Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:59:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818816.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_SRR1818816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:59:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,572,186
Mapped reads	1,530,630 / 97.36%
Unmapped reads	41,556 / 2.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,024 / 0.64%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	574,285 / 36.53%
Duplication rate	31.91%
Clipped reads	1,531,948 / 97.44%

2.2. ACGT Content

Number/percentage of A's	30,543,012 / 29.36%
Number/percentage of C's	22,064,655 / 21.21%
Number/percentage of T's	28,431,403 / 27.33%
Number/percentage of G's	22,969,415 / 22.08%
Number/percentage of N's	6,099 / 0.01%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.4435

2.4. Mapping Quality

Mean Mapping Quality	47.65

2.5. Mismatches and indels

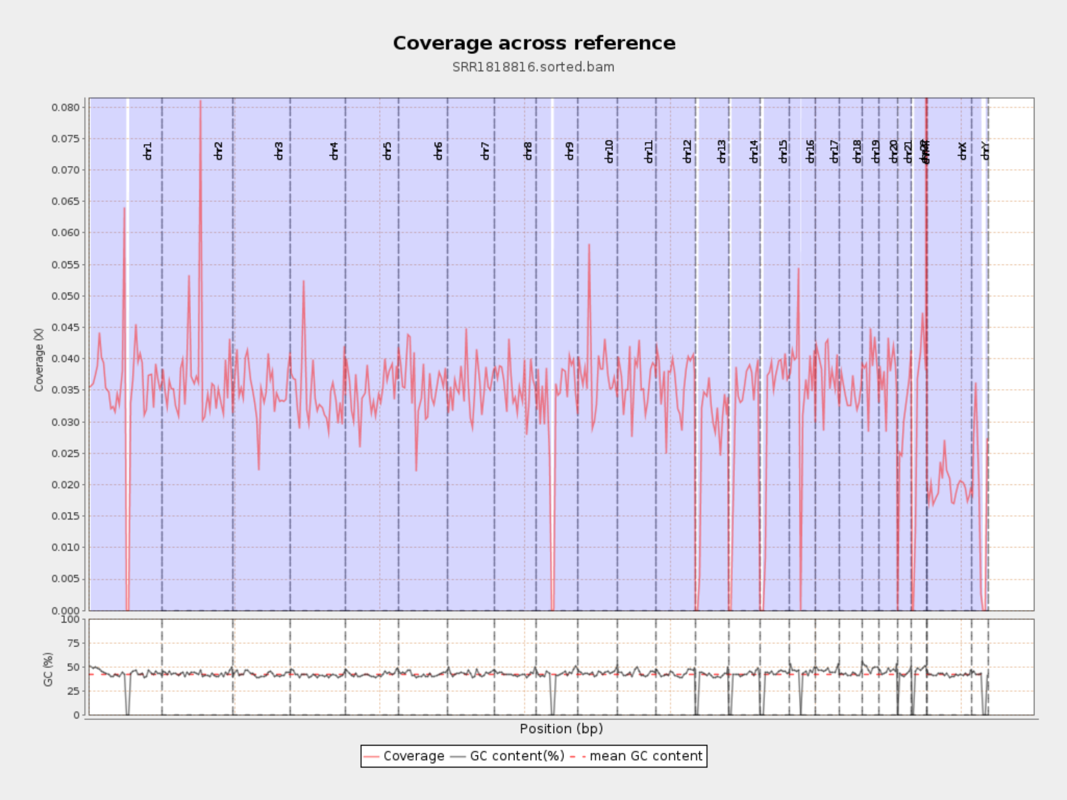
General error rate	0.53%
Mismatches	523,432
Insertions	12,097
Mapped reads with at least one insertion	0.78%
Deletions	25,441
Mapped reads with at least one deletion	1.64%
Homopolymer indels	40.55%

2.6. Chromosome stats

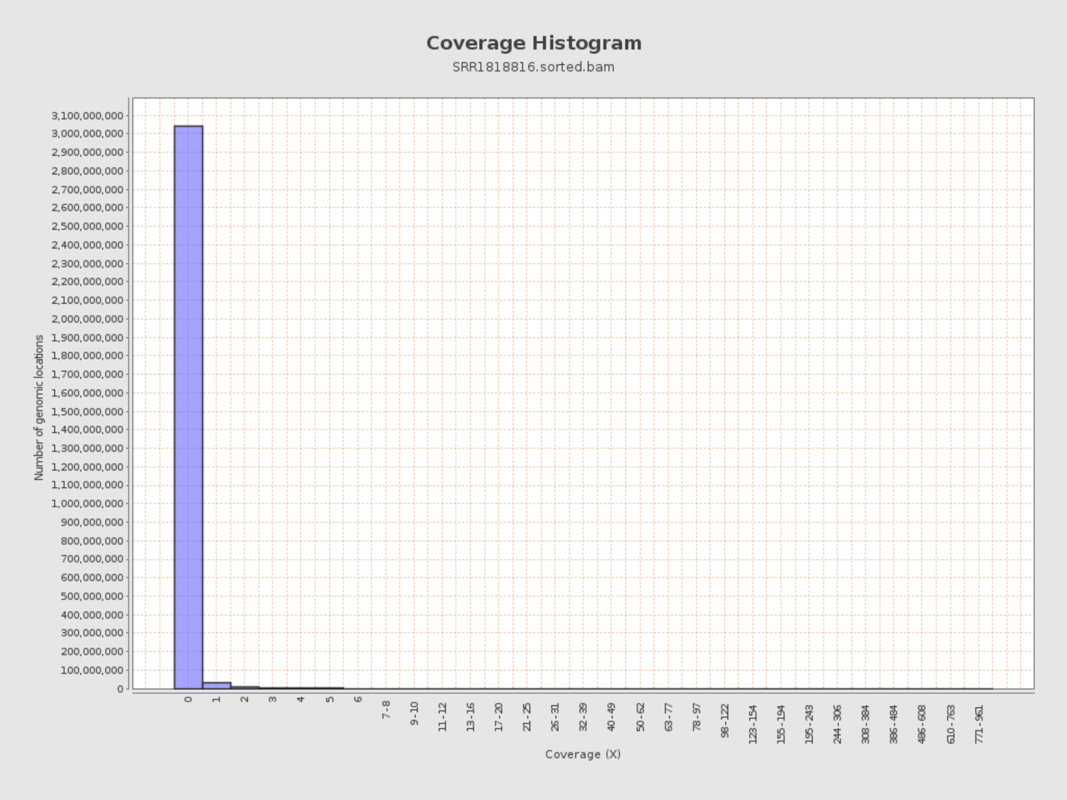
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8754156	0.0351	0.6821
chr2	243199373	9055349	0.0372	0.7209
chr3	198022430	6939799	0.035	0.3118
chr4	191154276	6559116	0.0343	0.3585
chr5	180915260	6308266	0.0349	0.327
chr6	171115067	6128381	0.0358	0.3537
chr7	159138663	5642071	0.0355	0.3959

chr8	146364022	5253064	0.0359	0.3544
chr9	141213431	4434094	0.0314	0.3509
chr10	135534747	5111084	0.0377	0.4905
chr11	135006516	4925156	0.0365	0.363
chr12	133851895	4859579	0.0363	0.3338
chr13	115169878	3062660	0.0266	0.2701
chr14	107349540	3241748	0.0302	0.3269
chr15	102531392	3120969	0.0304	0.2992
chr16	90354753	3241060	0.0359	0.4807
chr17	81195210	3102844	0.0382	0.3513
chr18	78077248	2685246	0.0344	0.4412
chr19	59128983	2278177	0.0385	0.5441
chr20	63025520	2375065	0.0377	0.3456
chr21	48129895	1370229	0.0285	0.3052
chr22	51304566	1458454	0.0284	0.3079
chrMT	16571	104732	6.3202	6.2397
chrX	155270560	3068424	0.0198	0.2712
chrY	59373566	977434	0.0165	0.7533

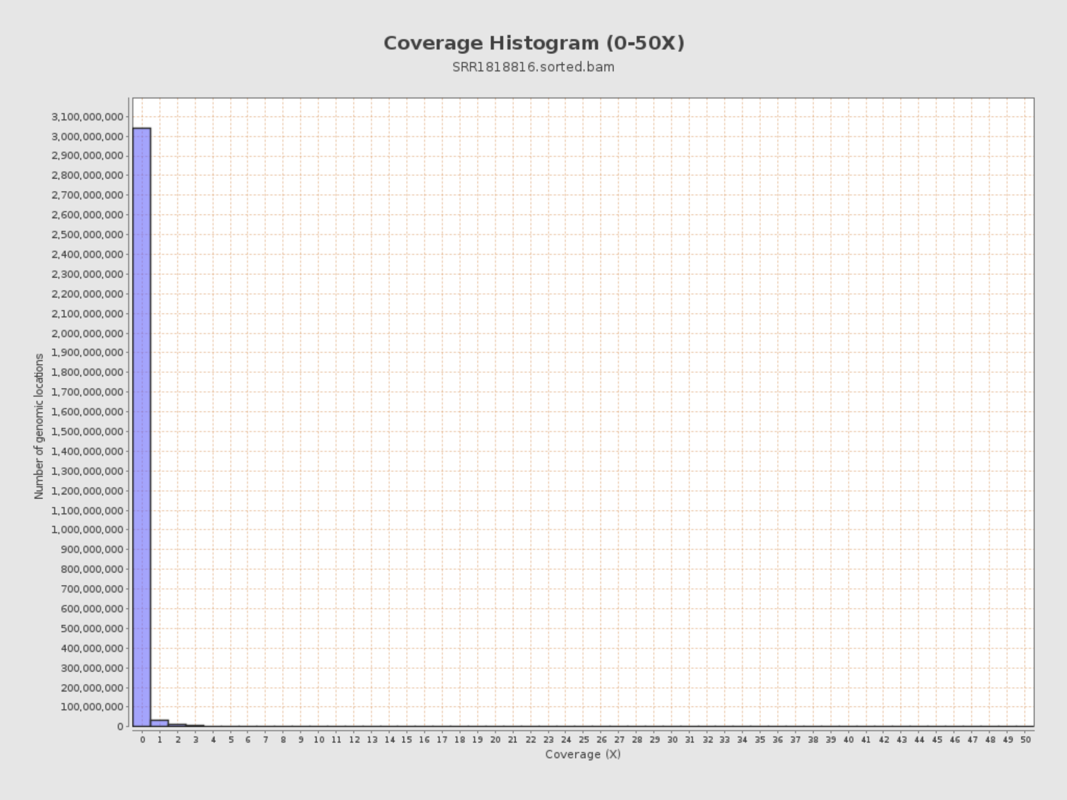
3. Results : Coverage across reference



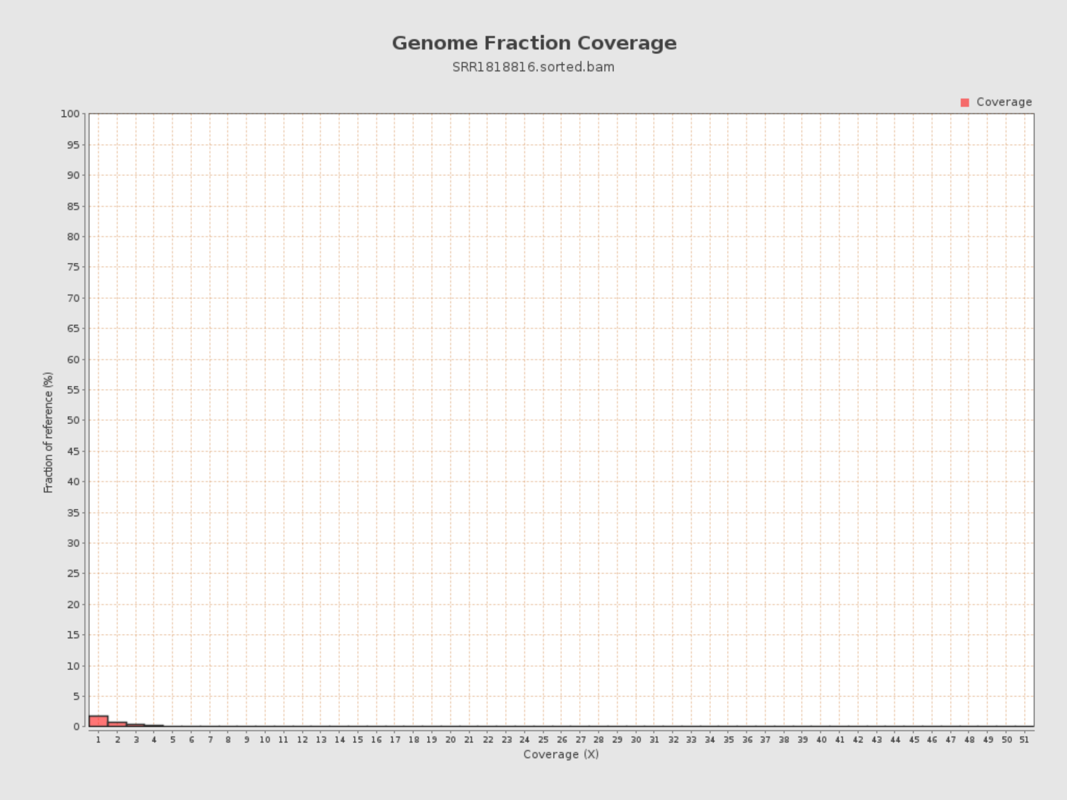
4. Results : Coverage Histogram



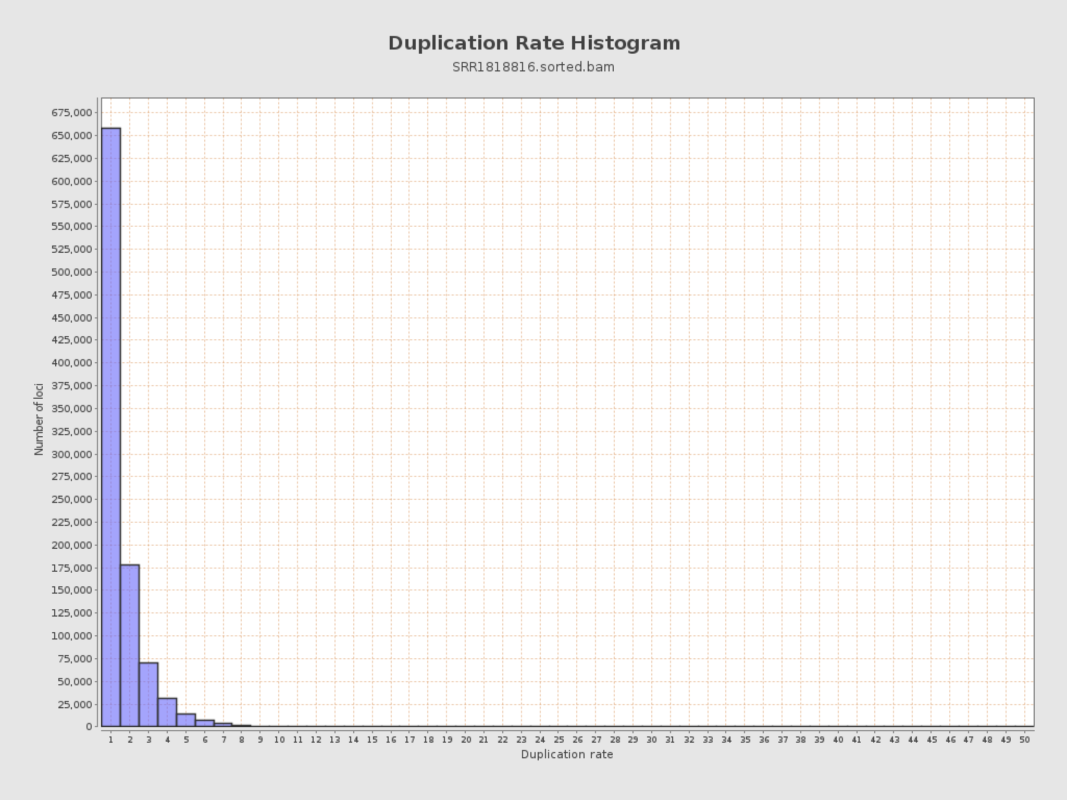
5. Results : Coverage Histogram (0-50X)



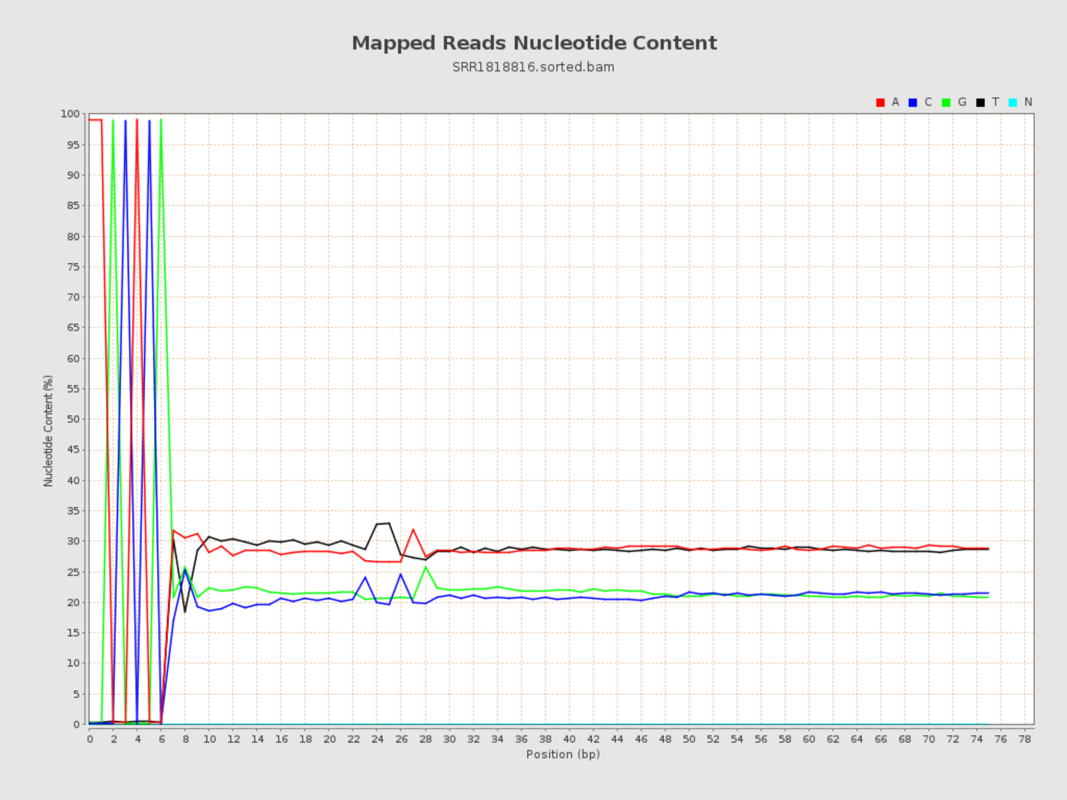
6. Results : Genome Fraction Coverage



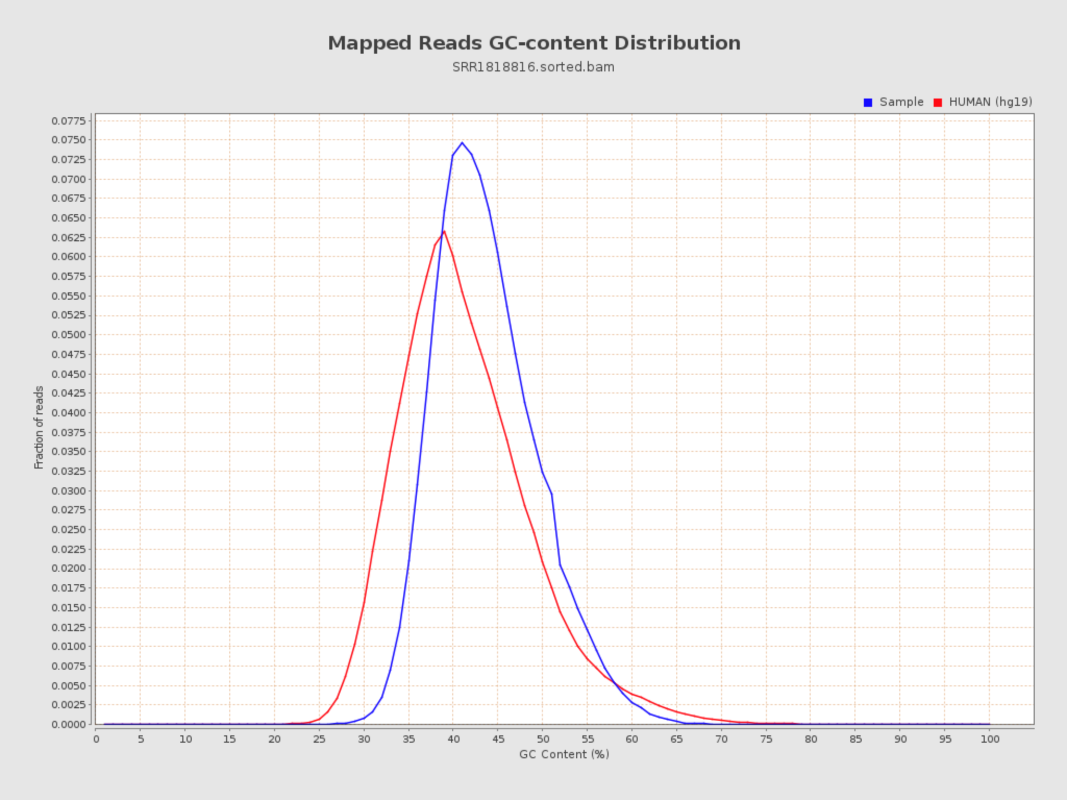
7. Results : Duplication Rate Histogram



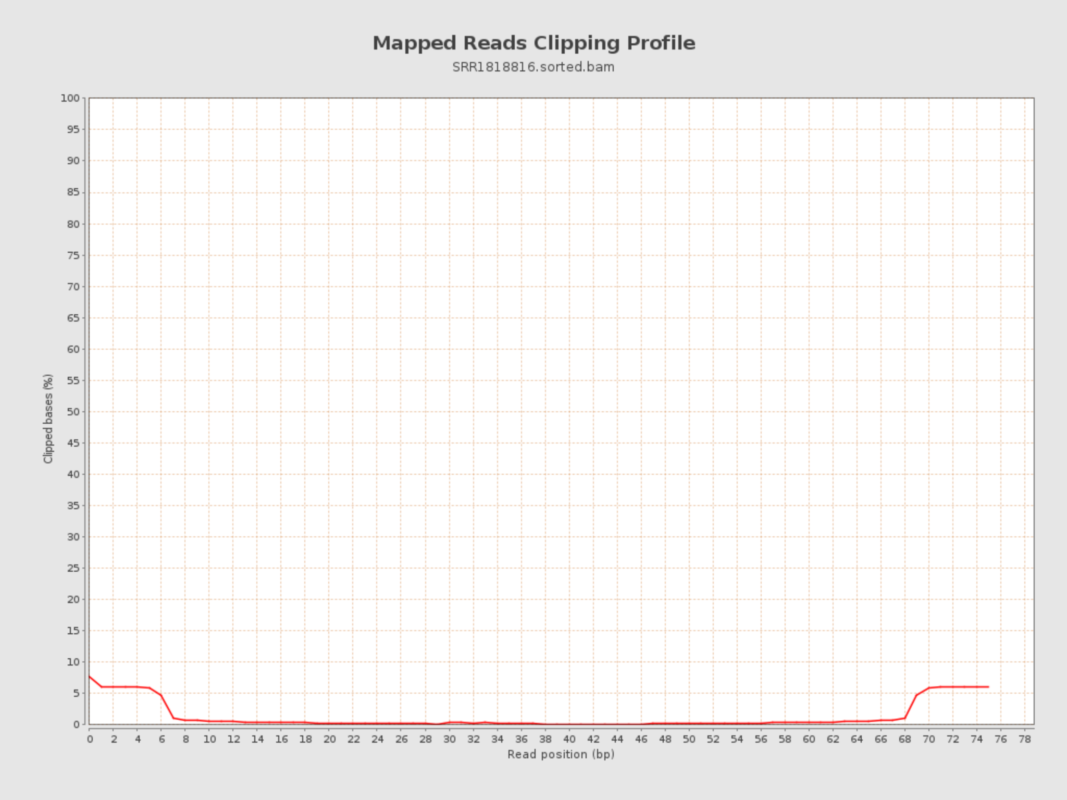
8. Results : Mapped Reads Nucleotide Content



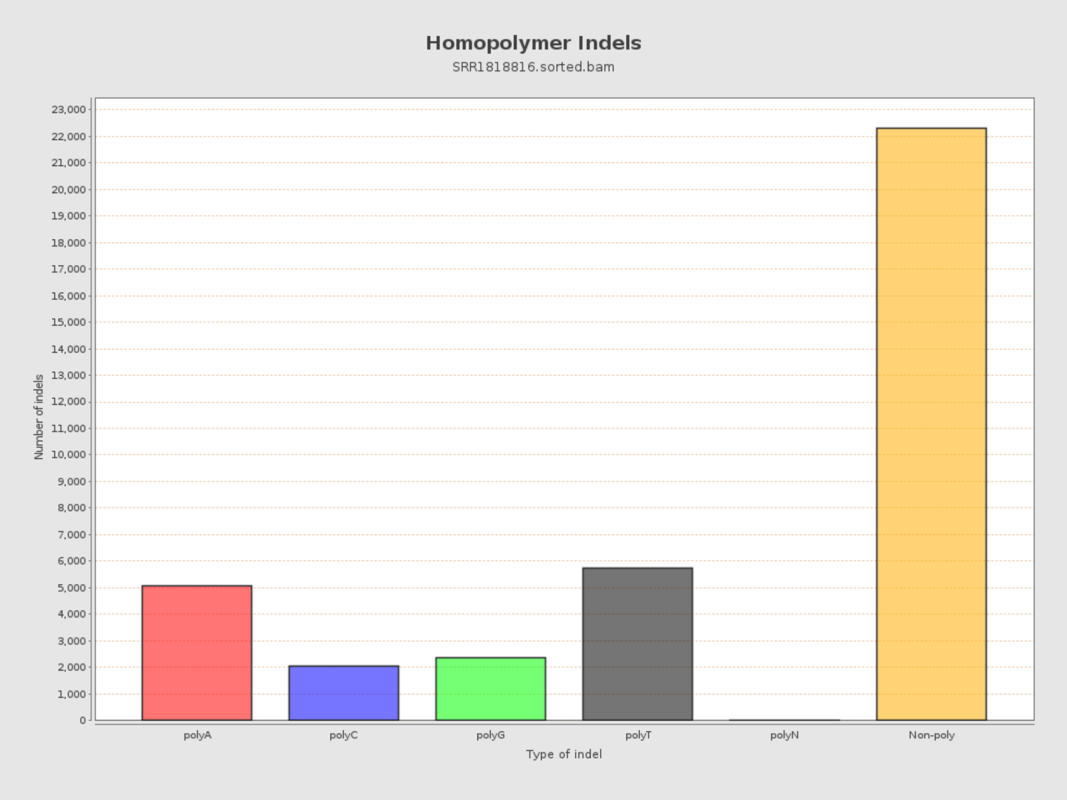
9. Results : Mapped Reads GC-content Distribution



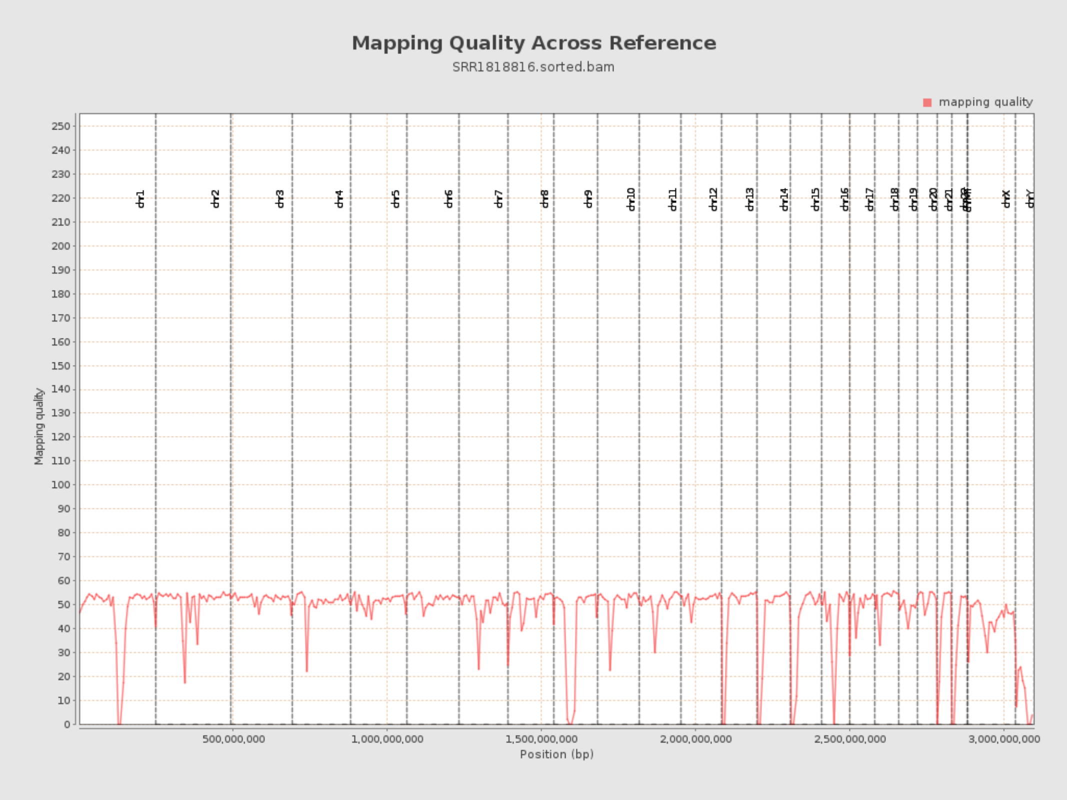
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram