Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:58:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818821.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_SRR1818821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:58:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,872,733
Mapped reads	1,824,540 / 97.43%
Unmapped reads	48,193 / 2.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,084 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	794,289 / 42.41%
Duplication rate	36.58%
Clipped reads	1,829,474 / 97.69%

2.2. ACGT Content

Number/percentage of A's	34,938,205 / 28.21%
Number/percentage of C's	28,002,642 / 22.61%
Number/percentage of T's	35,490,205 / 28.66%
Number/percentage of G's	25,389,370 / 20.5%
Number/percentage of N's	8,348 / 0.01%
GC Percentage	43.12%

2.3. Coverage

Mean	0.04

Standard Deviation	0.4784

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

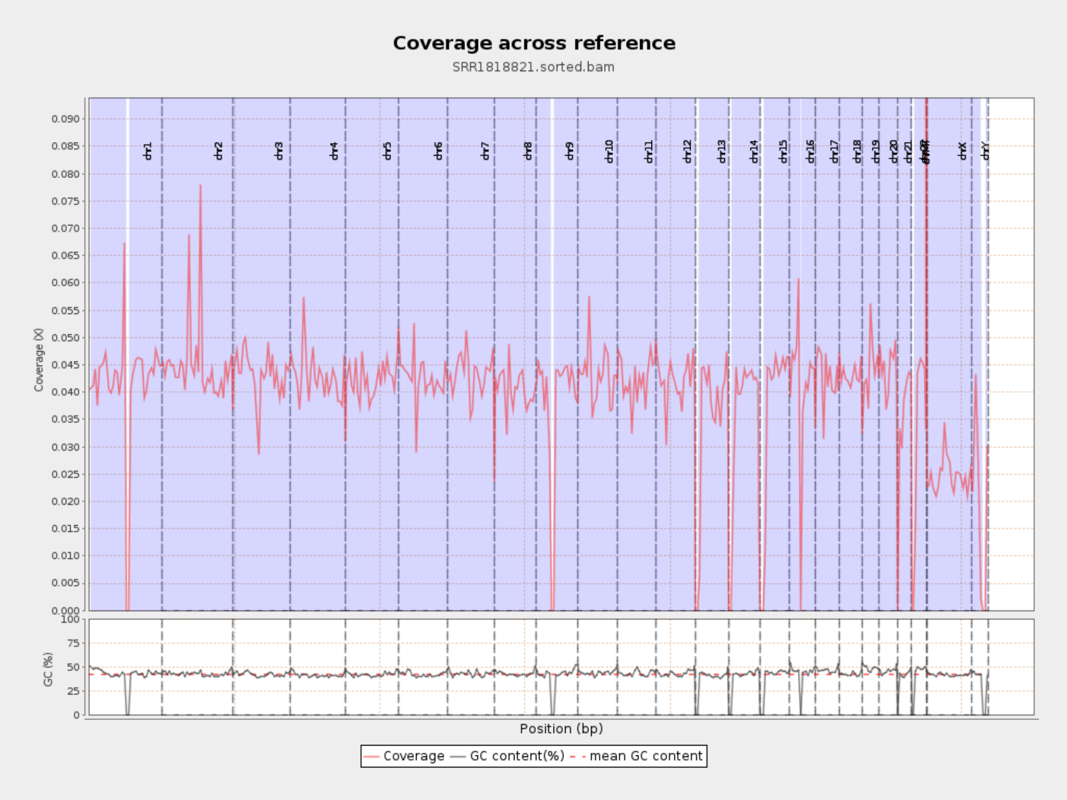
General error rate	0.53%
Mismatches	629,348
Insertions	13,567
Mapped reads with at least one insertion	0.73%
Deletions	30,725
Mapped reads with at least one deletion	1.67%
Homopolymer indels	42.52%

2.6. Chromosome stats

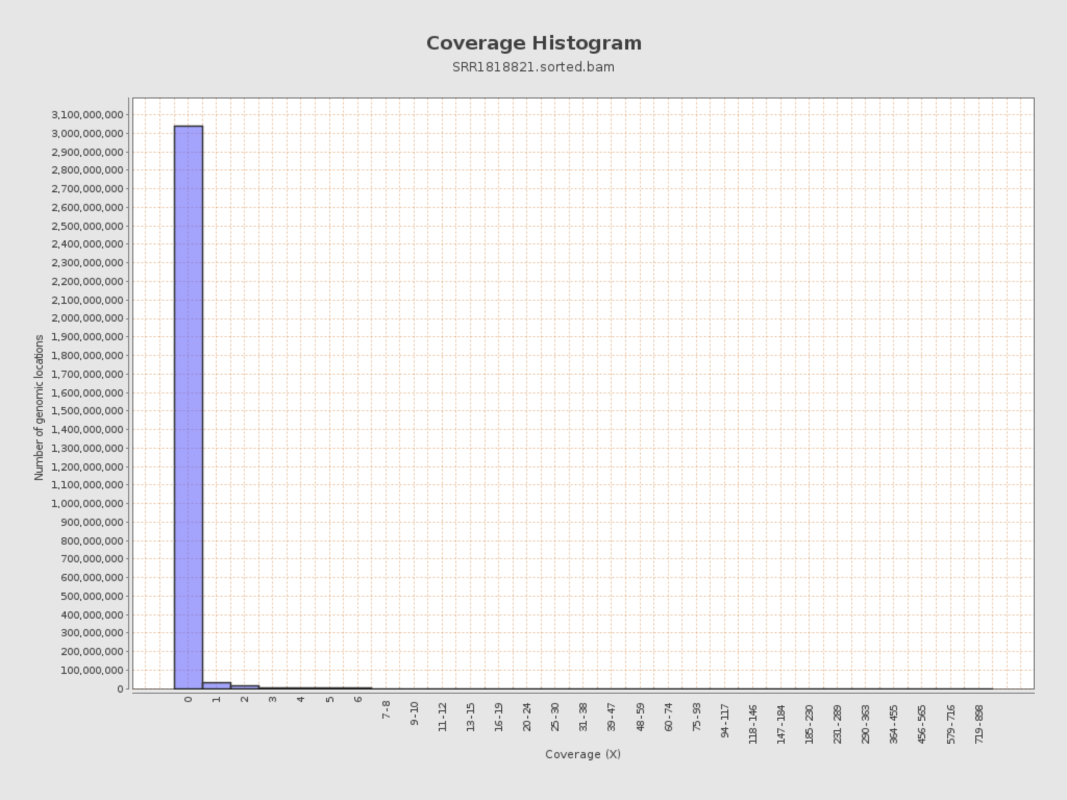
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10313269	0.0414	0.7054
chr2	243199373	11016126	0.0453	0.6966
chr3	198022430	8536927	0.0431	0.3805
chr4	191154276	8177115	0.0428	0.4196
chr5	180915260	7637472	0.0422	0.3878
chr6	171115067	7299230	0.0427	0.4143
chr7	159138663	6900537	0.0434	0.4665

chr8	146364022	5936140	0.0406	0.4236
chr9	141213431	5280201	0.0374	0.4092
chr10	135534747	5818597	0.0429	0.4732
chr11	135006516	5707112	0.0423	0.4106
chr12	133851895	5645109	0.0422	0.3987
chr13	115169878	3910783	0.034	0.3356
chr14	107349540	3770726	0.0351	0.3674
chr15	102531392	3669268	0.0358	0.3518
chr16	90354753	3725160	0.0412	0.5151
chr17	81195210	3480534	0.0429	0.4072
chr18	78077248	3368133	0.0431	0.5022
chr19	59128983	2625188	0.0444	0.609
chr20	63025520	2793018	0.0443	0.4086
chr21	48129895	1664319	0.0346	0.3602
chr22	51304566	1563827	0.0305	0.3499
chrMT	16571	124870	7.5355	6.7827
chrX	155270560	3828971	0.0247	0.3163
chrY	59373566	1085234	0.0183	0.6983

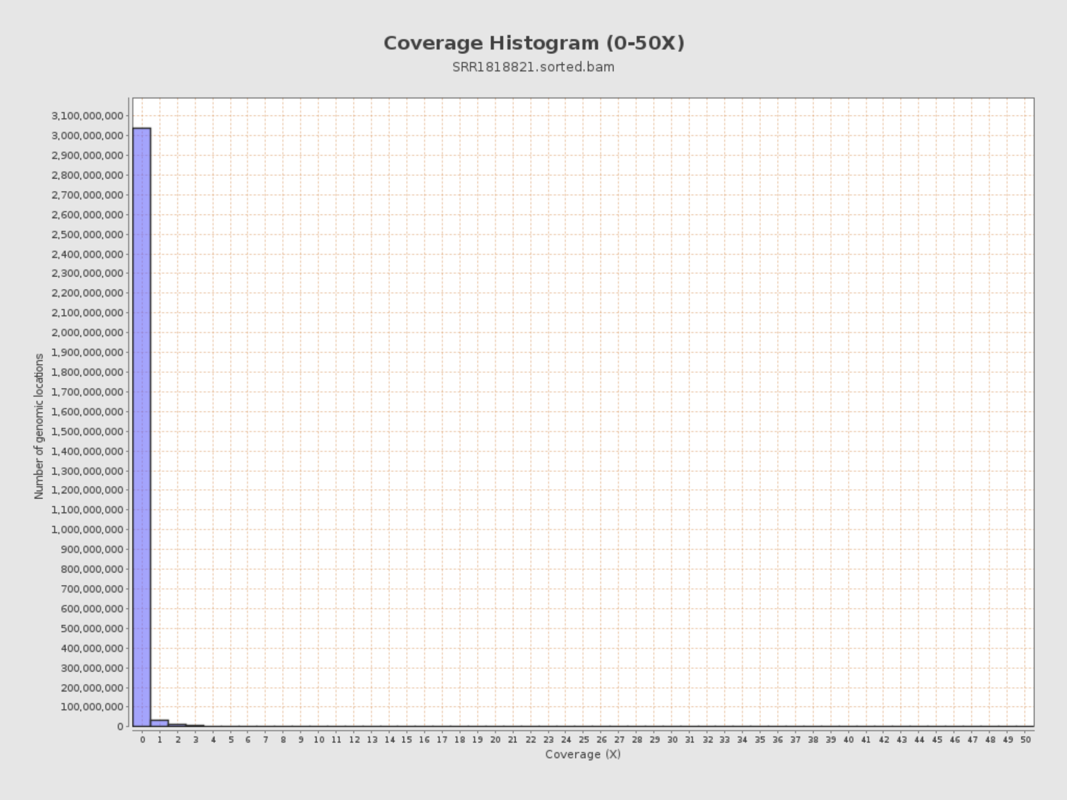
3. Results : Coverage across reference



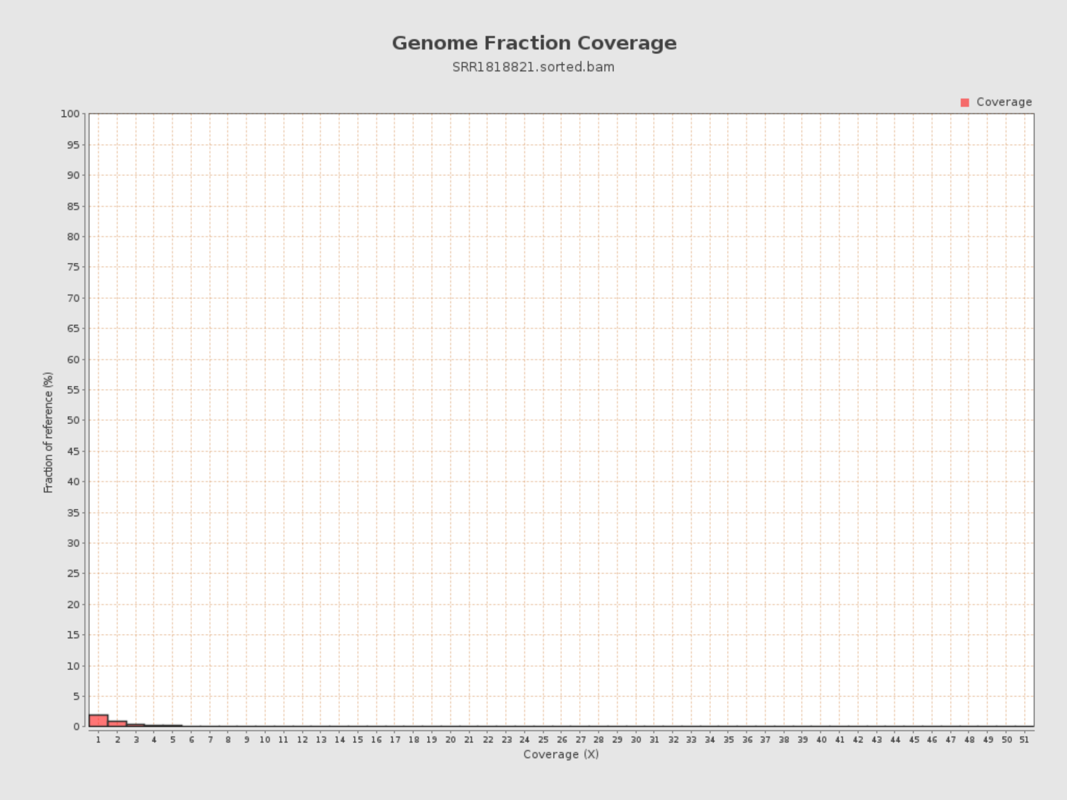
4. Results : Coverage Histogram



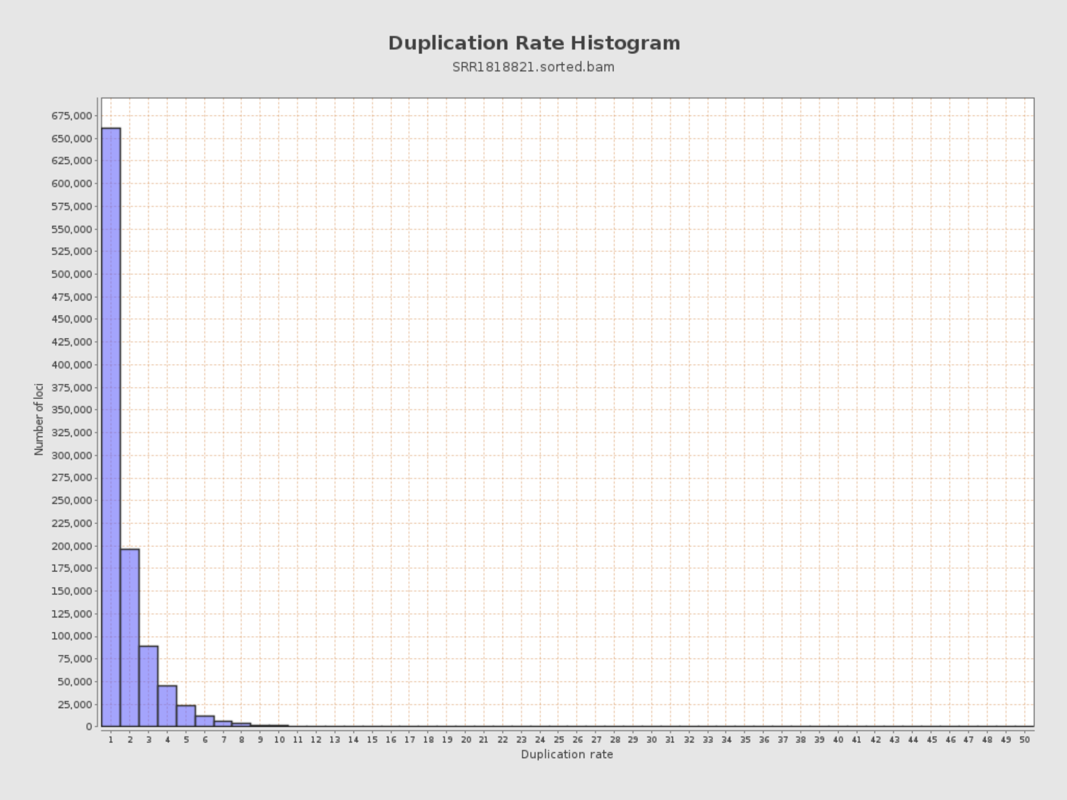
5. Results : Coverage Histogram (0-50X)



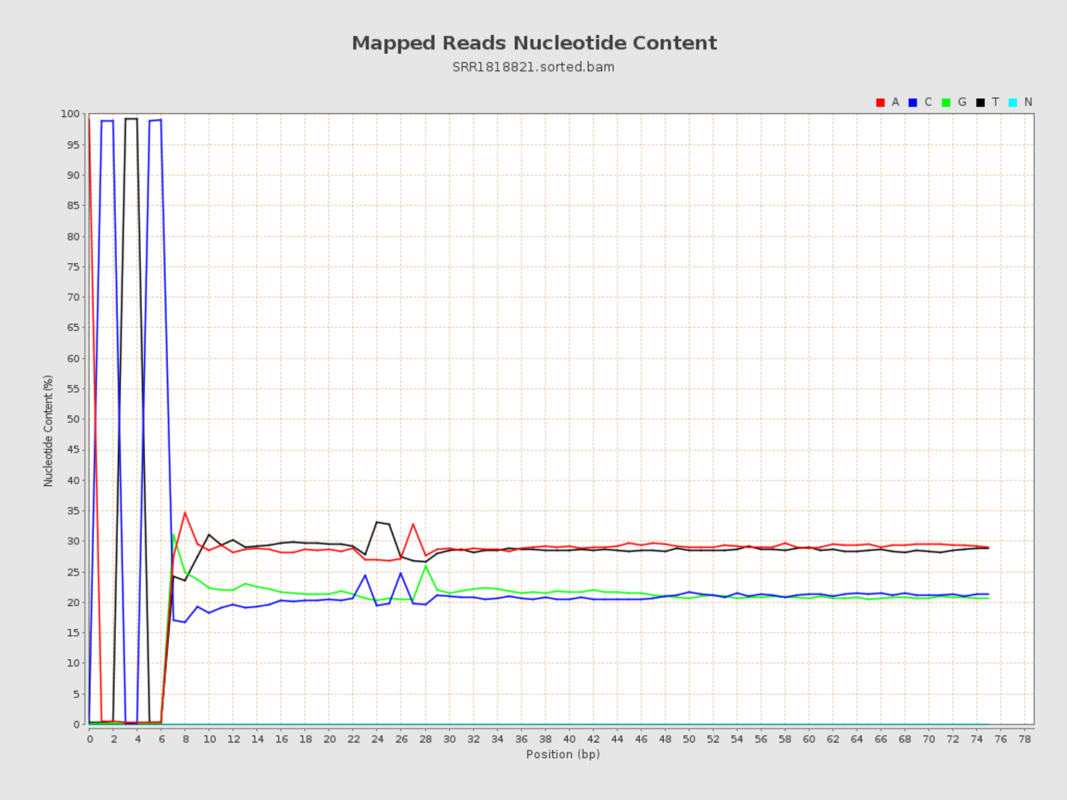
6. Results : Genome Fraction Coverage



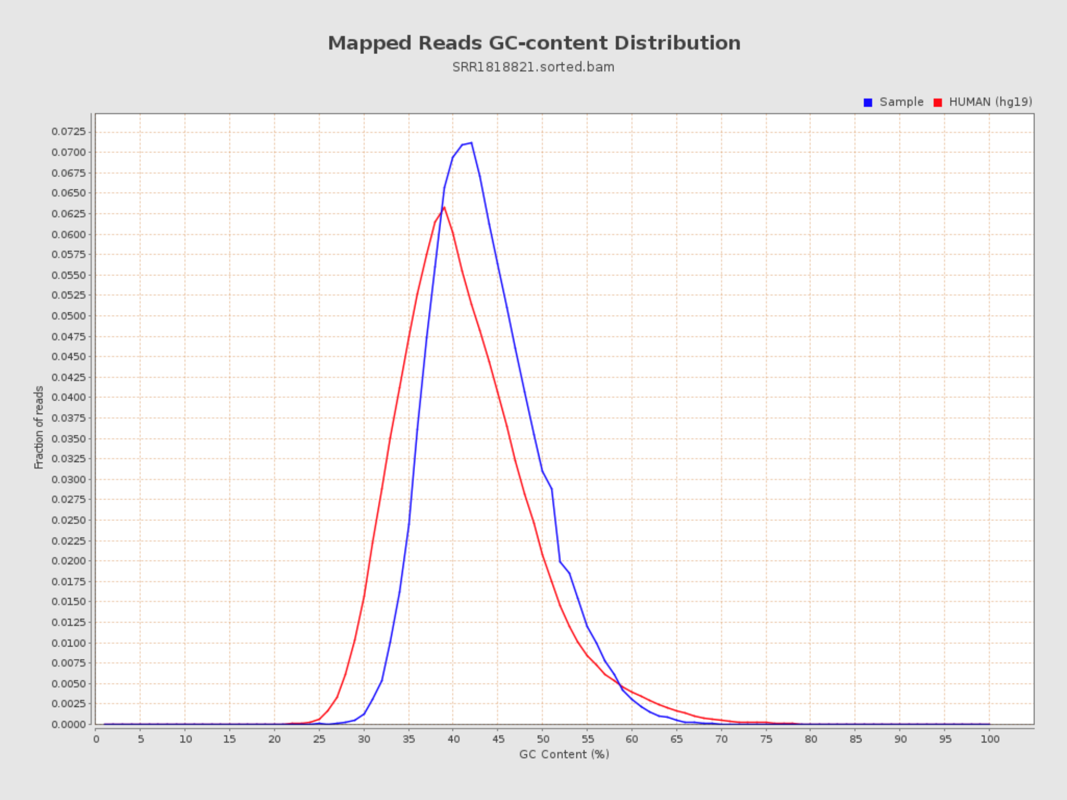
7. Results : Duplication Rate Histogram



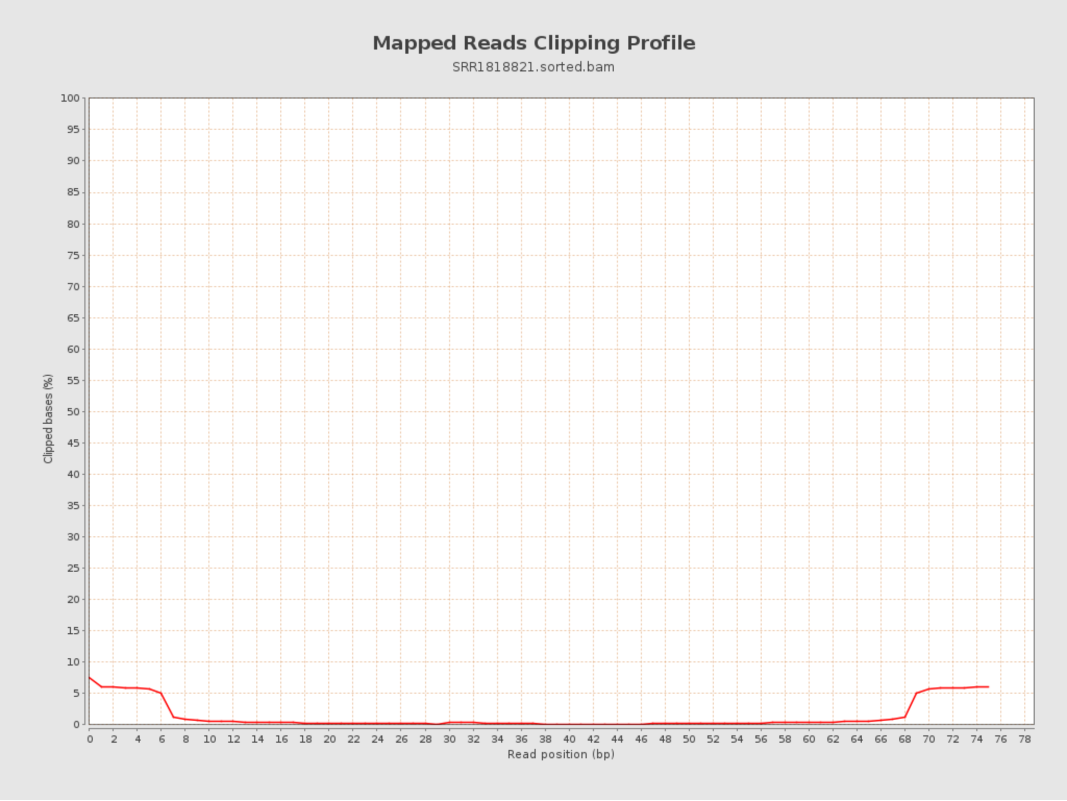
8. Results : Mapped Reads Nucleotide Content



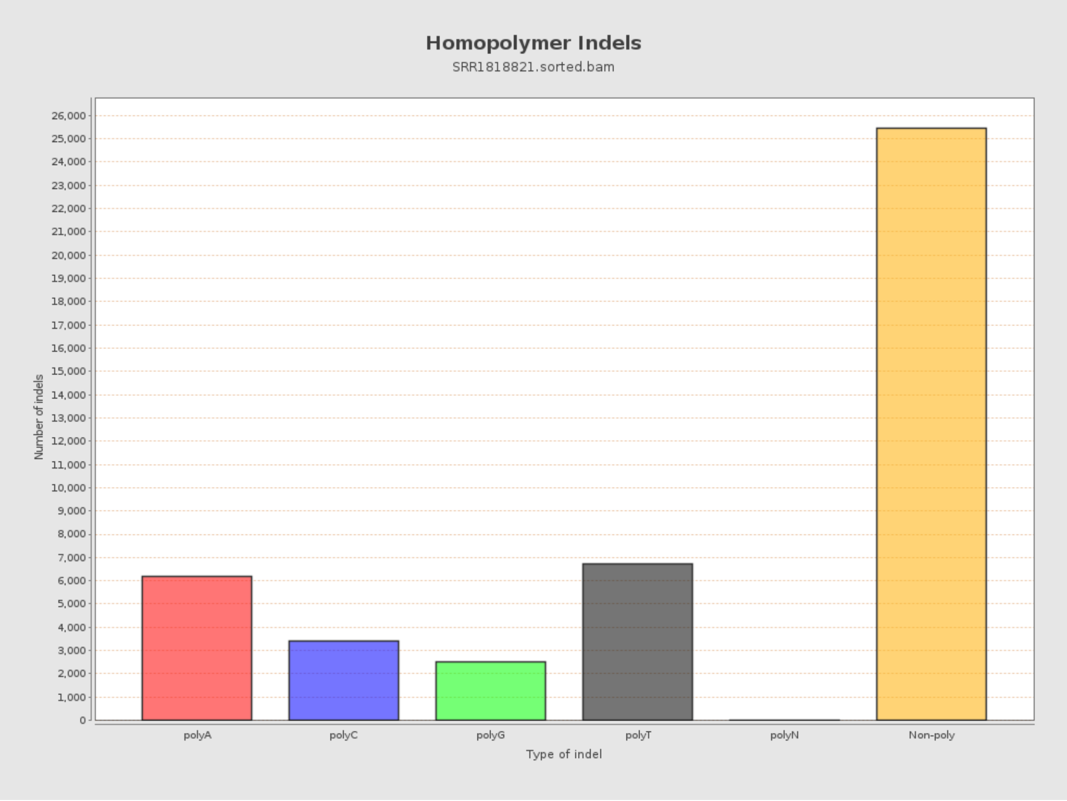
9. Results : Mapped Reads GC-content Distribution



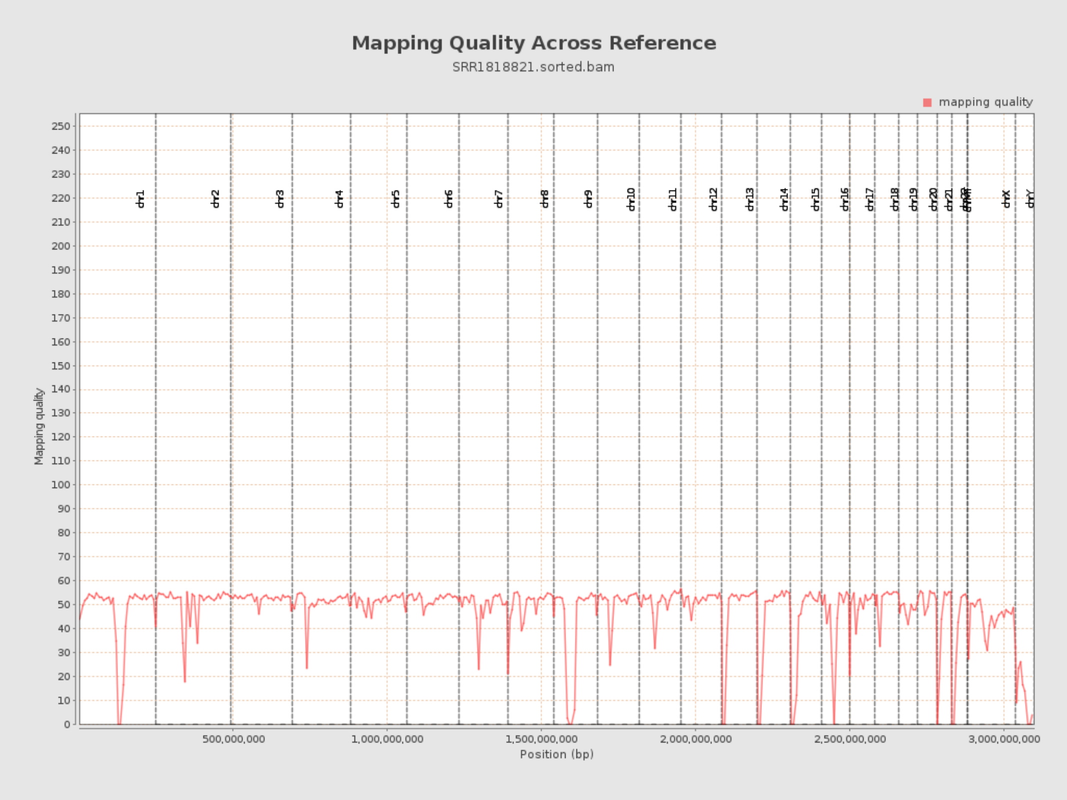
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram