Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818784.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_SRR1818784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,280,166
Mapped reads	2,146,230 / 94.13%
Unmapped reads	133,936 / 5.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,775 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,022,563 / 44.85%
Duplication rate	39.87%
Clipped reads	2,152,122 / 94.38%

2.2. ACGT Content

Number/percentage of A's	42,355,018 / 29.07%
Number/percentage of C's	30,591,125 / 21%
Number/percentage of T's	42,222,465 / 28.98%
Number/percentage of G's	30,504,215 / 20.94%
Number/percentage of N's	9,012 / 0.01%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.5813

2.4. Mapping Quality

Mean Mapping Quality	47.79

2.5. Mismatches and indels

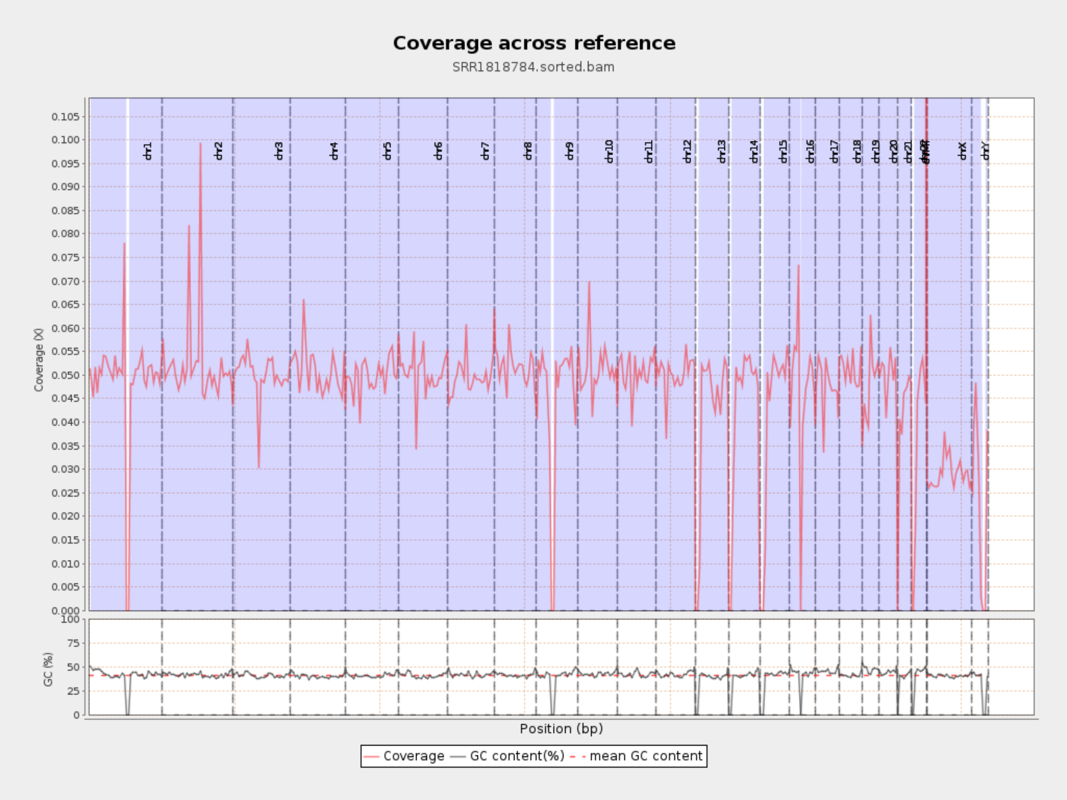
General error rate	0.52%
Mismatches	725,543
Insertions	16,062
Mapped reads with at least one insertion	0.74%
Deletions	36,374
Mapped reads with at least one deletion	1.68%
Homopolymer indels	40.38%

2.6. Chromosome stats

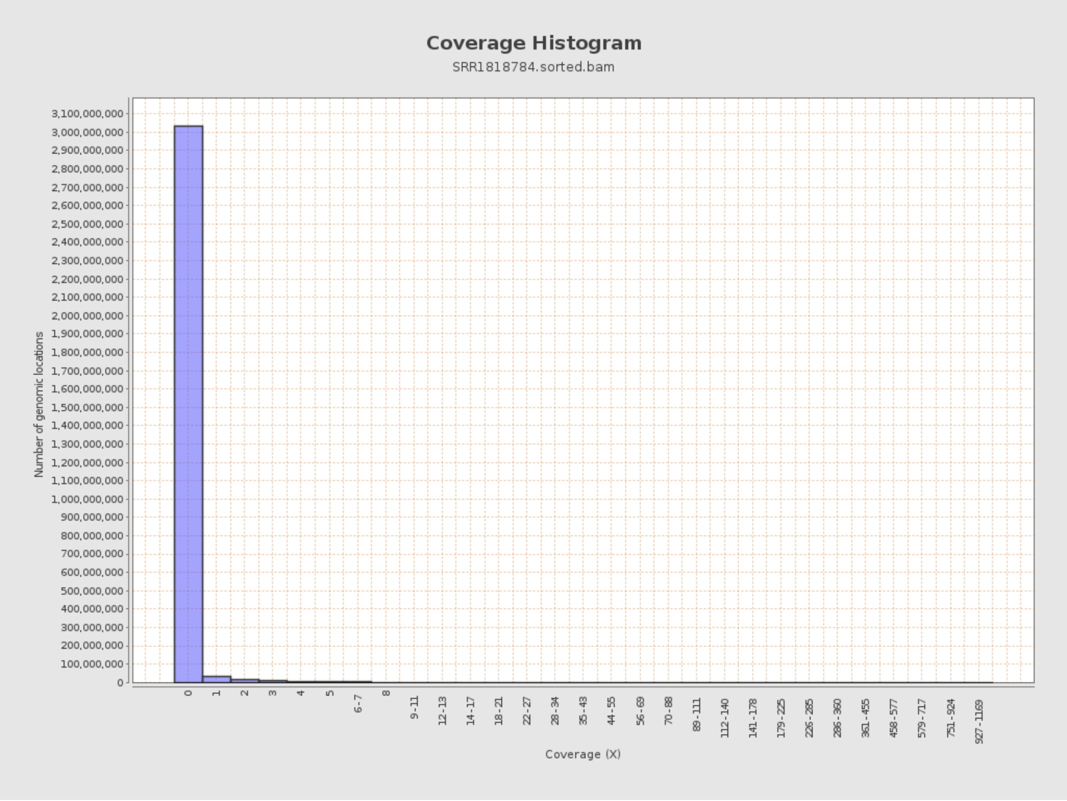
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12037204	0.0483	0.8523
chr2	243199373	12810443	0.0527	0.9173
chr3	198022430	9911345	0.0501	0.4336
chr4	191154276	9720693	0.0509	0.4928
chr5	180915260	8986875	0.0497	0.4509
chr6	171115067	8656448	0.0506	0.483
chr7	159138663	7876780	0.0495	0.5172

chr8	146364022	7603265	0.0519	0.5044
chr9	141213431	6310381	0.0447	0.4826
chr10	135534747	6965515	0.0514	0.579
chr11	135006516	6838698	0.0507	0.4859
chr12	133851895	6721300	0.0502	0.4575
chr13	115169878	4695735	0.0408	0.3939
chr14	107349540	4526612	0.0422	0.4377
chr15	102531392	4202290	0.041	0.4002
chr16	90354753	4261616	0.0472	0.6547
chr17	81195210	3863249	0.0476	0.4502
chr18	78077248	3996923	0.0512	0.6388
chr19	59128983	2846363	0.0481	0.7367
chr20	63025520	3142733	0.0499	0.458
chr21	48129895	1952201	0.0406	0.4114
chr22	51304566	1748721	0.0341	0.3912
chrMT	16571	198589	11.9841	11.2811
chrX	155270560	4527107	0.0292	0.3575
chrY	59373566	1339242	0.0226	0.9556

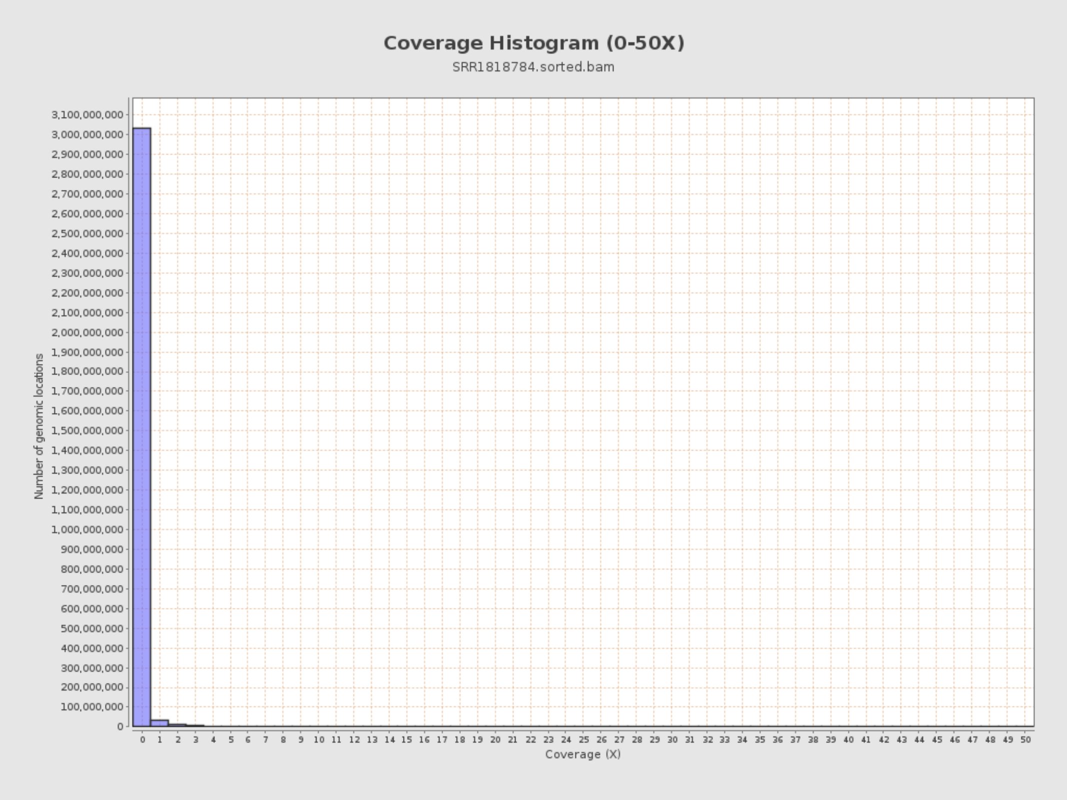
3. Results : Coverage across reference



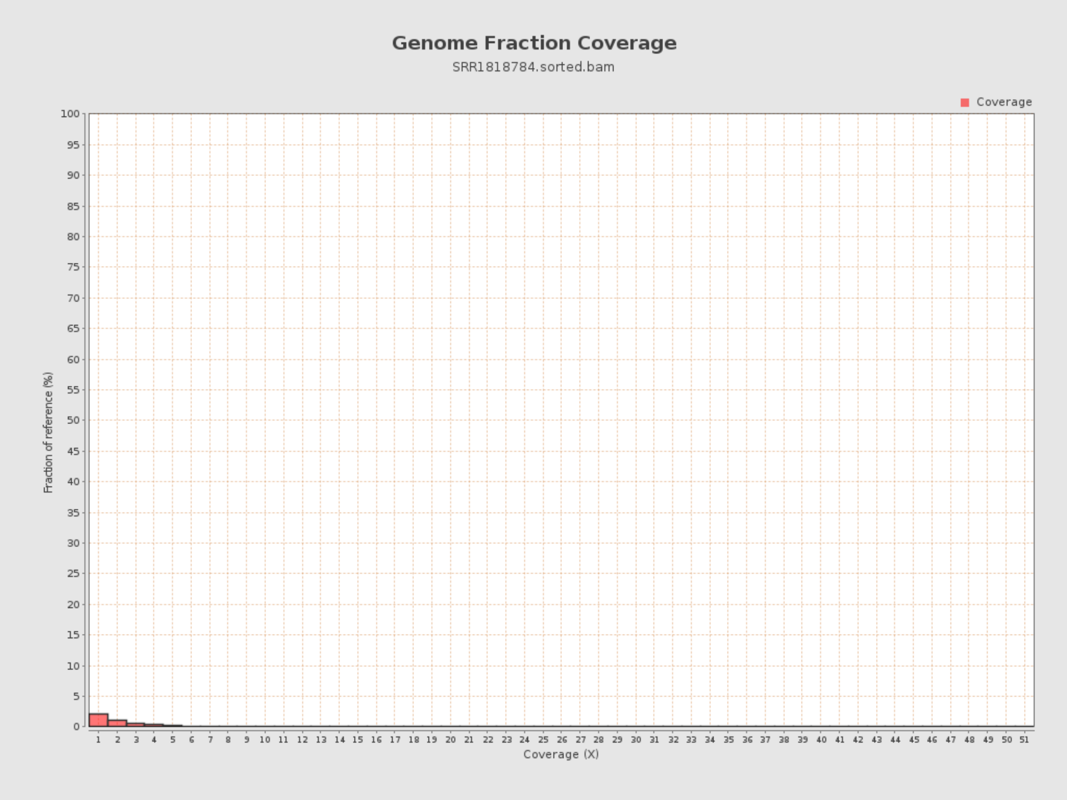
4. Results : Coverage Histogram



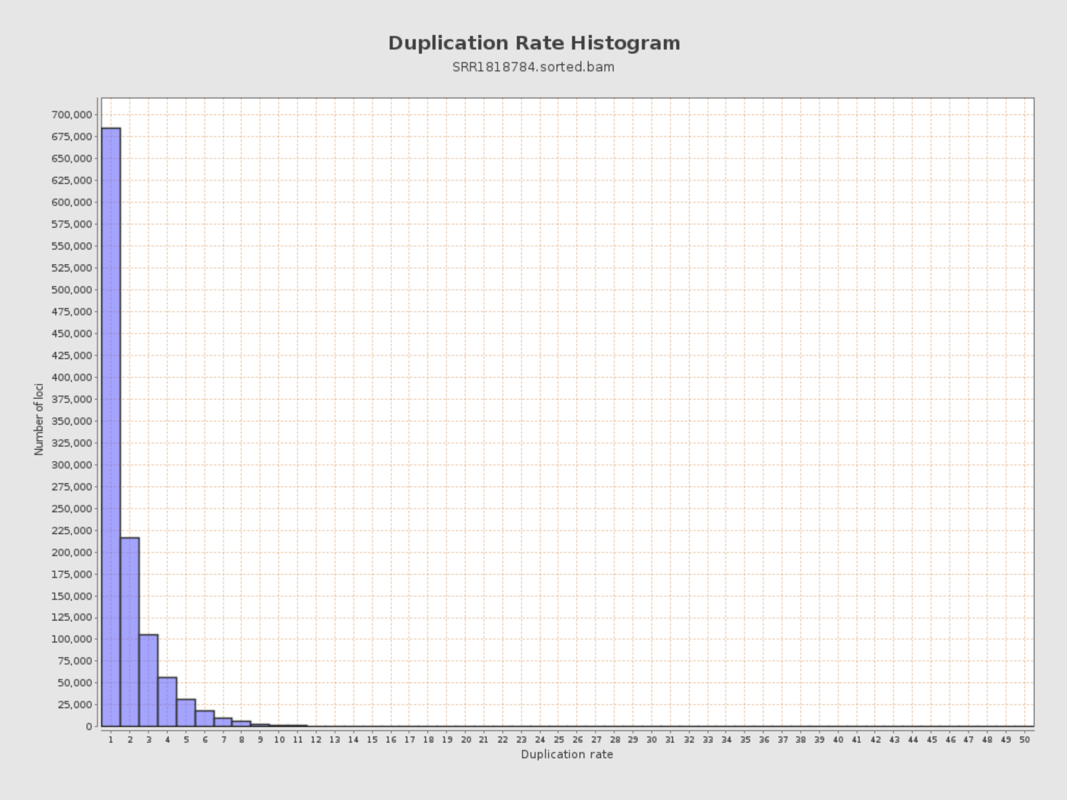
5. Results : Coverage Histogram (0-50X)



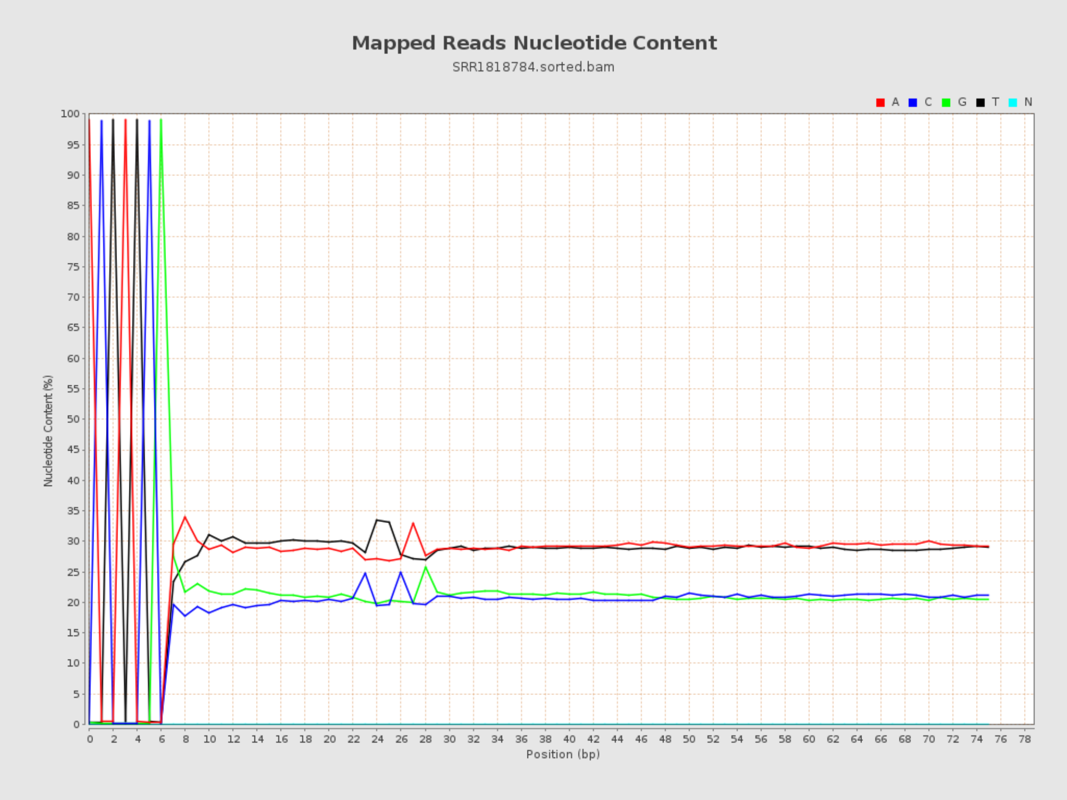
6. Results : Genome Fraction Coverage



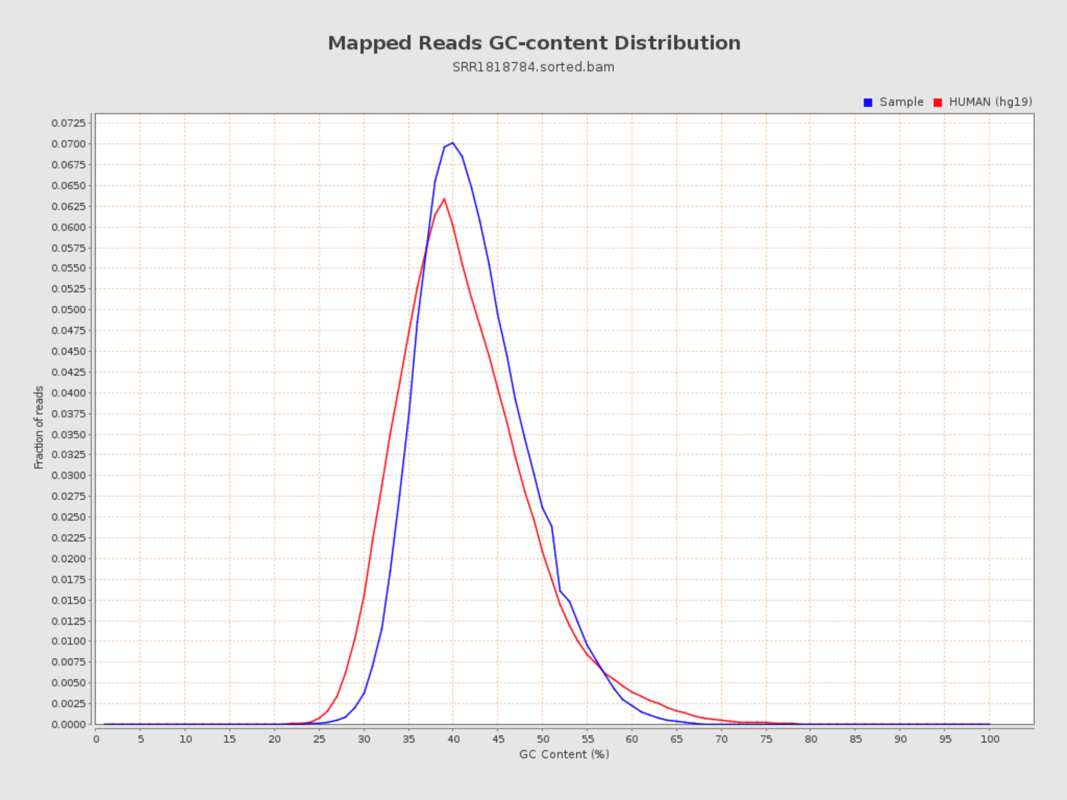
7. Results : Duplication Rate Histogram



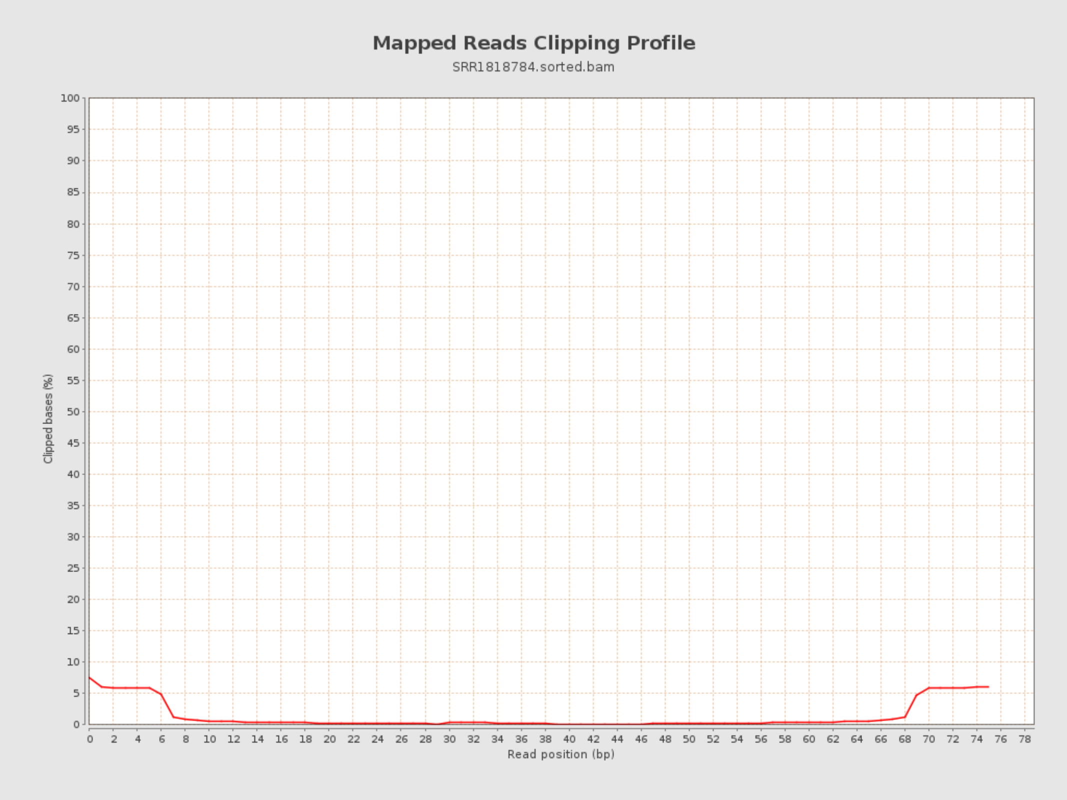
8. Results : Mapped Reads Nucleotide Content



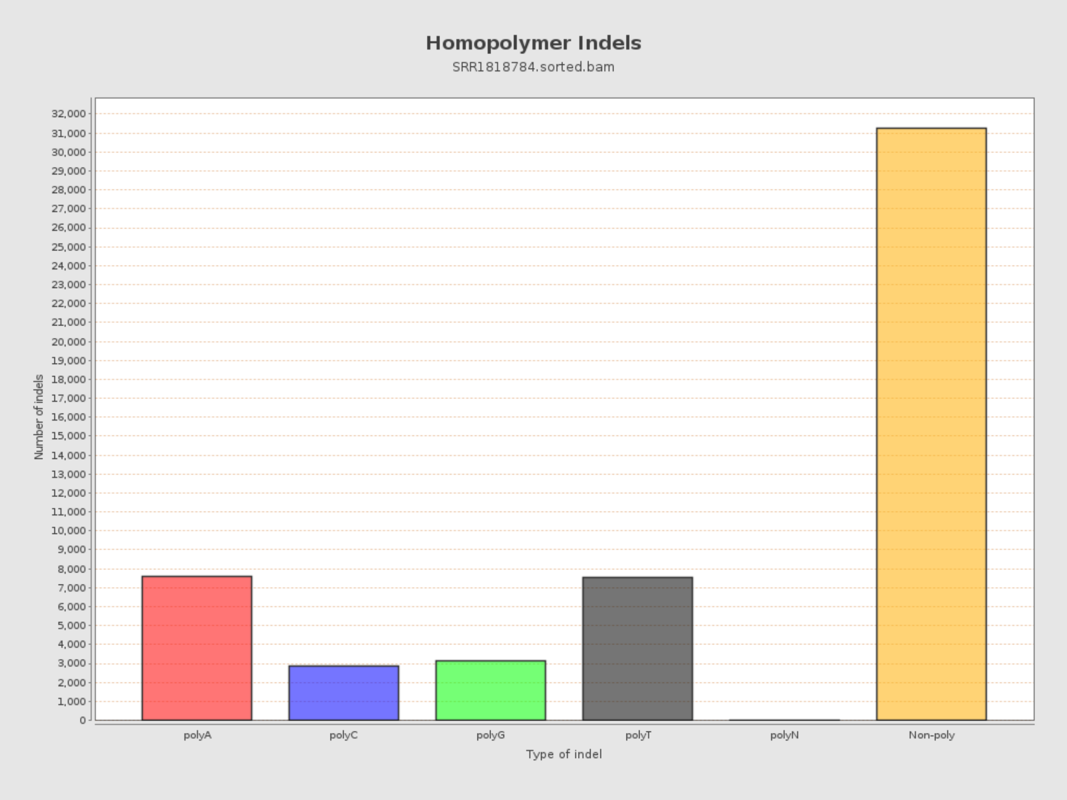
9. Results : Mapped Reads GC-content Distribution



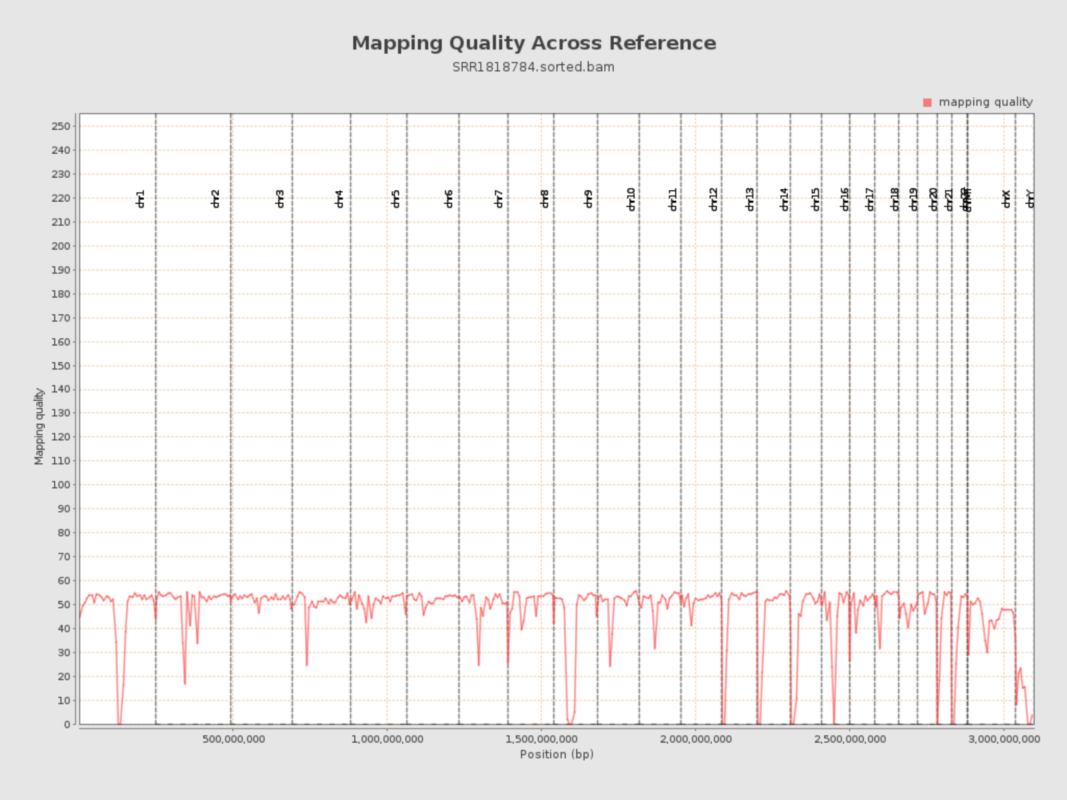
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram