Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:13:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818781.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_SRR1818781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818781.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:13:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,608,617
Mapped reads	1,518,673 / 94.41%
Unmapped reads	89,944 / 5.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,849 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	762,202 / 47.38%
Duplication rate	42.51%
Clipped reads	1,522,578 / 94.65%

2.2. ACGT Content

Number/percentage of A's	29,825,520 / 28.97%
Number/percentage of C's	21,992,016 / 21.36%
Number/percentage of T's	29,787,054 / 28.93%
Number/percentage of G's	21,353,892 / 20.74%
Number/percentage of N's	6,360 / 0.01%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.467

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

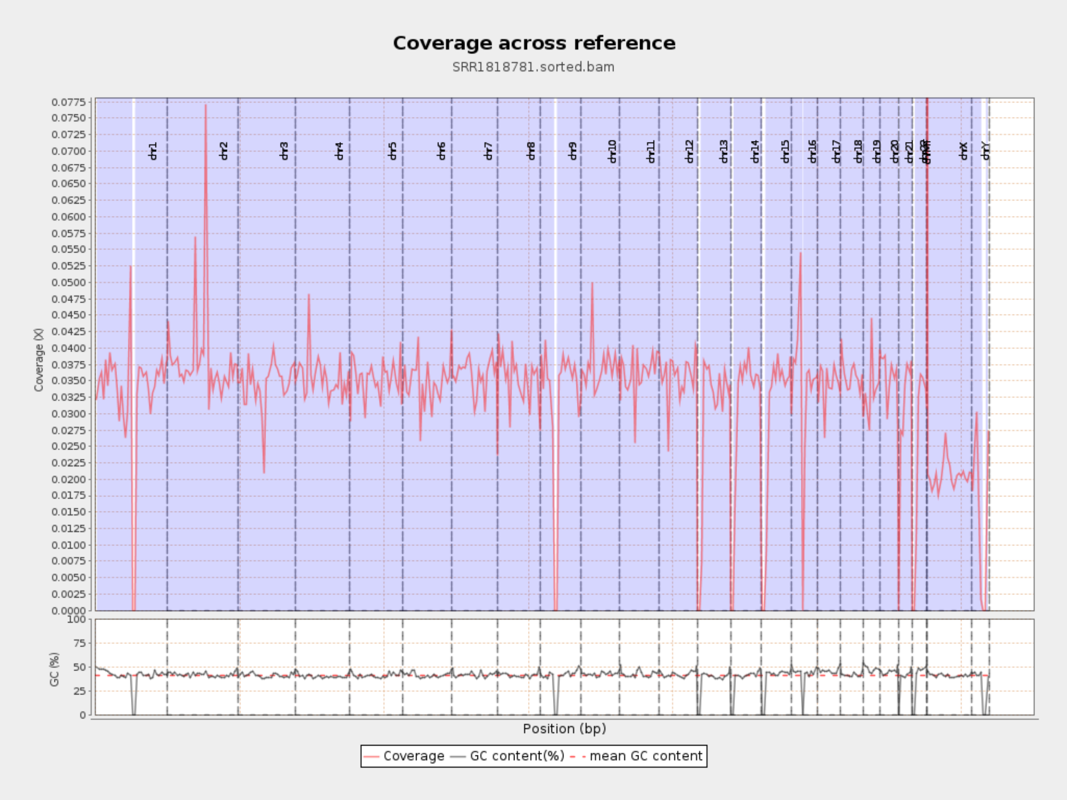
General error rate	0.54%
Mismatches	523,322
Insertions	13,551
Mapped reads with at least one insertion	0.88%
Deletions	26,768
Mapped reads with at least one deletion	1.75%
Homopolymer indels	39.81%

2.6. Chromosome stats

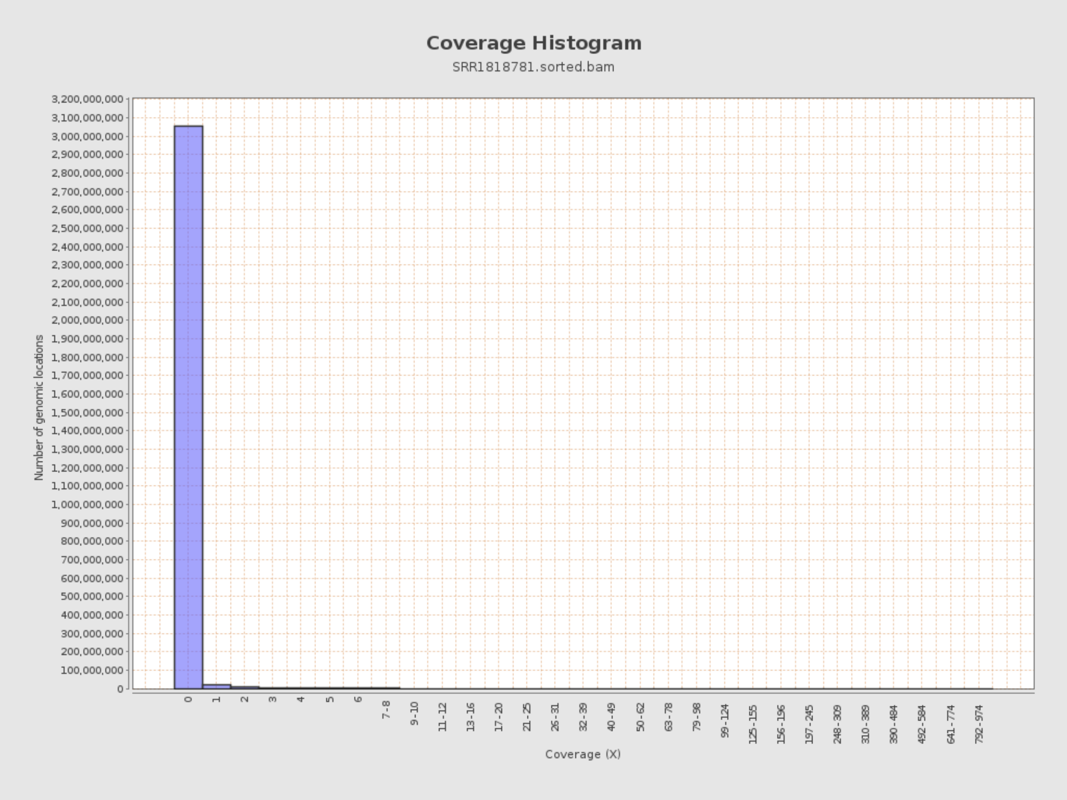
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8195968	0.0329	0.5643
chr2	243199373	9347301	0.0384	0.7576
chr3	198022430	6856730	0.0346	0.3665
chr4	191154276	6797784	0.0356	0.4156
chr5	180915260	6447272	0.0356	0.384
chr6	171115067	5925245	0.0346	0.3969
chr7	159138663	5737475	0.0361	0.4463

chr8	146364022	5201825	0.0355	0.4119
chr9	141213431	4493922	0.0318	0.3939
chr10	135534747	5055035	0.0373	0.5219
chr11	135006516	4884254	0.0362	0.4035
chr12	133851895	4770853	0.0356	0.3841
chr13	115169878	3322199	0.0288	0.3384
chr14	107349540	3215175	0.03	0.3746
chr15	102531392	2938702	0.0287	0.3358
chr16	90354753	3053322	0.0338	0.5305
chr17	81195210	2790513	0.0344	0.3872
chr18	78077248	2803944	0.0359	0.4676
chr19	59128983	1995070	0.0337	0.5201
chr20	63025520	2245768	0.0356	0.4016
chr21	48129895	1444595	0.03	0.3627
chr22	51304566	1220278	0.0238	0.3445
chrMT	16571	175435	10.5869	10.6513
chrX	155270560	3219685	0.0207	0.2994
chrY	59373566	869945	0.0147	0.7685

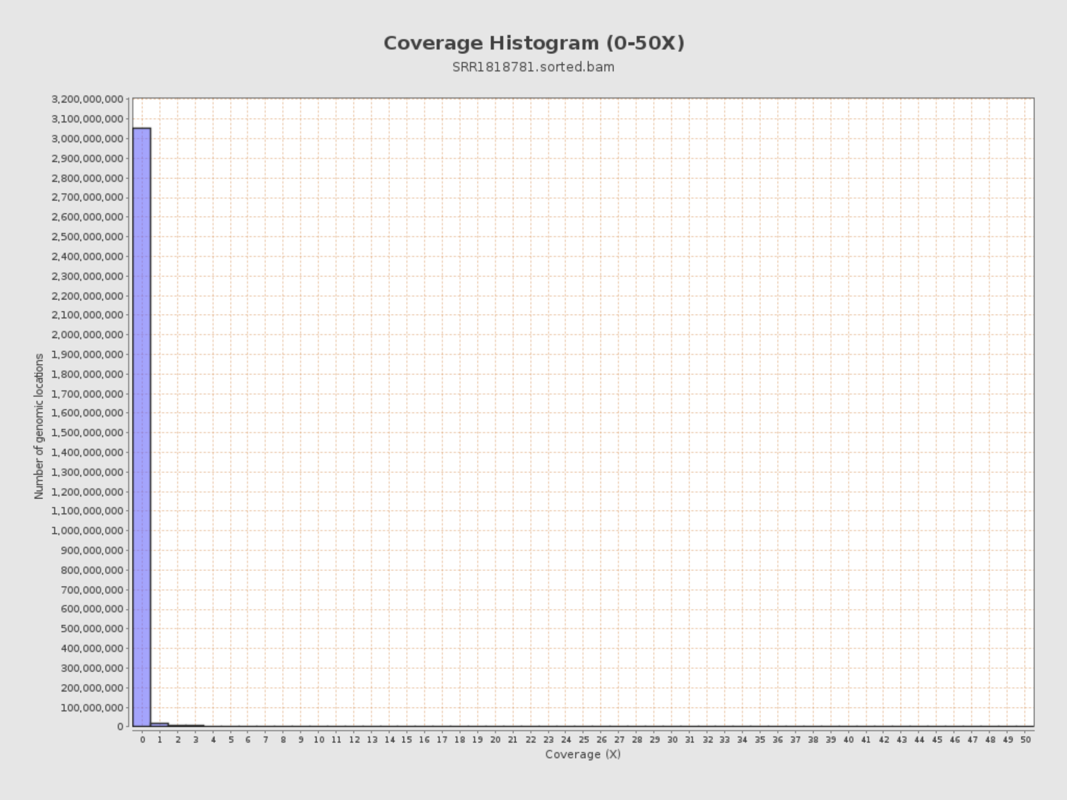
3. Results : Coverage across reference



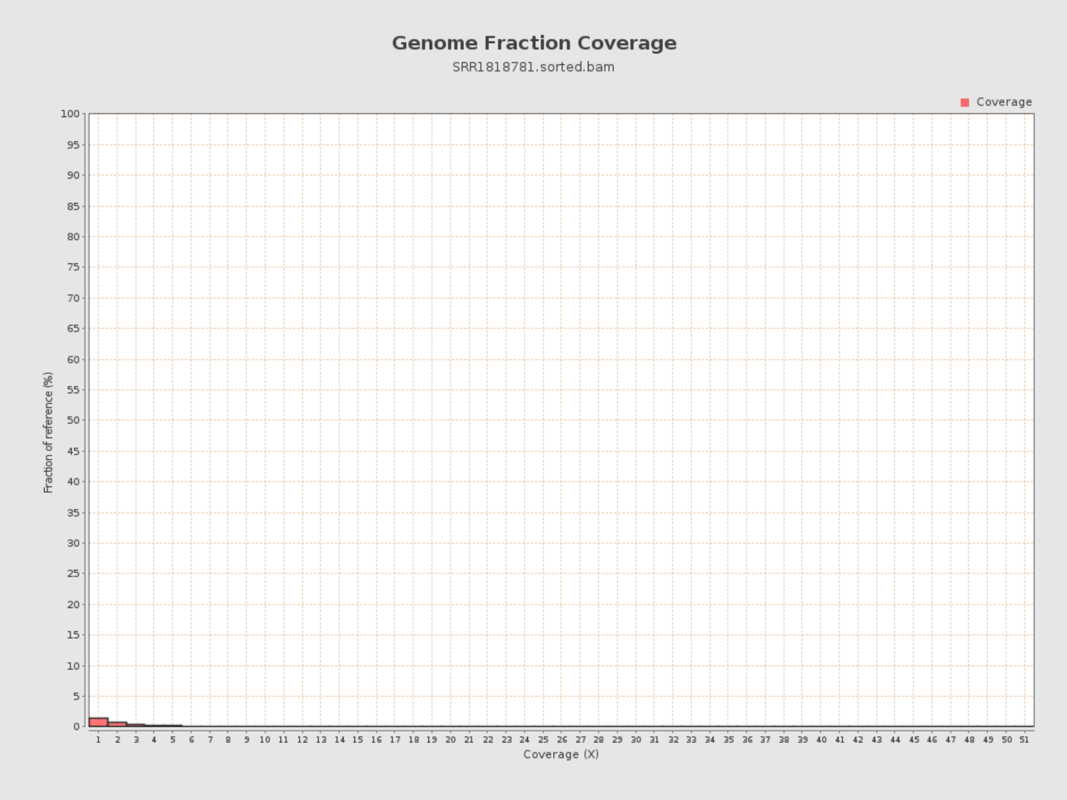
4. Results : Coverage Histogram



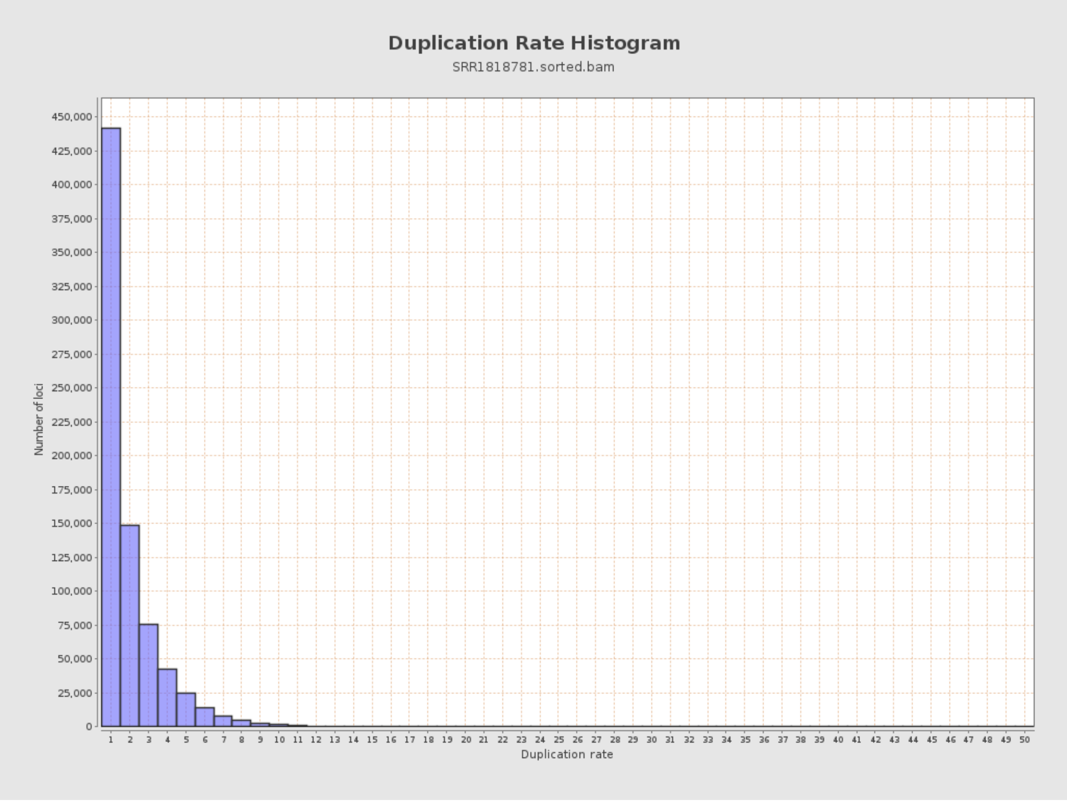
5. Results : Coverage Histogram (0-50X)



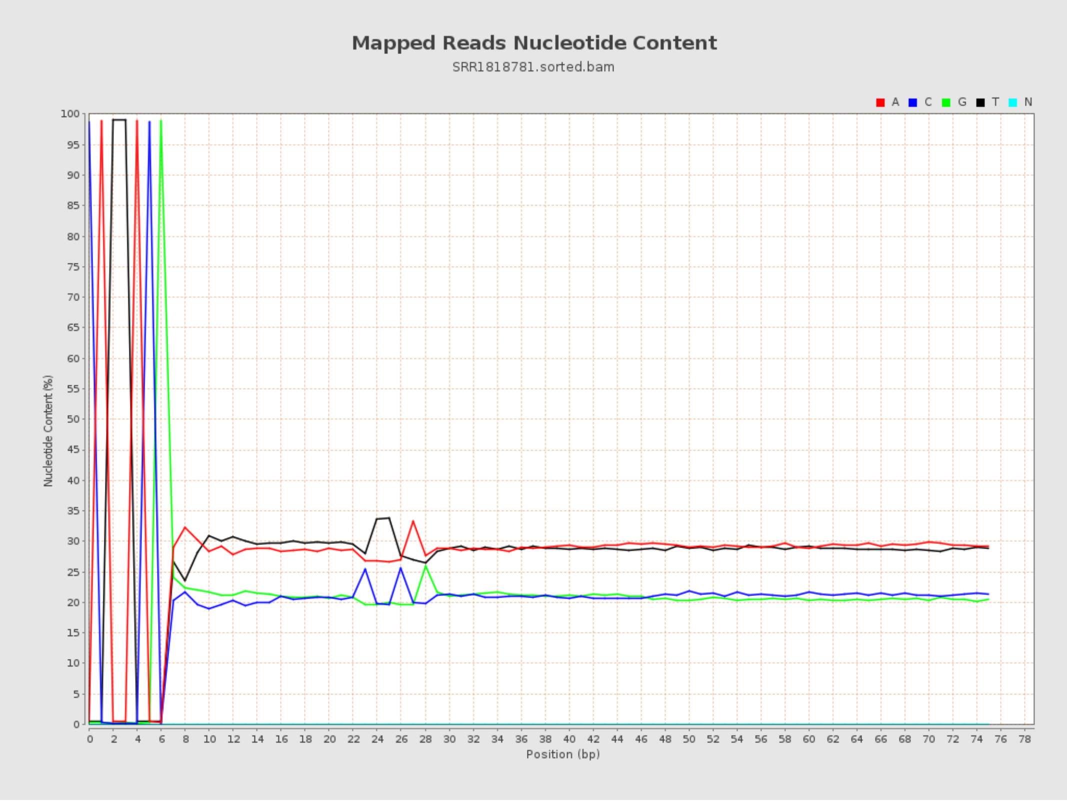
6. Results : Genome Fraction Coverage



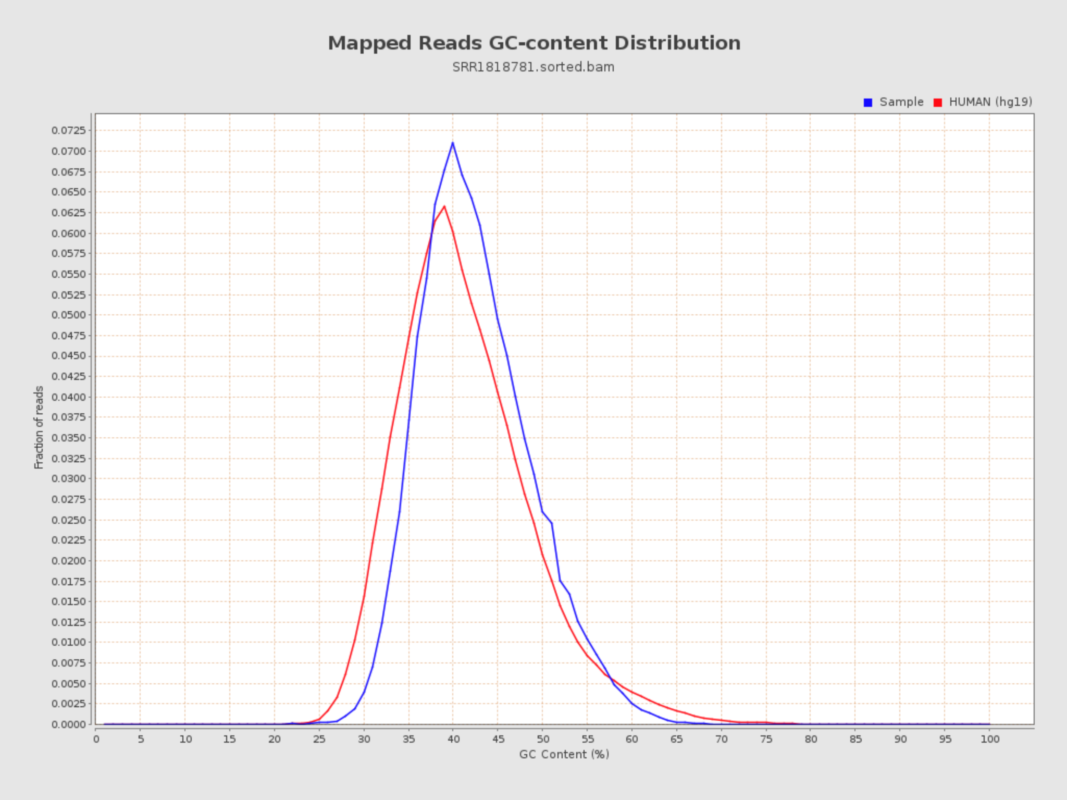
7. Results : Duplication Rate Histogram



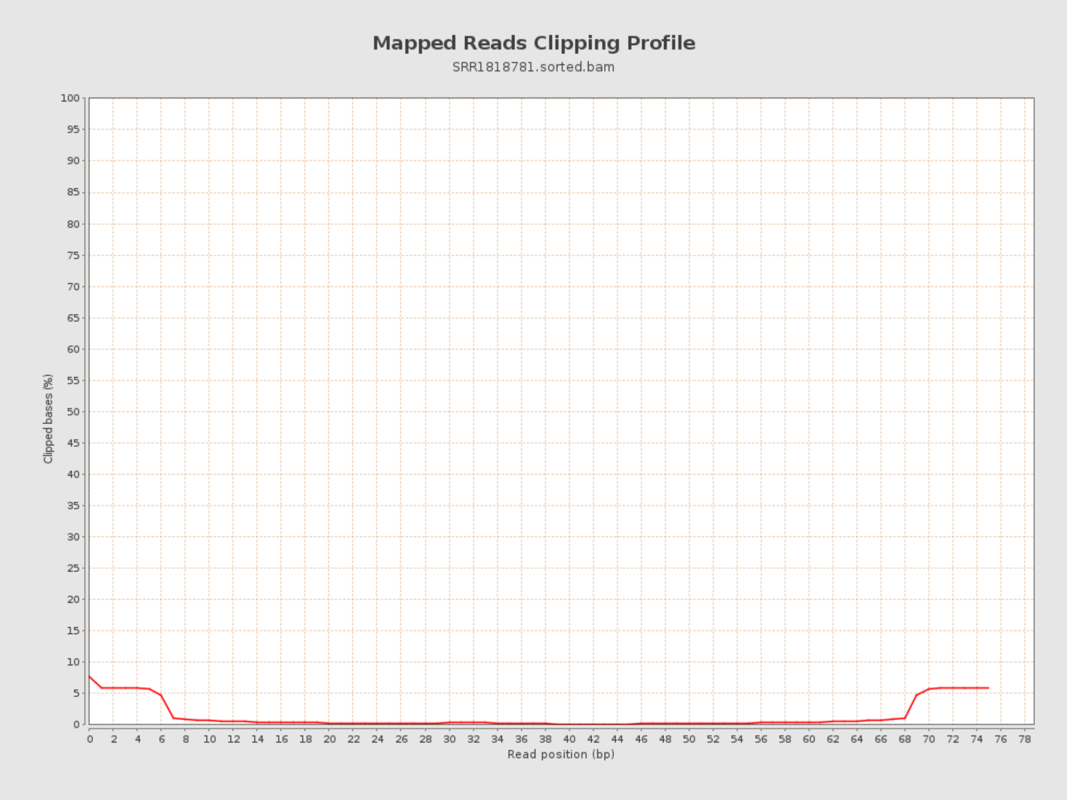
8. Results : Mapped Reads Nucleotide Content



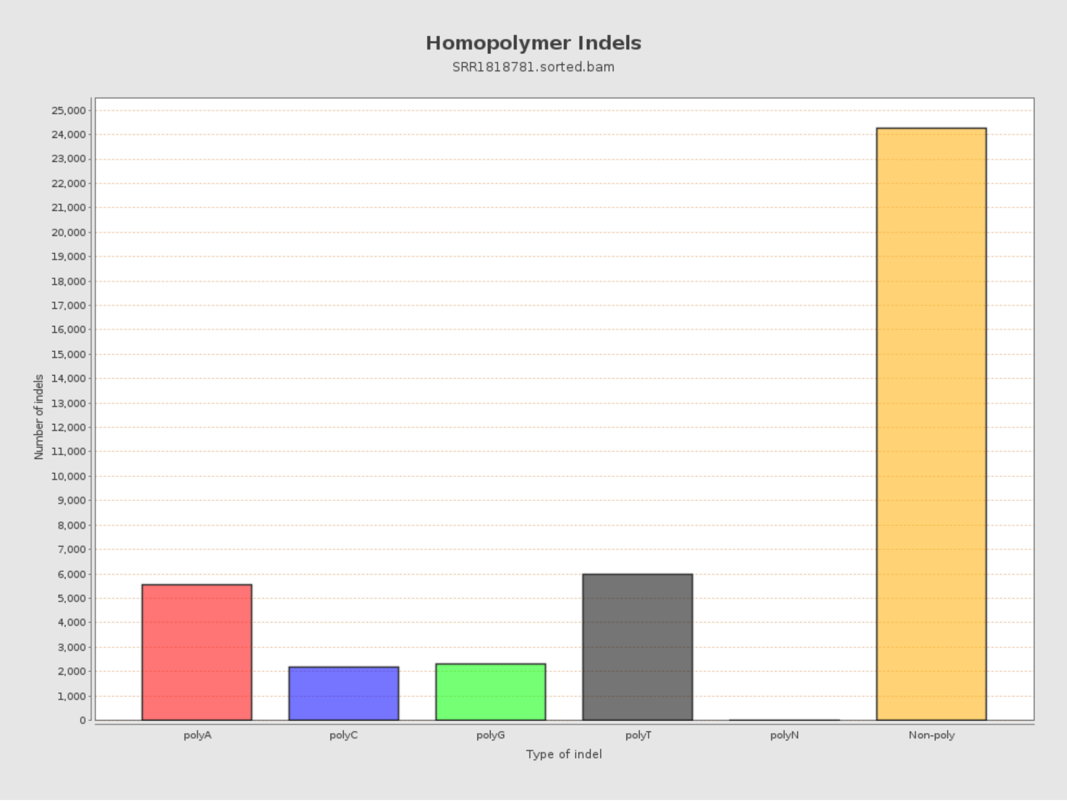
9. Results : Mapped Reads GC-content Distribution



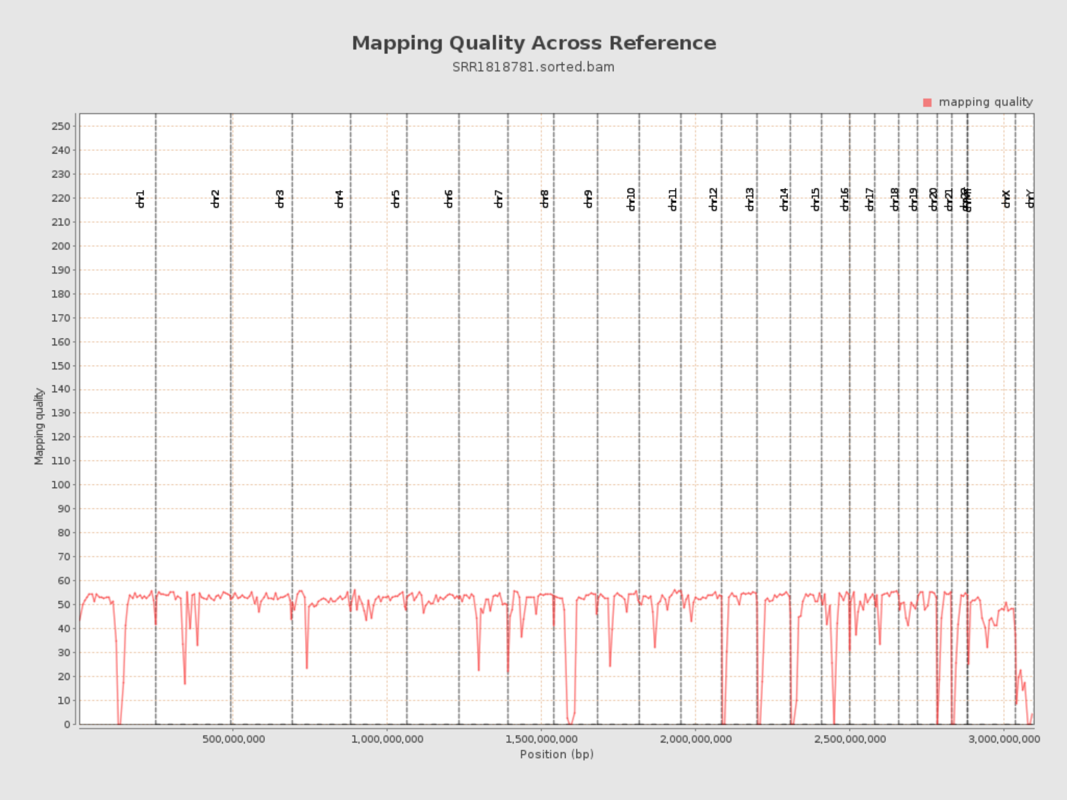
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram