Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:57:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818944.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_SRR1818944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,211,066
Mapped reads	1,193,554 / 98.55%
Unmapped reads	17,512 / 1.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,645 / 1.21%
Read min/max/mean length	30 / 101 / 101.46
Duplicated reads (estimated)	427,874 / 35.33%
Duplication rate	29.39%
Clipped reads	1,200,445 / 99.12%

2.2. ACGT Content

Number/percentage of A's	30,559,197 / 27.63%
Number/percentage of C's	23,739,407 / 21.46%
Number/percentage of T's	31,734,058 / 28.69%
Number/percentage of G's	24,558,977 / 22.21%
Number/percentage of N's	4,553 / 0%
GC Percentage	43.67%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.447

2.4. Mapping Quality

Mean Mapping Quality	48.97

2.5. Mismatches and indels

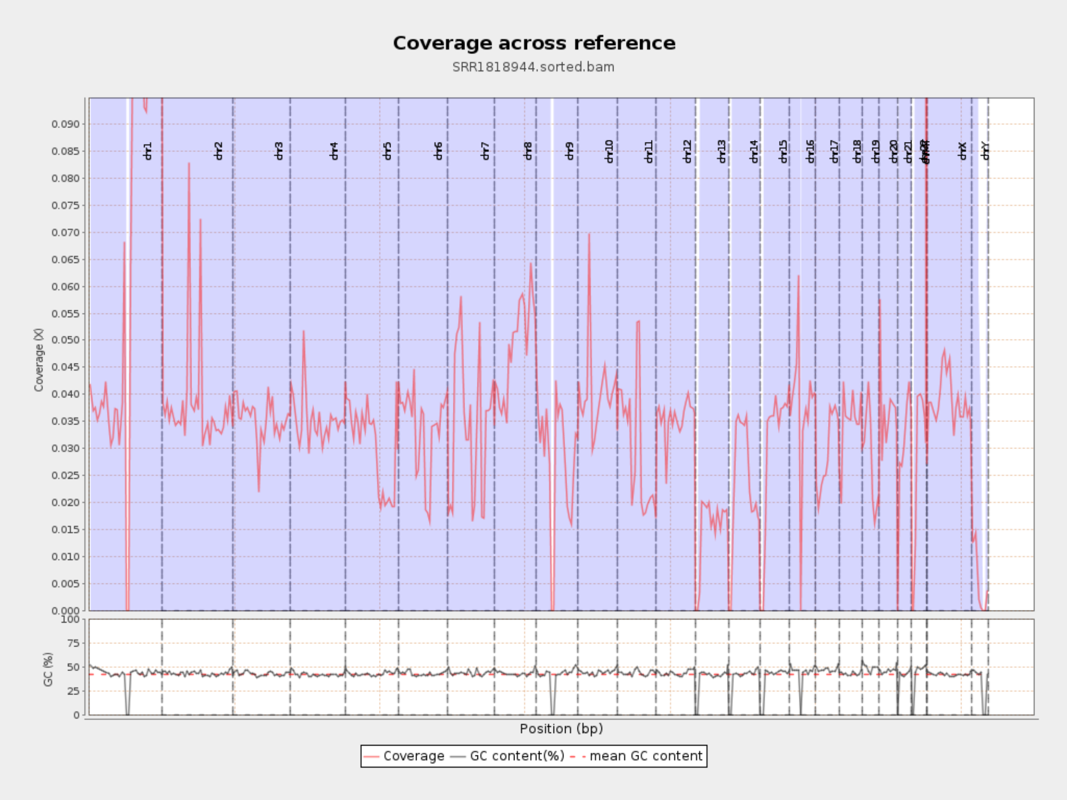
General error rate	0.66%
Mismatches	702,803
Insertions	13,532
Mapped reads with at least one insertion	1.1%
Deletions	34,496
Mapped reads with at least one deletion	2.83%
Homopolymer indels	42%

2.6. Chromosome stats

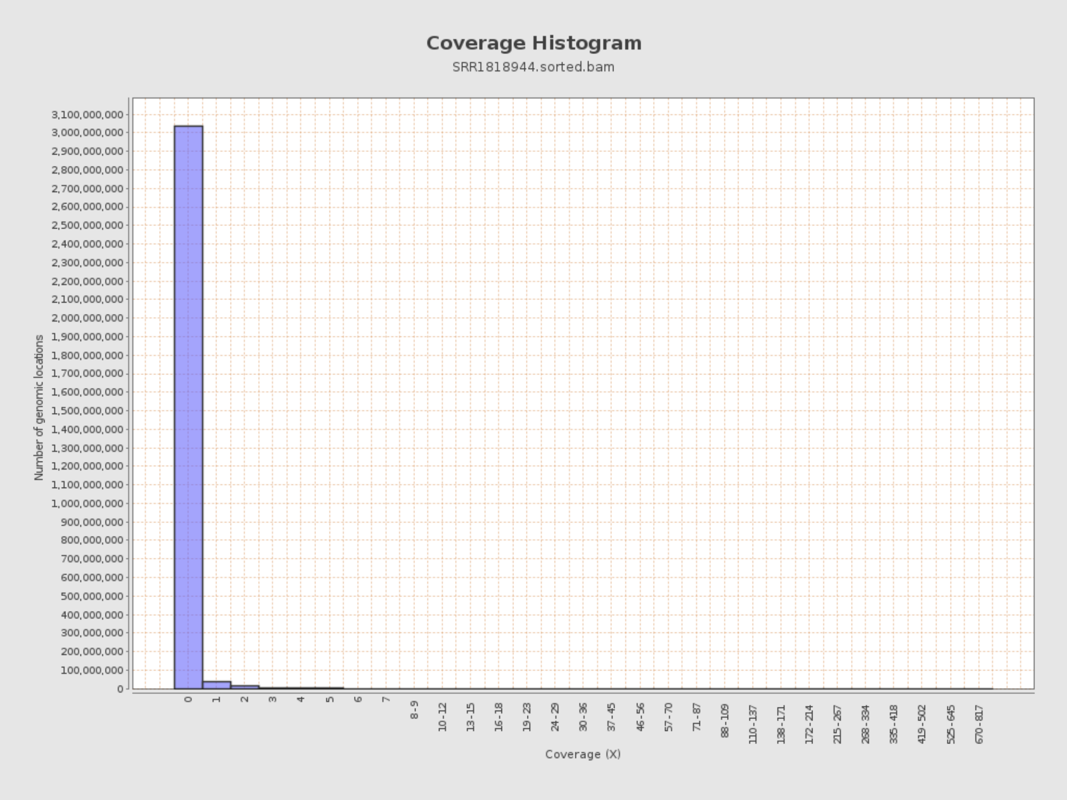
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16271076	0.0653	0.7451
chr2	243199373	9324310	0.0383	0.6516
chr3	198022430	7013978	0.0354	0.3088
chr4	191154276	6721886	0.0352	0.3249
chr5	180915260	5495561	0.0304	0.2997
chr6	171115067	5788823	0.0338	0.3226
chr7	159138663	5450011	0.0342	0.36

chr8	146364022	7178099	0.049	0.3959
chr9	141213431	3843860	0.0272	0.4268
chr10	135534747	5462915	0.0403	0.5713
chr11	135006516	4119075	0.0305	0.3139
chr12	133851895	4769693	0.0356	0.3128
chr13	115169878	1722878	0.015	0.1944
chr14	107349540	2508427	0.0234	0.2827
chr15	102531392	3076362	0.03	0.2853
chr16	90354753	3419520	0.0378	0.4965
chr17	81195210	2395964	0.0295	0.3182
chr18	78077248	2724418	0.0349	0.6197
chr19	59128983	1696224	0.0287	0.6961
chr20	63025520	2339730	0.0371	0.3332
chr21	48129895	1458613	0.0303	0.3249
chr22	51304566	1350397	0.0263	0.2871
chrMT	16571	180640	10.901	9.8469
chrX	155270560	6021842	0.0388	0.3888
chrY	59373566	325726	0.0055	0.4041

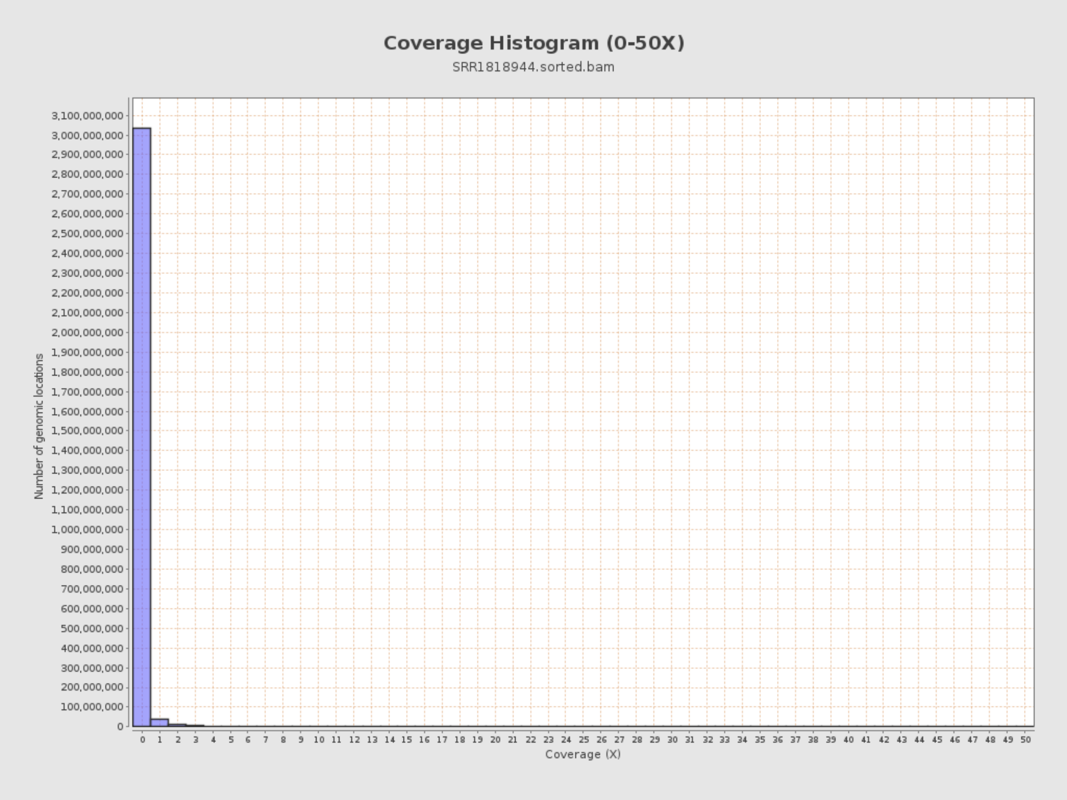
3. Results : Coverage across reference



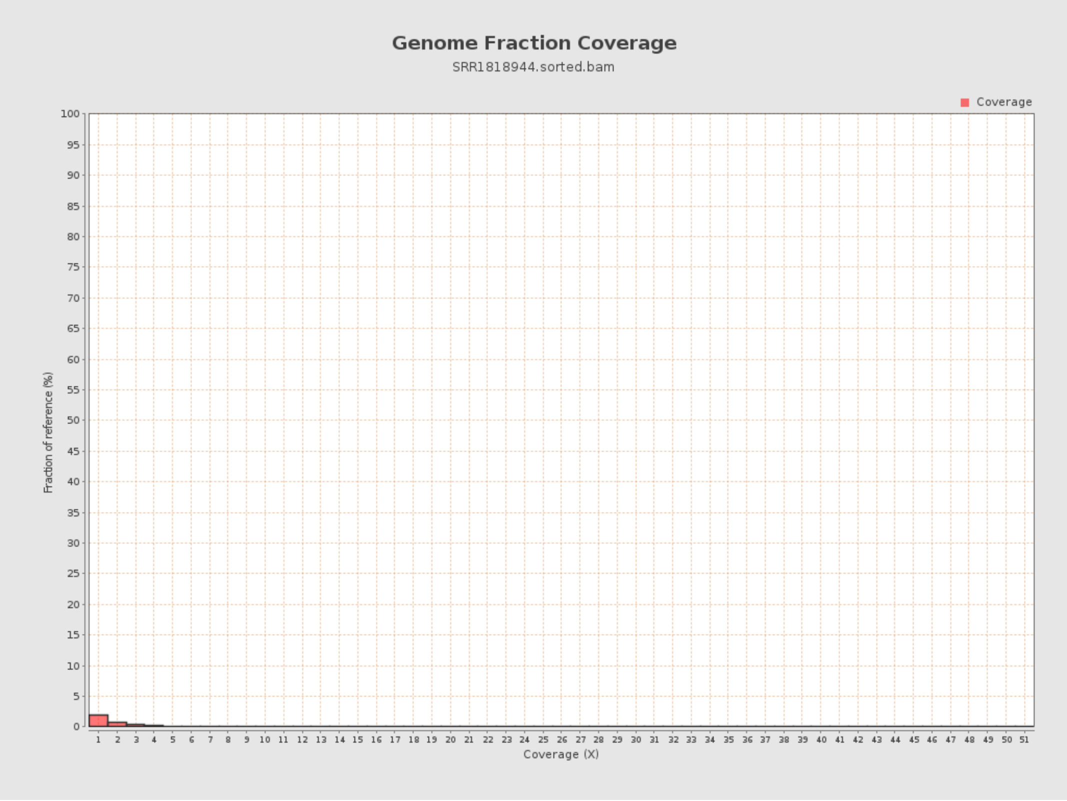
4. Results : Coverage Histogram



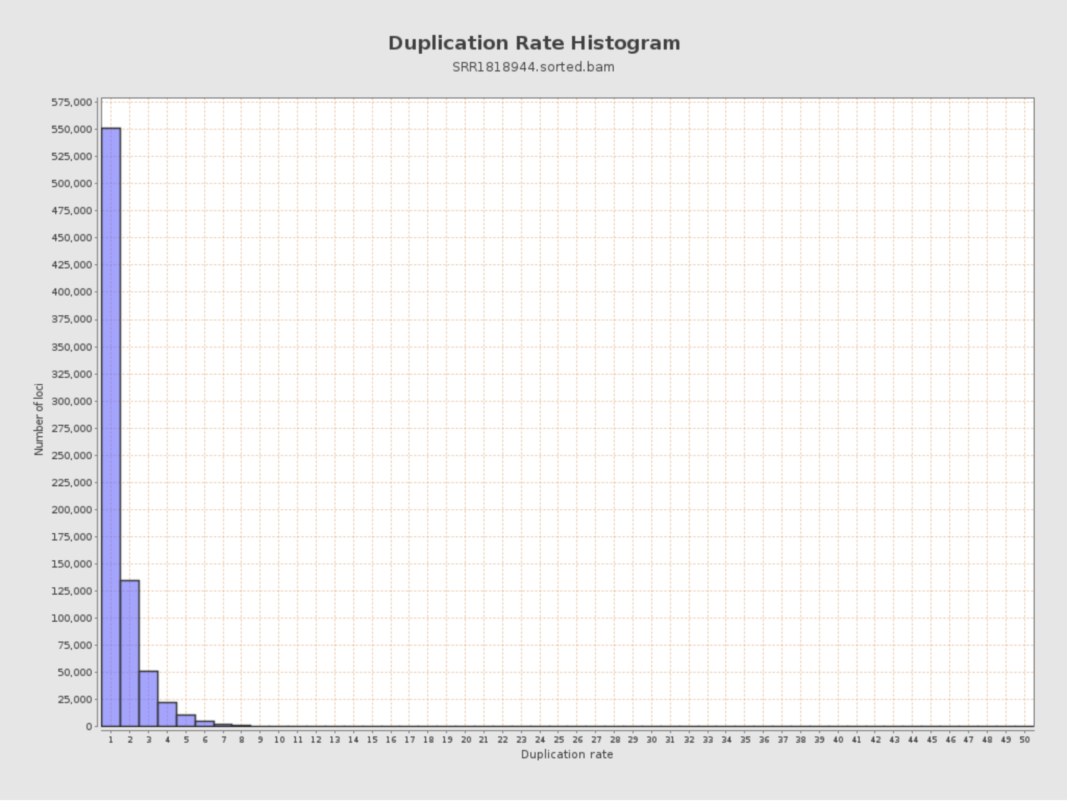
5. Results : Coverage Histogram (0-50X)



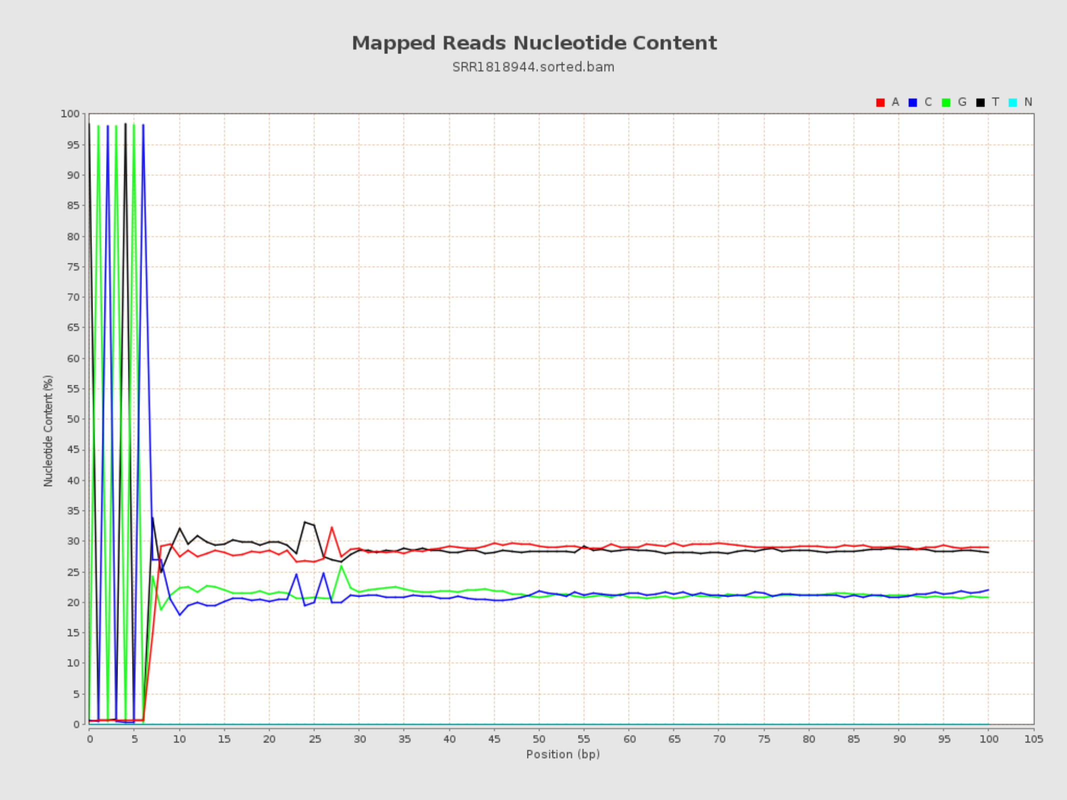
6. Results : Genome Fraction Coverage



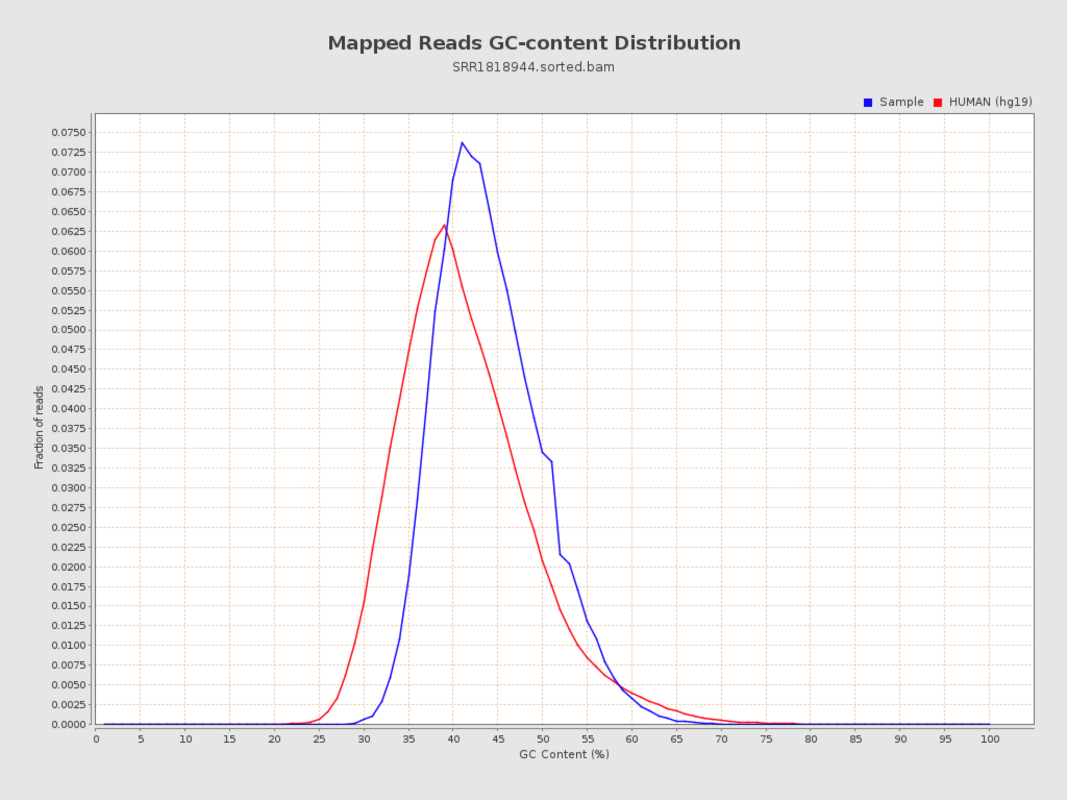
7. Results : Duplication Rate Histogram



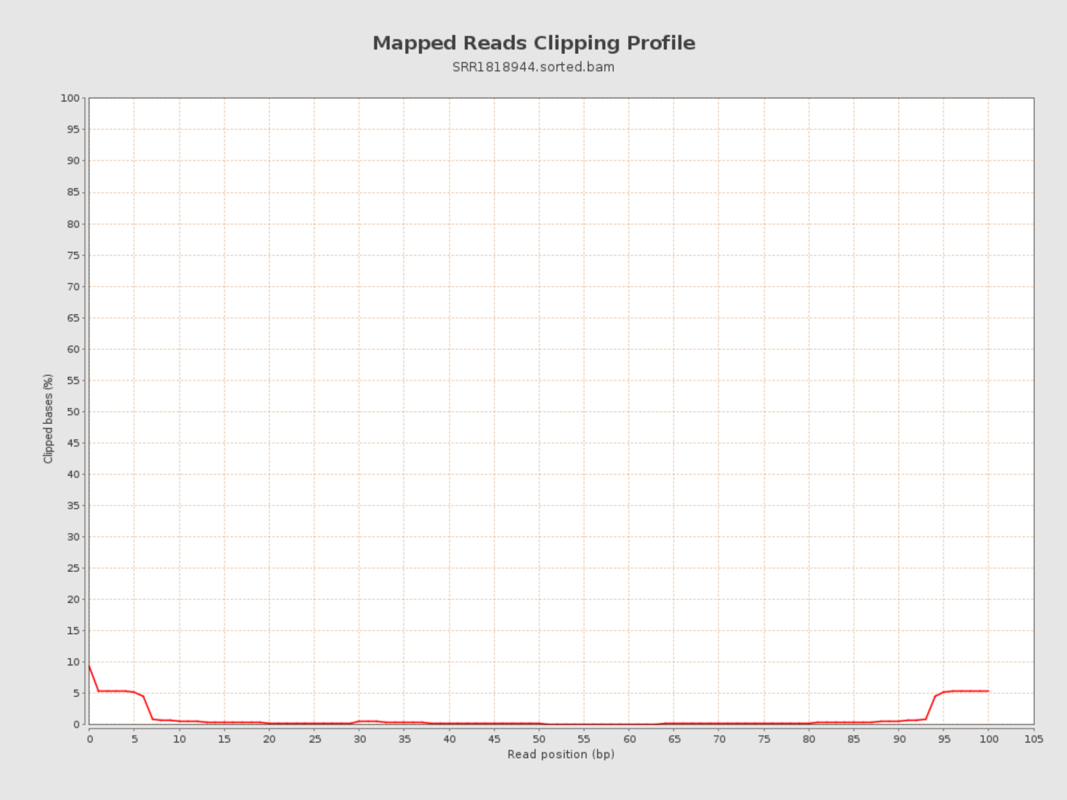
8. Results : Mapped Reads Nucleotide Content



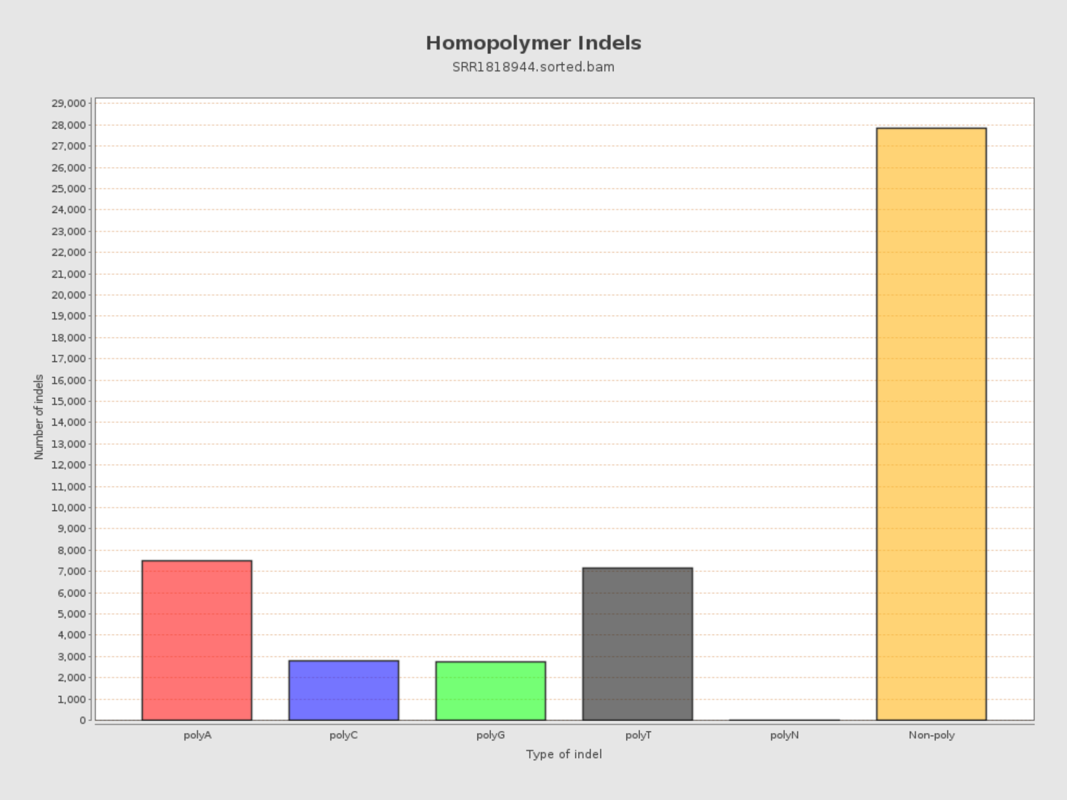
9. Results : Mapped Reads GC-content Distribution



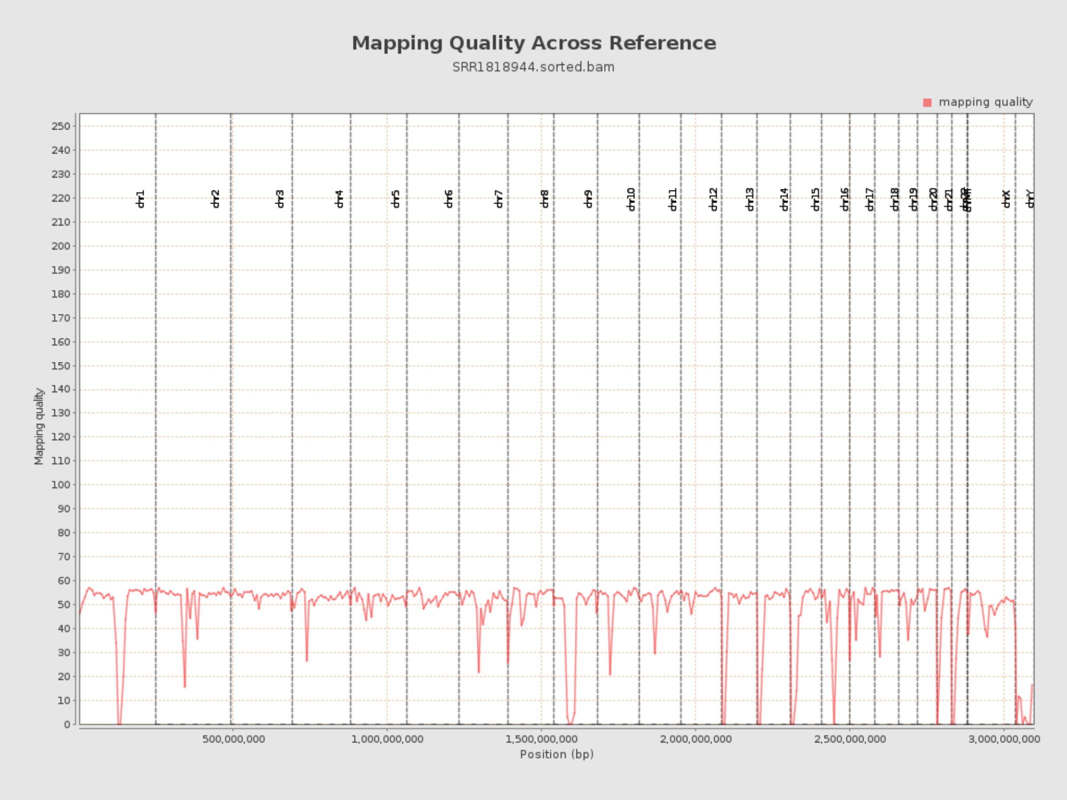
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram