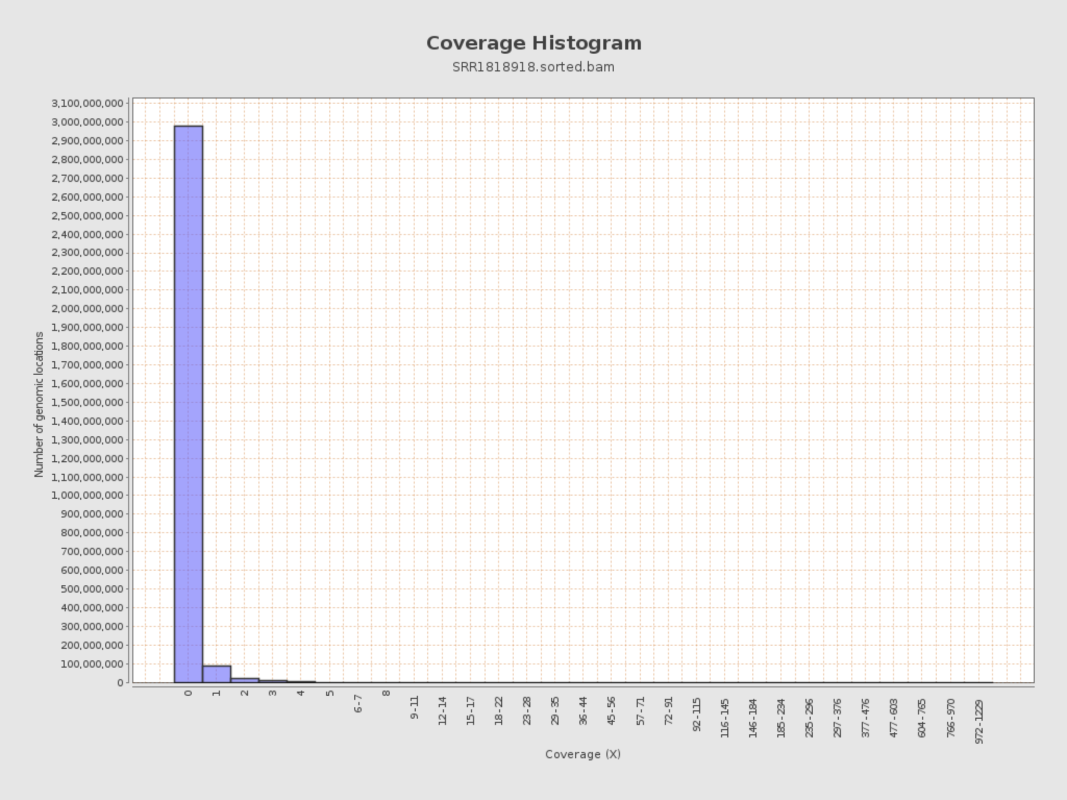
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16315984	0.0655	1.0032
chr2	243199373	13147765	0.0541	1.113
chr3	198022430	10529948	0.0532	0.3187
chr4	191154276	10255206	0.0536	0.405
chr5	180915260	8231151	0.0455	0.3302
chr6	171115067	8584105	0.0502	0.3464
chr7	159138663	15551129	0.0977	1.6931

chr8	146364022	14823142	0.1013	0.5562
chr9	141213431	6386377	0.0452	0.6159
chr10	135534747	7915043	0.0584	0.8817
chr11	135006516	7613943	0.0564	0.4027
chr12	133851895	7839972	0.0586	0.3421
chr13	115169878	4342333	0.0377	0.2626
chr14	107349540	5100748	0.0475	0.3478
chr15	102531392	4832169	0.0471	0.3004
chr16	90354753	4418468	0.0489	0.8362
chr17	81195210	4368537	0.0538	0.4423
chr18	78077248	3078434	0.0394	0.6942
chr19	59128983	3089278	0.0522	0.8954
chr20	63025520	7227069	0.1147	0.5177
chr21	48129895	2068617	0.043	0.334
chr22	51304566	1596806	0.0311	0.2755
chrMT	16571	370061	22.3318	13.9347
chrX	155270560	7092658	0.0457	0.3622
chrY	59373566	603448	0.0102	0.8734

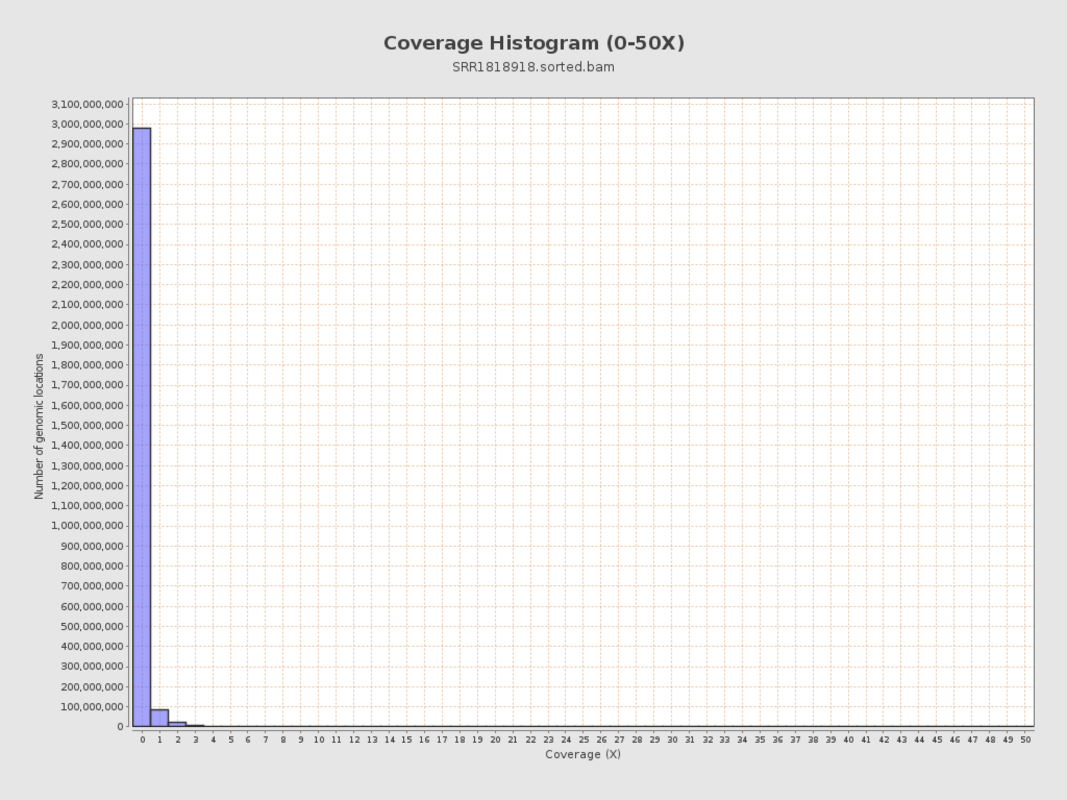
3. Results : Coverage across reference



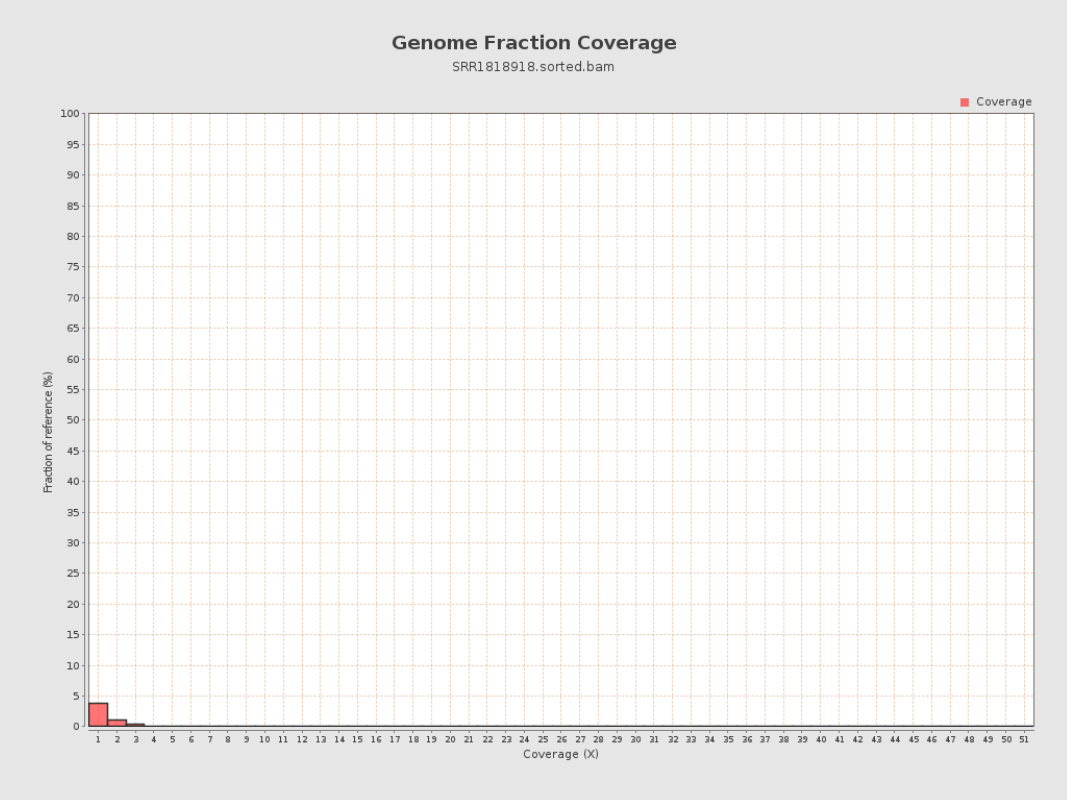
4. Results : Coverage Histogram



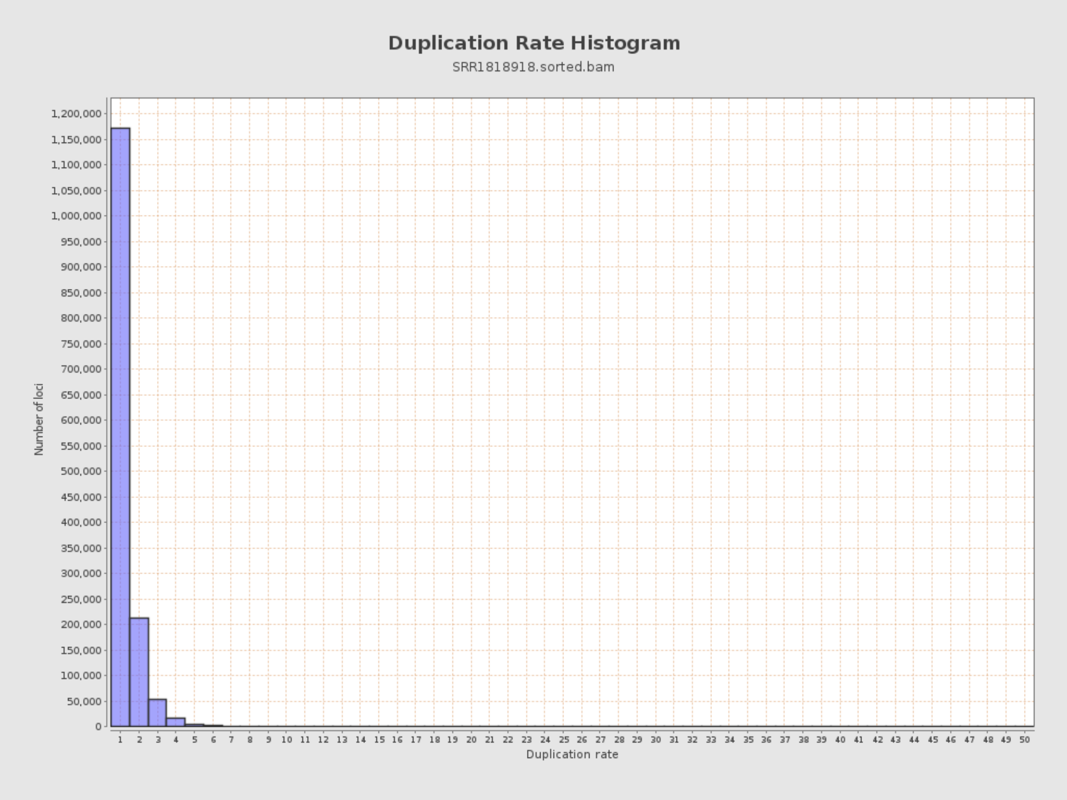
5. Results : Coverage Histogram (0-50X)



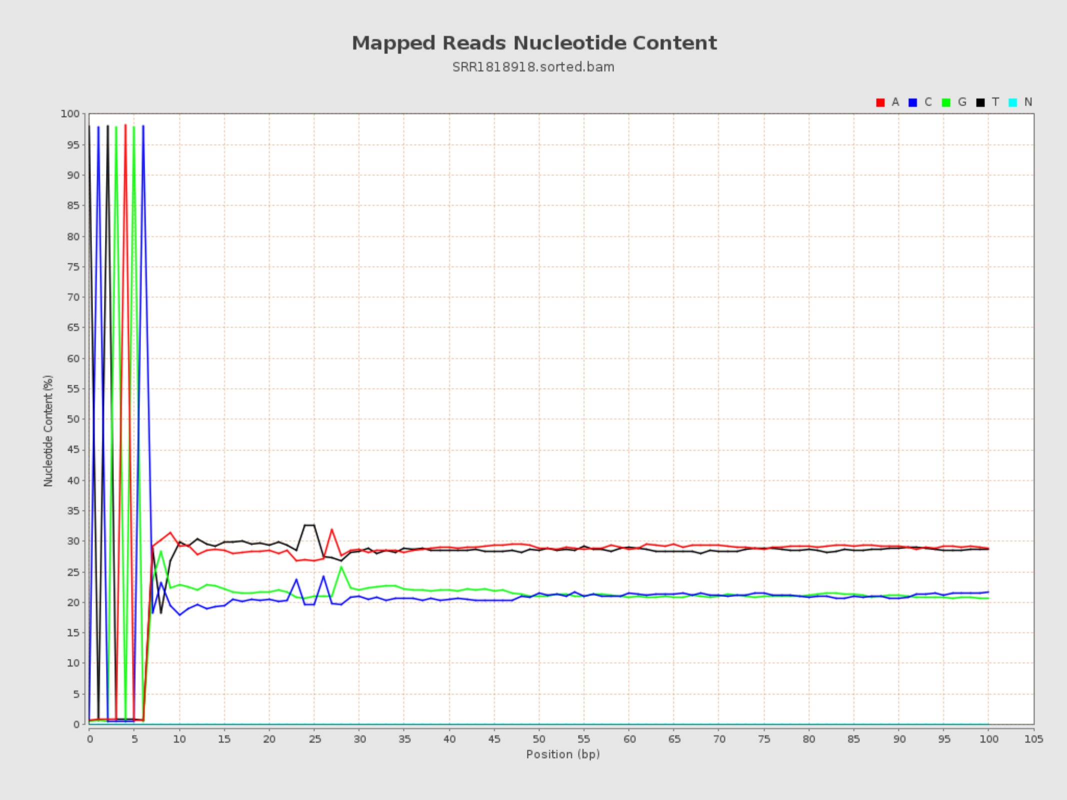
6. Results : Genome Fraction Coverage



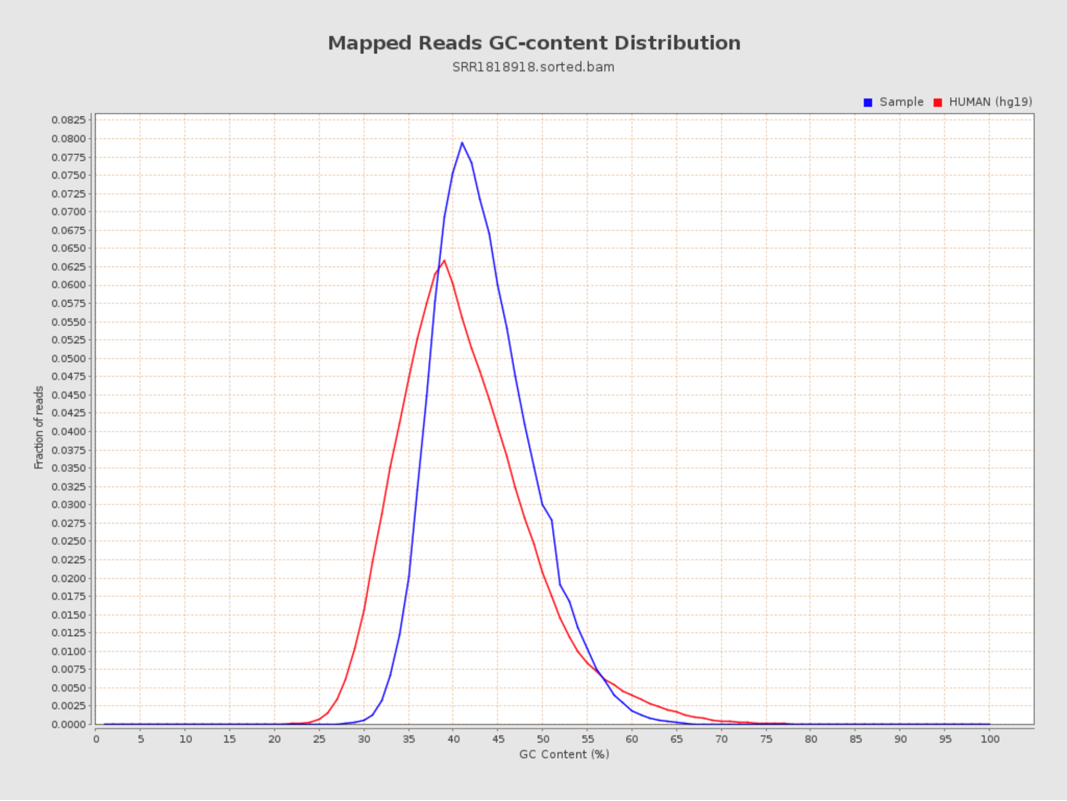
7. Results : Duplication Rate Histogram



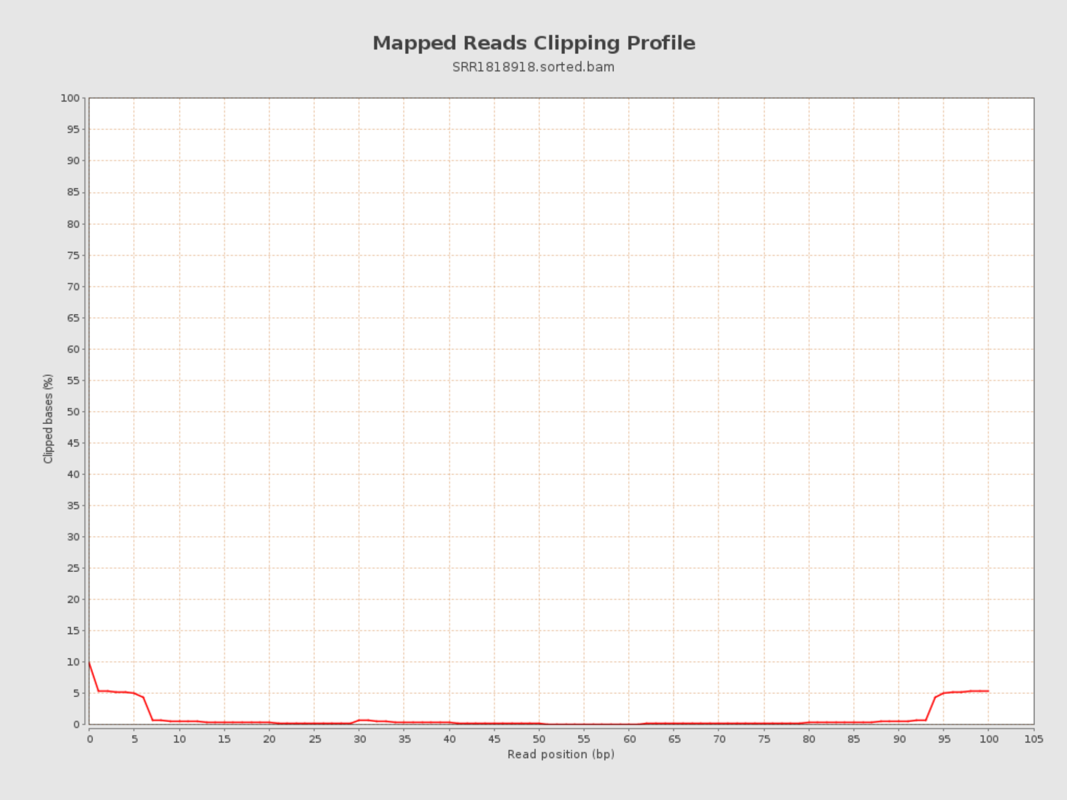
8. Results : Mapped Reads Nucleotide Content



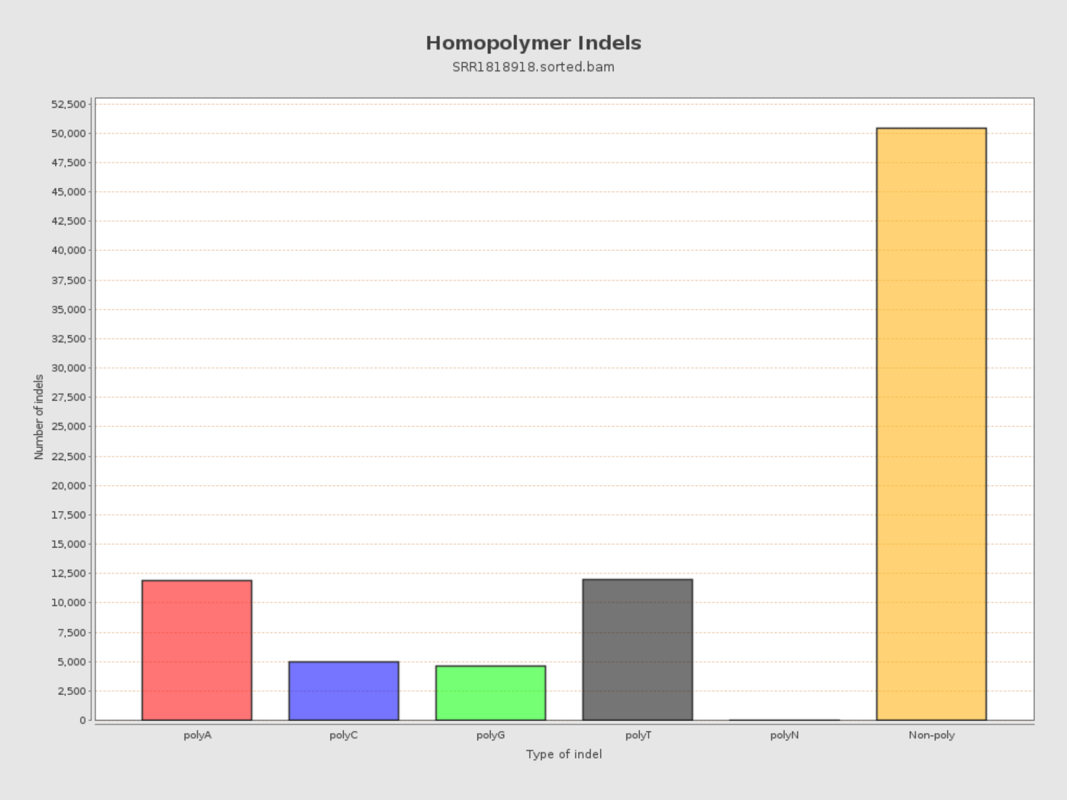
9. Results : Mapped Reads GC-content Distribution



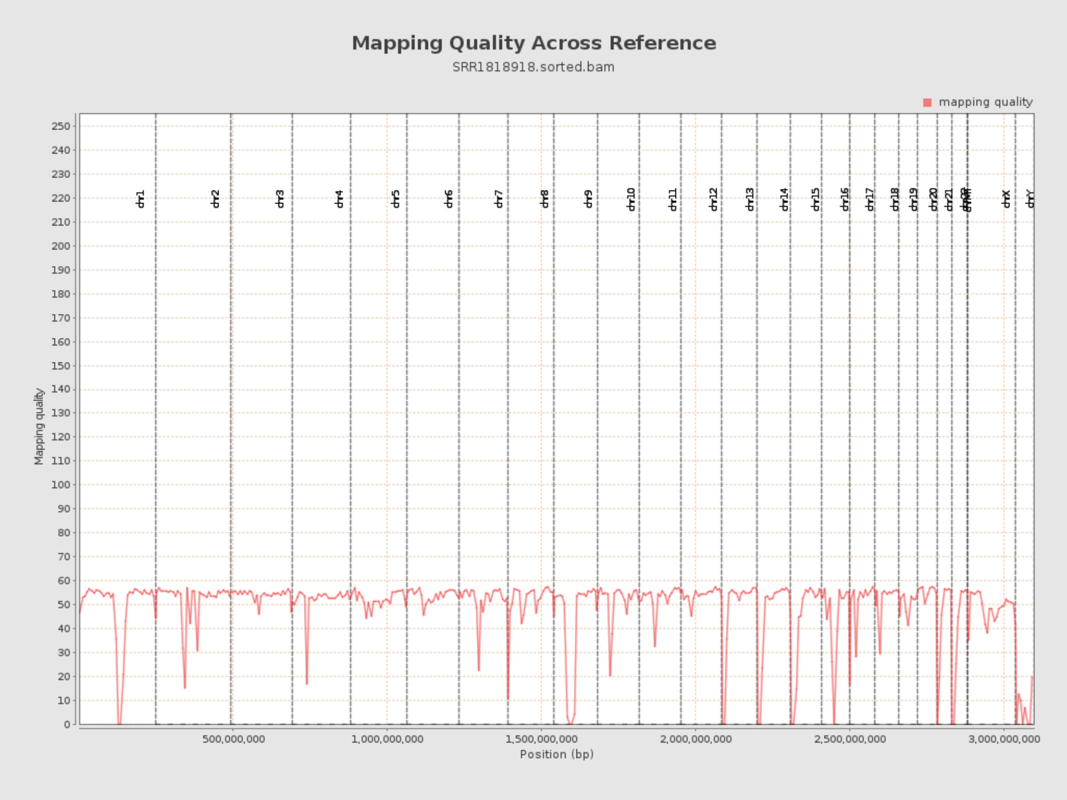
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram