Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:25:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818949.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_SRR1818949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:25:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,065,102
Mapped reads	2,037,188 / 98.65%
Unmapped reads	27,914 / 1.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,565 / 1.24%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	851,489 / 41.23%
Duplication rate	35.12%
Clipped reads	2,043,476 / 98.95%

2.2. ACGT Content

Number/percentage of A's	53,940,184 / 28.58%
Number/percentage of C's	41,810,796 / 22.16%
Number/percentage of T's	51,869,159 / 27.49%
Number/percentage of G's	41,089,661 / 21.77%
Number/percentage of N's	8,221 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.061

Standard Deviation	0.6938

2.4. Mapping Quality

Mean Mapping Quality	49.19

2.5. Mismatches and indels

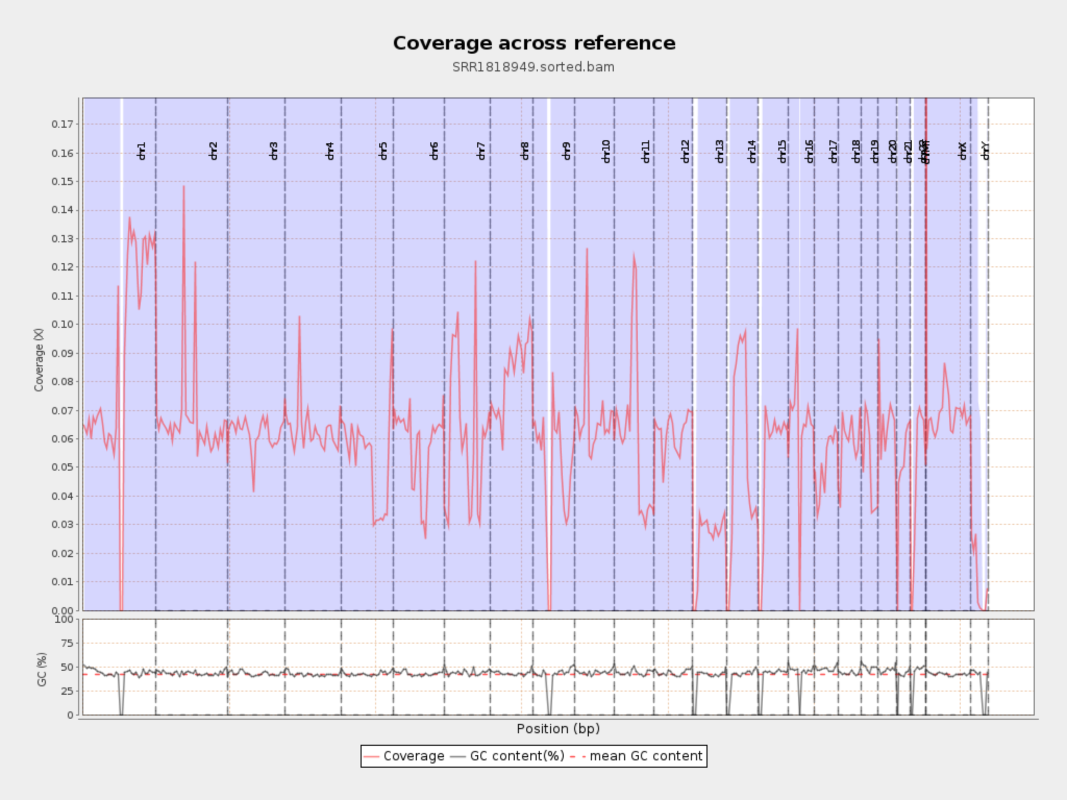
General error rate	0.69%
Mismatches	1,252,702
Insertions	24,812
Mapped reads with at least one insertion	1.18%
Deletions	58,738
Mapped reads with at least one deletion	2.82%
Homopolymer indels	42.41%

2.6. Chromosome stats

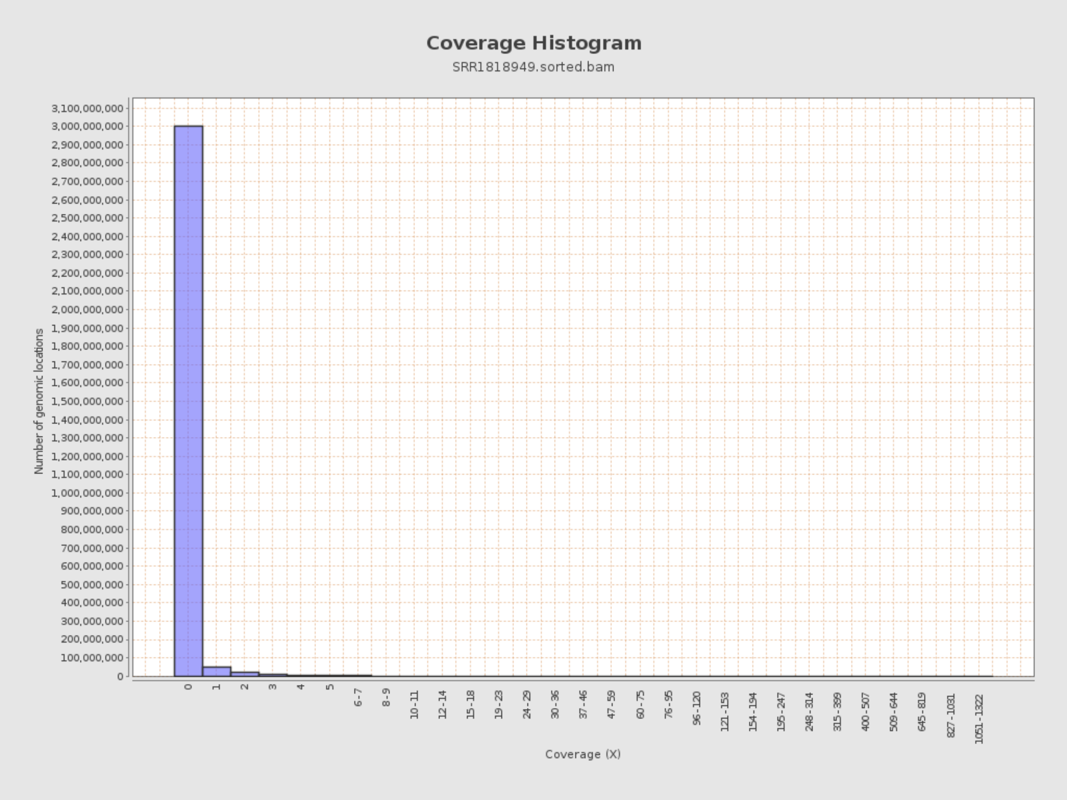
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21780720	0.0874	1.206
chr2	243199373	16418984	0.0675	1.0477
chr3	198022430	12260958	0.0619	0.4408
chr4	191154276	12222937	0.0639	0.497
chr5	180915260	9782507	0.0541	0.4214
chr6	171115067	9889422	0.0578	0.4605
chr7	159138663	9836612	0.0618	0.5699

chr8	146364022	12138253	0.0829	0.5722
chr9	141213431	6944662	0.0492	0.789
chr10	135534747	9108499	0.0672	0.8269
chr11	135006516	8212723	0.0608	0.5322
chr12	133851895	8399604	0.0628	0.46
chr13	115169878	2847296	0.0247	0.2733
chr14	107349540	5909374	0.055	0.4493
chr15	102531392	5345672	0.0521	0.405
chr16	90354753	5733633	0.0635	0.7906
chr17	81195210	4206855	0.0518	0.456
chr18	78077248	4559197	0.0584	0.9224
chr19	59128983	3003305	0.0508	1.0803
chr20	63025520	4164120	0.0661	0.4887
chr21	48129895	2423582	0.0504	0.4572
chr22	51304566	2378283	0.0464	0.4267
chrMT	16571	8687	0.5242	1.4219
chrX	155270560	10658279	0.0686	0.5519
chrY	59373566	590886	0.01	0.5999

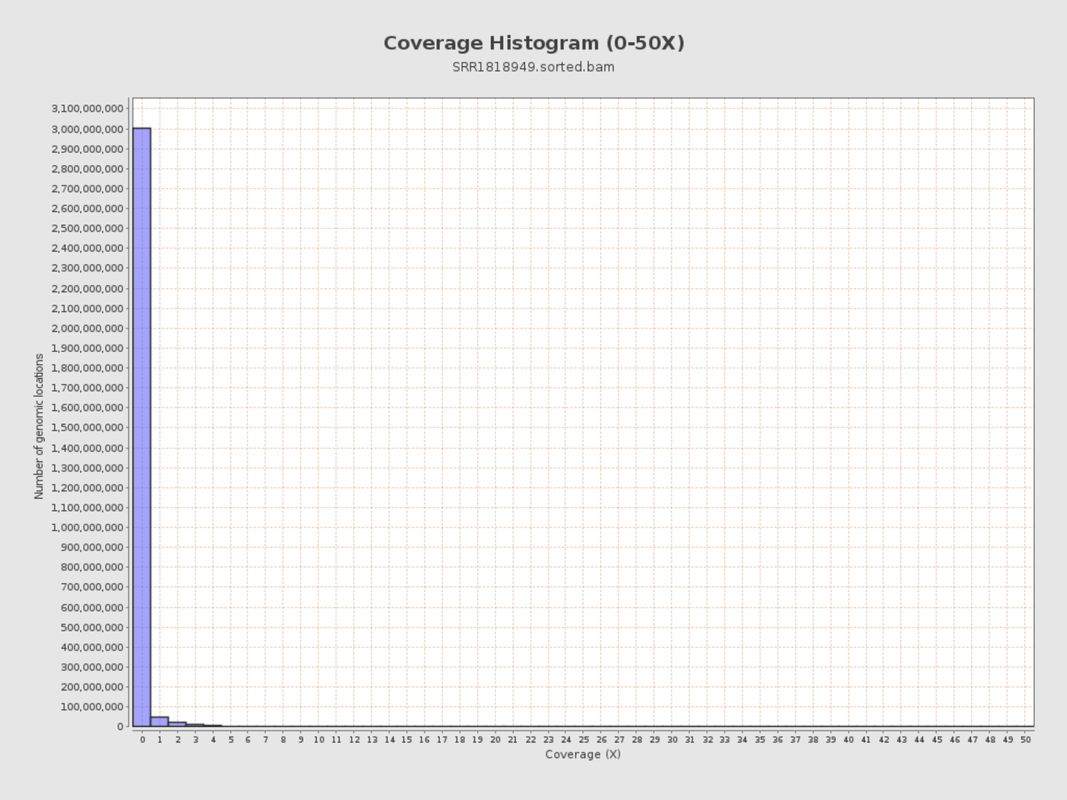
3. Results : Coverage across reference



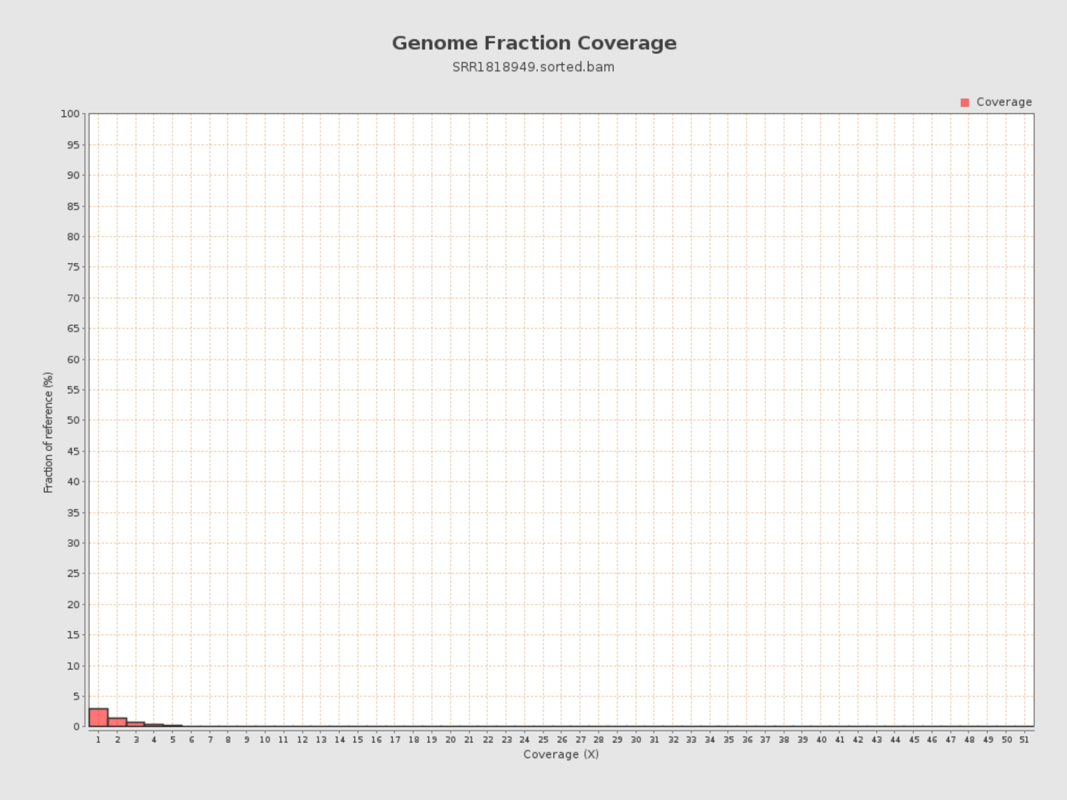
4. Results : Coverage Histogram



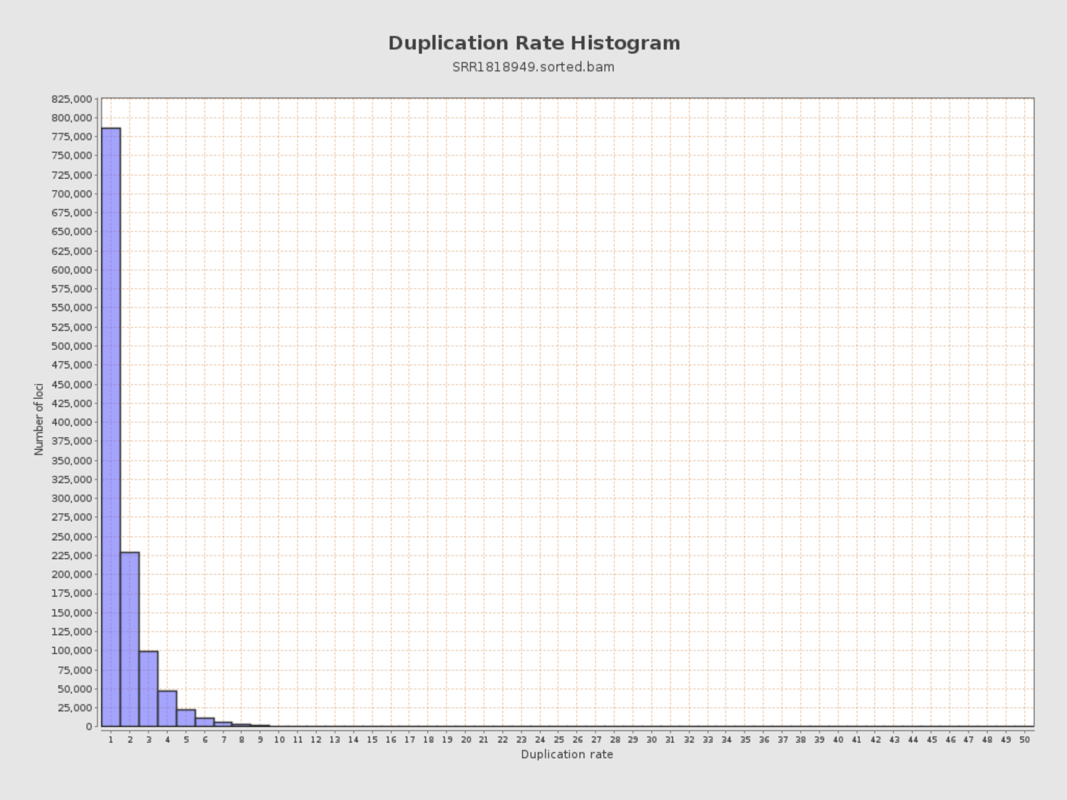
5. Results : Coverage Histogram (0-50X)



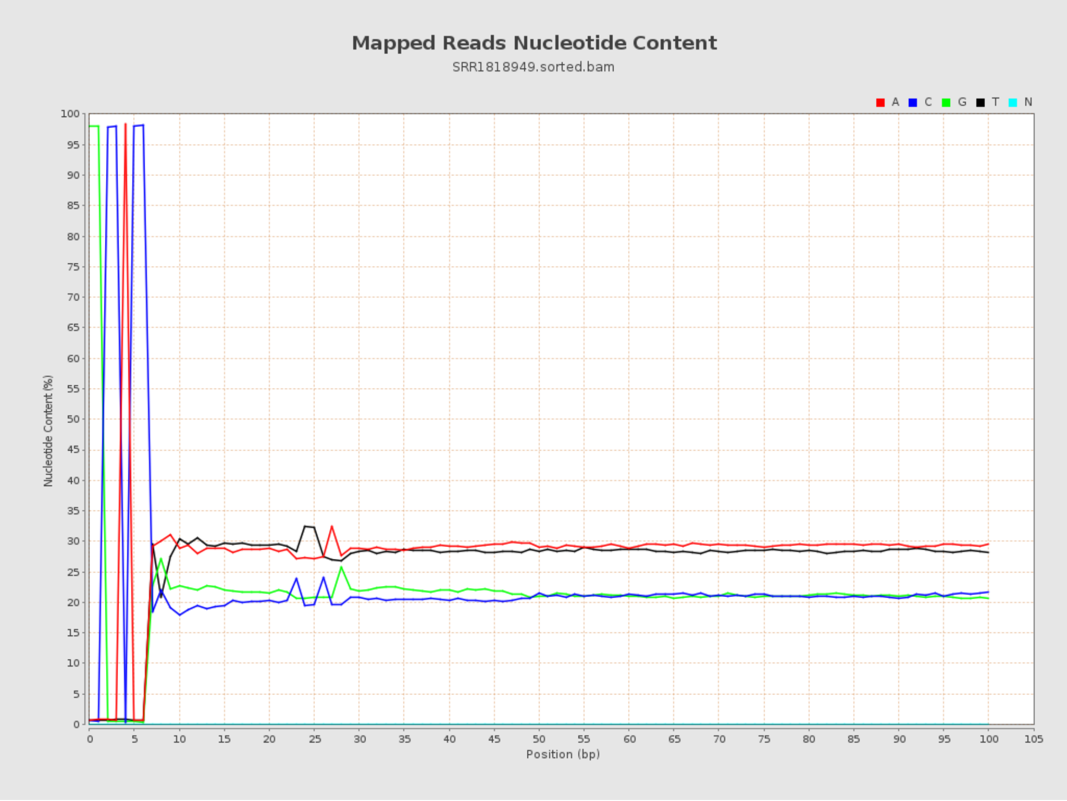
6. Results : Genome Fraction Coverage



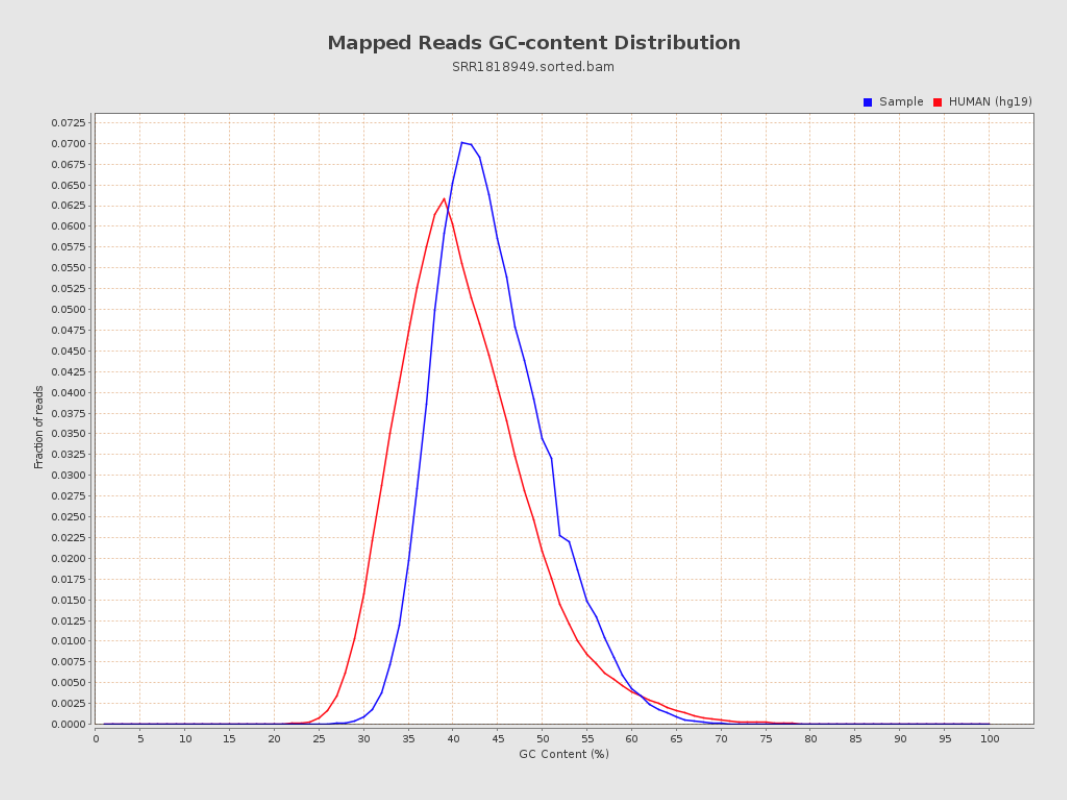
7. Results : Duplication Rate Histogram



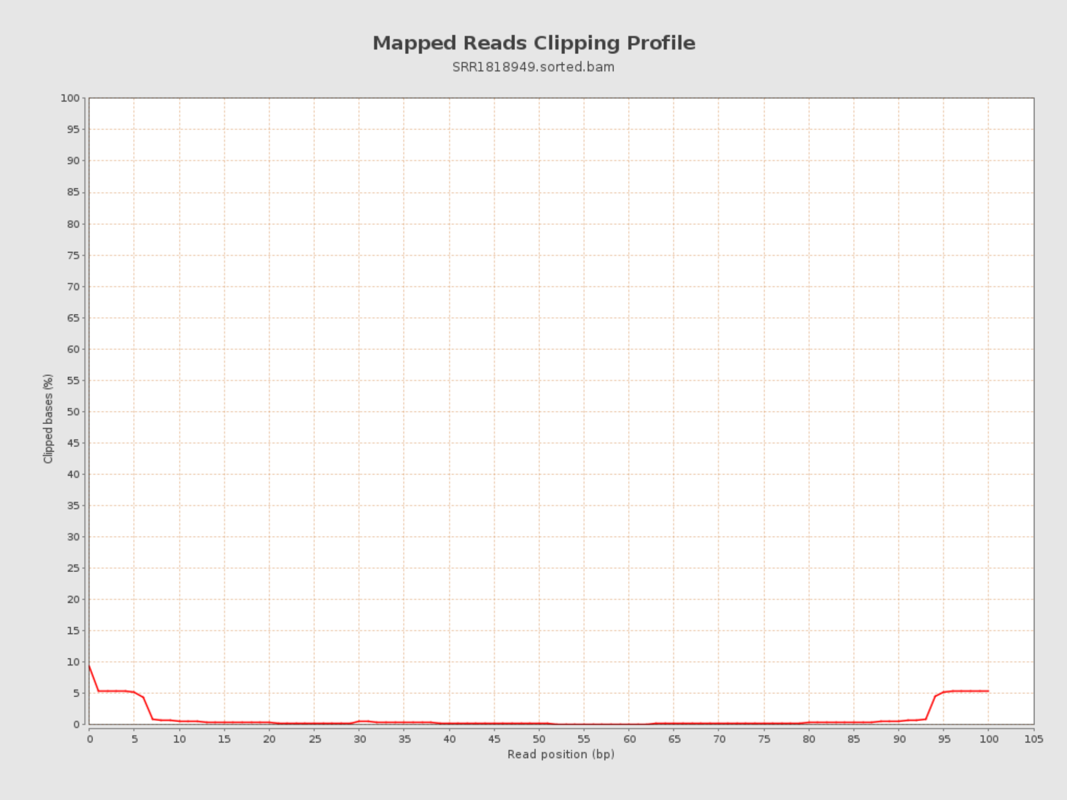
8. Results : Mapped Reads Nucleotide Content



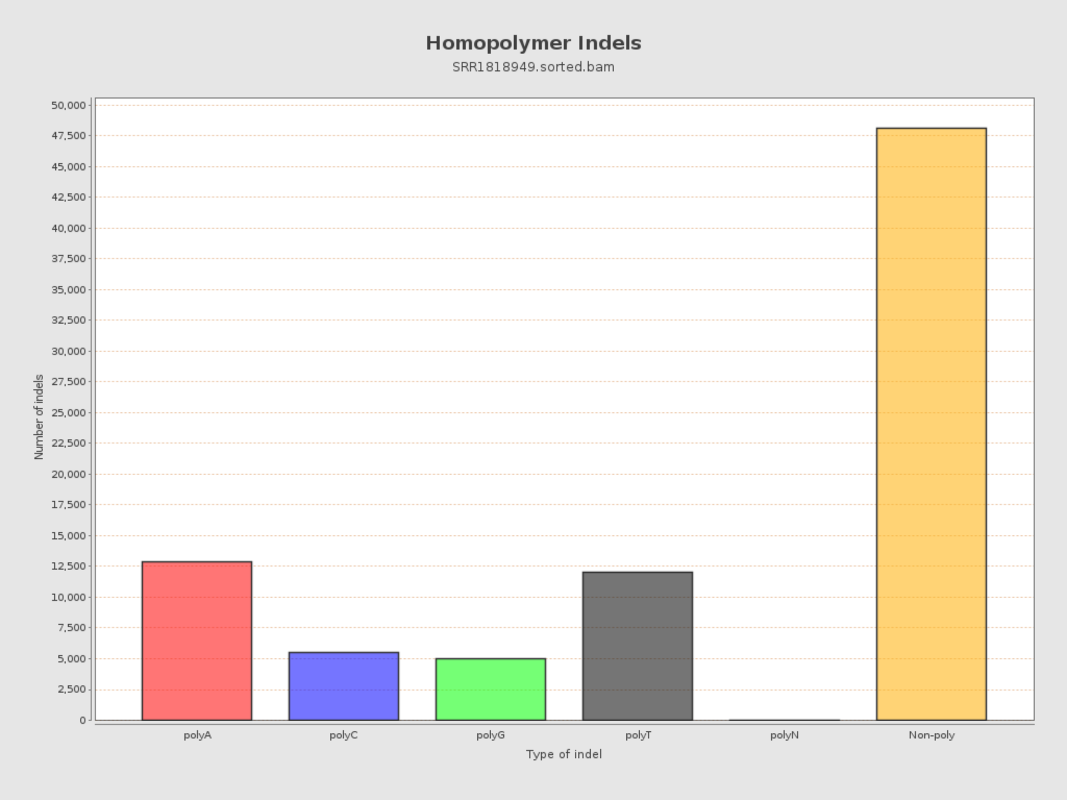
9. Results : Mapped Reads GC-content Distribution



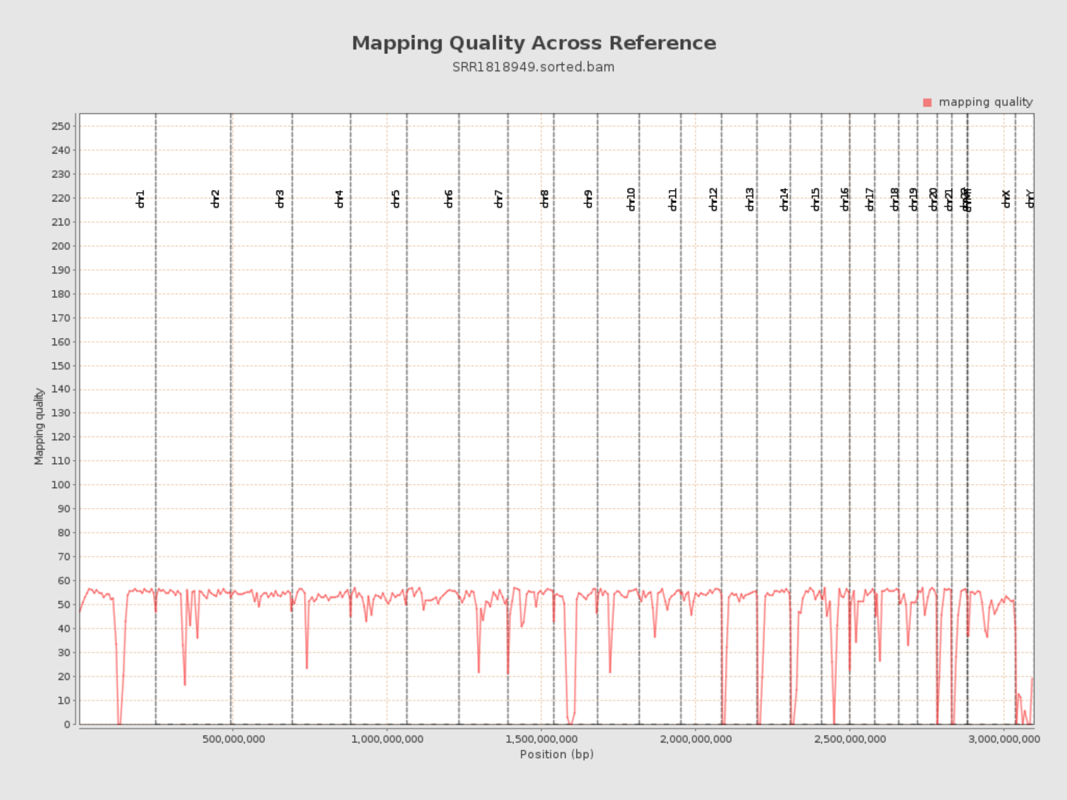
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram