Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818851.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_SRR1818851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:15:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,183,382
Mapped reads	1,889,076 / 86.52%
Unmapped reads	294,306 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,809 / 1.41%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	494,032 / 22.63%
Duplication rate	22.78%
Clipped reads	1,903,060 / 87.16%

2.2. ACGT Content

Number/percentage of A's	51,816,310 / 29.62%
Number/percentage of C's	35,503,317 / 20.3%
Number/percentage of T's	50,022,414 / 28.6%
Number/percentage of G's	37,567,895 / 21.48%
Number/percentage of N's	2,743 / 0%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.6479

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

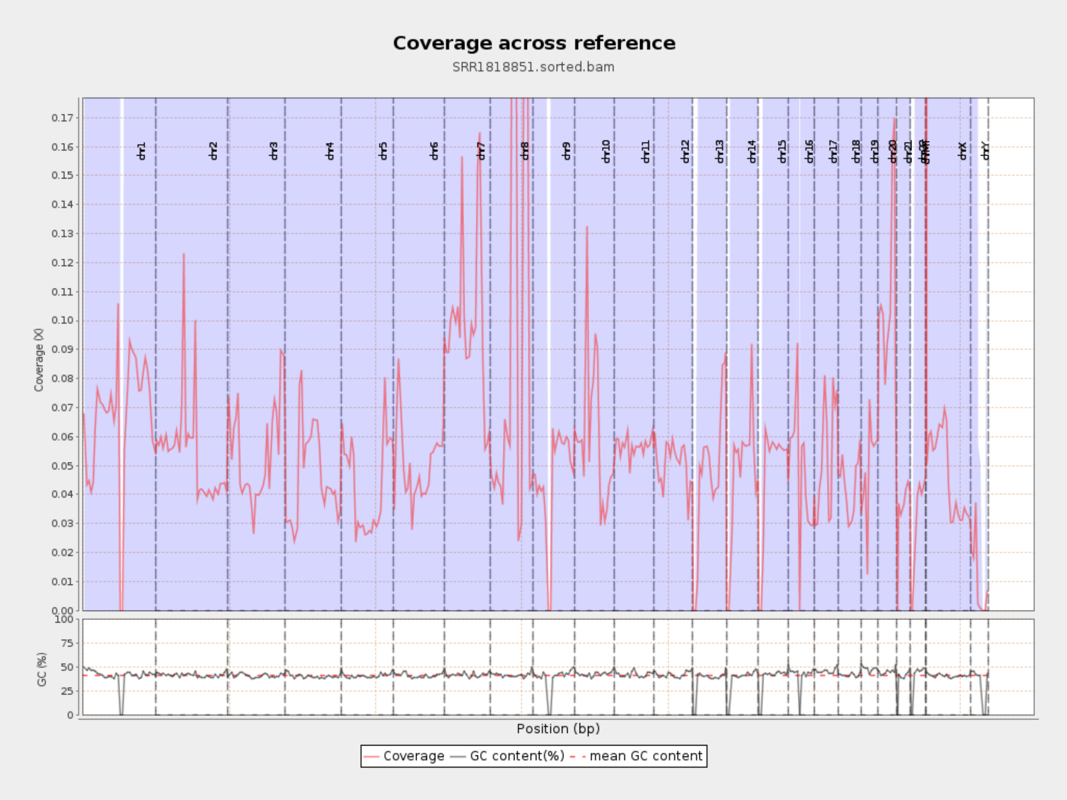
General error rate	0.64%
Mismatches	1,058,027
Insertions	23,329
Mapped reads with at least one insertion	1.19%
Deletions	57,486
Mapped reads with at least one deletion	2.98%
Homopolymer indels	41.97%

2.6. Chromosome stats

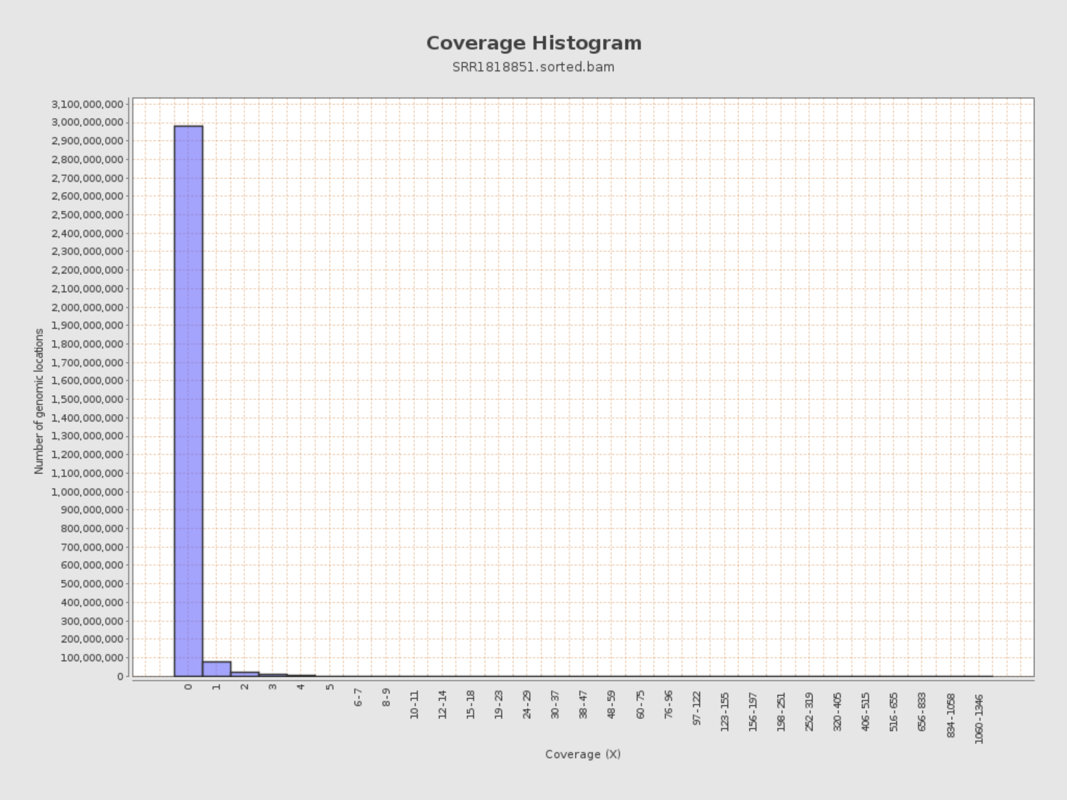
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16596711	0.0666	1.029
chr2	243199373	13250433	0.0545	0.9233
chr3	198022430	10852856	0.0548	0.331
chr4	191154276	8952233	0.0468	0.3901
chr5	180915260	7868122	0.0435	0.3075
chr6	171115067	8618505	0.0504	0.3377
chr7	159138663	15774223	0.0991	1.3393

chr8	146364022	15599228	0.1066	0.581
chr9	141213431	6427650	0.0455	0.5405
chr10	135534747	8123802	0.0599	0.8296
chr11	135006516	7651496	0.0567	0.4109
chr12	133851895	6811851	0.0509	0.3205
chr13	115169878	5427512	0.0471	0.3051
chr14	107349540	5129091	0.0478	0.3381
chr15	102531392	4756924	0.0464	0.2986
chr16	90354753	4232262	0.0468	0.6569
chr17	81195210	4253764	0.0524	0.4086
chr18	78077248	3374772	0.0432	0.6193
chr19	59128983	2900062	0.049	0.8004
chr20	63025520	7087101	0.1124	0.5067
chr21	48129895	1698152	0.0353	0.3186
chr22	51304566	1500310	0.0292	0.2729
chrMT	16571	248852	15.0173	9.9067
chrX	155270560	7271204	0.0468	0.3585
chrY	59373566	614910	0.0104	0.7243

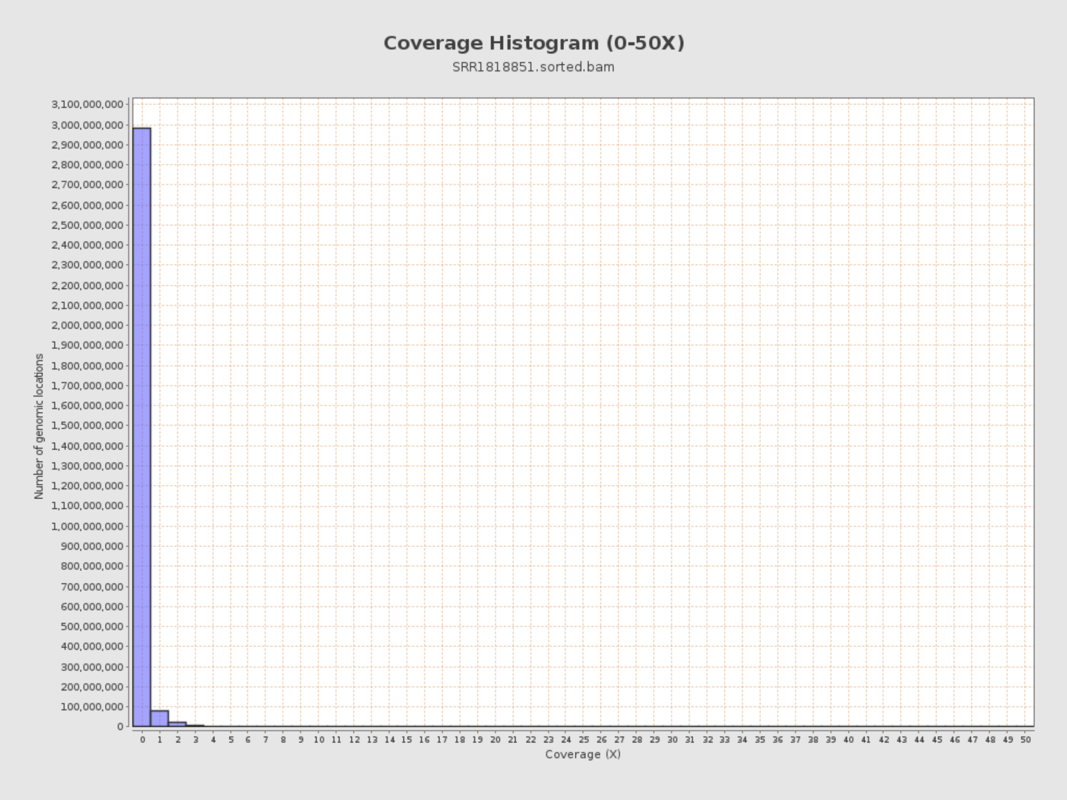
3. Results : Coverage across reference



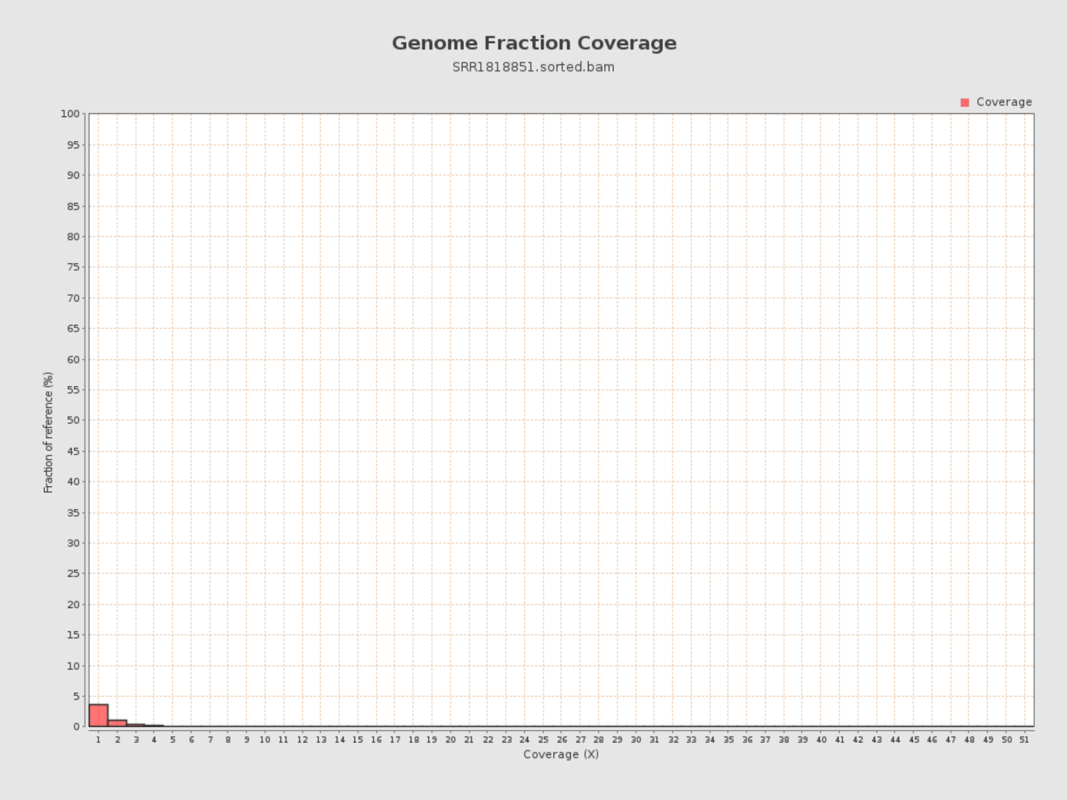
4. Results : Coverage Histogram



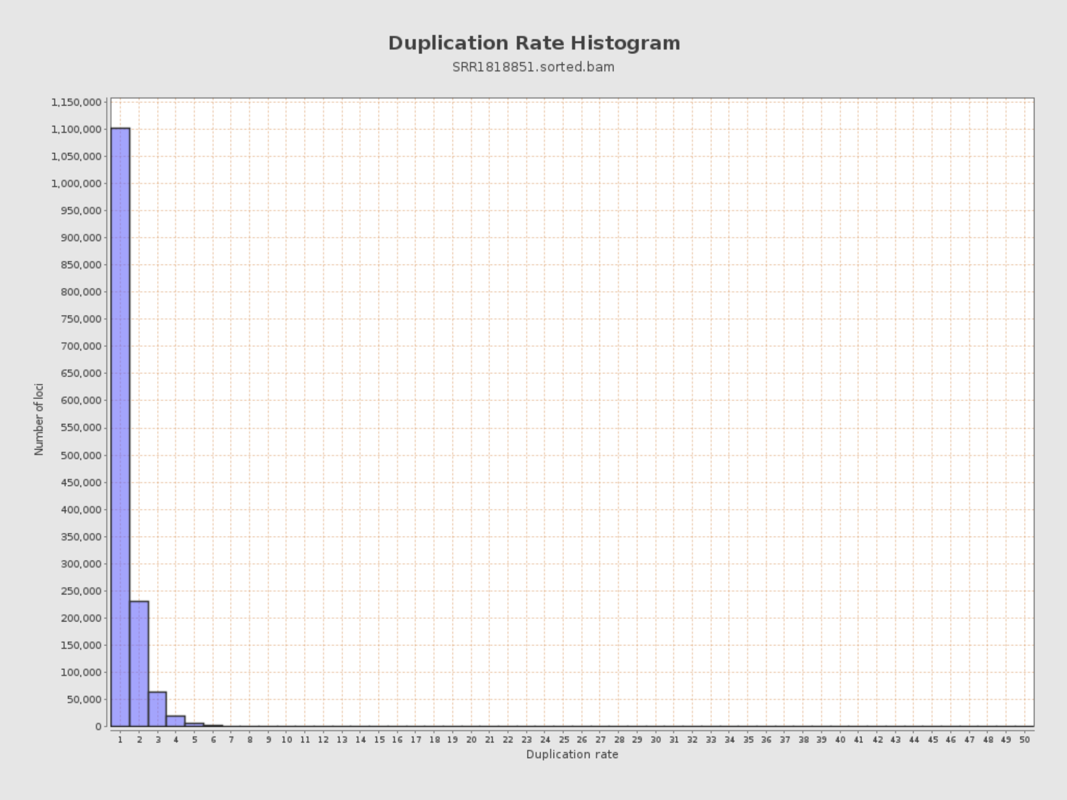
5. Results : Coverage Histogram (0-50X)



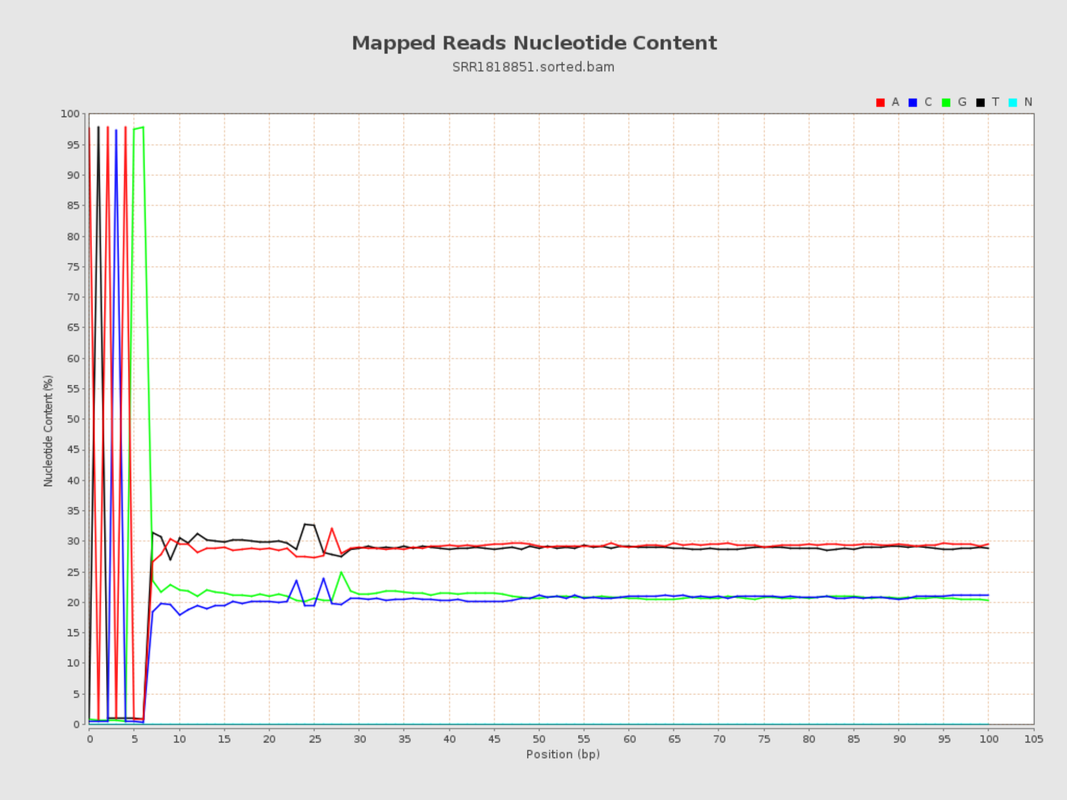
6. Results : Genome Fraction Coverage



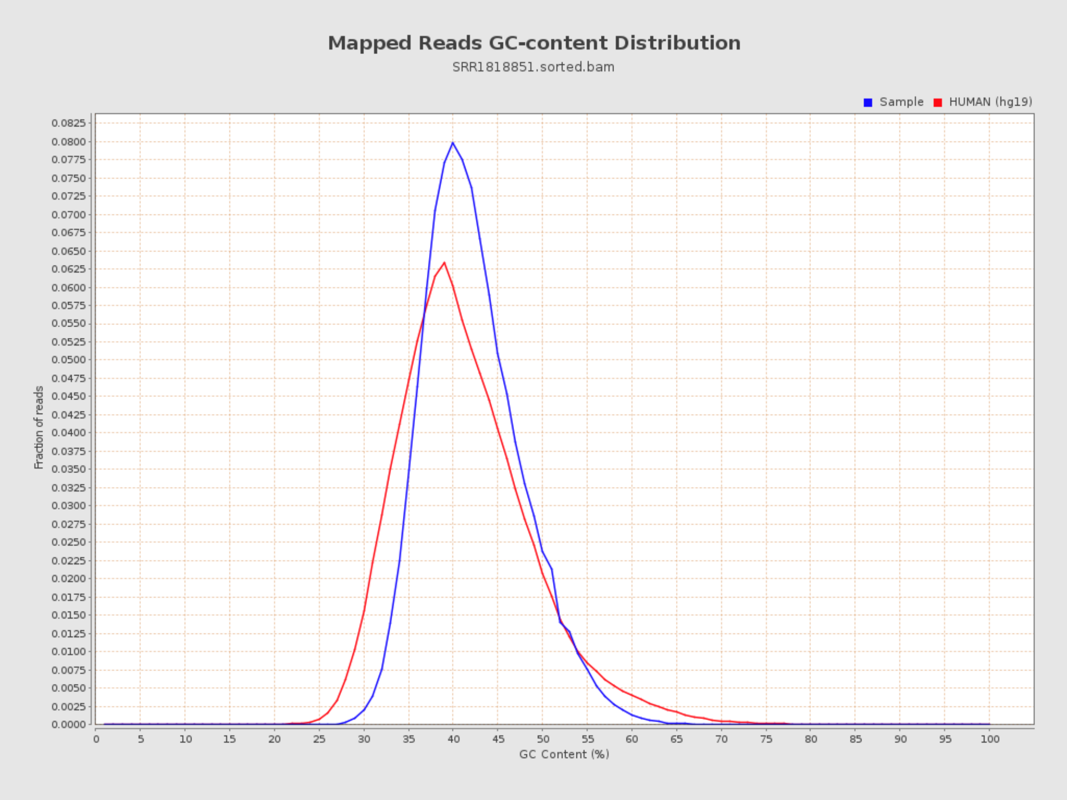
7. Results : Duplication Rate Histogram



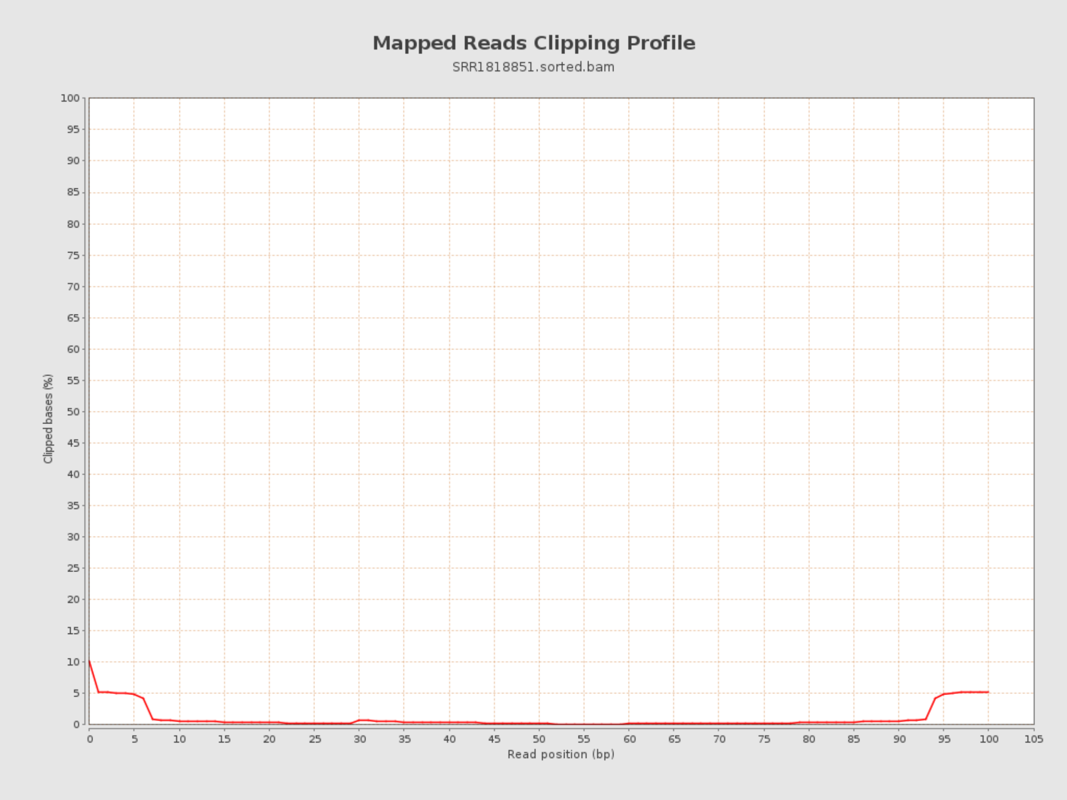
8. Results : Mapped Reads Nucleotide Content



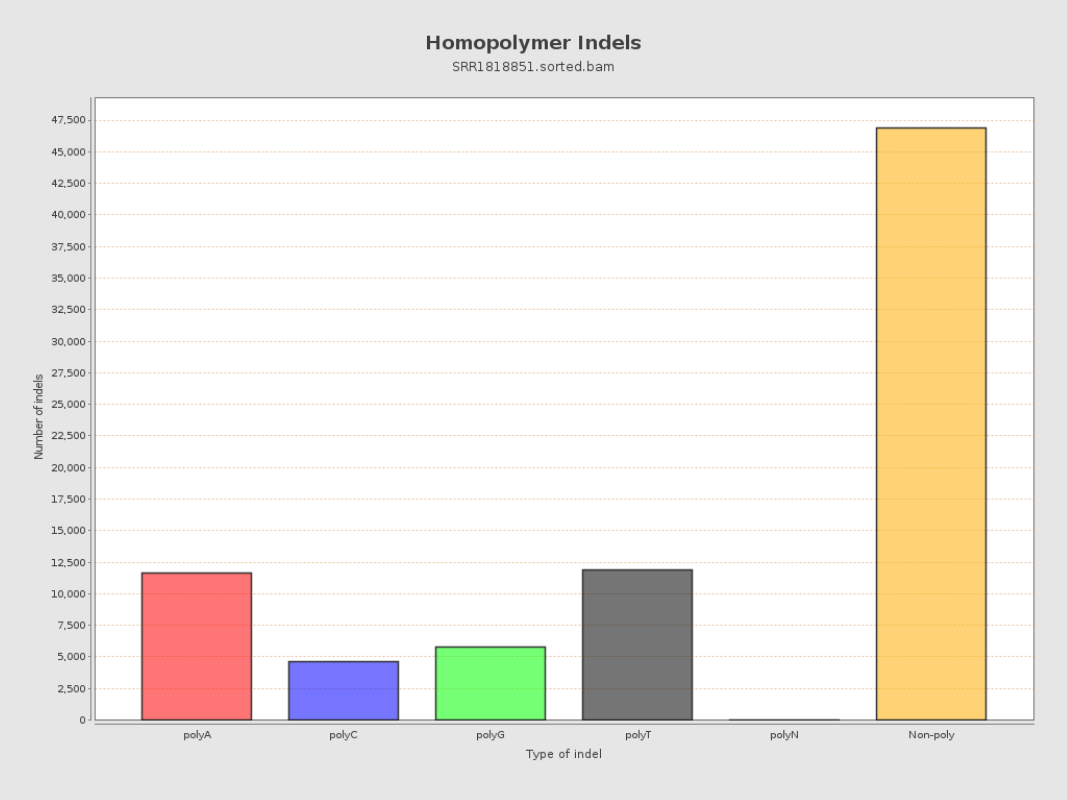
9. Results : Mapped Reads GC-content Distribution



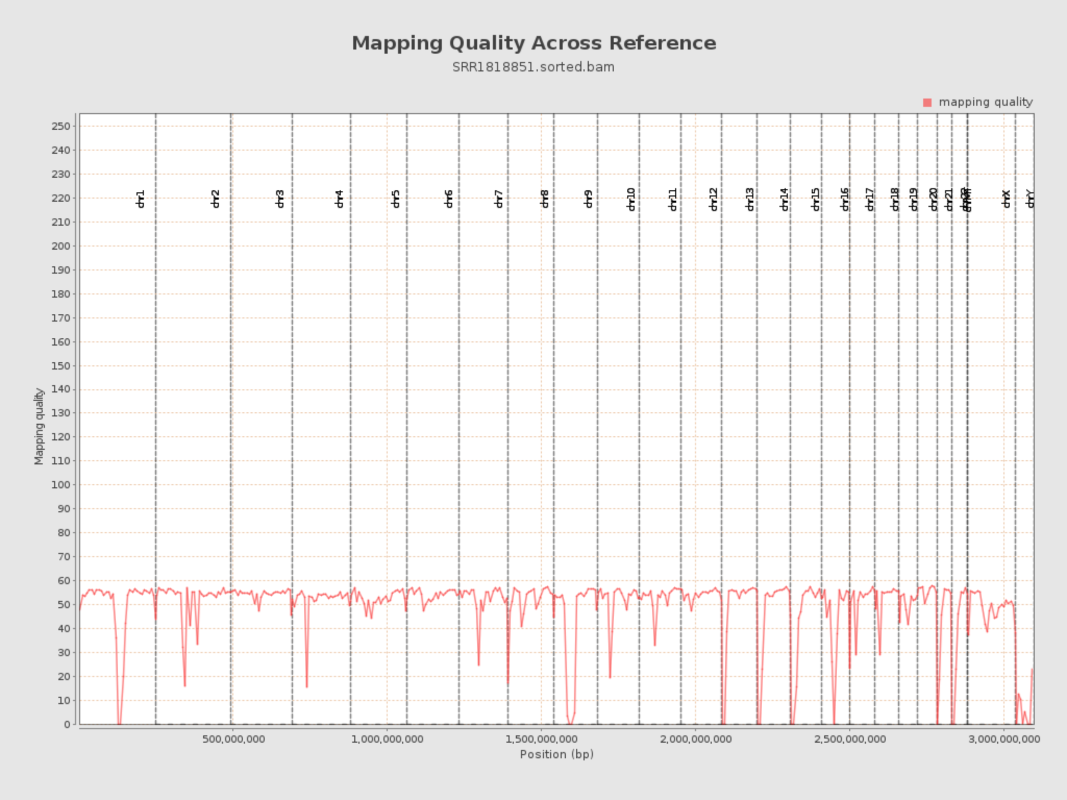
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram