Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:26:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818852.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_SRR1818852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:26:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,118,235
Mapped reads	2,088,799 / 98.61%
Unmapped reads	29,436 / 1.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,844 / 1.6%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	576,401 / 27.21%
Duplication rate	23.99%
Clipped reads	2,116,850 / 99.93%

2.2. ACGT Content

Number/percentage of A's	56,246,448 / 29.12%
Number/percentage of C's	41,491,834 / 21.48%
Number/percentage of T's	54,875,016 / 28.41%
Number/percentage of G's	40,531,958 / 20.98%
Number/percentage of N's	2,729 / 0%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0624

Standard Deviation	0.7153

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

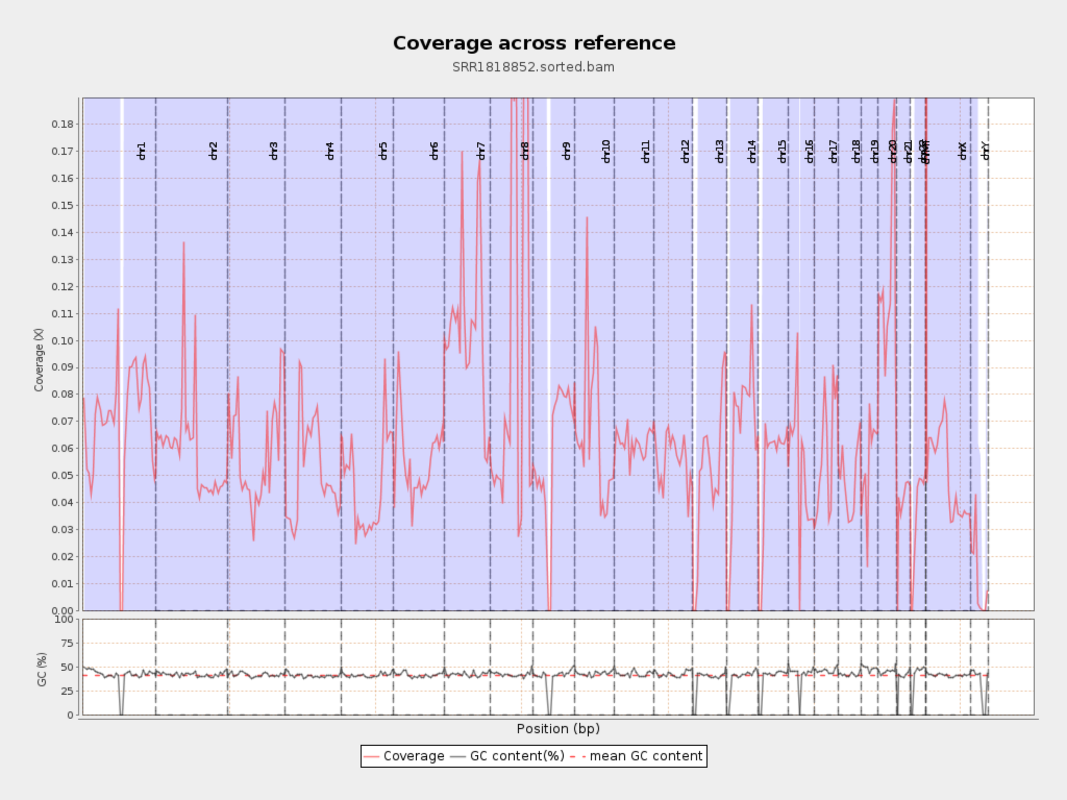
General error rate	0.64%
Mismatches	1,163,548
Insertions	24,564
Mapped reads with at least one insertion	1.14%
Deletions	63,056
Mapped reads with at least one deletion	2.95%
Homopolymer indels	41.95%

2.6. Chromosome stats

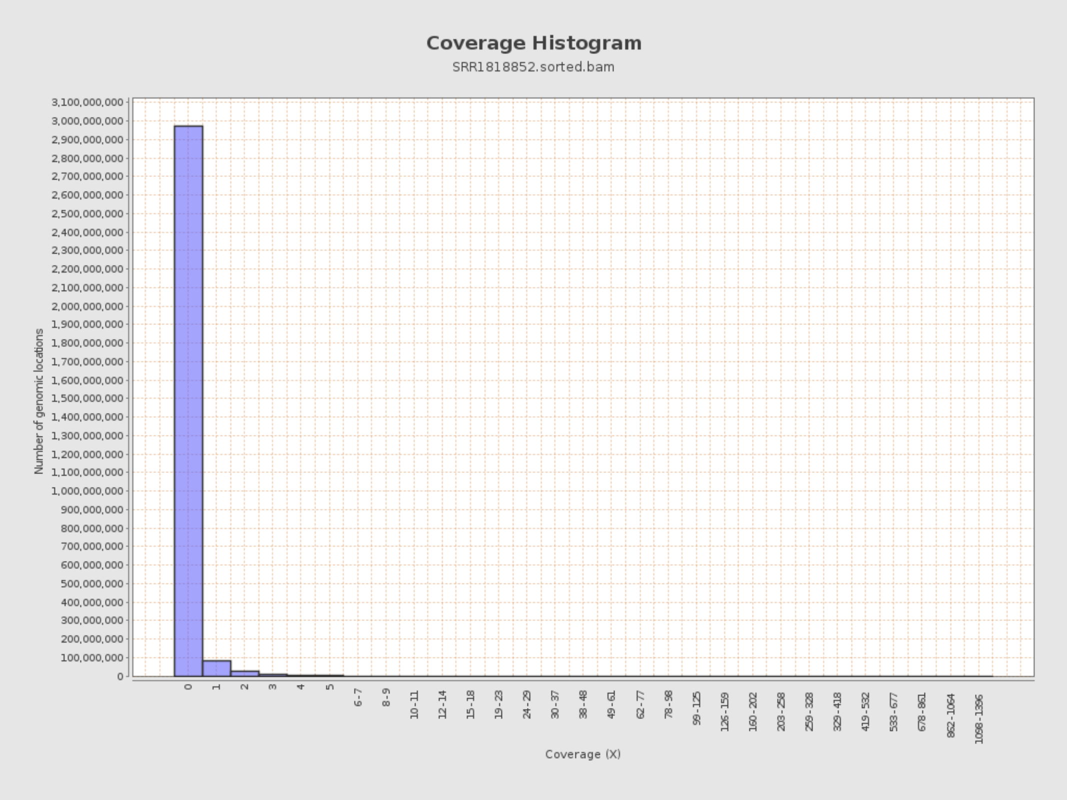
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17367324	0.0697	1.1091
chr2	243199373	14511016	0.0597	1.0193
chr3	198022430	11669643	0.0589	0.3474
chr4	191154276	9947770	0.052	0.4486
chr5	180915260	8449979	0.0467	0.3282
chr6	171115067	9563775	0.0559	0.3695
chr7	159138663	16720567	0.1051	1.5055

chr8	146364022	16981821	0.116	0.6248
chr9	141213431	8315277	0.0589	0.6155
chr10	135534747	8854450	0.0653	0.8875
chr11	135006516	8344087	0.0618	0.4458
chr12	133851895	7495448	0.056	0.3447
chr13	115169878	5872788	0.051	0.3213
chr14	107349540	7100161	0.0661	0.3939
chr15	102531392	5245220	0.0512	0.3217
chr16	90354753	4649124	0.0515	0.7456
chr17	81195210	4727992	0.0582	0.4303
chr18	78077248	3784975	0.0485	0.694
chr19	59128983	3215531	0.0544	0.906
chr20	63025520	7971712	0.1265	0.5588
chr21	48129895	1885293	0.0392	0.3621
chr22	51304566	1725427	0.0336	0.31
chrMT	16571	369347	22.2888	13.4154
chrX	155270560	7806108	0.0503	0.3908
chrY	59373566	693816	0.0117	0.8295

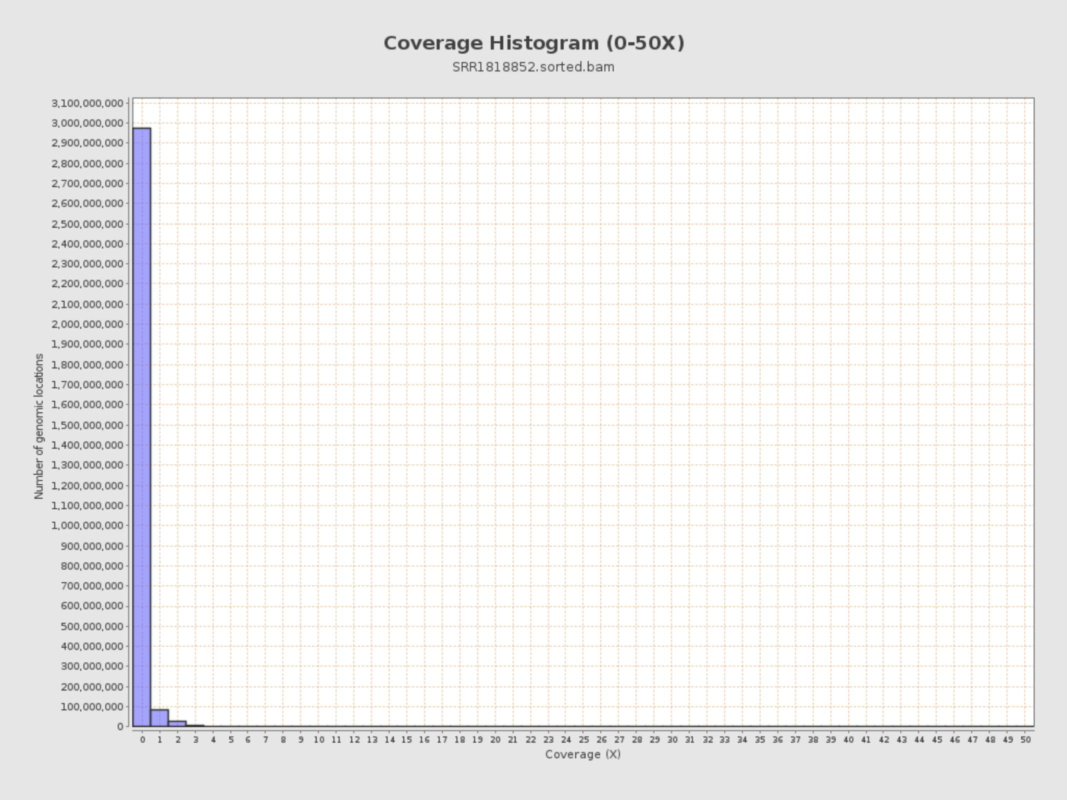
3. Results : Coverage across reference



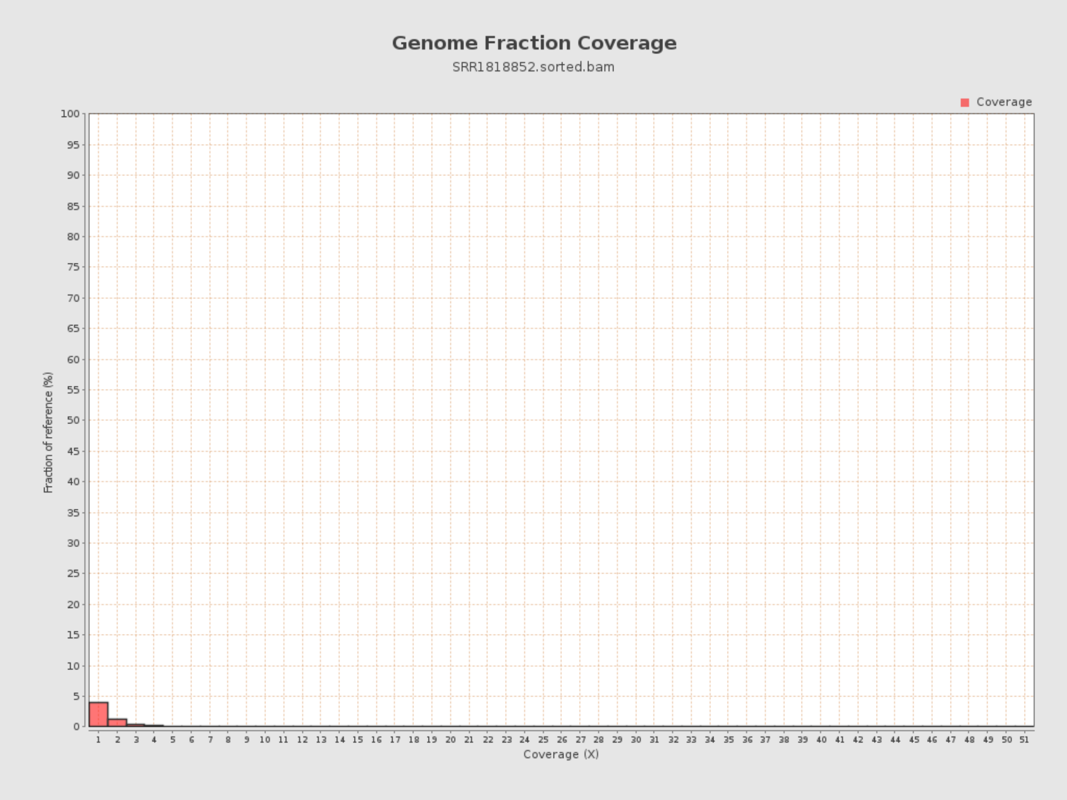
4. Results : Coverage Histogram



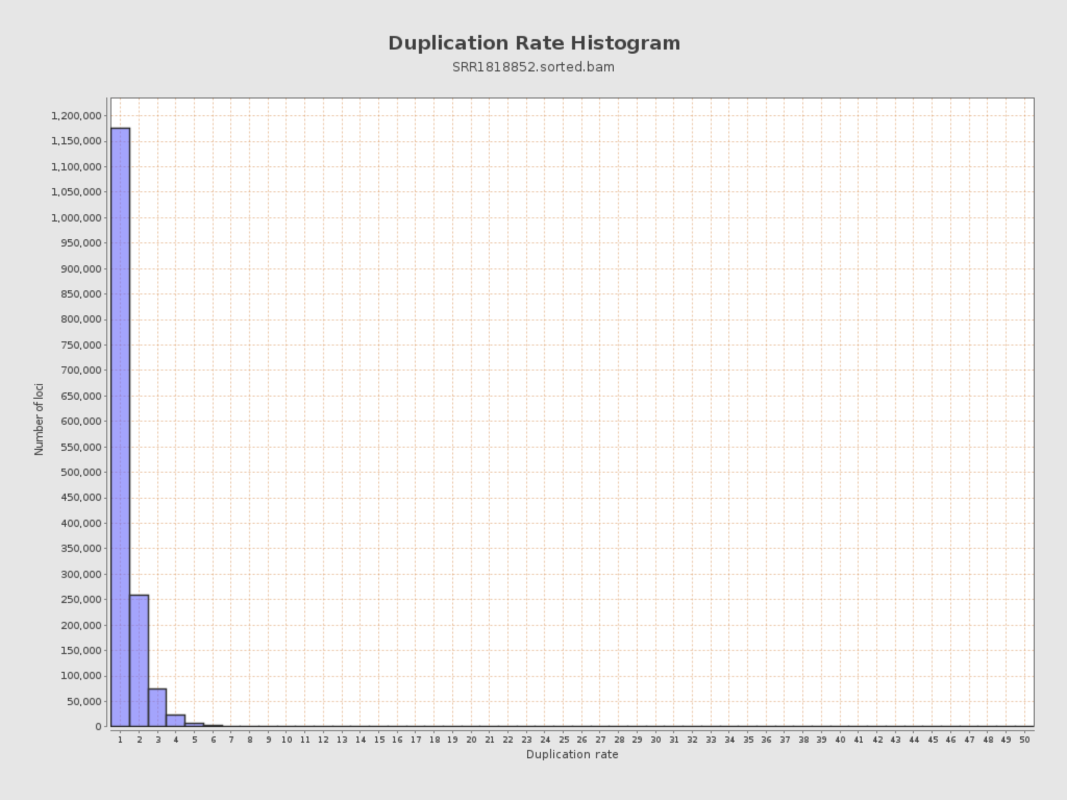
5. Results : Coverage Histogram (0-50X)



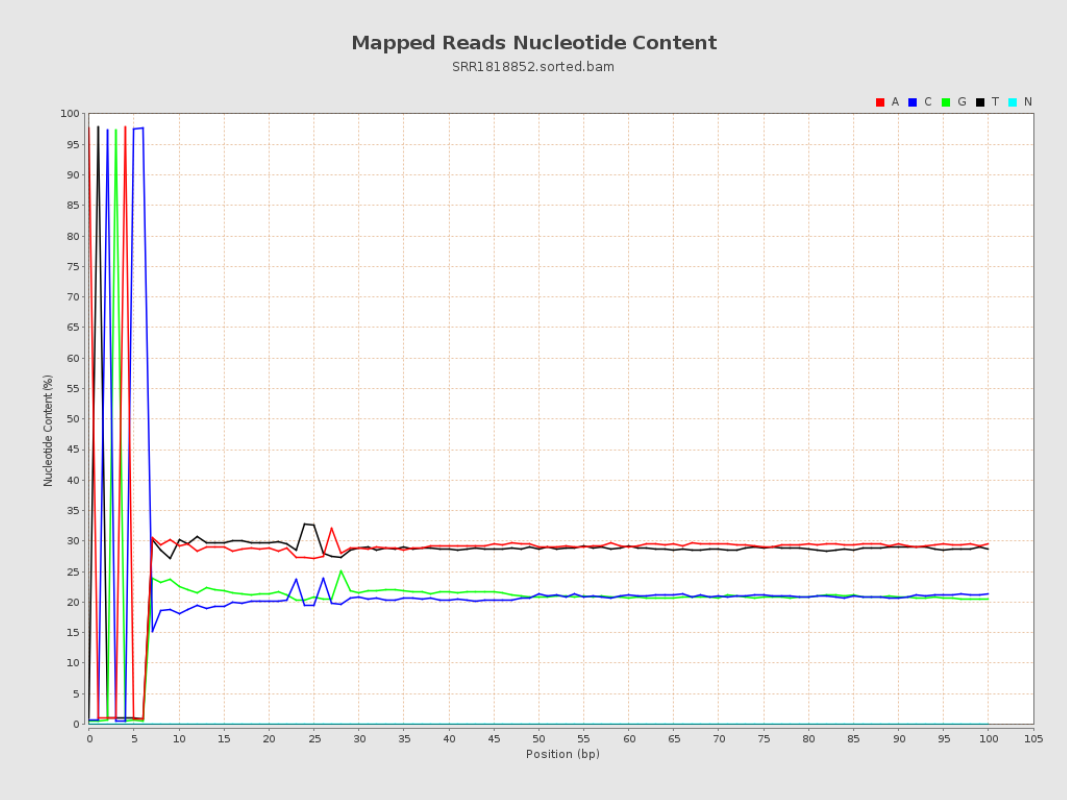
6. Results : Genome Fraction Coverage



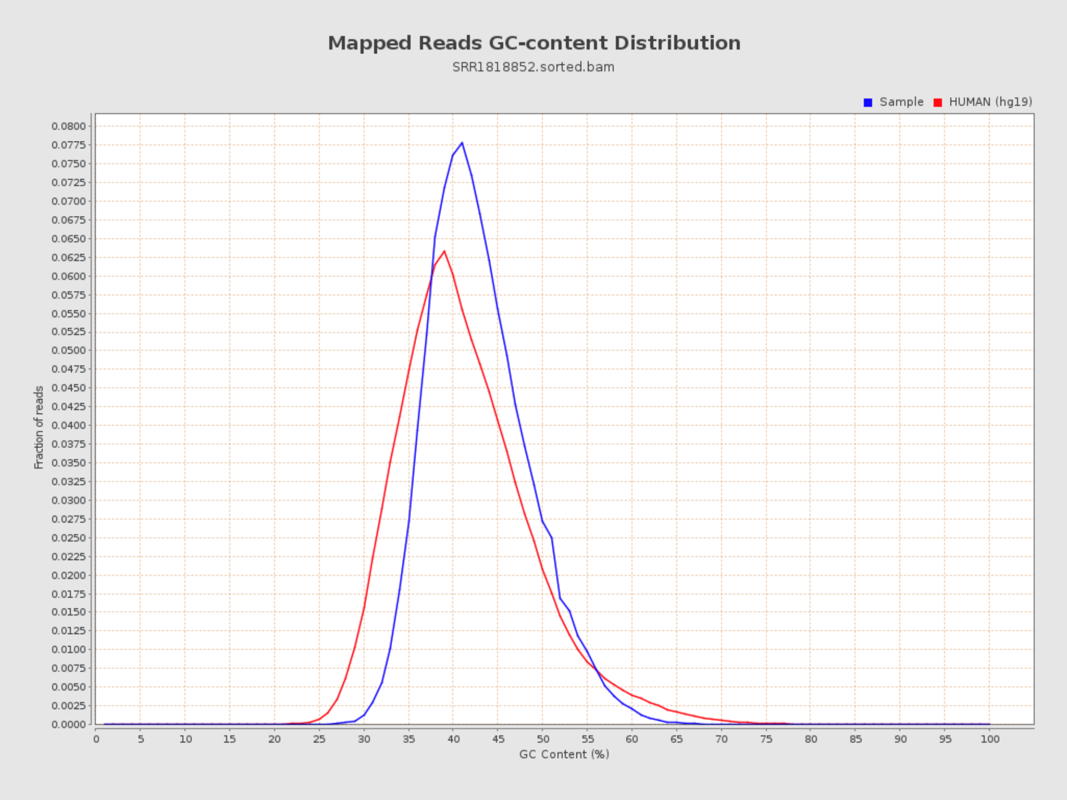
7. Results : Duplication Rate Histogram



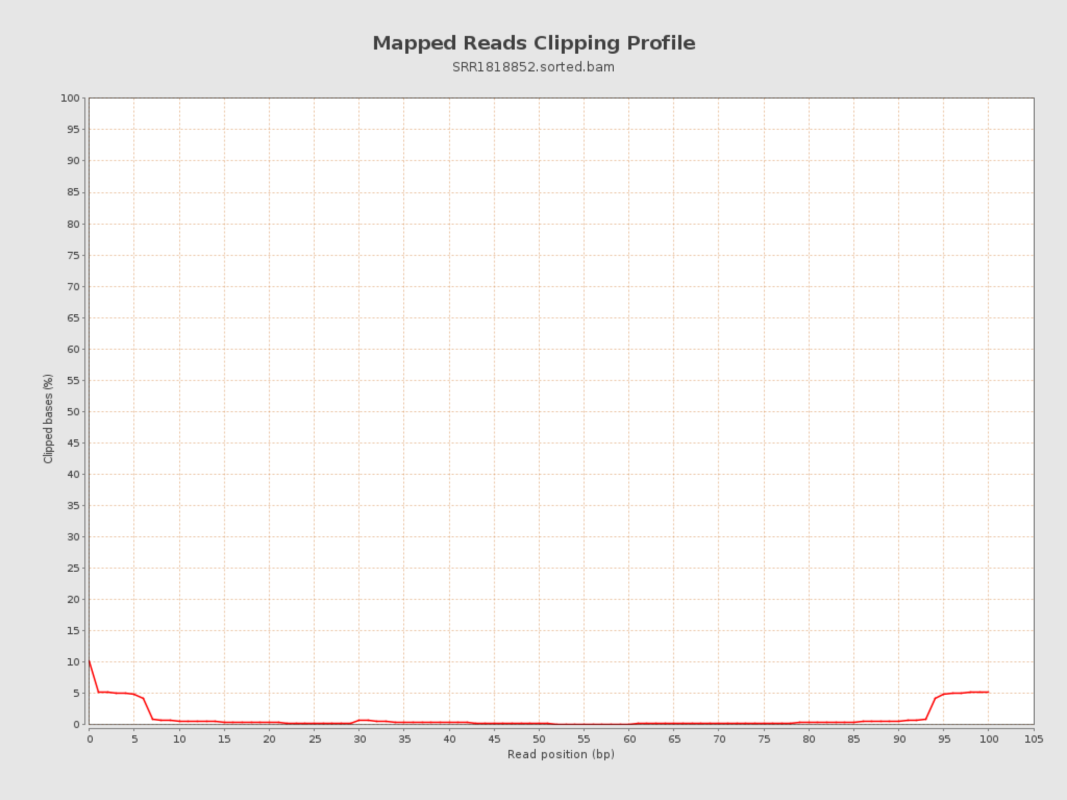
8. Results : Mapped Reads Nucleotide Content



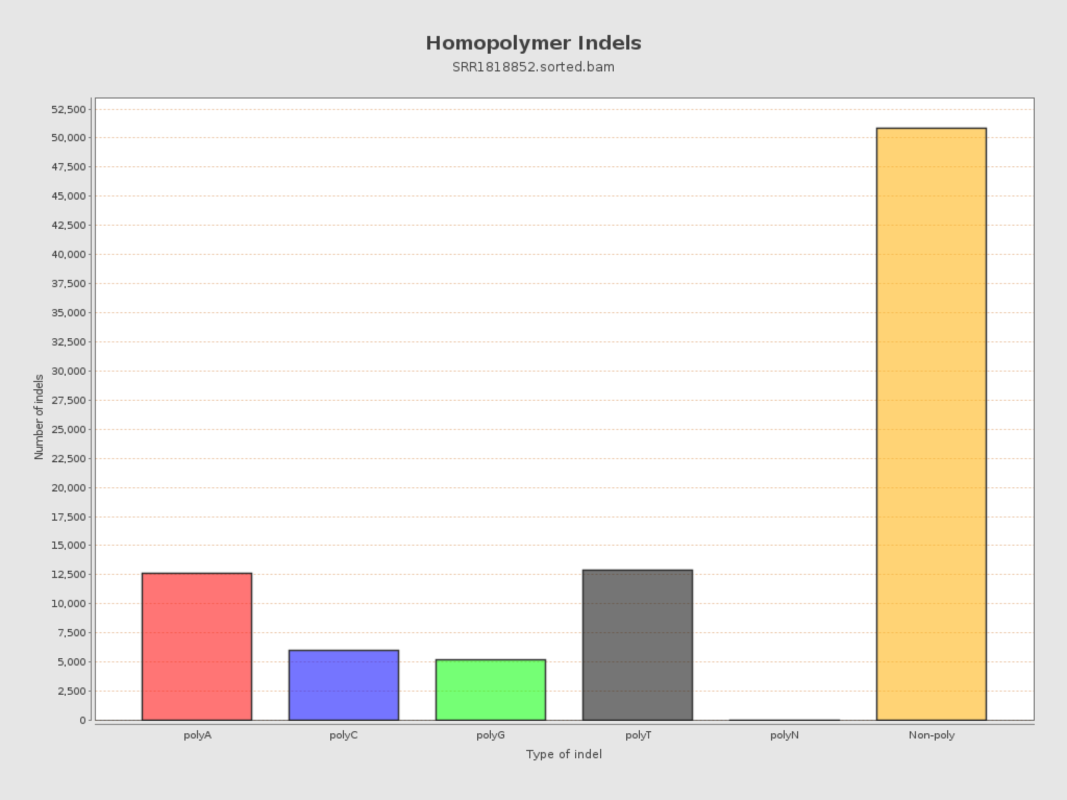
9. Results : Mapped Reads GC-content Distribution



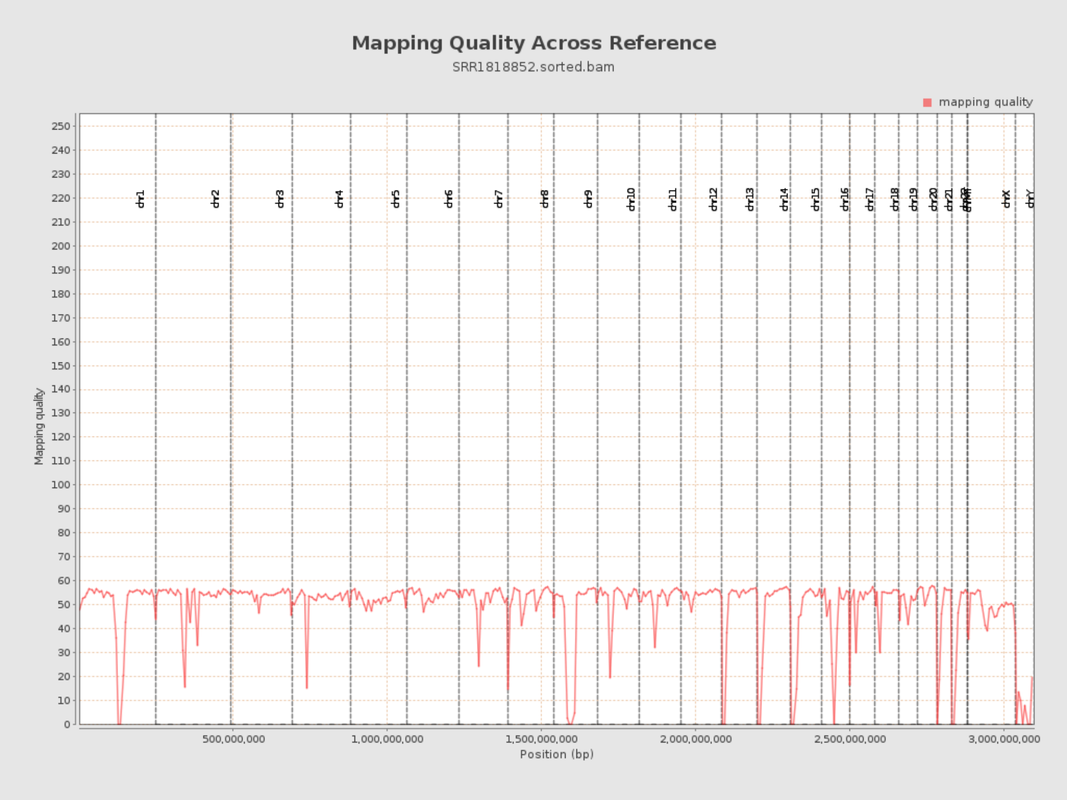
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram