Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:23:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084280.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_SRR3084280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:23:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,412,890
Mapped reads	2,151,493 / 89.17%
Unmapped reads	261,397 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,353 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	69,741 / 2.89%
Duplication rate	2.57%
Clipped reads	1,091,941 / 45.25%

2.2. ACGT Content

Number/percentage of A's	39,012,583 / 27.64%
Number/percentage of C's	27,036,425 / 19.16%
Number/percentage of T's	43,177,919 / 30.59%
Number/percentage of G's	31,746,827 / 22.49%
Number/percentage of N's	164,189 / 0.12%
GC Percentage	41.65%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.34

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

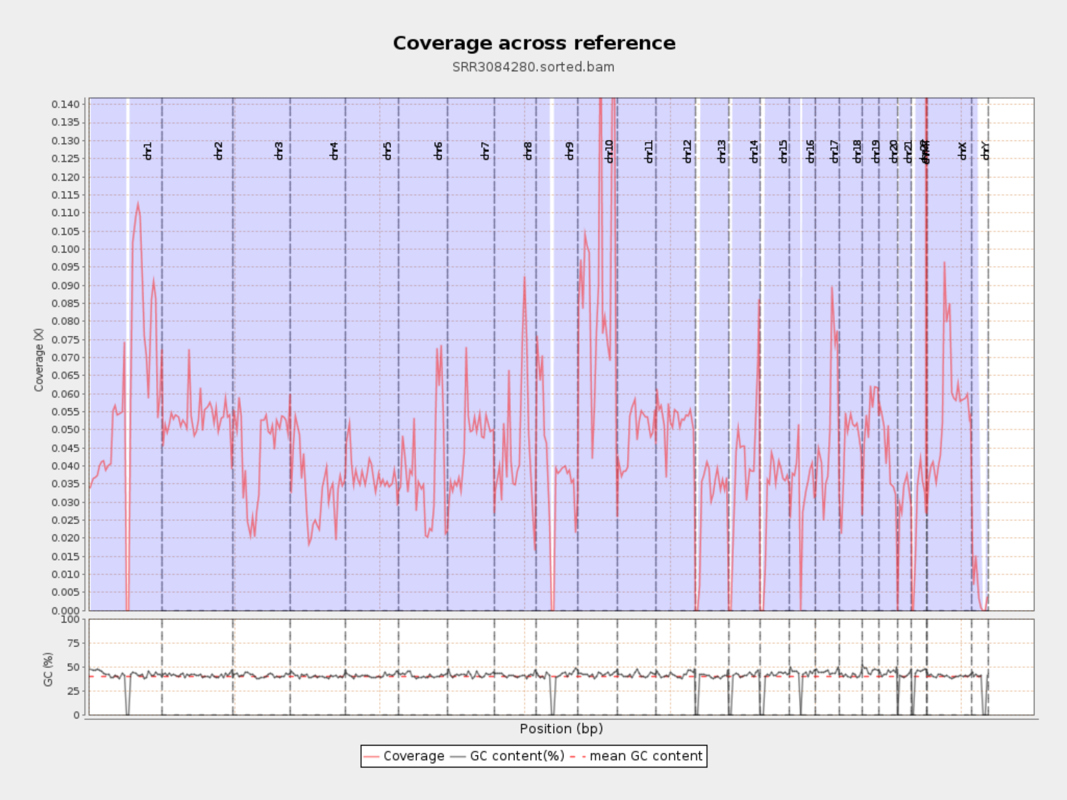
General error rate	1.05%
Mismatches	1,464,239
Insertions	10,963
Mapped reads with at least one insertion	0.51%
Deletions	31,676
Mapped reads with at least one deletion	1.46%
Homopolymer indels	45.55%

2.6. Chromosome stats

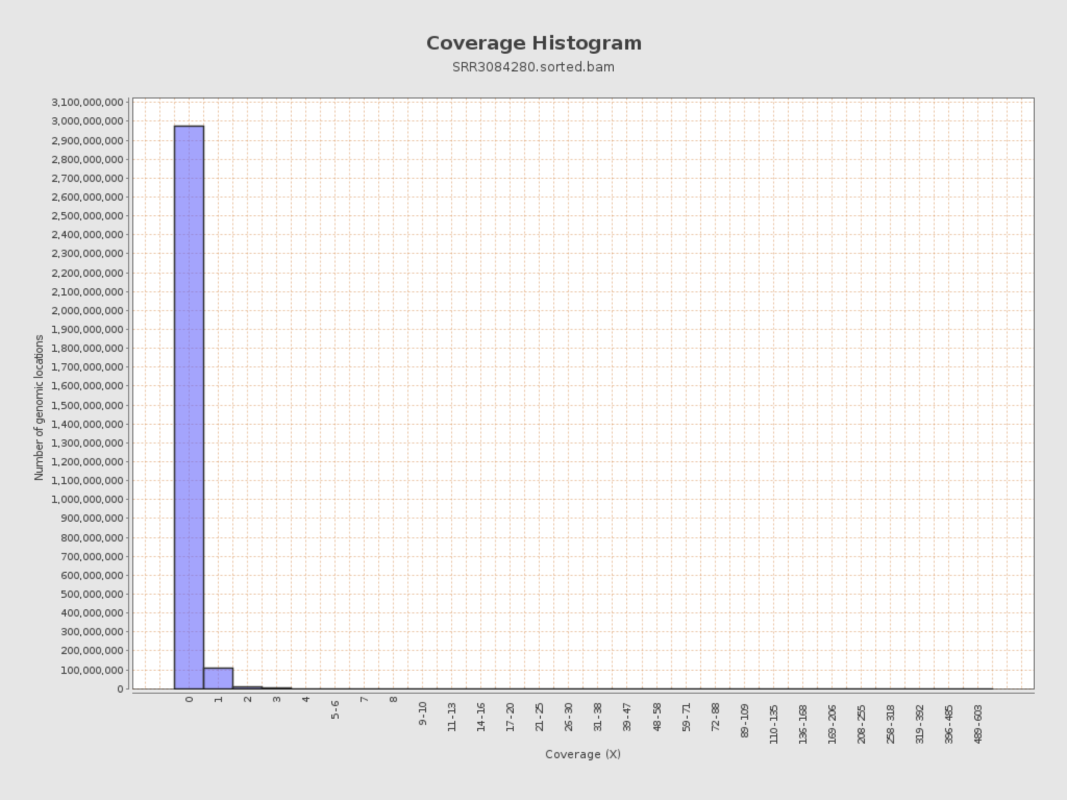
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14844748	0.0596	0.5934
chr2	243199373	12987389	0.0534	0.3941
chr3	198022430	8792449	0.0444	0.2442
chr4	191154276	6438478	0.0337	0.214
chr5	180915260	6819076	0.0377	0.2153
chr6	171115067	6583928	0.0385	0.251
chr7	159138663	7367840	0.0463	0.4363

chr8	146364022	6639234	0.0454	0.3169
chr9	141213431	5443114	0.0385	0.2731
chr10	135534747	12589747	0.0929	0.5305
chr11	135006516	6550407	0.0485	0.3237
chr12	133851895	7038386	0.0526	0.2574
chr13	115169878	3433681	0.0298	0.193
chr14	107349540	4106988	0.0383	0.2243
chr15	102531392	3151357	0.0307	0.1994
chr16	90354753	3036441	0.0336	0.2286
chr17	81195210	4163602	0.0513	0.2669
chr18	78077248	3558962	0.0456	0.4725
chr19	59128983	3208989	0.0543	0.4241
chr20	63025520	2692773	0.0427	0.2333
chr21	48129895	1396066	0.029	0.199
chr22	51304566	1284057	0.025	0.1753
chrMT	16571	120510	7.2723	4.9725
chrX	155270560	8622387	0.0555	0.2992
chrY	59373566	318422	0.0054	0.1134

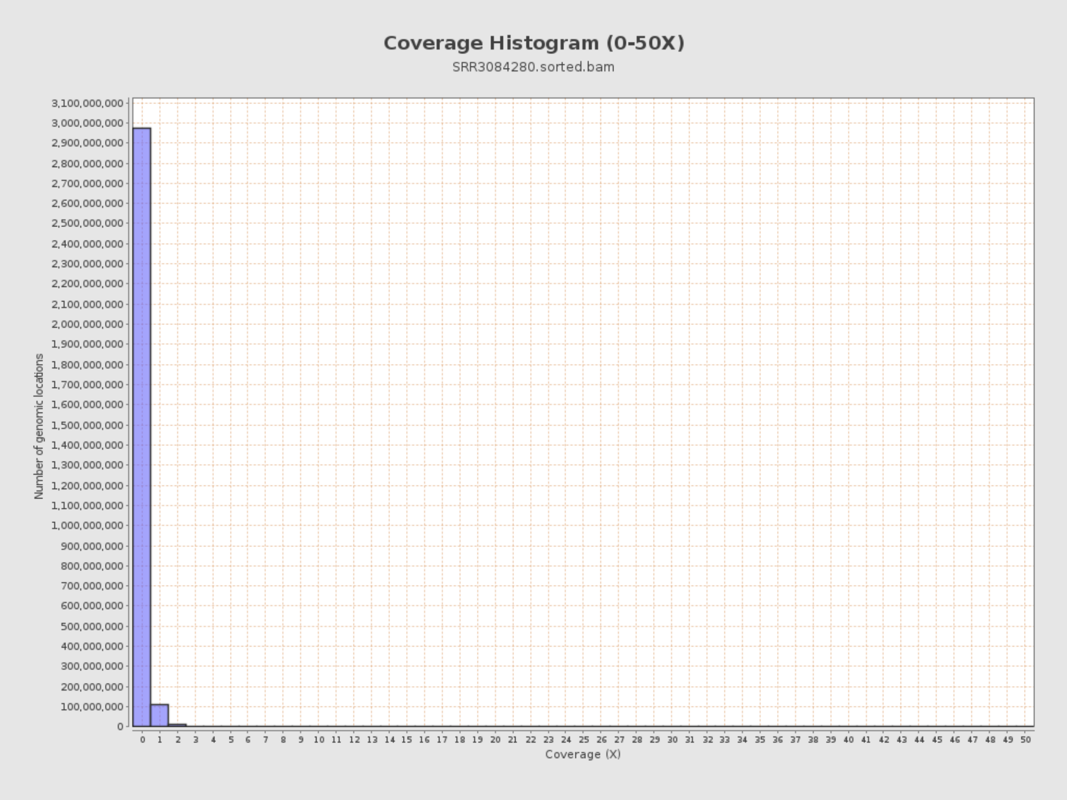
3. Results : Coverage across reference



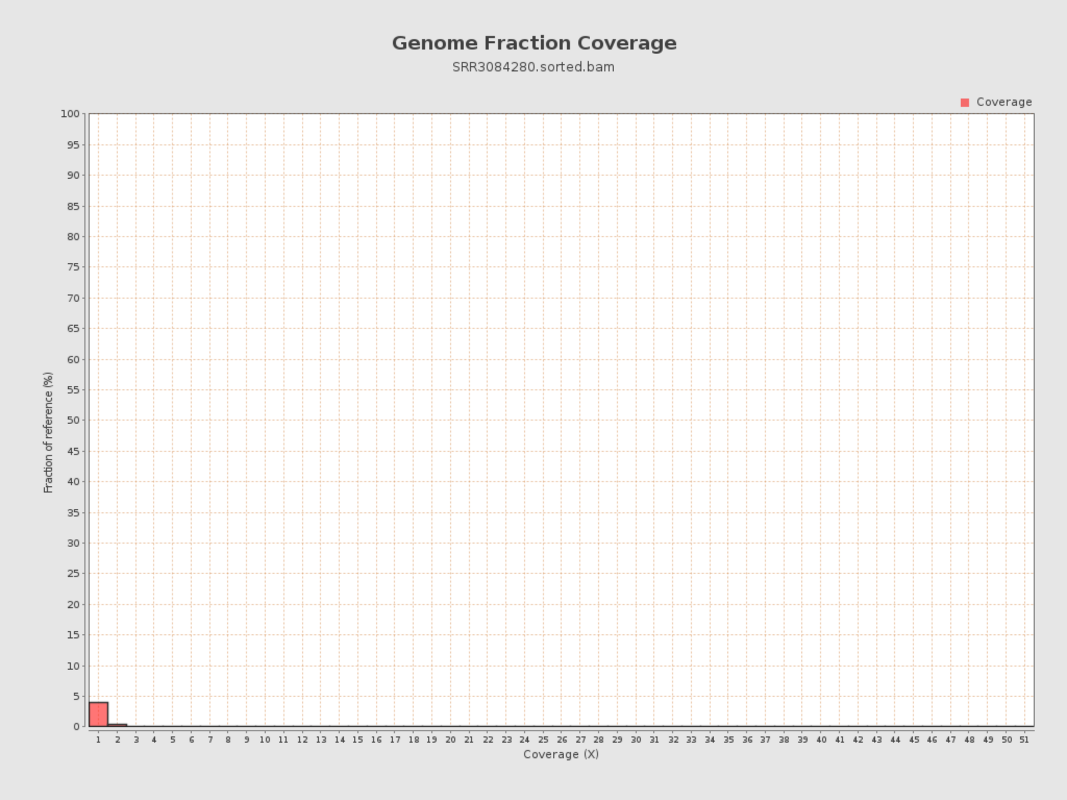
4. Results : Coverage Histogram



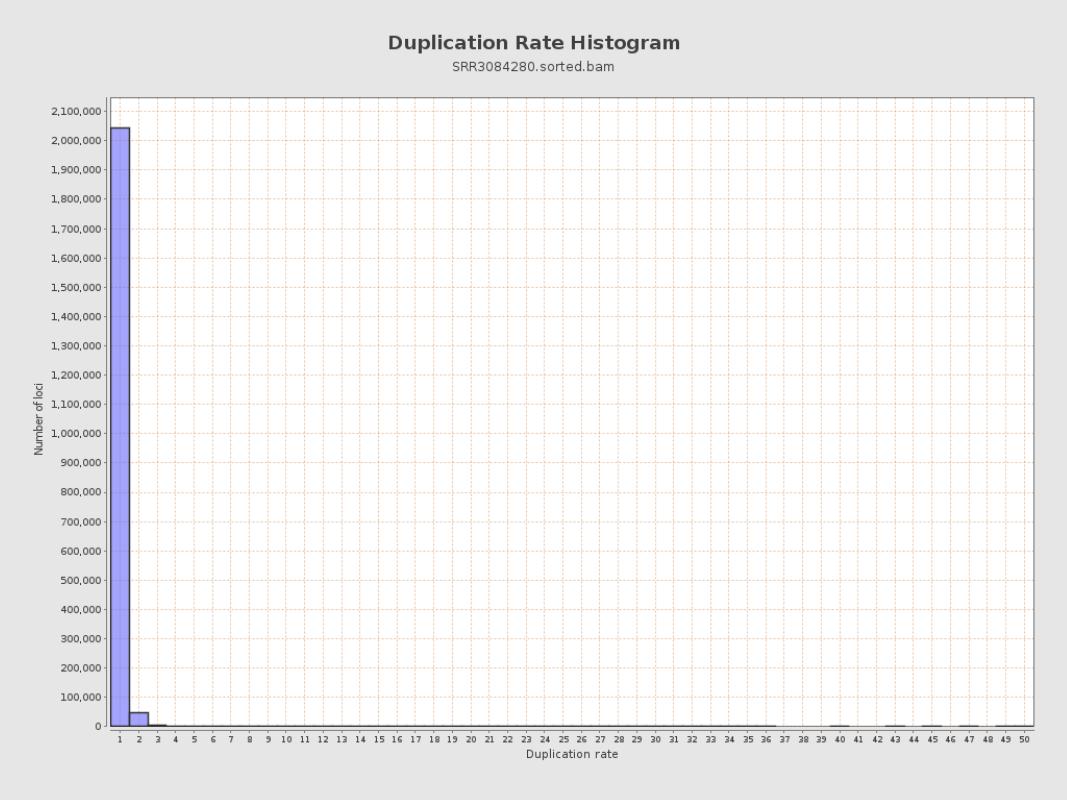
5. Results : Coverage Histogram (0-50X)



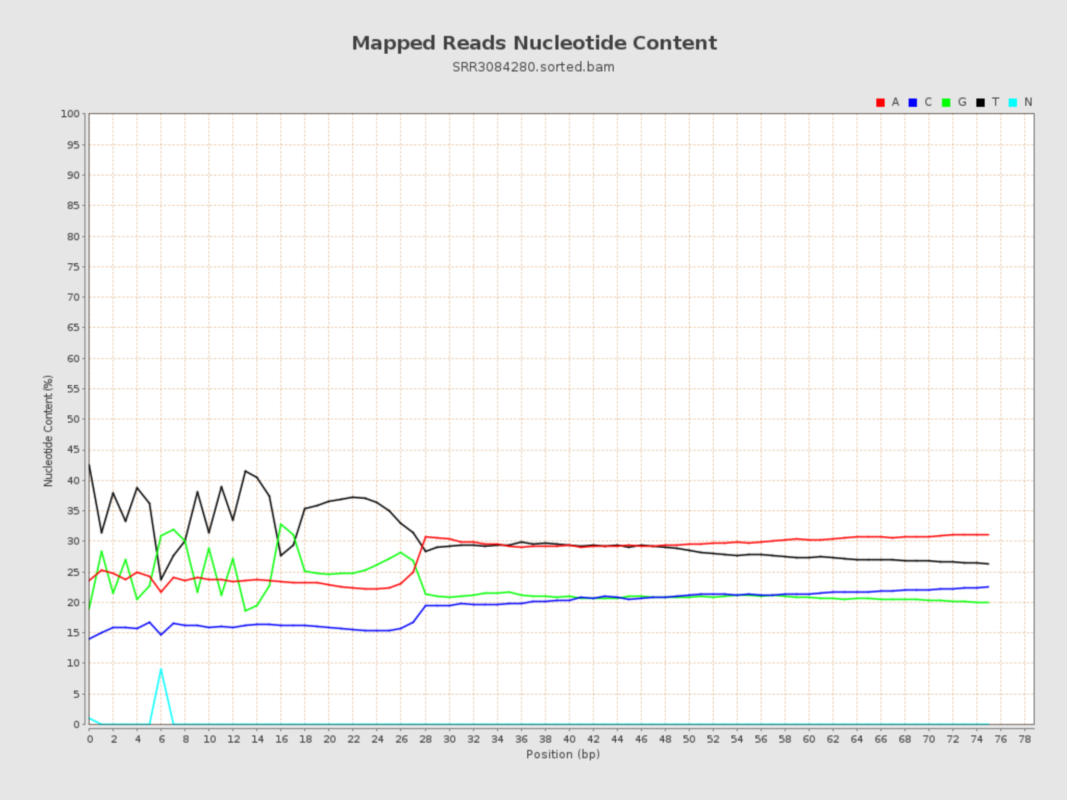
6. Results : Genome Fraction Coverage



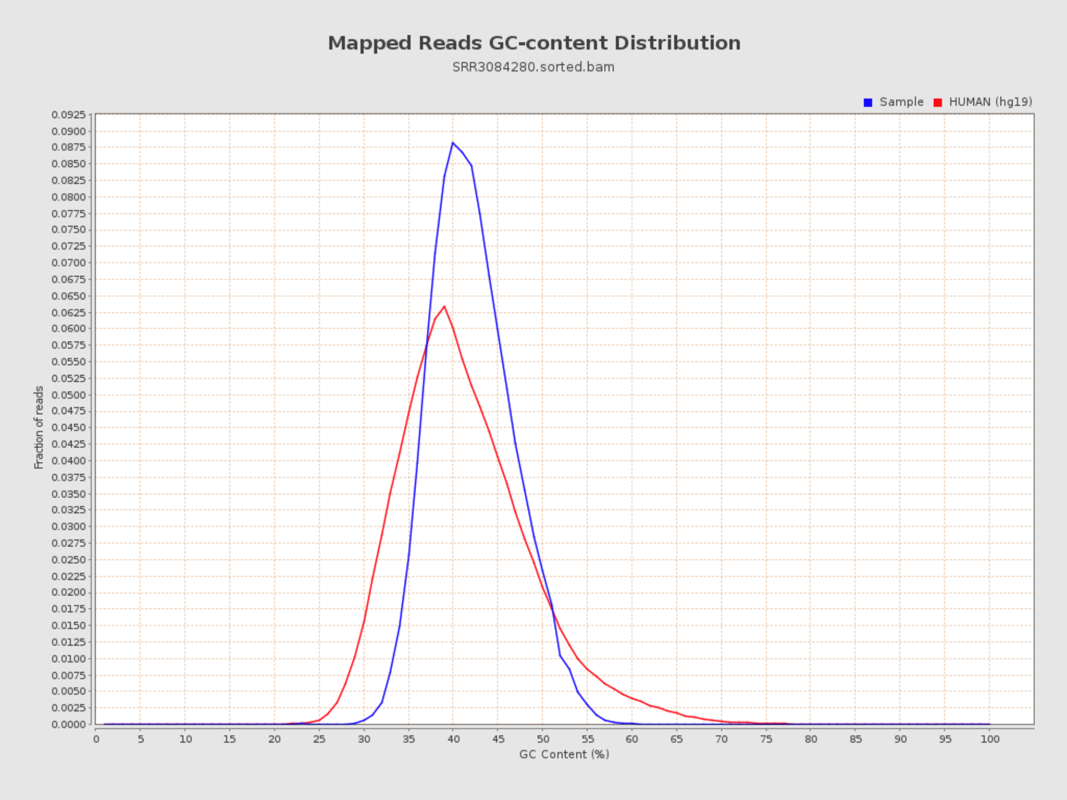
7. Results : Duplication Rate Histogram



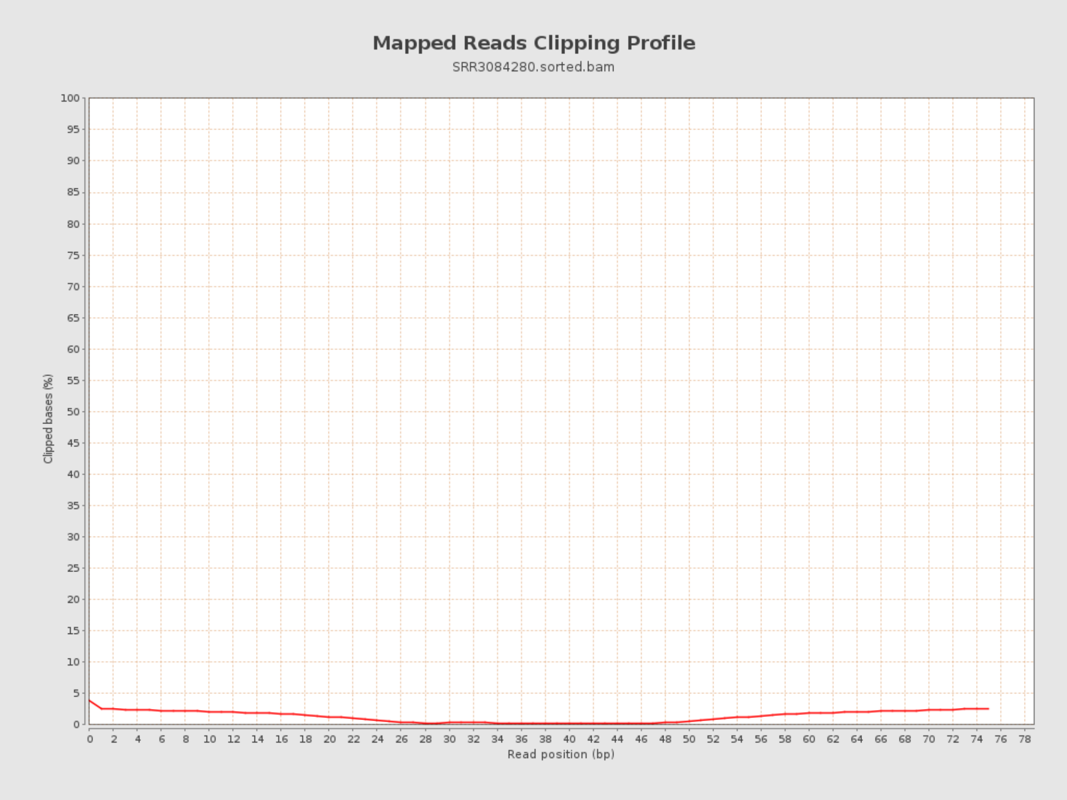
8. Results : Mapped Reads Nucleotide Content



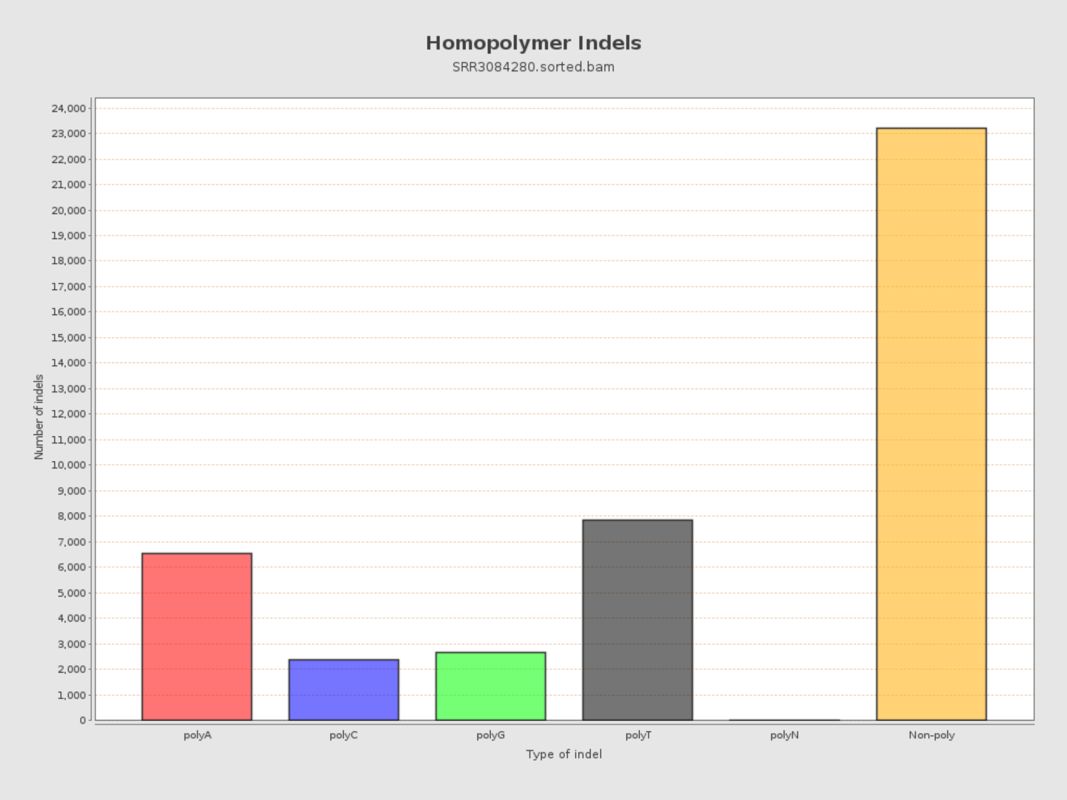
9. Results : Mapped Reads GC-content Distribution



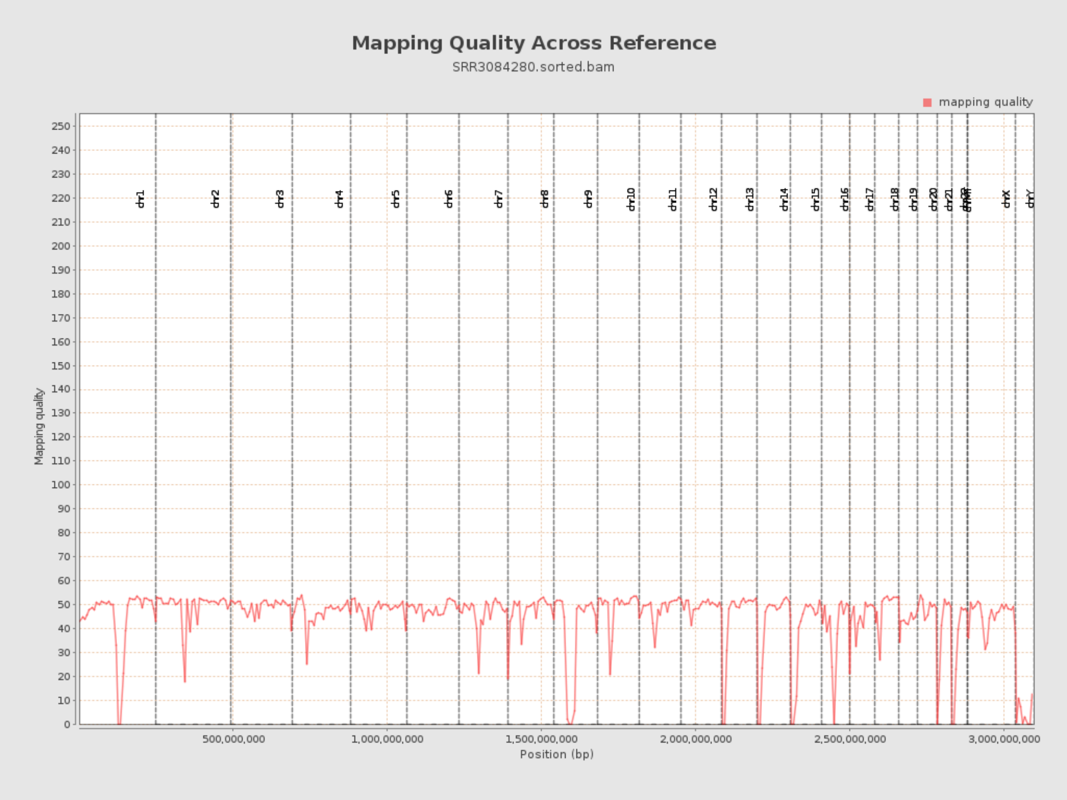
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram