Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:16:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818775.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_SRR1818775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:16:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,457,445
Mapped reads	2,396,504 / 97.52%
Unmapped reads	60,941 / 2.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,601 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,569,936 / 63.88%
Duplication rate	50.84%
Clipped reads	2,400,639 / 97.69%

2.2. ACGT Content

Number/percentage of A's	46,332,955 / 28.48%
Number/percentage of C's	37,065,691 / 22.78%
Number/percentage of T's	47,226,818 / 29.03%
Number/percentage of G's	32,042,976 / 19.7%
Number/percentage of N's	10,286 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.7123

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

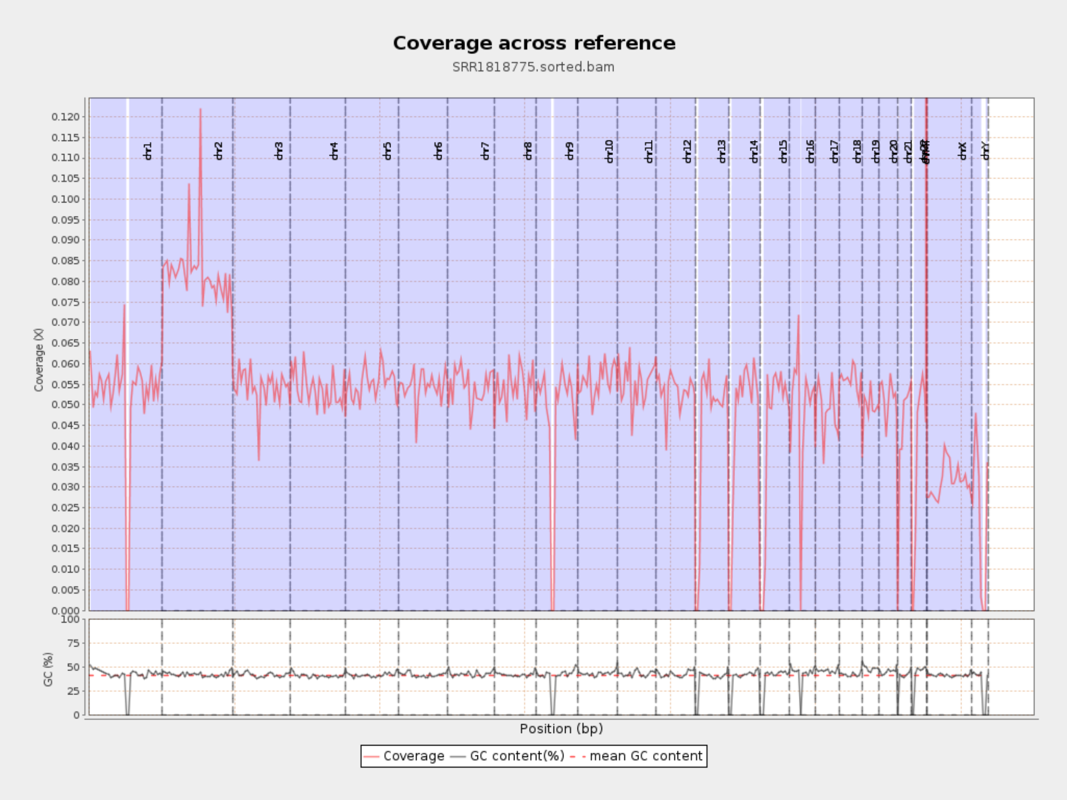
General error rate	0.53%
Mismatches	832,258
Insertions	15,801
Mapped reads with at least one insertion	0.65%
Deletions	41,003
Mapped reads with at least one deletion	1.7%
Homopolymer indels	43.19%

2.6. Chromosome stats

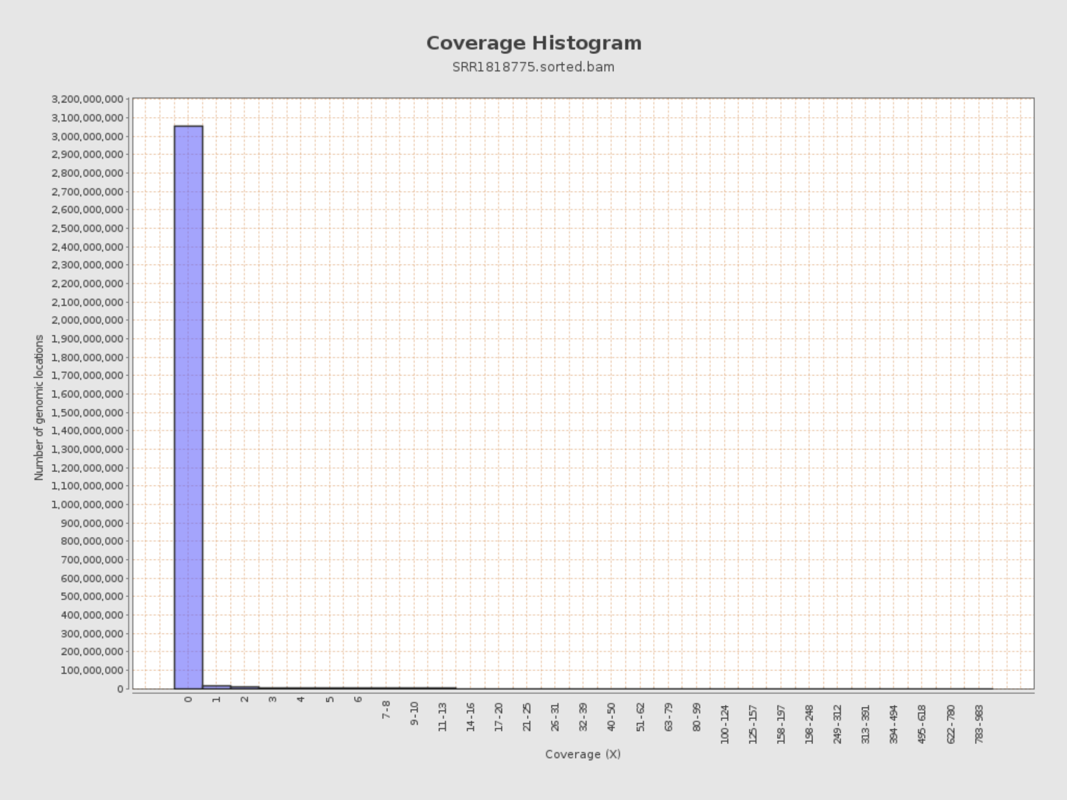
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12987055	0.0521	0.8106
chr2	243199373	20126876	0.0828	1.0716
chr3	198022430	10761853	0.0543	0.6288
chr4	191154276	10288899	0.0538	0.6738
chr5	180915260	9989700	0.0552	0.6389
chr6	171115067	9333233	0.0545	0.6535
chr7	159138663	8671238	0.0545	0.6951

chr8	146364022	7952729	0.0543	0.6697
chr9	141213431	6635507	0.047	0.6489
chr10	135534747	7594788	0.056	0.7347
chr11	135006516	7490245	0.0555	0.6815
chr12	133851895	7144460	0.0534	0.6584
chr13	115169878	5140148	0.0446	0.5712
chr14	107349540	4922438	0.0459	0.6065
chr15	102531392	4423141	0.0431	0.5598
chr16	90354753	4445201	0.0492	0.7103
chr17	81195210	3936131	0.0485	0.6226
chr18	78077248	4392140	0.0563	0.8117
chr19	59128983	2938040	0.0497	0.7616
chr20	63025520	3262227	0.0518	0.6374
chr21	48129895	2091394	0.0435	0.5833
chr22	51304566	1868717	0.0364	0.5738
chrMT	16571	126201	7.6158	9.5426
chrX	155270560	4884617	0.0315	0.4868
chrY	59373566	1336281	0.0225	0.9107

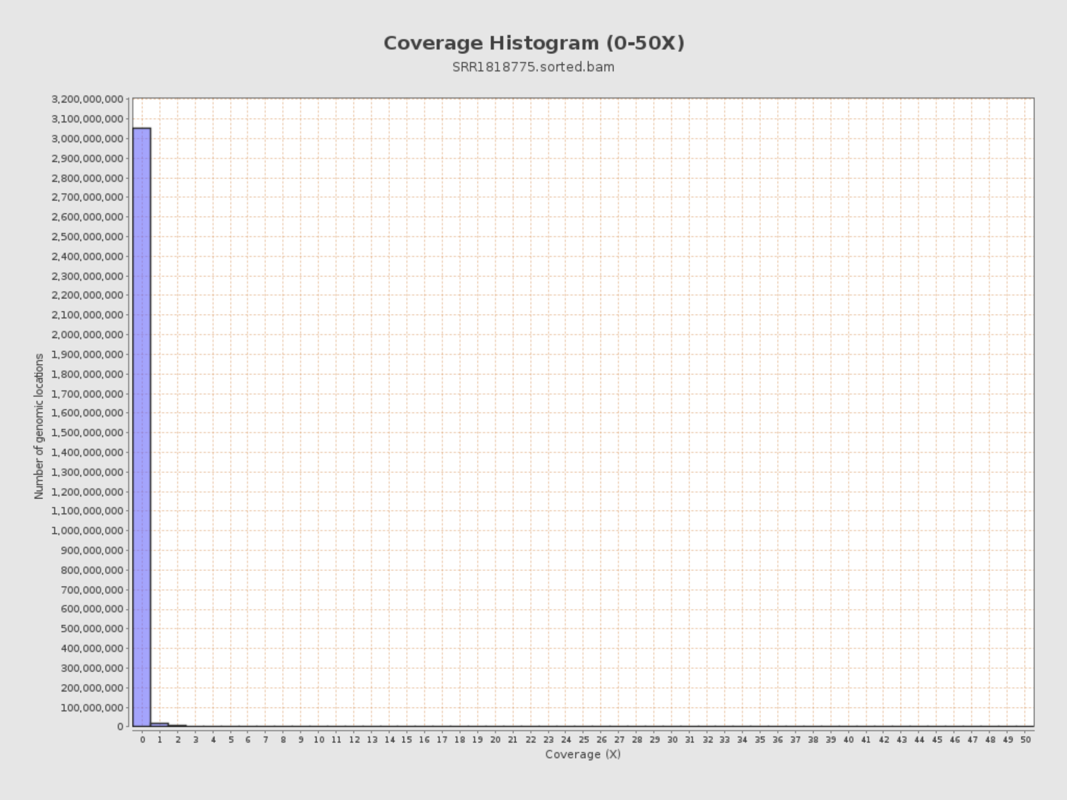
3. Results : Coverage across reference



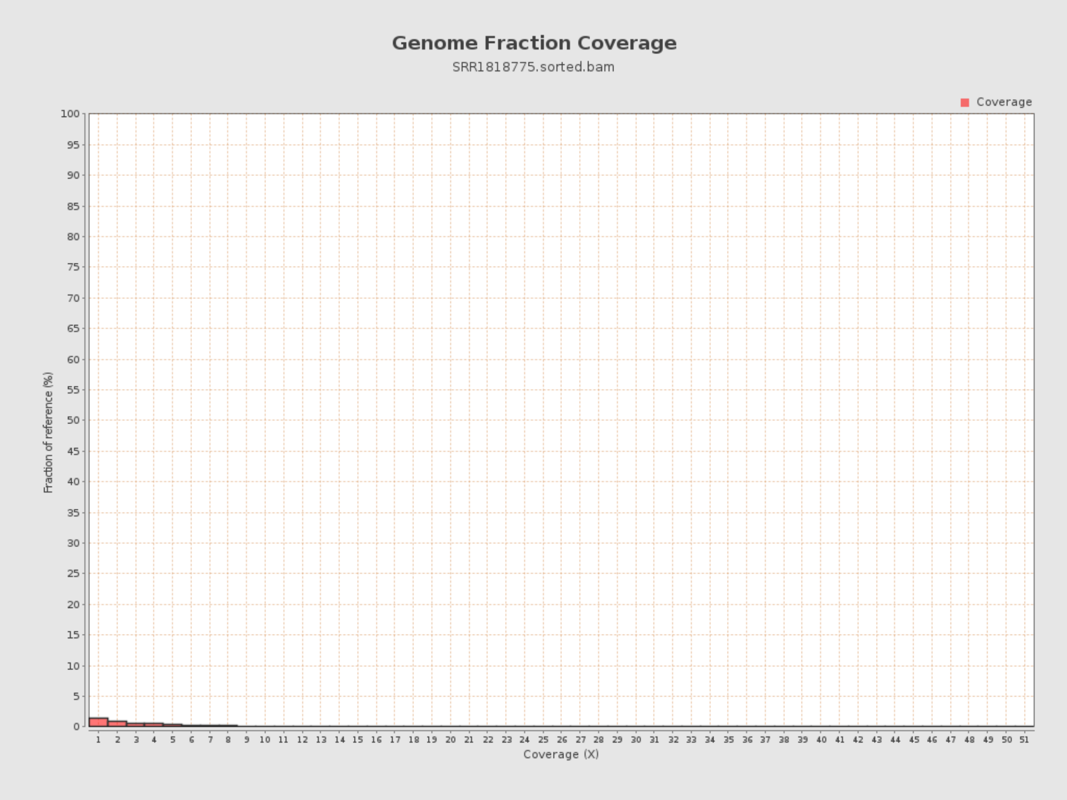
4. Results : Coverage Histogram



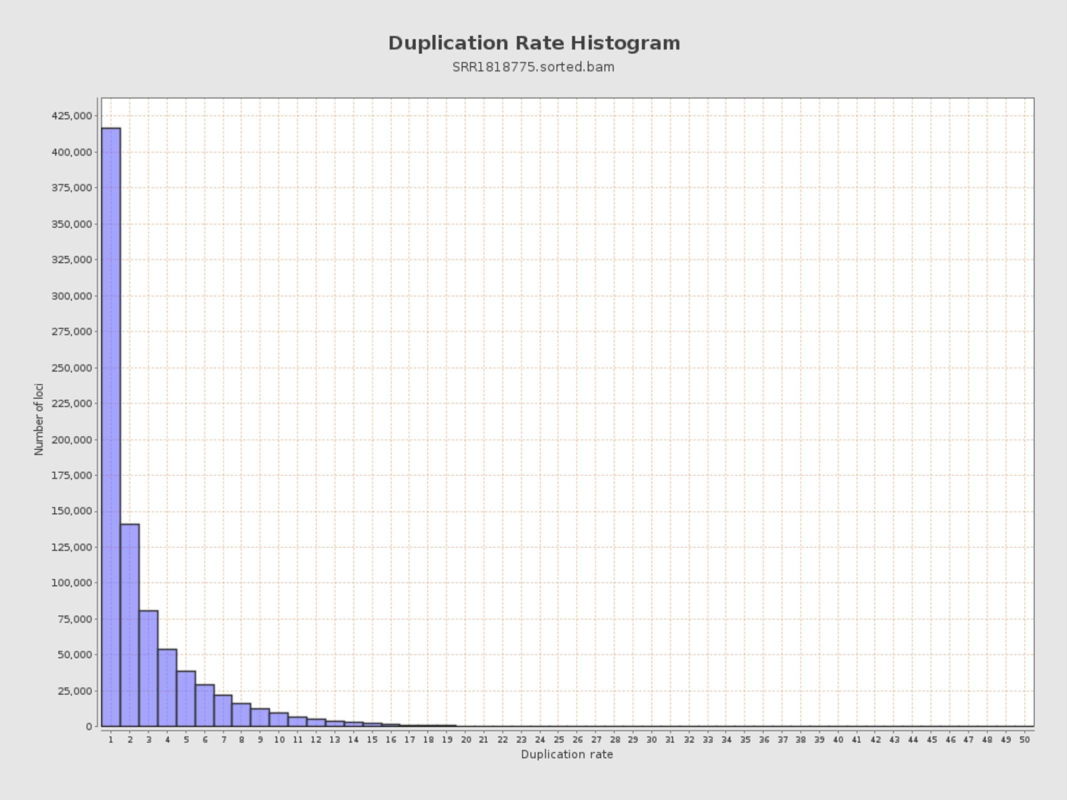
5. Results : Coverage Histogram (0-50X)



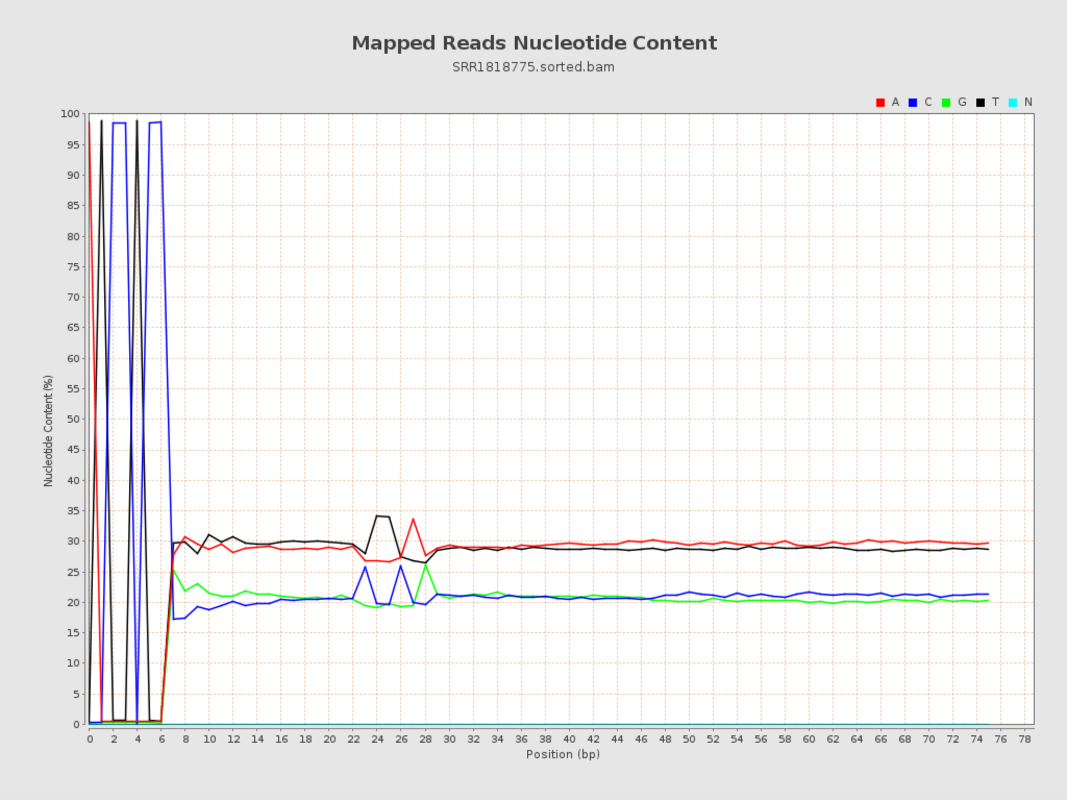
6. Results : Genome Fraction Coverage



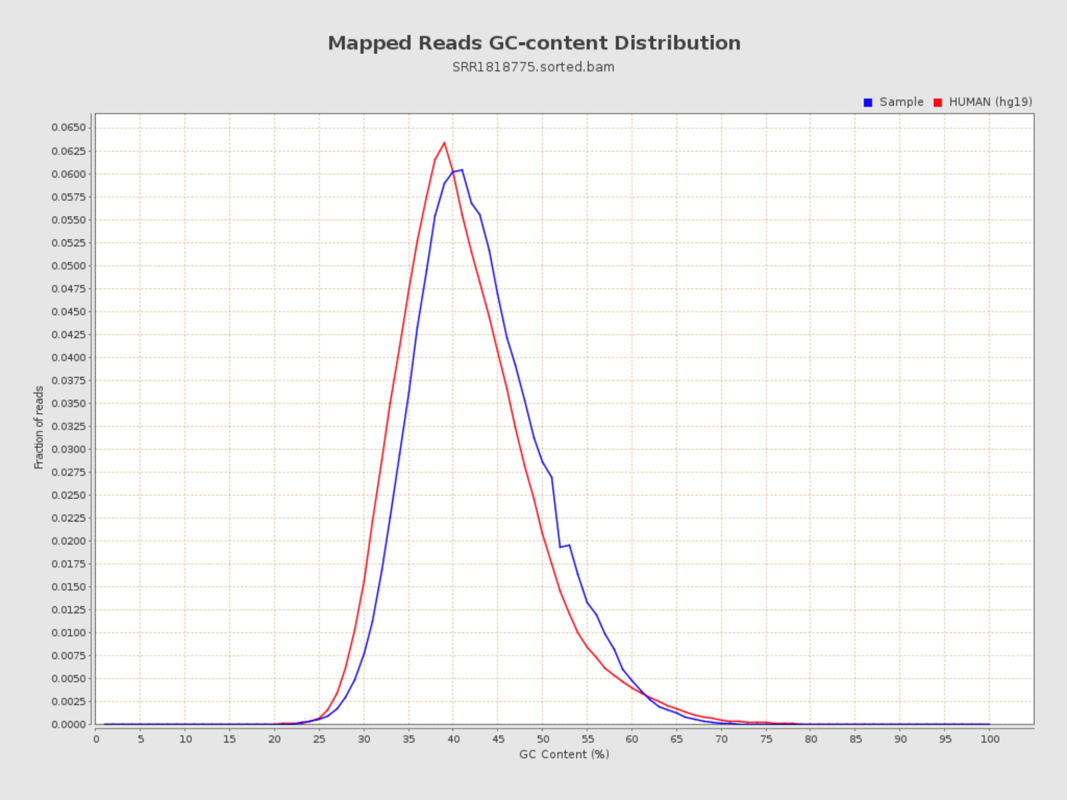
7. Results : Duplication Rate Histogram



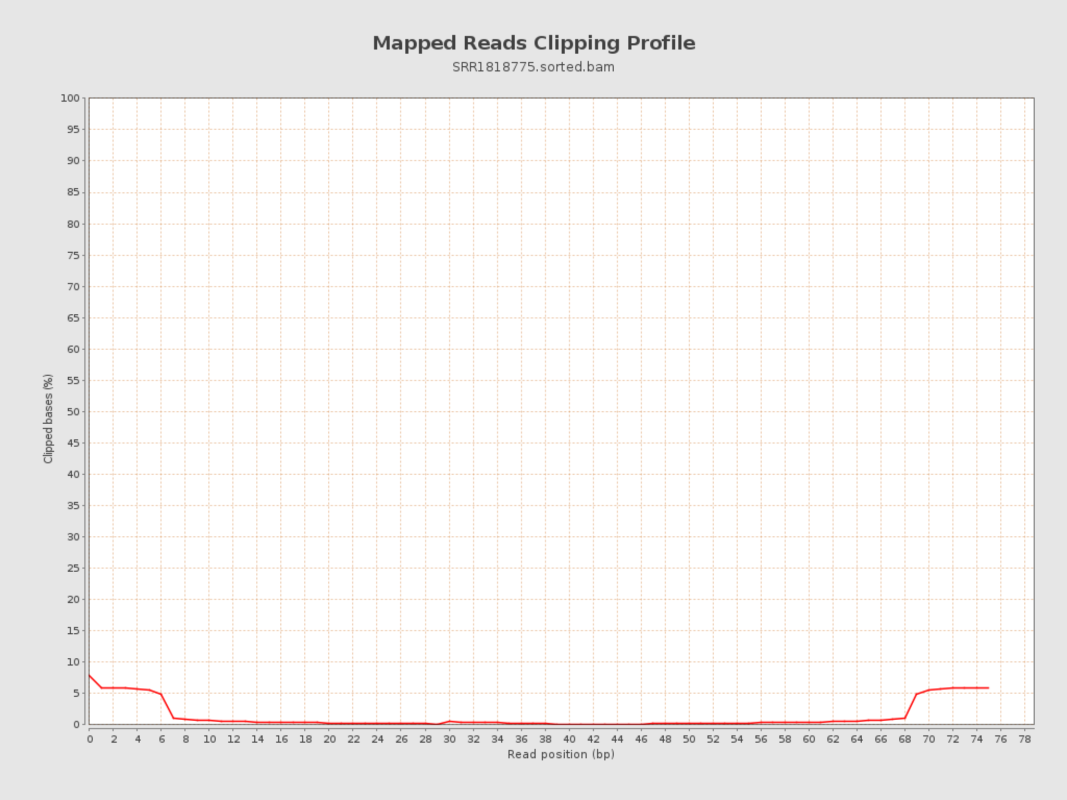
8. Results : Mapped Reads Nucleotide Content



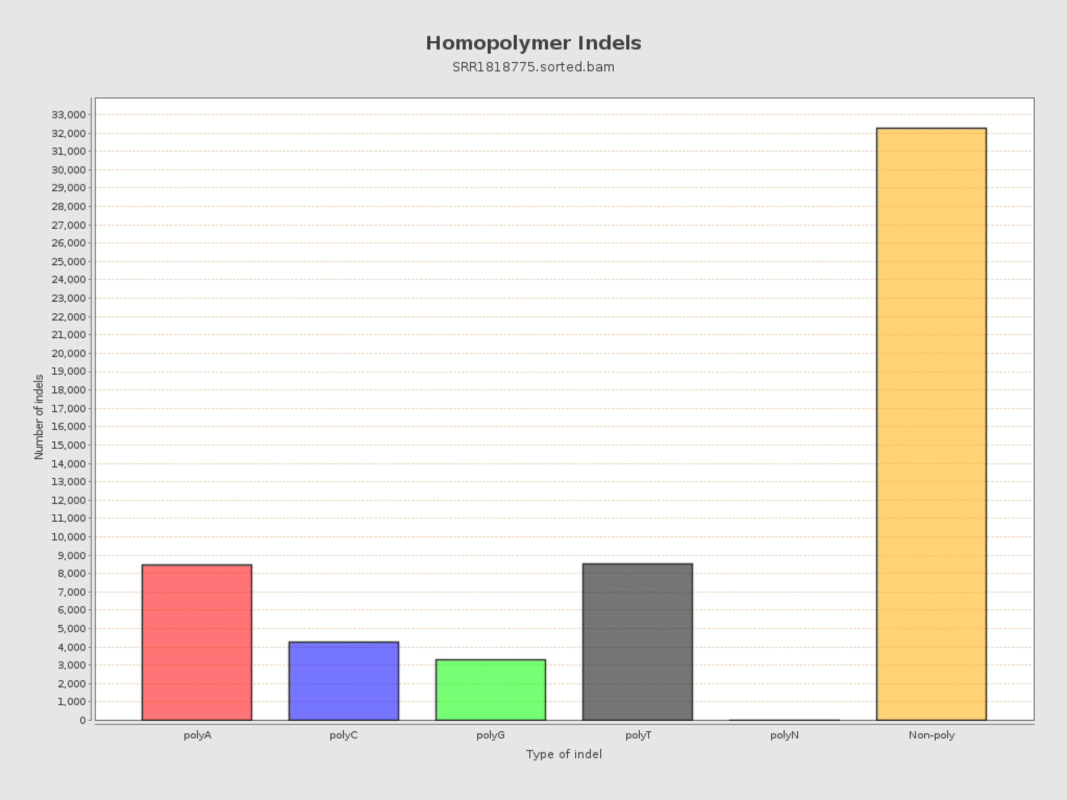
9. Results : Mapped Reads GC-content Distribution



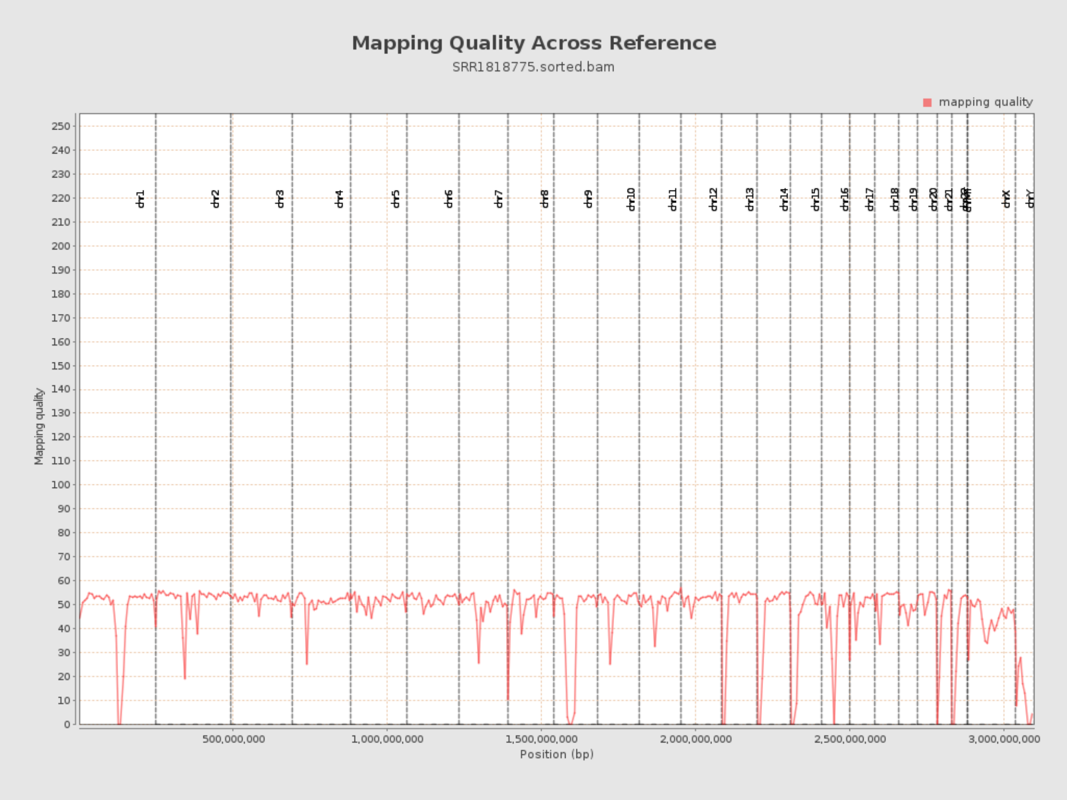
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram