Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:51:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818994.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_SRR1818994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:50:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,528,243
Mapped reads	2,496,068 / 98.73%
Unmapped reads	32,175 / 1.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,362 / 1.56%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	1,219,697 / 48.24%
Duplication rate	41.02%
Clipped reads	2,503,910 / 99.04%

2.2. ACGT Content

Number/percentage of A's	65,944,721 / 28.56%
Number/percentage of C's	48,932,325 / 21.19%
Number/percentage of T's	66,353,797 / 28.73%
Number/percentage of G's	49,682,143 / 21.51%
Number/percentage of N's	10,943 / 0%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0746

Standard Deviation	0.8773

2.4. Mapping Quality

Mean Mapping Quality	49.13

2.5. Mismatches and indels

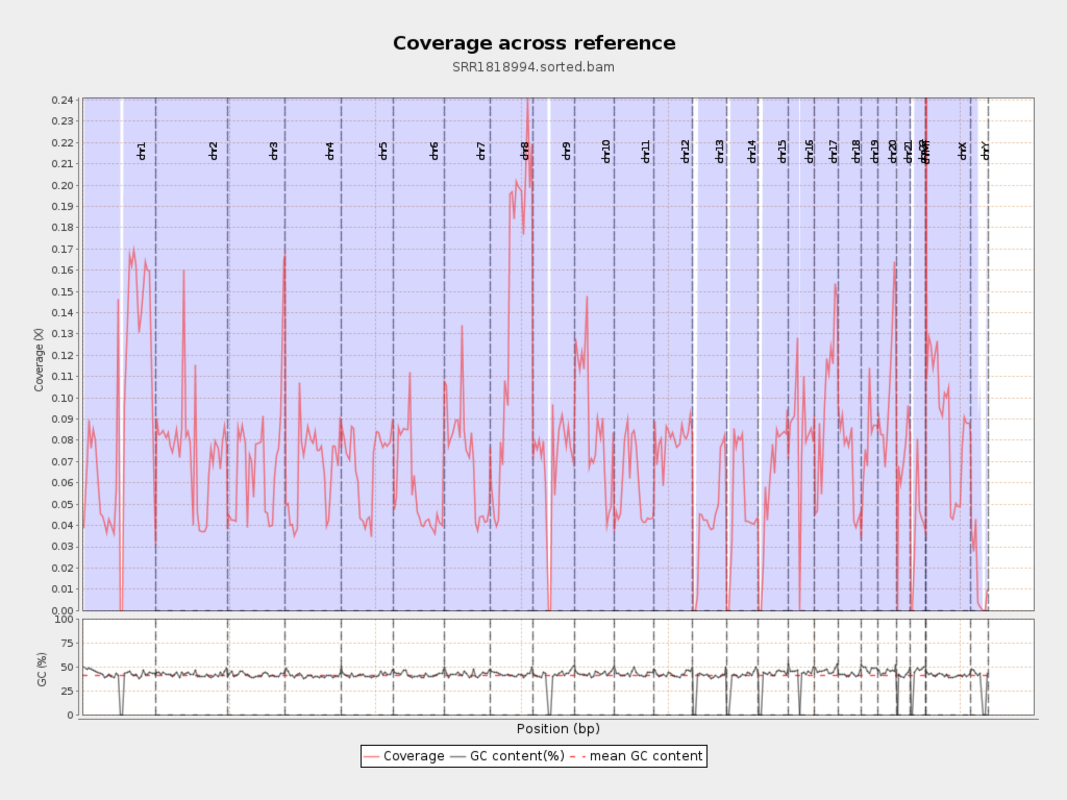
General error rate	0.67%
Mismatches	1,466,691
Insertions	36,800
Mapped reads with at least one insertion	1.43%
Deletions	74,276
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.76%

2.6. Chromosome stats

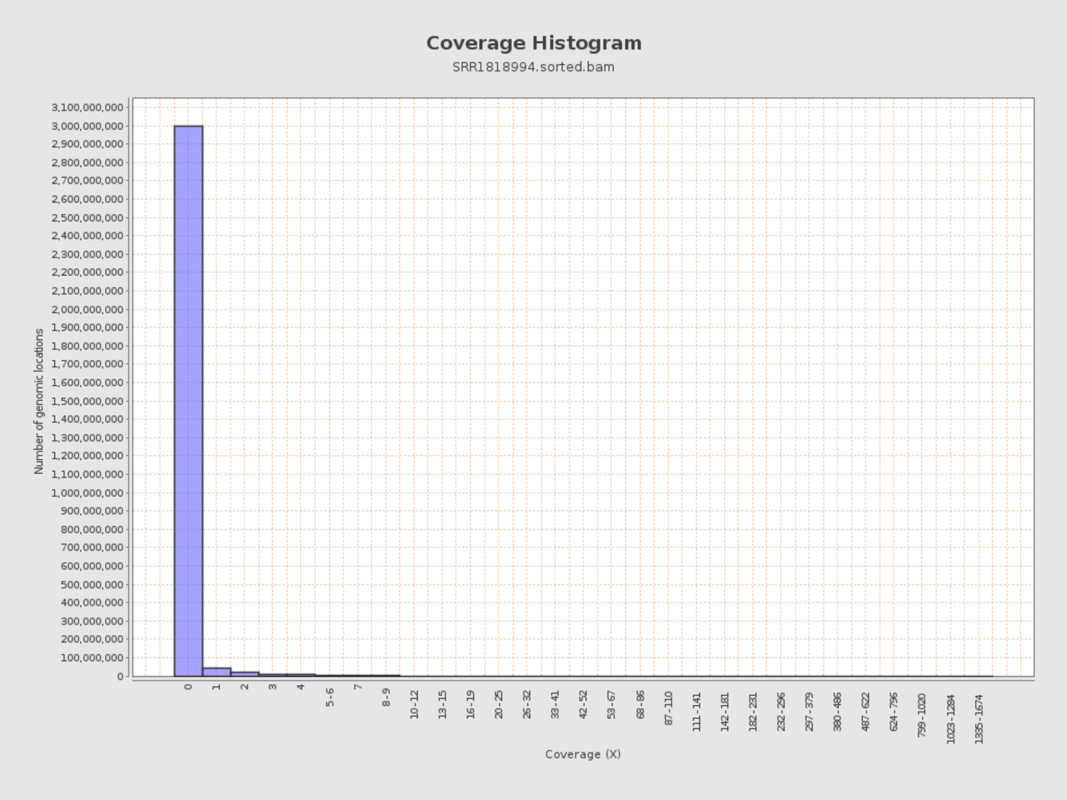
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22753718	0.0913	1.5059
chr2	243199373	18304076	0.0753	1.2643
chr3	198022430	13619259	0.0688	0.5131
chr4	191154276	12770159	0.0668	0.577
chr5	180915260	12459161	0.0689	0.537
chr6	171115067	9801390	0.0573	0.5807
chr7	159138663	11515731	0.0724	1.1214

chr8	146364022	21123195	0.1443	0.8451
chr9	141213431	9781227	0.0693	0.828
chr10	135534747	11791141	0.087	1.0199
chr11	135006516	7776643	0.0576	0.5607
chr12	133851895	10810839	0.0808	0.5691
chr13	115169878	5020449	0.0436	0.4018
chr14	107349540	5380201	0.0501	0.4666
chr15	102531392	5995621	0.0585	0.4772
chr16	90354753	7406929	0.082	1.108
chr17	81195210	7996382	0.0985	0.6985
chr18	78077248	5391903	0.0691	0.907
chr19	59128983	4737234	0.0801	1.3673
chr20	63025520	6628343	0.1052	0.6808
chr21	48129895	3307672	0.0687	0.586
chr22	51304566	1898727	0.037	0.4244
chrMT	16571	25378	1.5315	2.579
chrX	155270560	13903954	0.0895	0.6914
chrY	59373566	862368	0.0145	0.9479

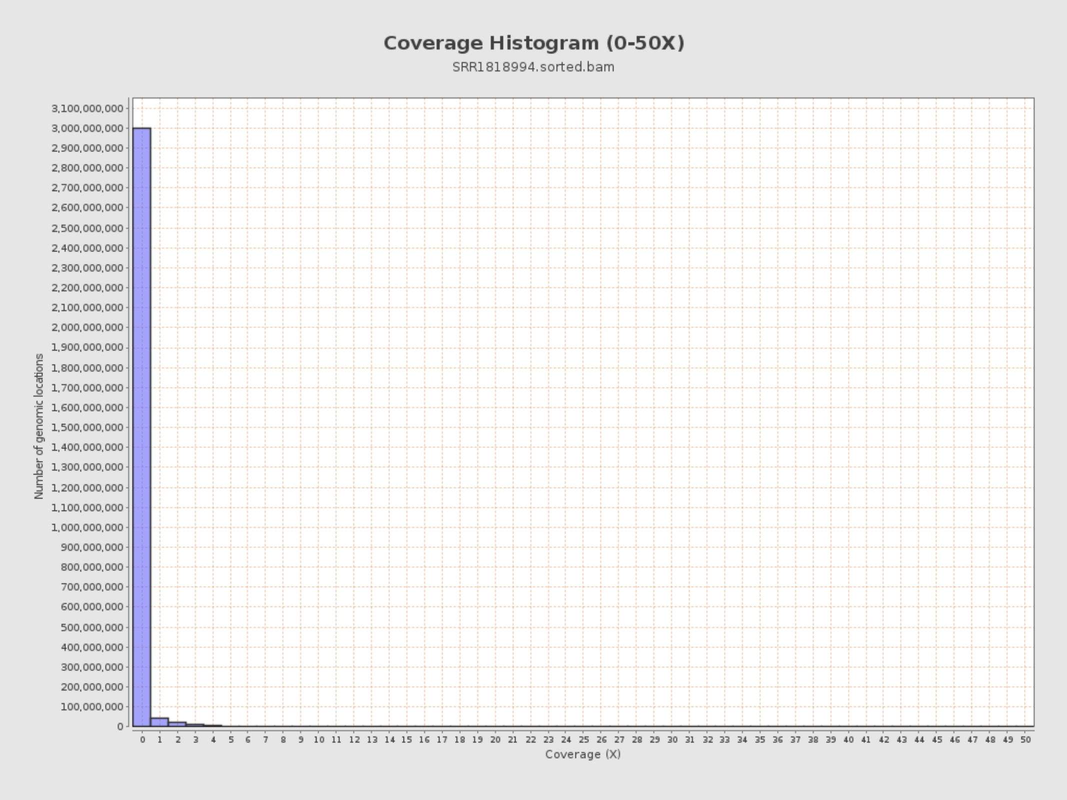
3. Results : Coverage across reference



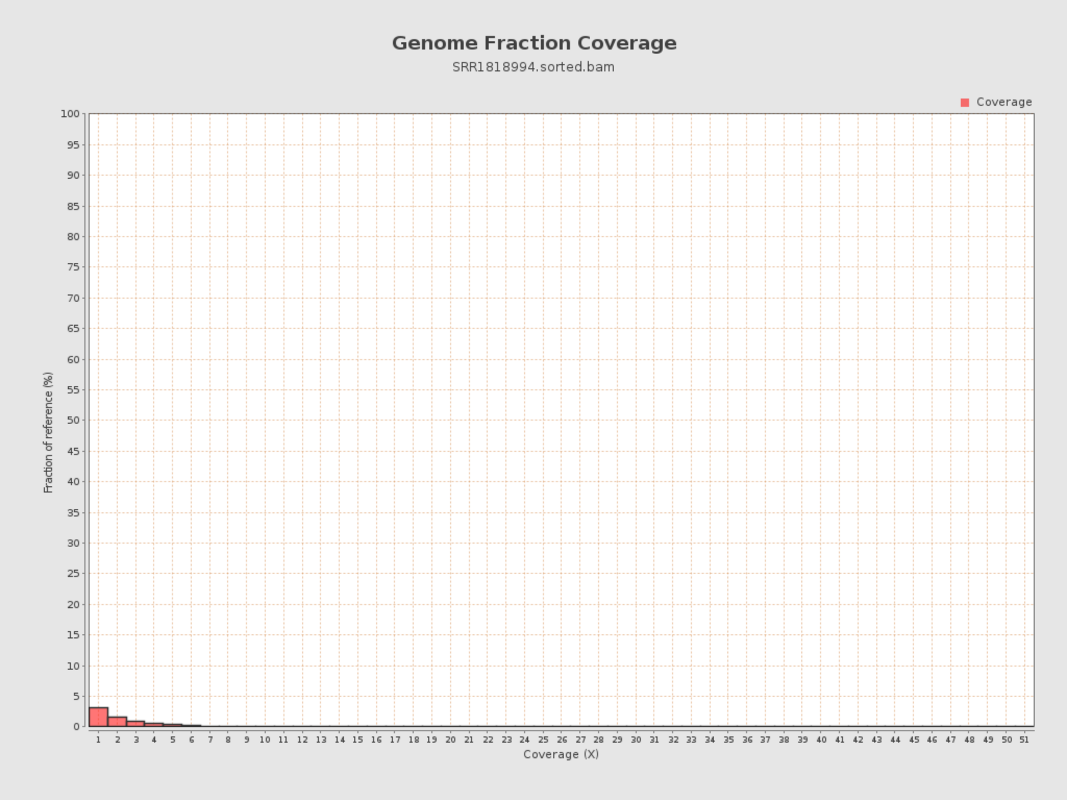
4. Results : Coverage Histogram



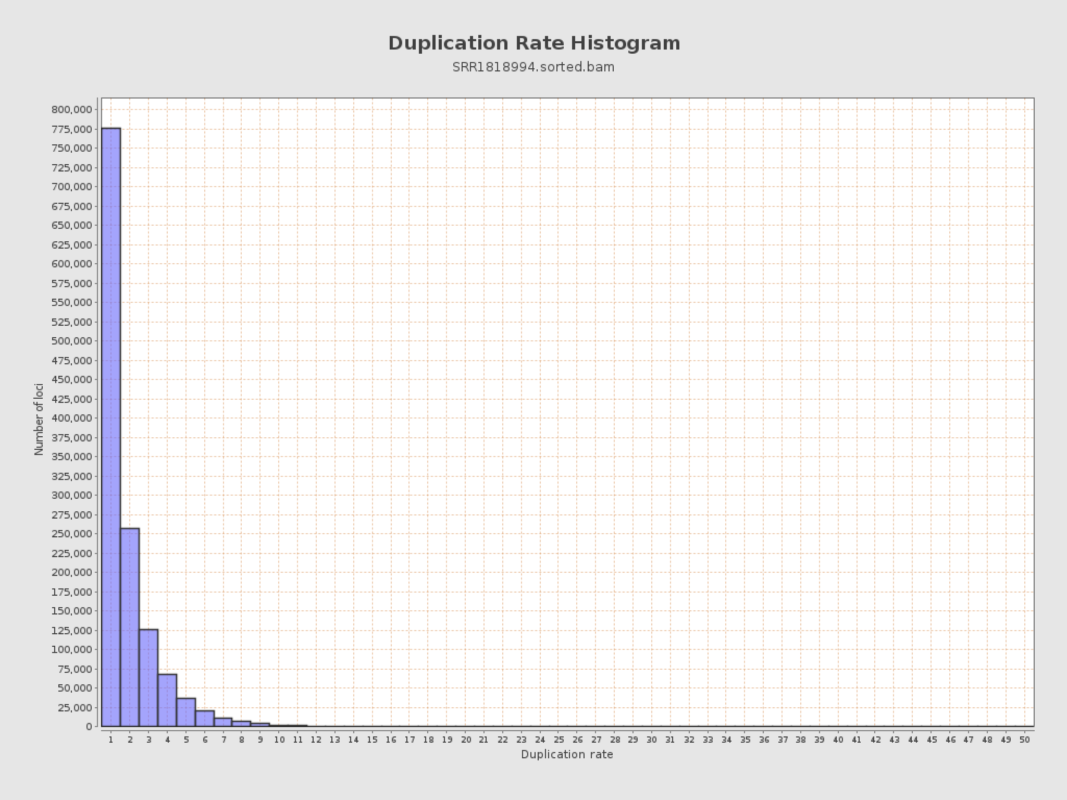
5. Results : Coverage Histogram (0-50X)



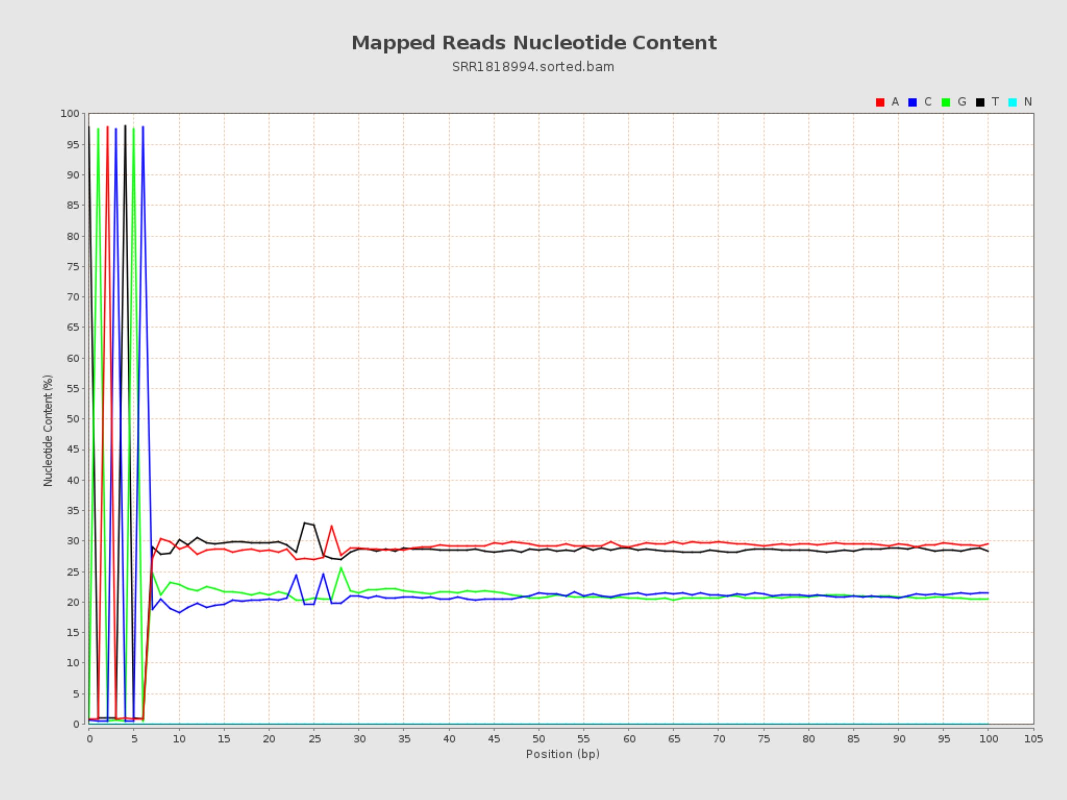
6. Results : Genome Fraction Coverage



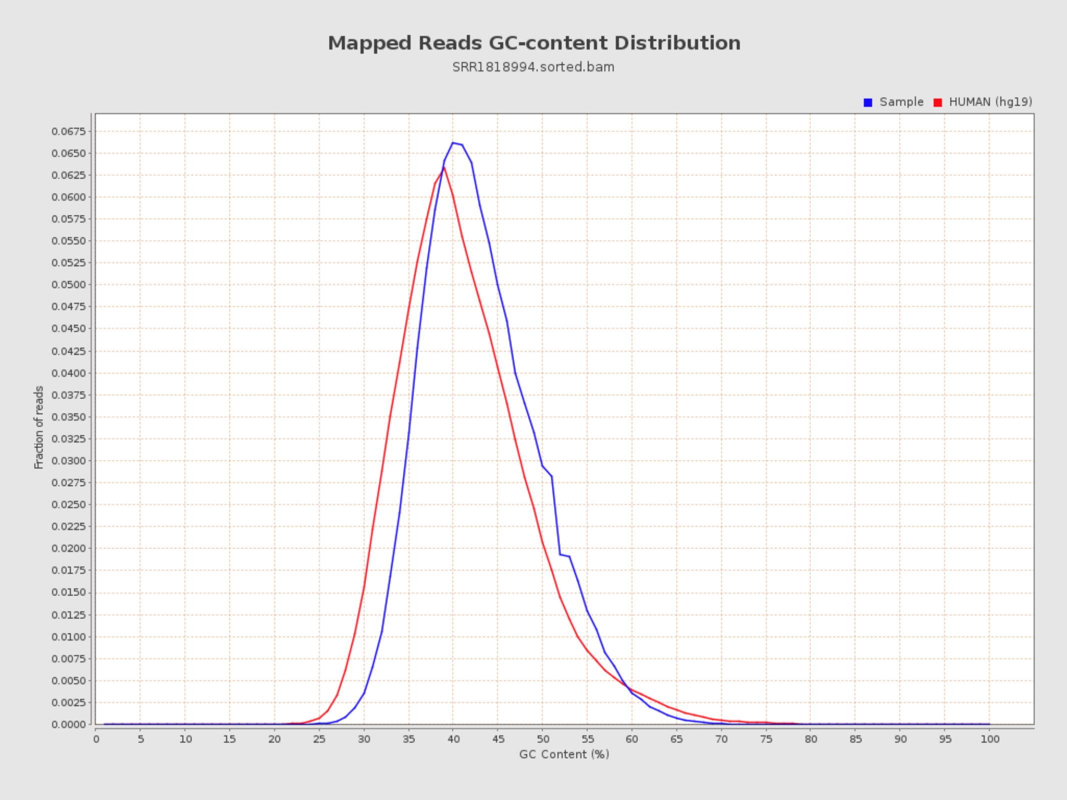
7. Results : Duplication Rate Histogram



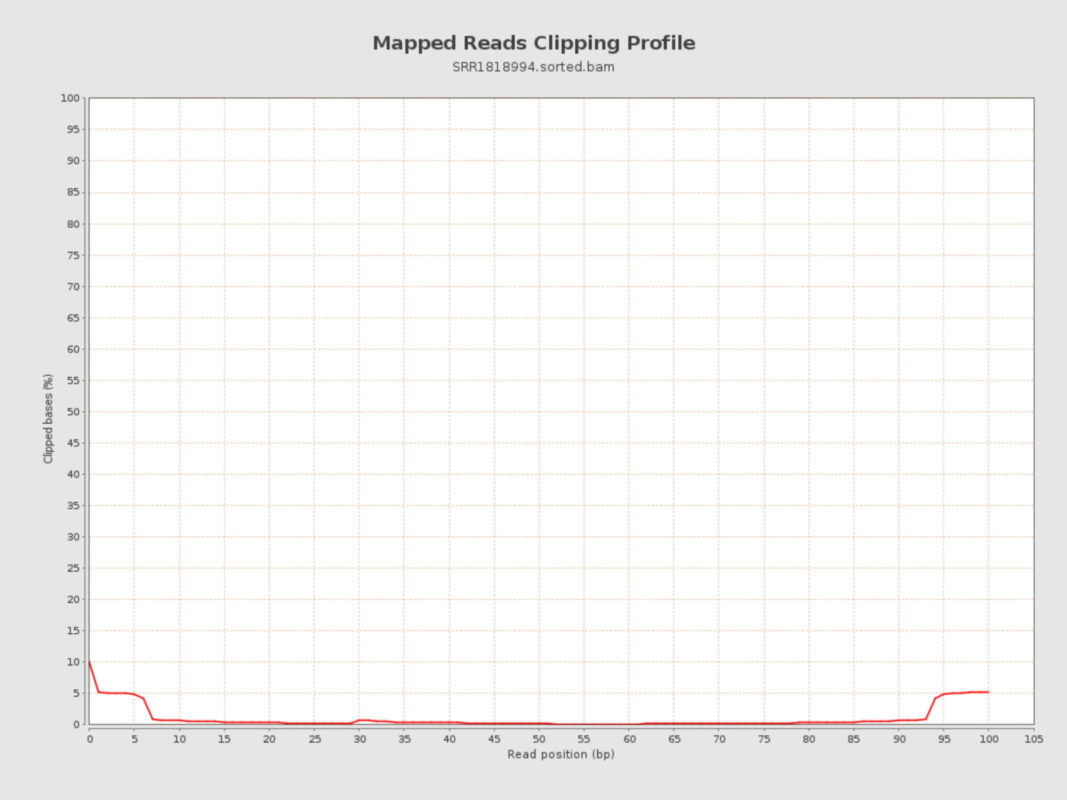
8. Results : Mapped Reads Nucleotide Content



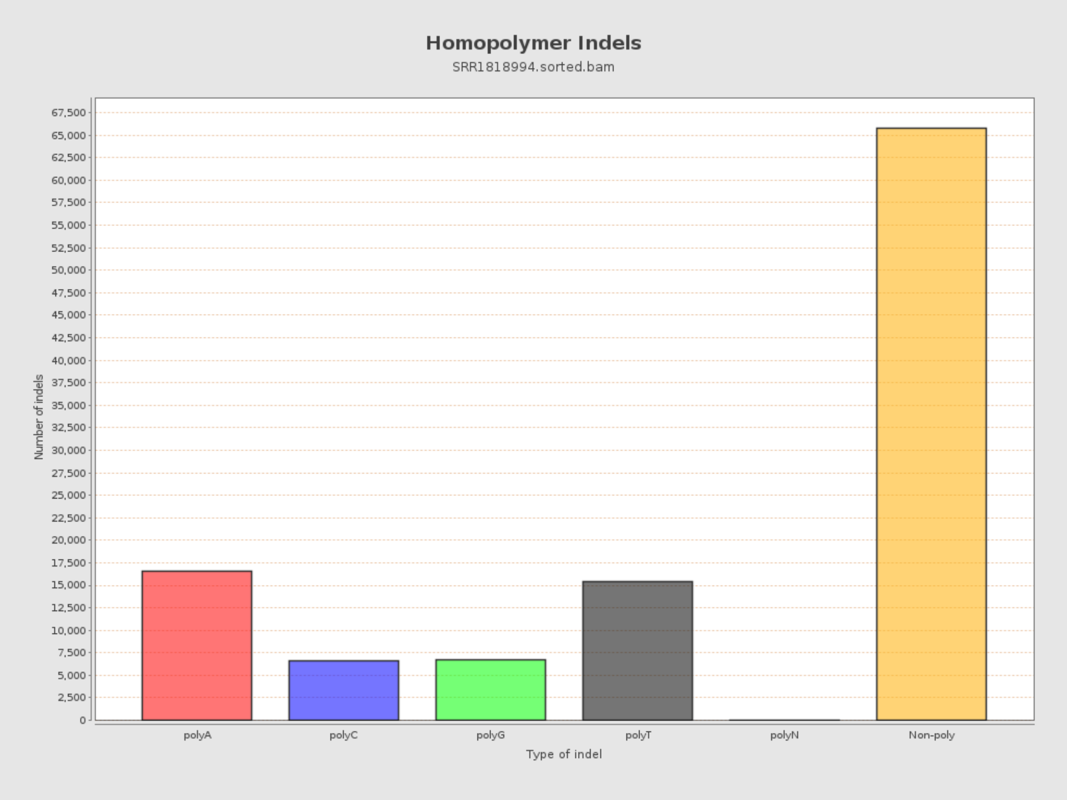
9. Results : Mapped Reads GC-content Distribution



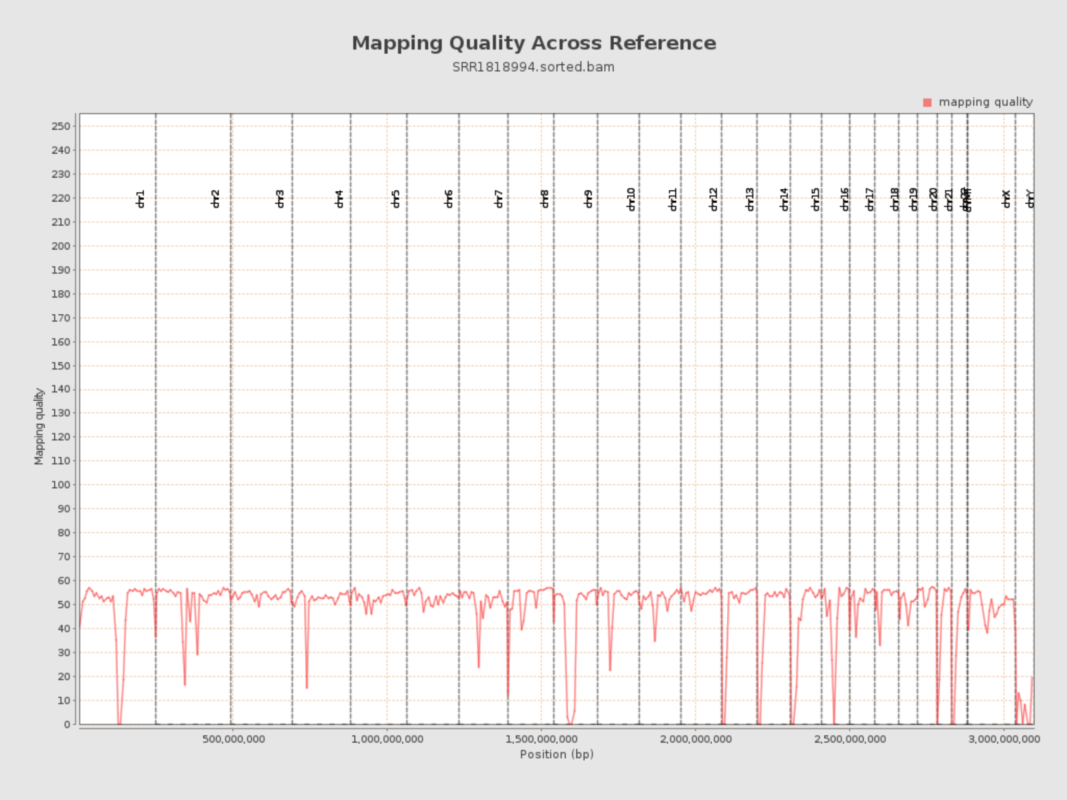
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram