Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:37:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818834.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_SRR1818834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:37:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,203,983
Mapped reads	2,176,649 / 98.76%
Unmapped reads	27,334 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,792 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	557,238 / 25.28%
Duplication rate	21.97%
Clipped reads	2,201,582 / 99.89%

2.2. ACGT Content

Number/percentage of A's	57,023,322 / 28.3%
Number/percentage of C's	43,305,479 / 21.5%
Number/percentage of T's	57,313,774 / 28.45%
Number/percentage of G's	43,814,844 / 21.75%
Number/percentage of N's	2,920 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0651

Standard Deviation	0.7247

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

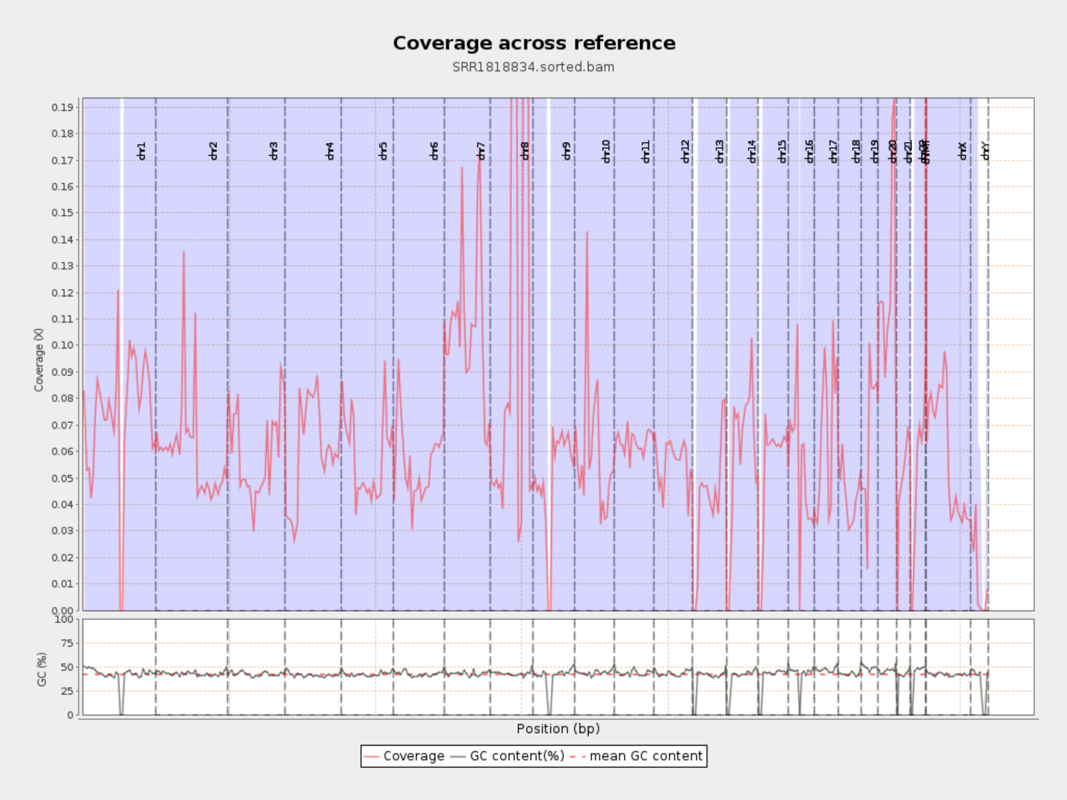
General error rate	0.62%
Mismatches	1,180,291
Insertions	28,464
Mapped reads with at least one insertion	1.27%
Deletions	63,681
Mapped reads with at least one deletion	2.86%
Homopolymer indels	40.26%

2.6. Chromosome stats

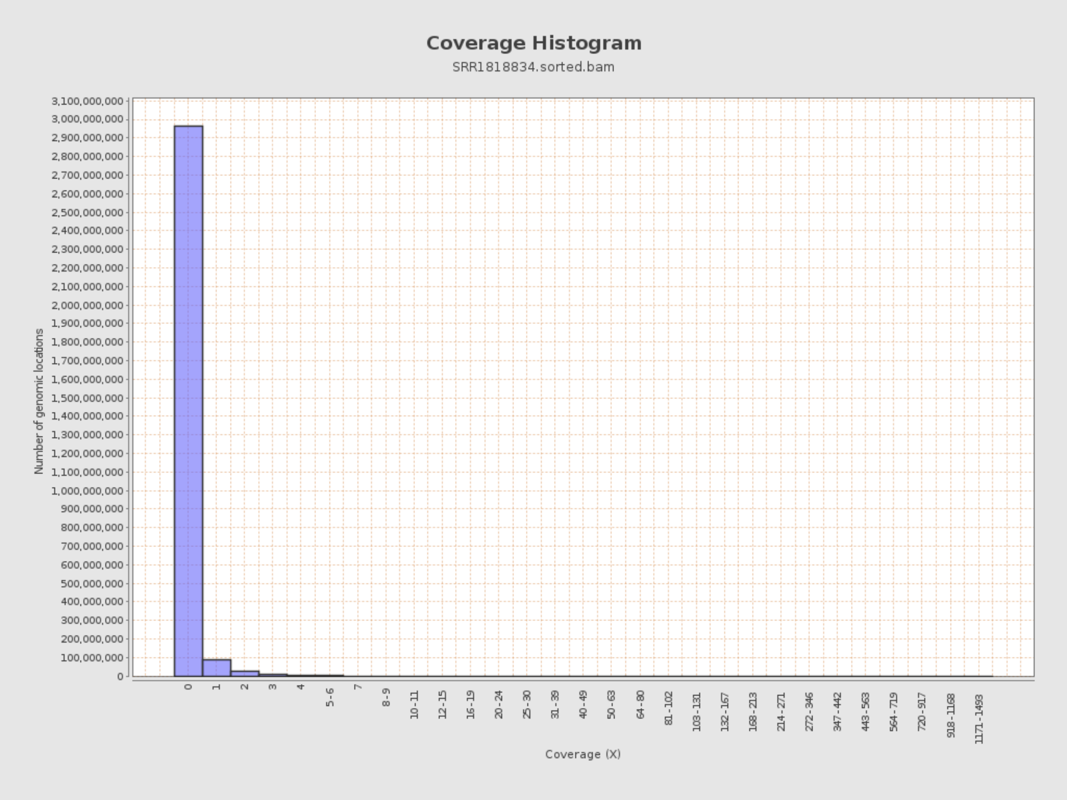
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18396828	0.0738	1.1539
chr2	243199373	14654376	0.0603	1.0432
chr3	198022430	11797990	0.0596	0.3442
chr4	191154276	11719902	0.0613	0.4364
chr5	180915260	10562692	0.0584	0.3553
chr6	171115067	9569063	0.0559	0.3725
chr7	159138663	17167632	0.1079	1.4251

chr8	146364022	19281462	0.1317	0.6581
chr9	141213431	7083297	0.0502	0.5984
chr10	135534747	7994045	0.059	0.8978
chr11	135006516	8577061	0.0635	0.4436
chr12	133851895	7499165	0.056	0.3371
chr13	115169878	4899085	0.0425	0.2897
chr14	107349540	6516119	0.0607	0.378
chr15	102531392	5370119	0.0524	0.3331
chr16	90354753	4800048	0.0531	0.7662
chr17	81195210	5282419	0.0651	0.4818
chr18	78077248	3443429	0.0441	0.7208
chr19	59128983	3872408	0.0655	1.0967
chr20	63025520	8062386	0.1279	0.5484
chr21	48129895	2391908	0.0497	0.3697
chr22	51304566	2424377	0.0473	0.3439
chrMT	16571	358114	21.6109	14.0506
chrX	155270560	9143262	0.0589	0.4144
chrY	59373566	716360	0.0121	0.8614

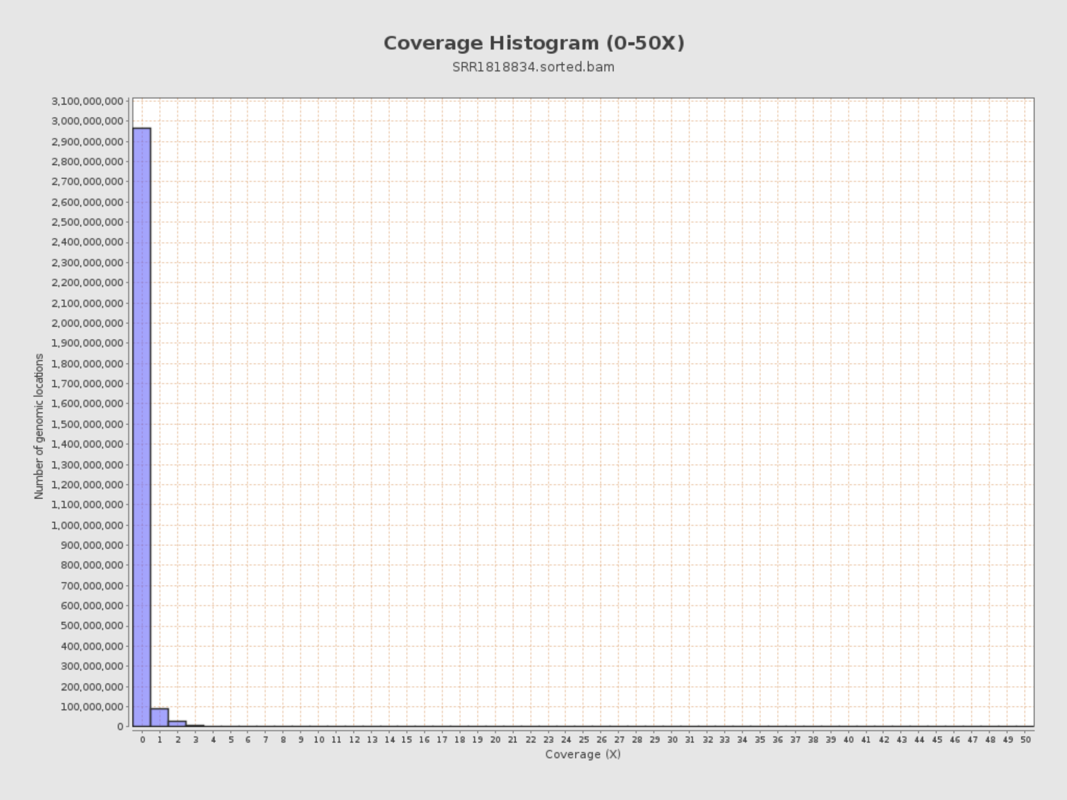
3. Results : Coverage across reference



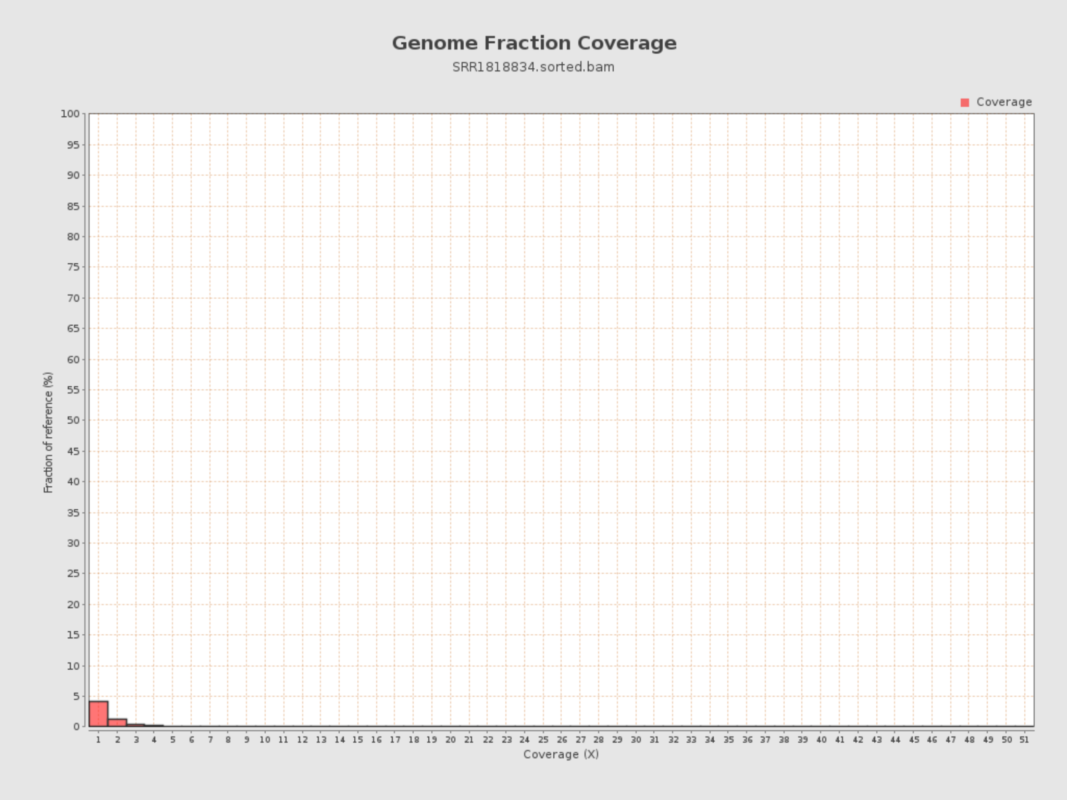
4. Results : Coverage Histogram



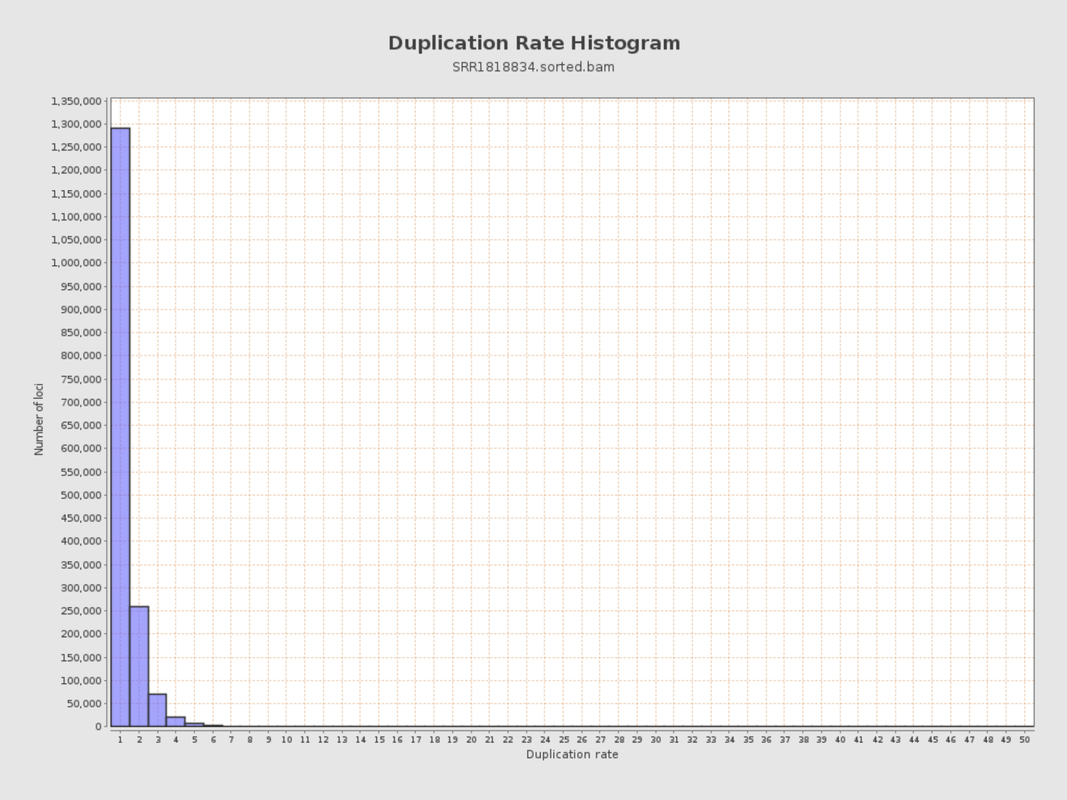
5. Results : Coverage Histogram (0-50X)



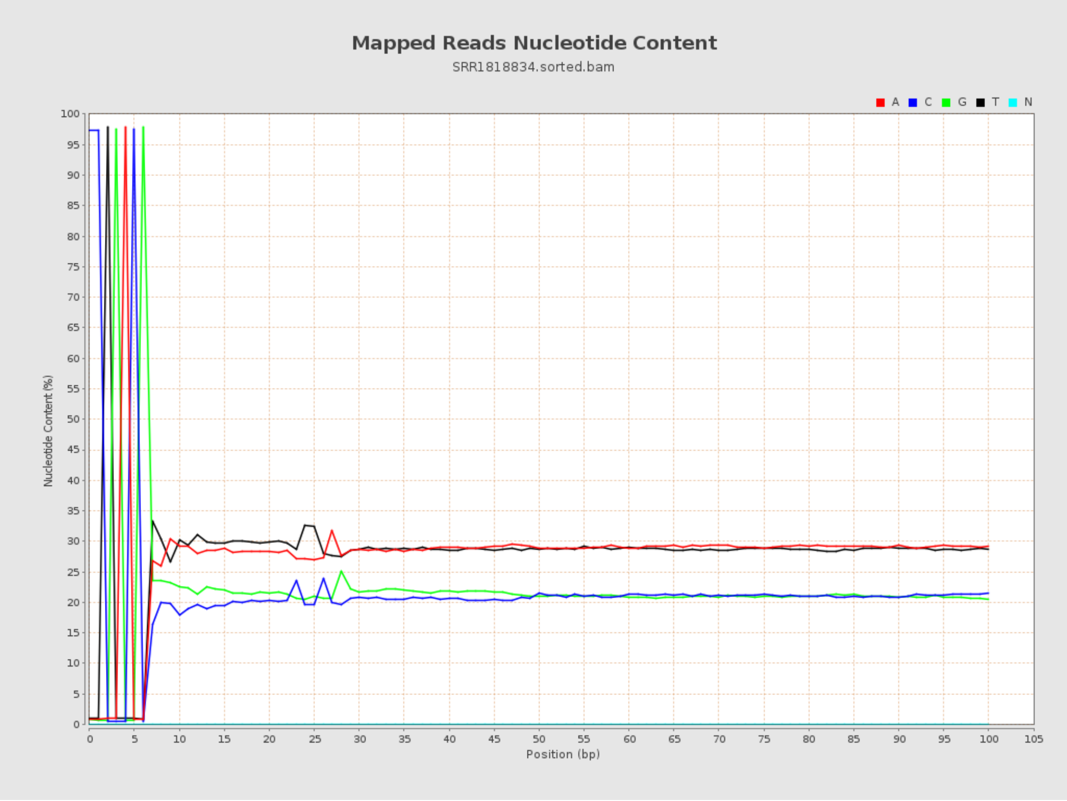
6. Results : Genome Fraction Coverage



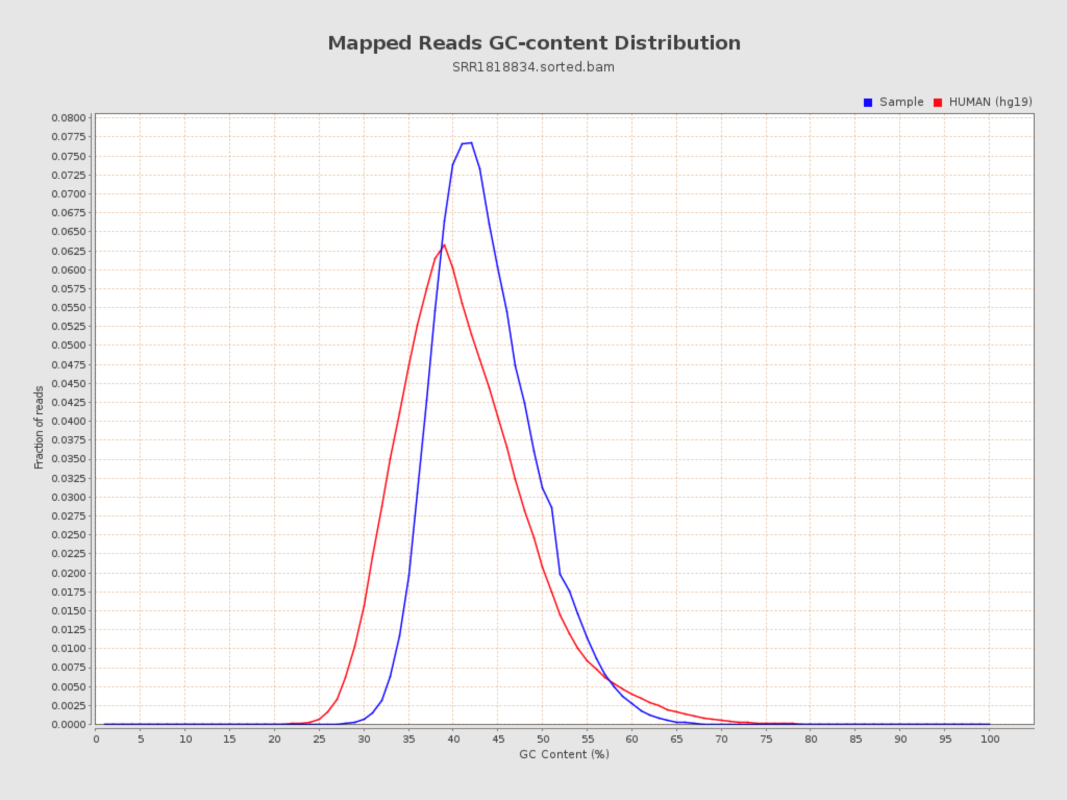
7. Results : Duplication Rate Histogram



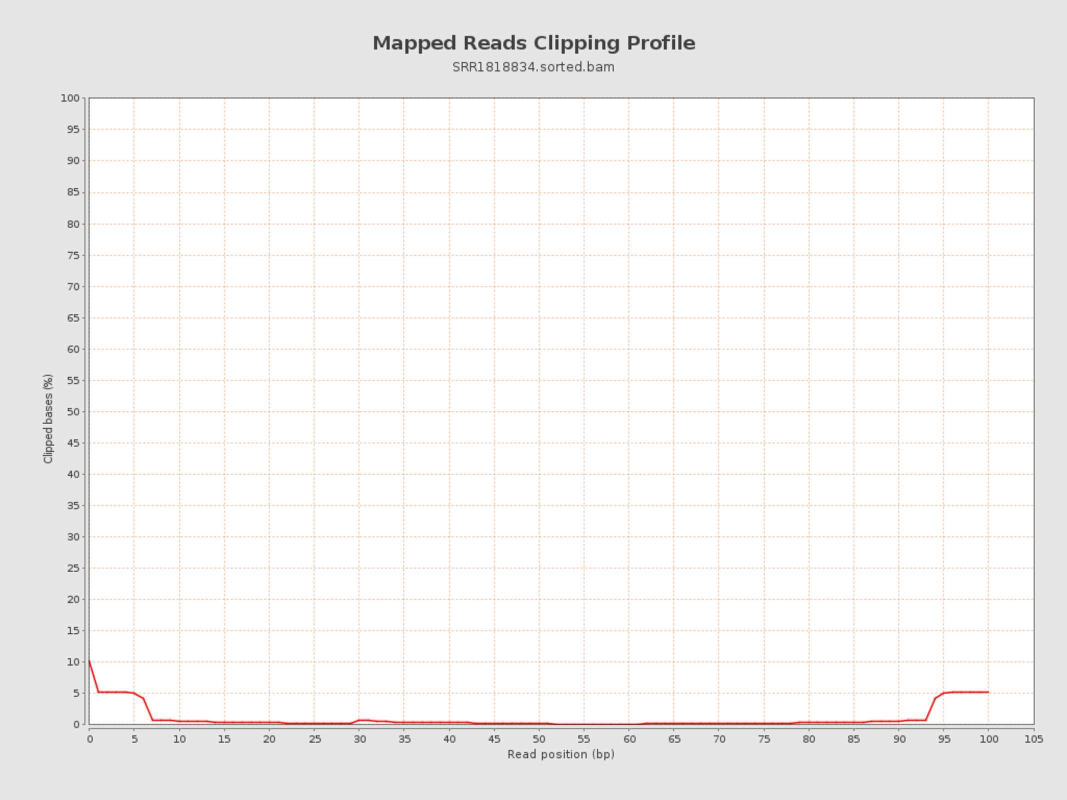
8. Results : Mapped Reads Nucleotide Content



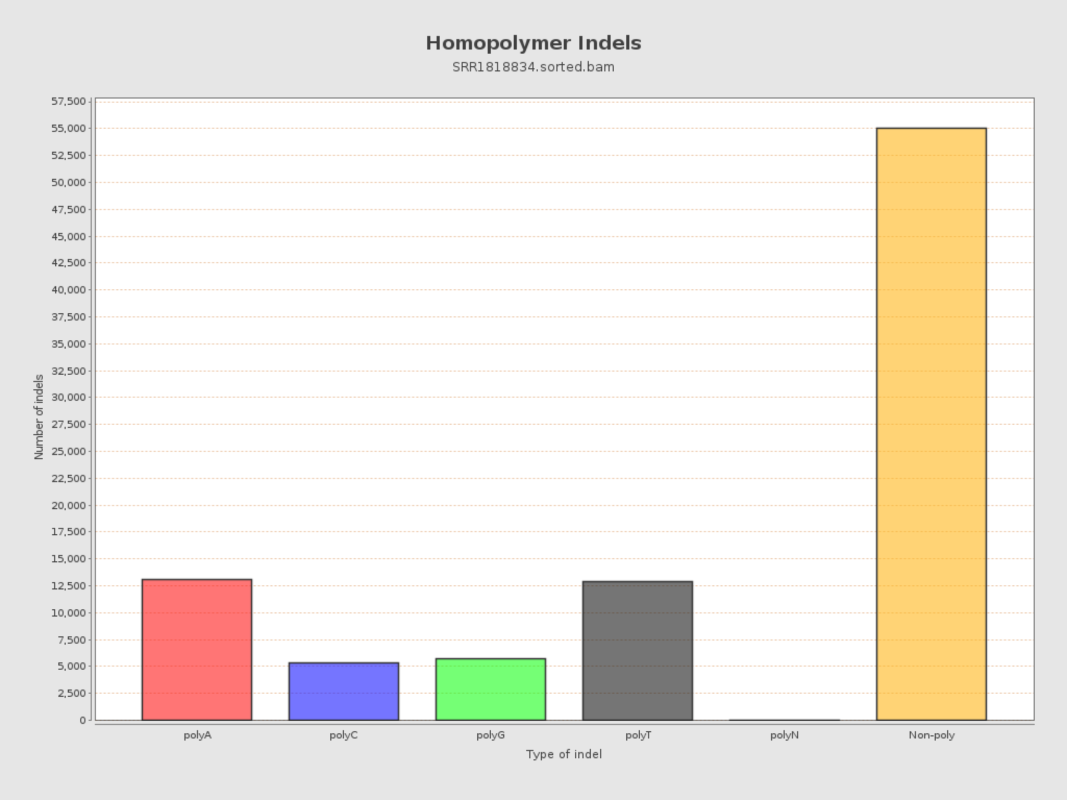
9. Results : Mapped Reads GC-content Distribution



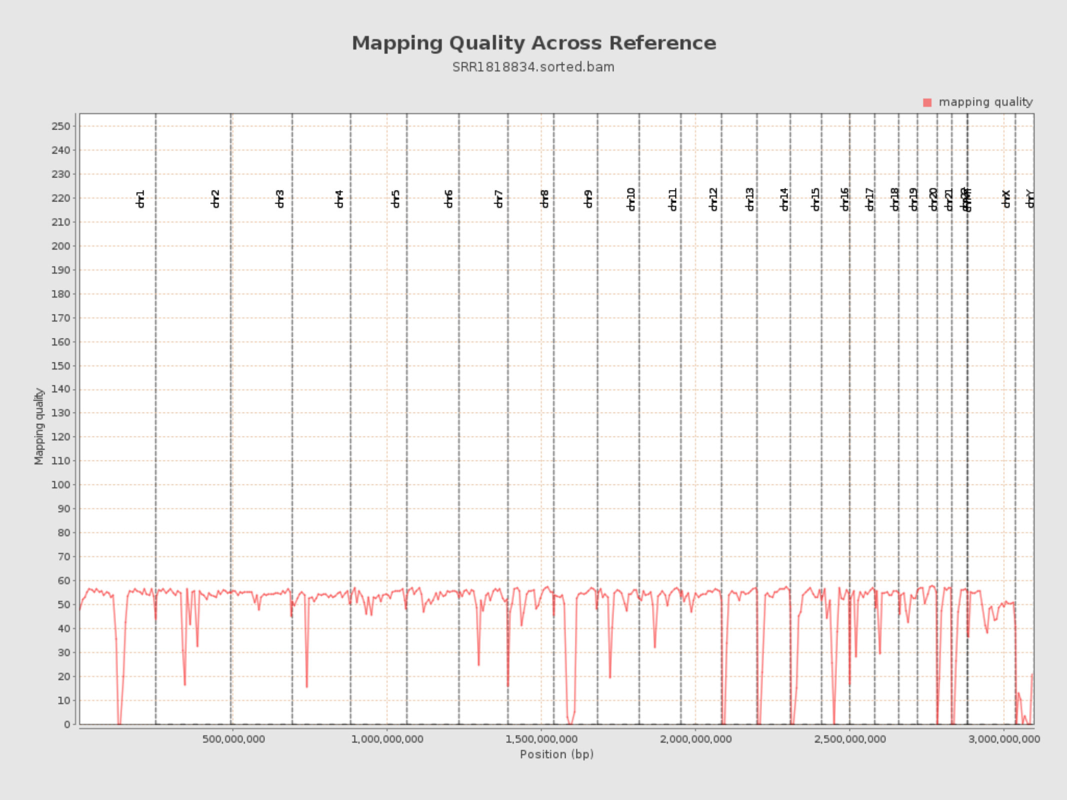
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram