Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:00:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525205.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_SRR10525205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:00:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,559,966
Mapped reads	3,286,063 / 92.31%
Unmapped reads	273,903 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,947 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	190,672 / 5.36%
Duplication rate	4.23%
Clipped reads	3,293,459 / 92.51%

2.2. ACGT Content

Number/percentage of A's	48,964,555 / 25.63%
Number/percentage of C's	35,128,246 / 18.39%
Number/percentage of T's	58,562,357 / 30.66%
Number/percentage of G's	48,359,713 / 25.32%
Number/percentage of N's	4,372 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0617

Standard Deviation	0.5384

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

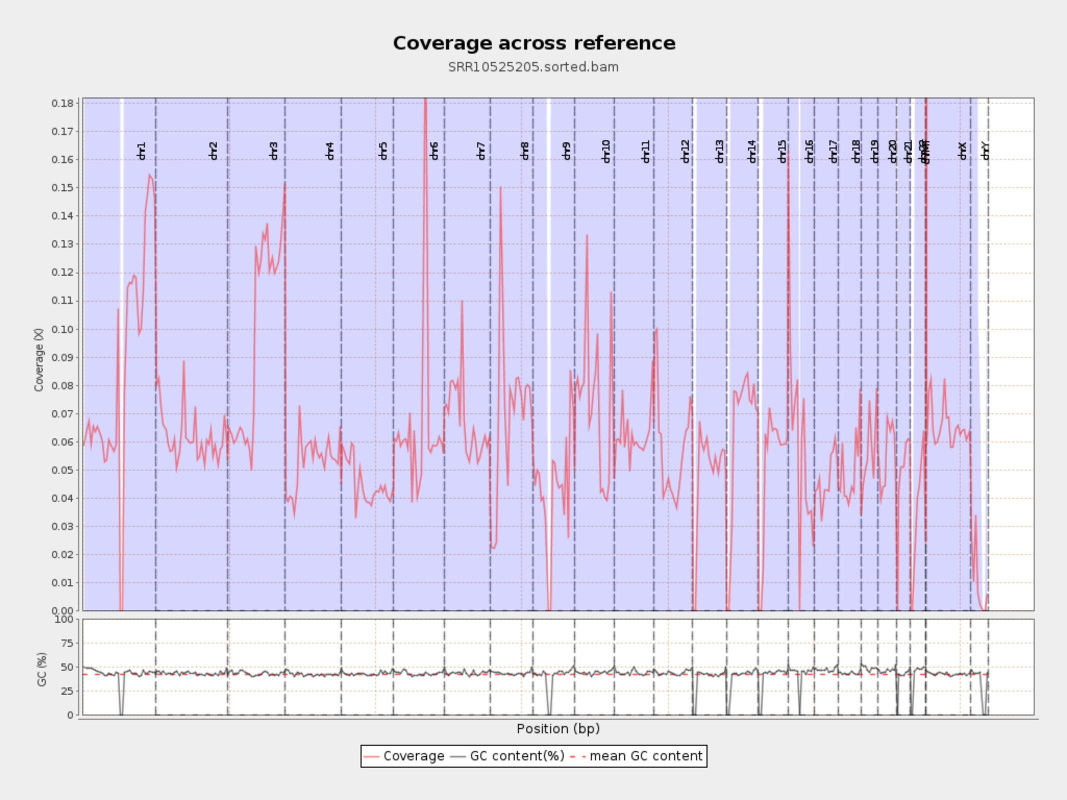
General error rate	0.52%
Mismatches	971,498
Insertions	11,995
Mapped reads with at least one insertion	0.36%
Deletions	39,318
Mapped reads with at least one deletion	1.19%
Homopolymer indels	43.33%

2.6. Chromosome stats

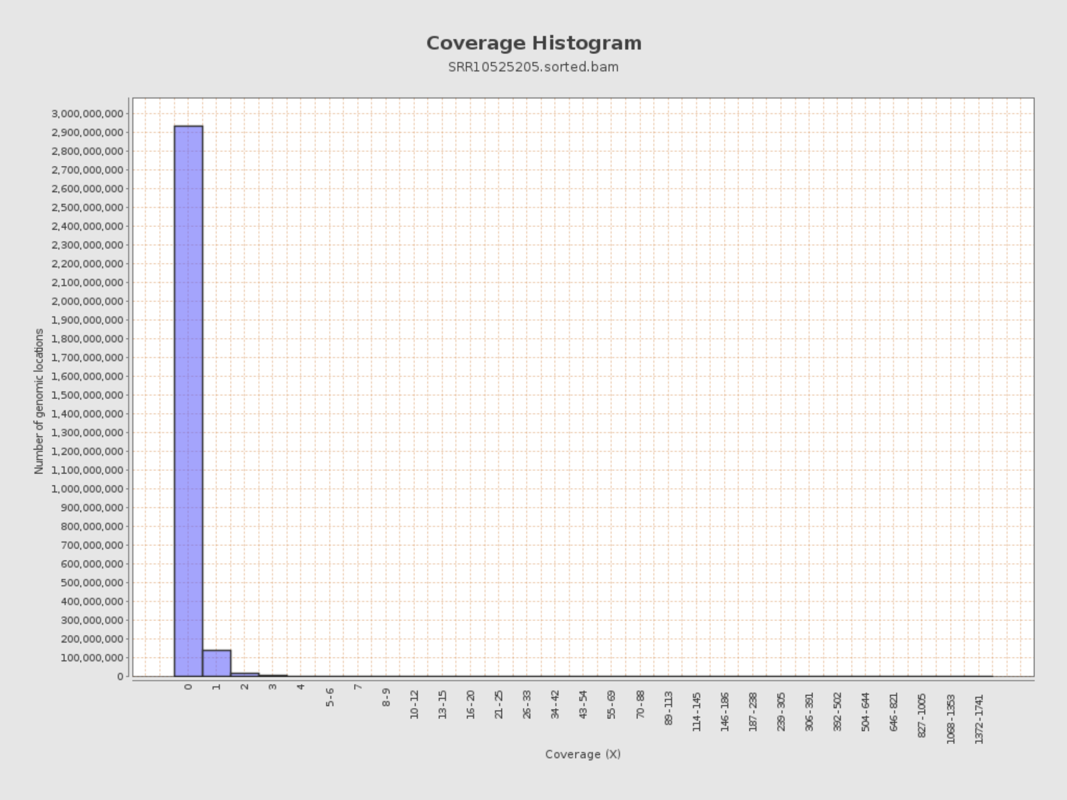
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21328706	0.0856	1.0789
chr2	243199373	15087524	0.062	0.7599
chr3	198022430	18964813	0.0958	0.3652
chr4	191154276	10177702	0.0532	0.3078
chr5	180915260	8157387	0.0451	0.25
chr6	171115067	11422734	0.0668	0.3543
chr7	159138663	10762316	0.0676	0.7817

chr8	146364022	10468105	0.0715	0.5192
chr9	141213431	6082177	0.0431	0.36
chr10	135534747	9936609	0.0733	0.5619
chr11	135006516	8392742	0.0622	0.4184
chr12	133851895	7718824	0.0577	0.2903
chr13	115169878	5579261	0.0484	0.2632
chr14	107349540	6884125	0.0641	0.3062
chr15	102531392	5124689	0.05	0.2691
chr16	90354753	5289294	0.0585	0.3258
chr17	81195210	3811263	0.0469	0.2692
chr18	78077248	3845513	0.0493	0.7266
chr19	59128983	3371733	0.057	0.7023
chr20	63025520	3474392	0.0551	0.2813
chr21	48129895	2342282	0.0487	0.3006
chr22	51304566	1743633	0.034	0.2163
chrMT	16571	358360	21.6257	12.1282
chrX	155270560	10168454	0.0655	0.3401
chrY	59373566	589438	0.0099	0.2847

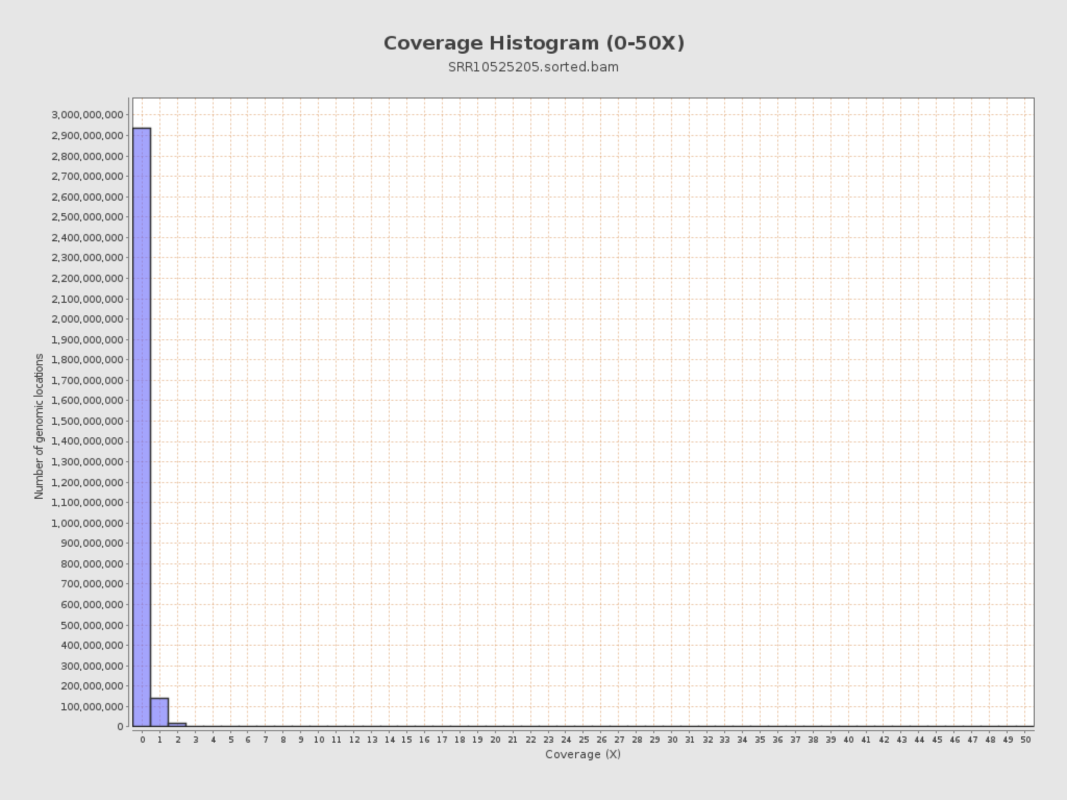
3. Results : Coverage across reference



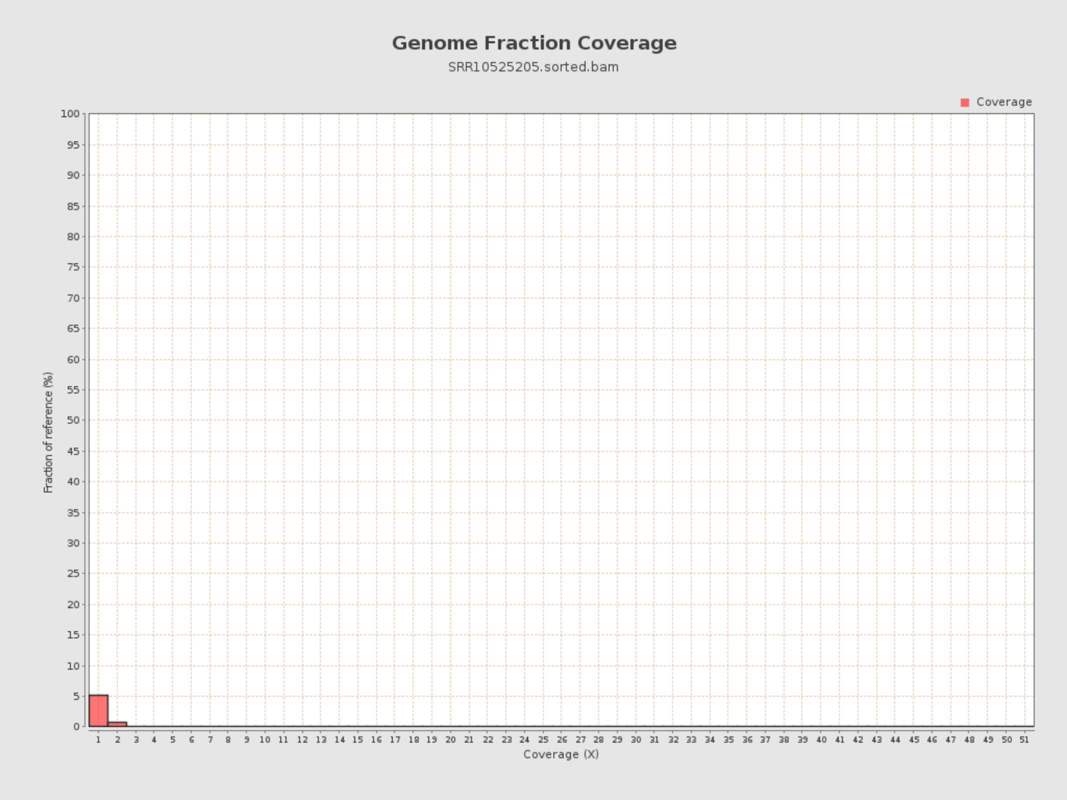
4. Results : Coverage Histogram



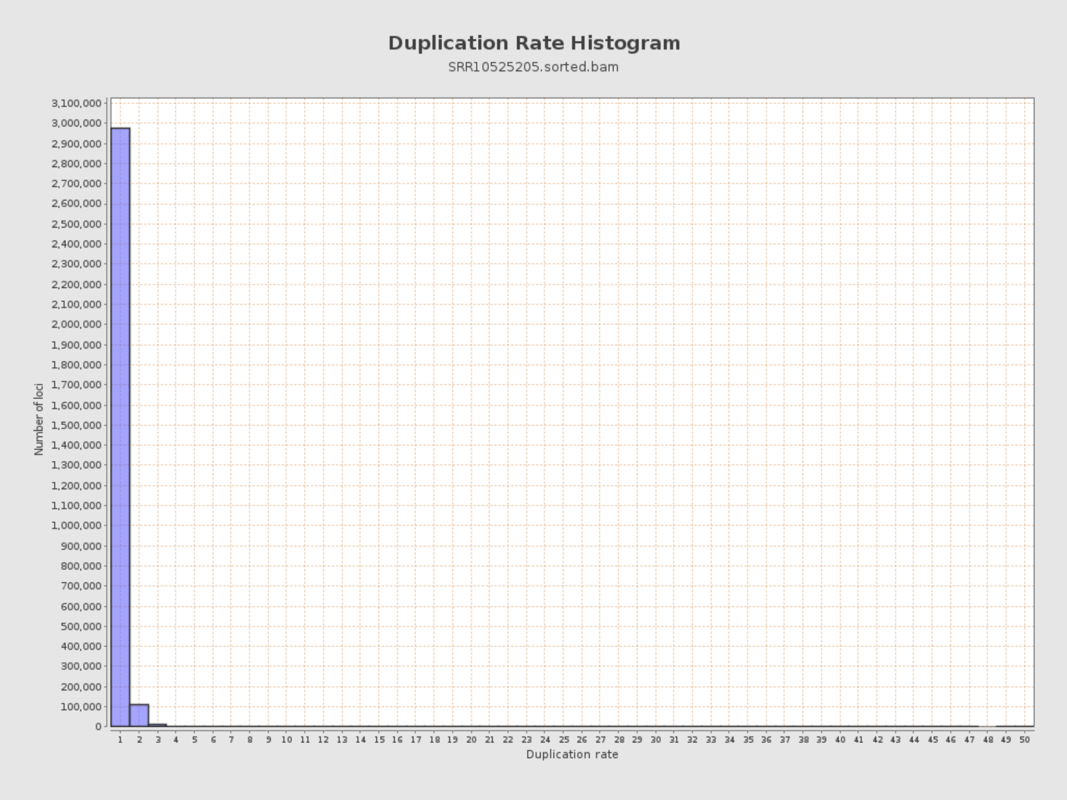
5. Results : Coverage Histogram (0-50X)



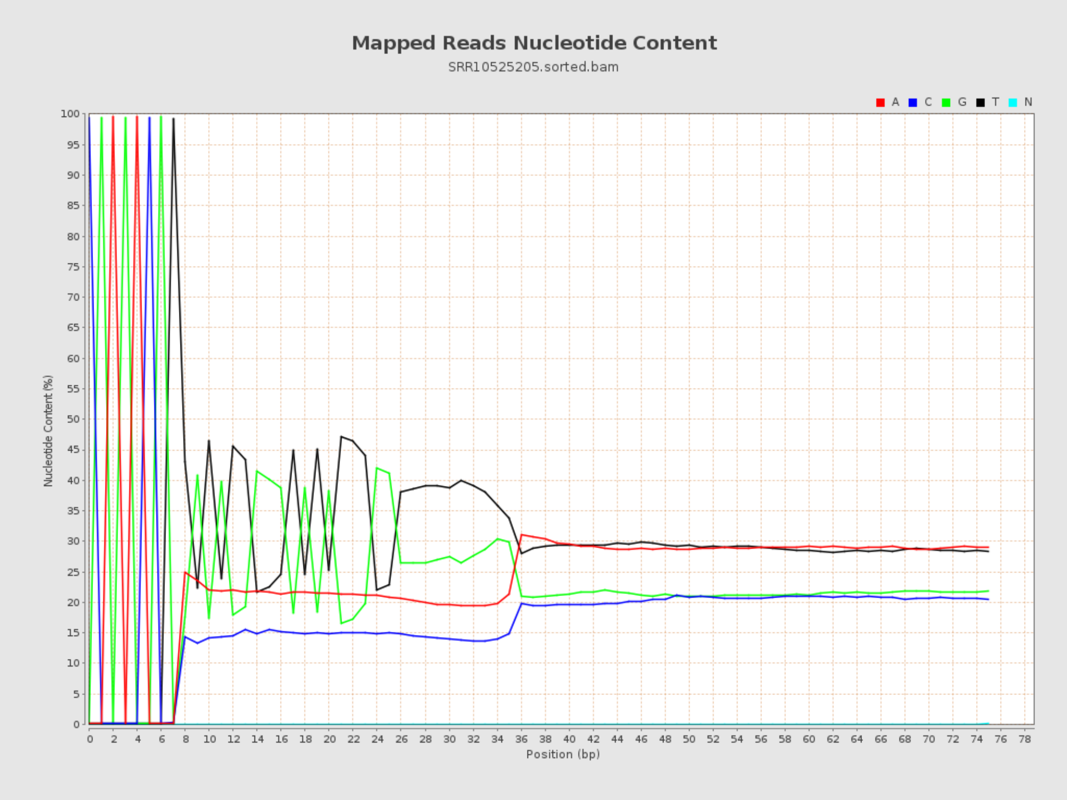
6. Results : Genome Fraction Coverage



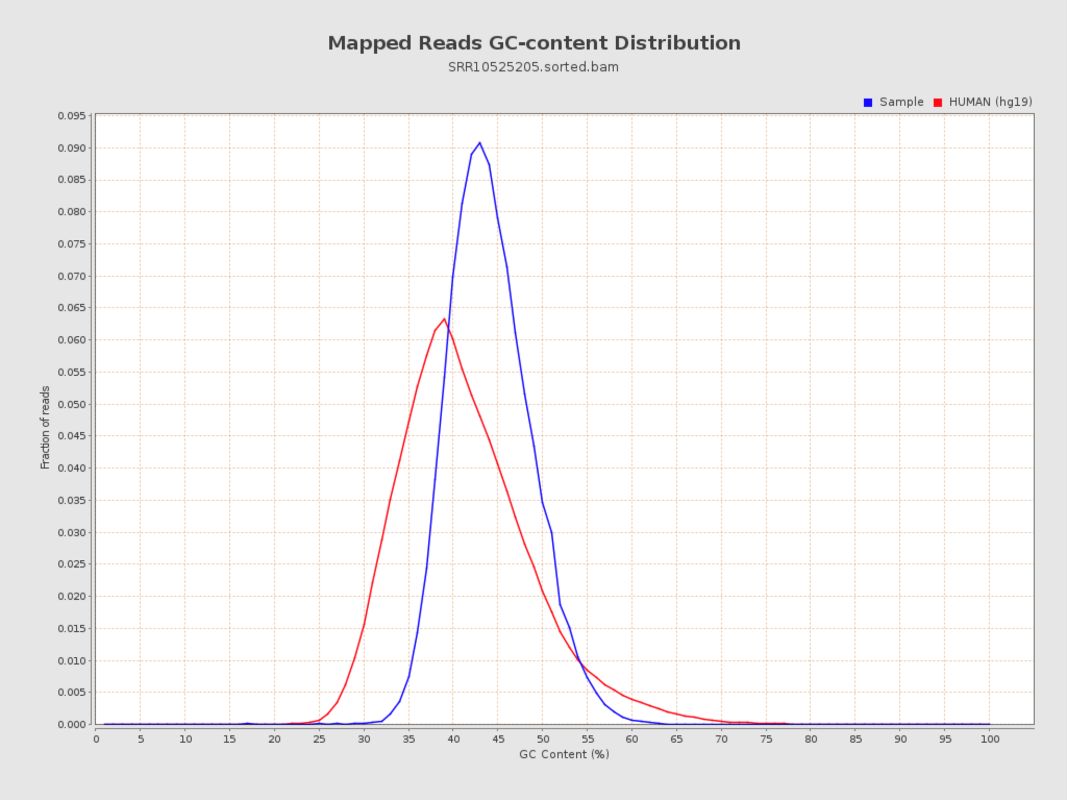
7. Results : Duplication Rate Histogram



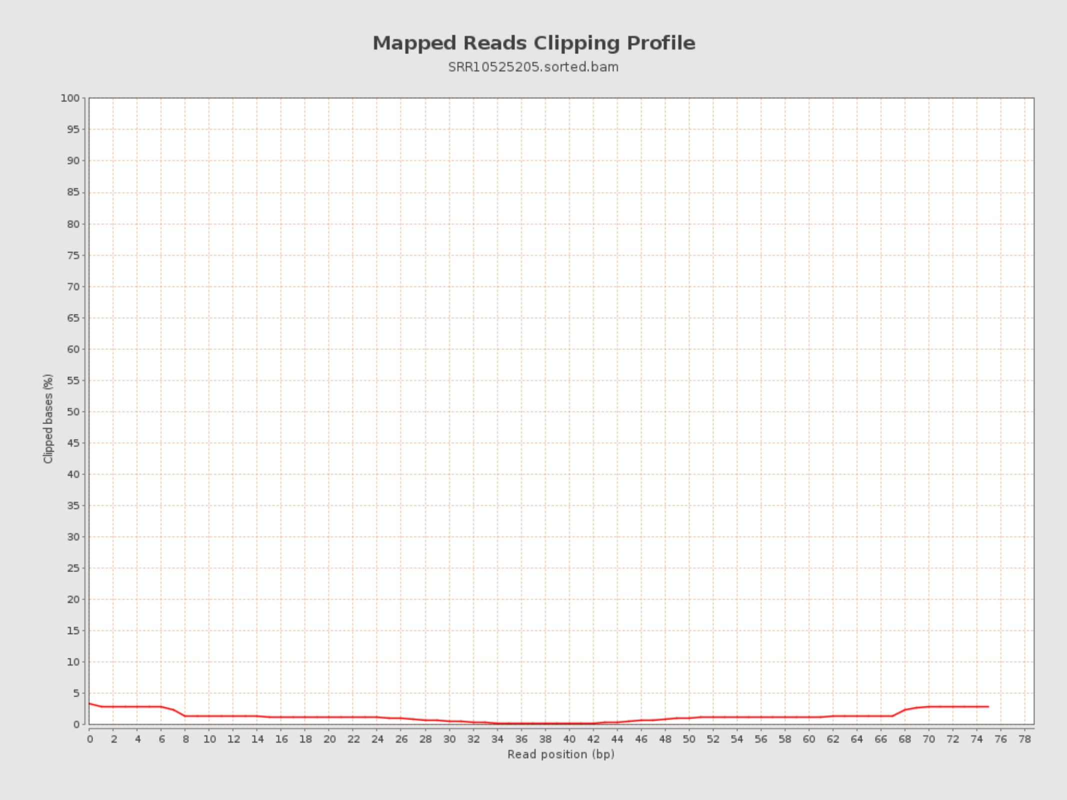
8. Results : Mapped Reads Nucleotide Content



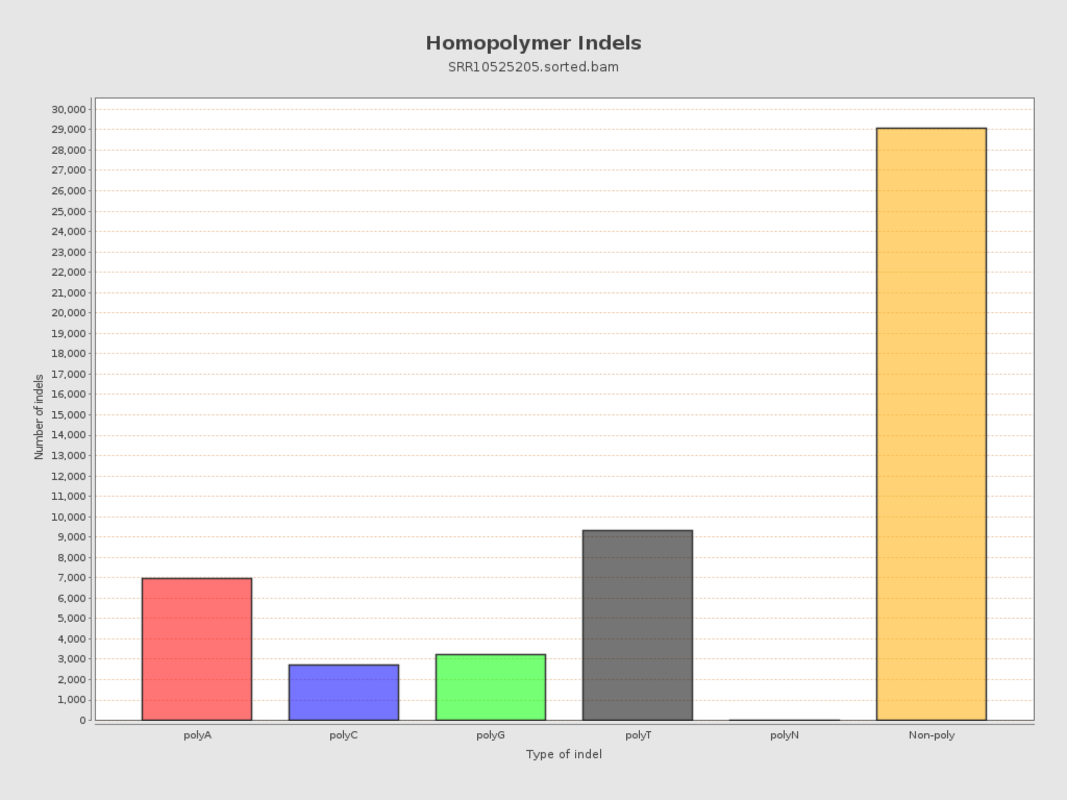
9. Results : Mapped Reads GC-content Distribution



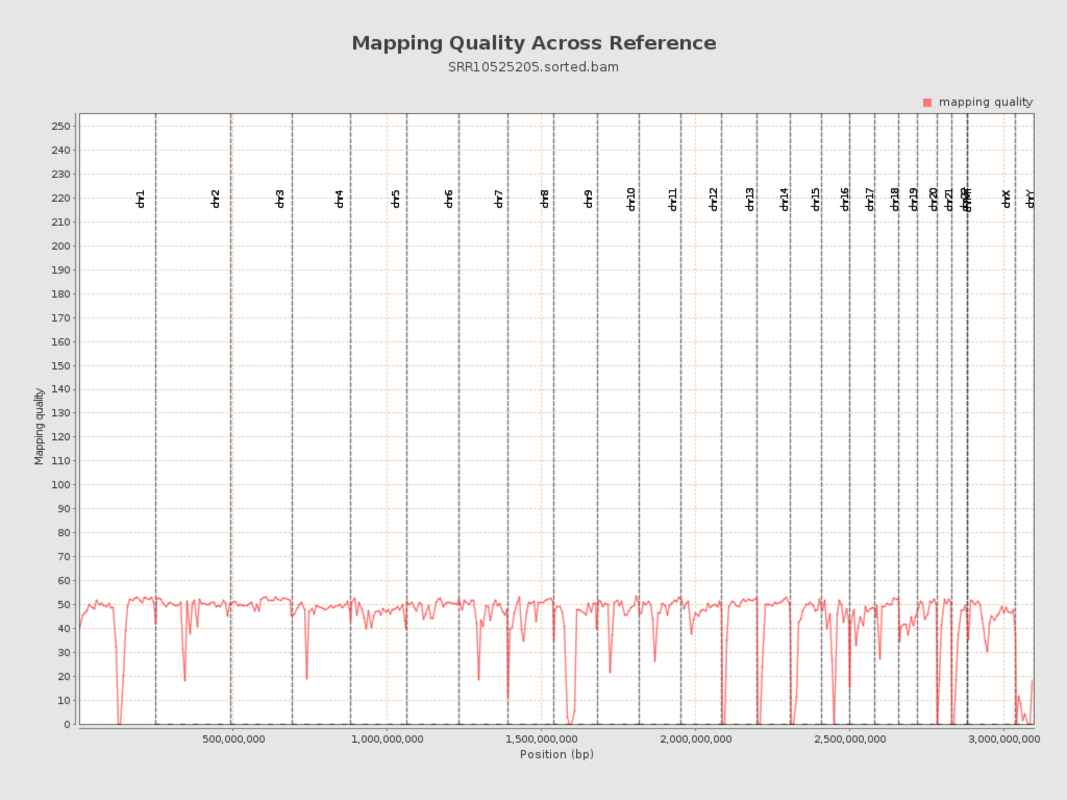
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram