Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/24 14:12:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082420.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_SRR3082420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082420.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:12:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,851,070
Mapped reads	2,540,407 / 89.1%
Unmapped reads	310,663 / 10.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,522 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	106,436 / 3.73%
Duplication rate	3.08%
Clipped reads	1,195,177 / 41.92%

2.2. ACGT Content

Number/percentage of A's	46,399,165 / 27.54%
Number/percentage of C's	31,643,395 / 18.78%
Number/percentage of T's	51,952,792 / 30.83%
Number/percentage of G's	38,499,671 / 22.85%
Number/percentage of N's	3,398 / 0%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.4706

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

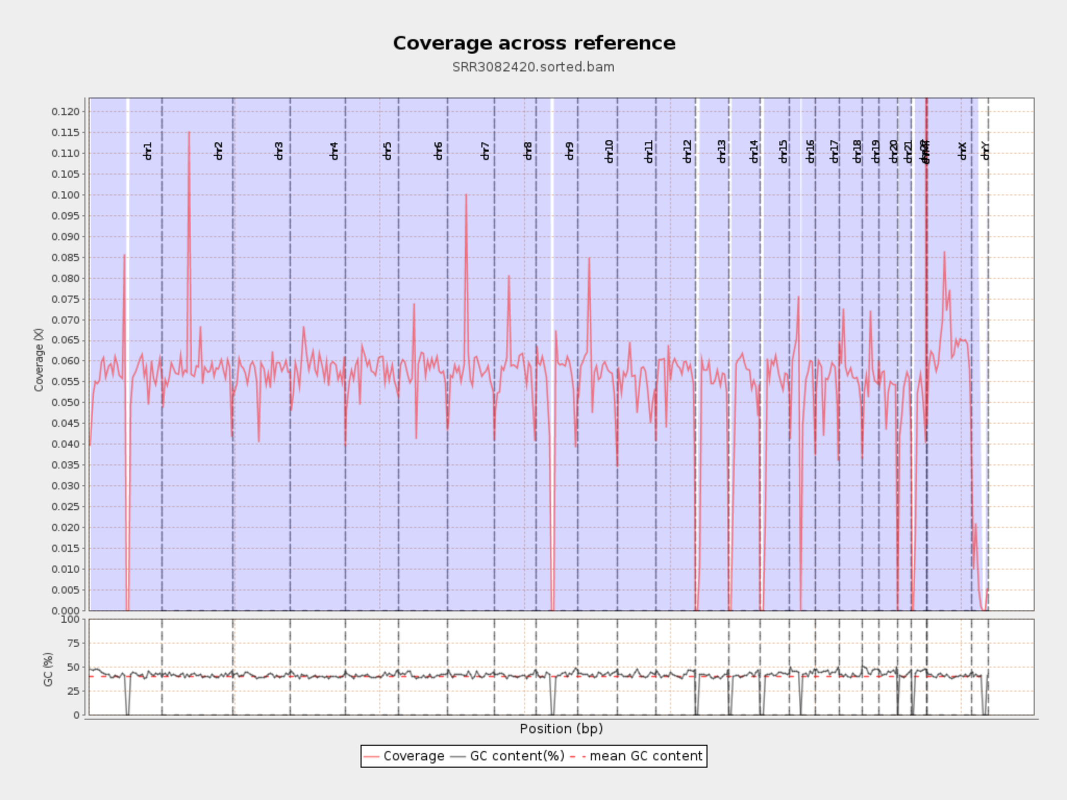
General error rate	0.85%
Mismatches	1,407,662
Insertions	13,636
Mapped reads with at least one insertion	0.53%
Deletions	37,495
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.07%

2.6. Chromosome stats

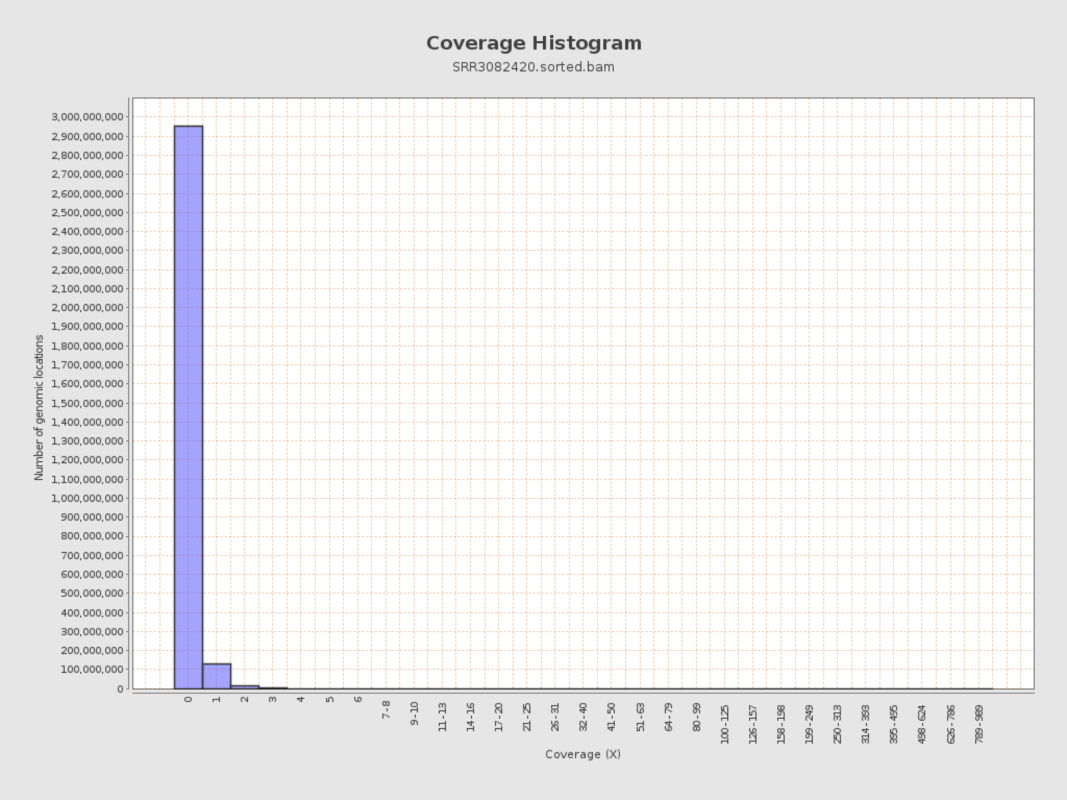
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13441131	0.0539	0.7612
chr2	243199373	14432884	0.0593	0.6842
chr3	198022430	11264203	0.0569	0.269
chr4	191154276	11127614	0.0582	0.2899
chr5	180915260	10376863	0.0574	0.2728
chr6	171115067	9917326	0.058	0.3369
chr7	159138663	9424797	0.0592	0.6925

chr8	146364022	8411168	0.0575	0.6035
chr9	141213431	7166668	0.0508	0.4575
chr10	135534747	7872320	0.0581	0.4135
chr11	135006516	7382187	0.0547	0.4071
chr12	133851895	7703503	0.0576	0.2789
chr13	115169878	5399442	0.0469	0.2433
chr14	107349540	5101658	0.0475	0.2811
chr15	102531392	4769350	0.0465	0.2565
chr16	90354753	4762714	0.0527	0.3028
chr17	81195210	4390119	0.0541	0.2926
chr18	78077248	4556385	0.0584	0.8733
chr19	59128983	3332423	0.0564	0.6137
chr20	63025520	3310268	0.0525	0.2712
chr21	48129895	2183152	0.0454	0.2601
chr22	51304566	1813892	0.0354	0.2113
chrMT	16571	10869	0.6559	0.9982
chrX	155270560	9966730	0.0642	0.3383
chrY	59373566	441983	0.0074	0.1583

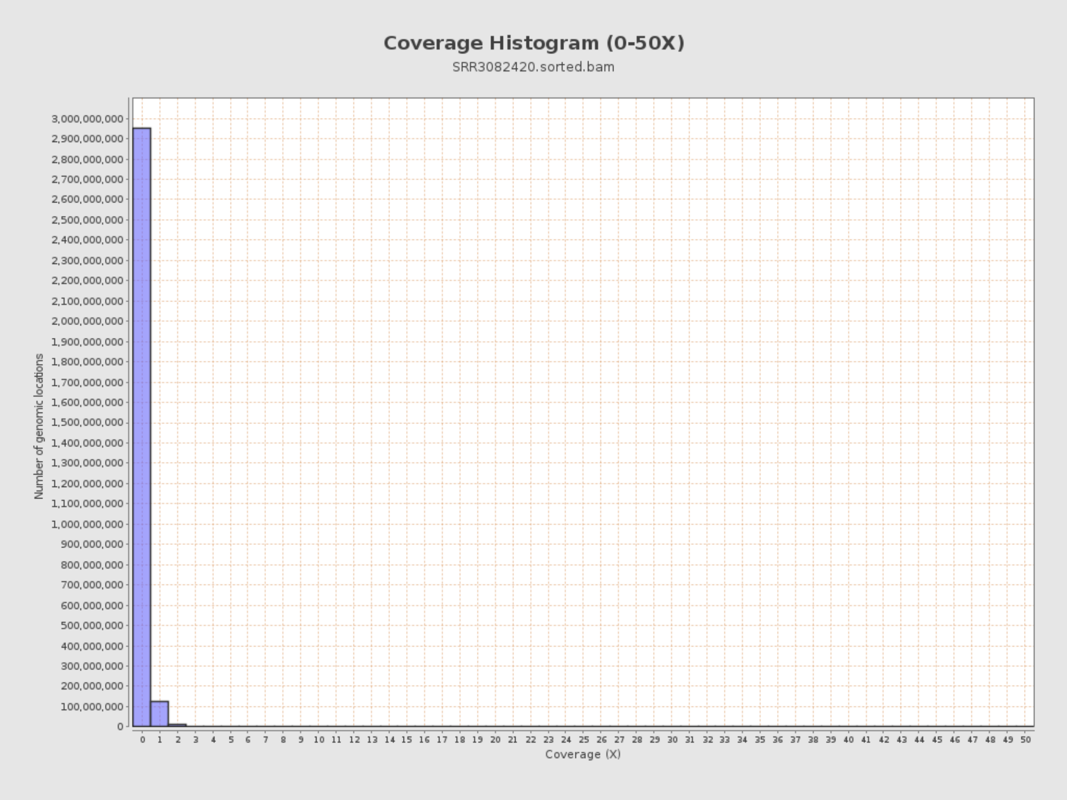
3. Results : Coverage across reference



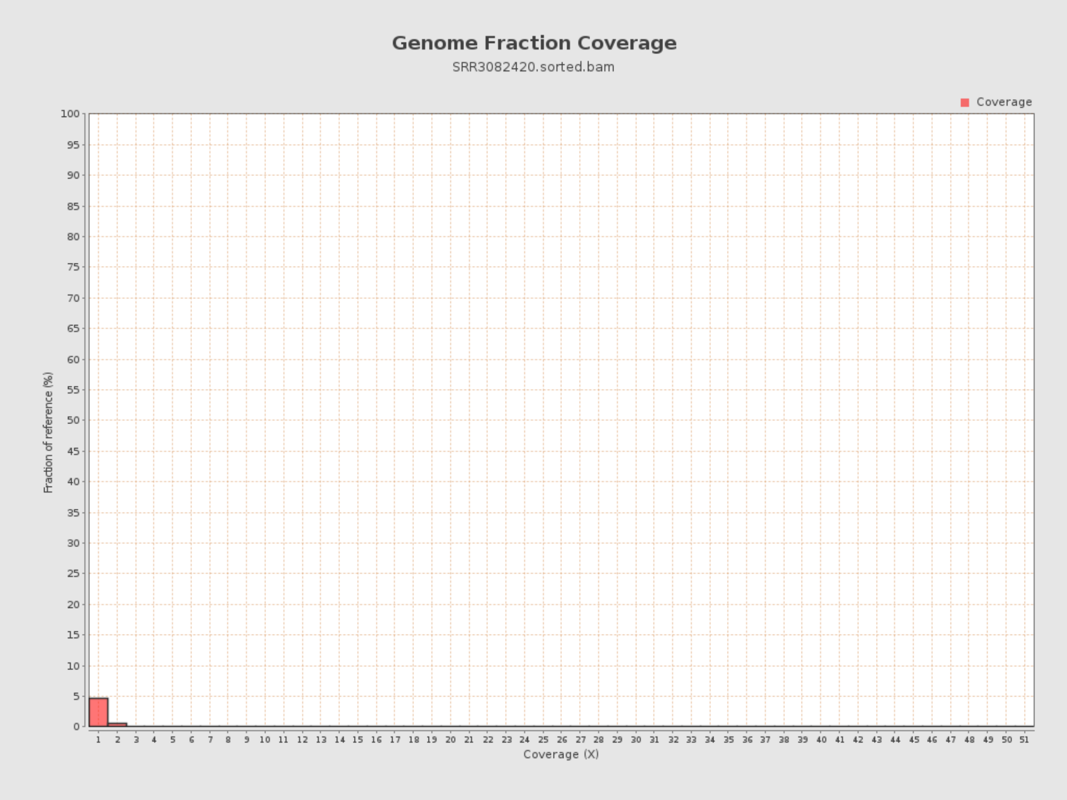
4. Results : Coverage Histogram



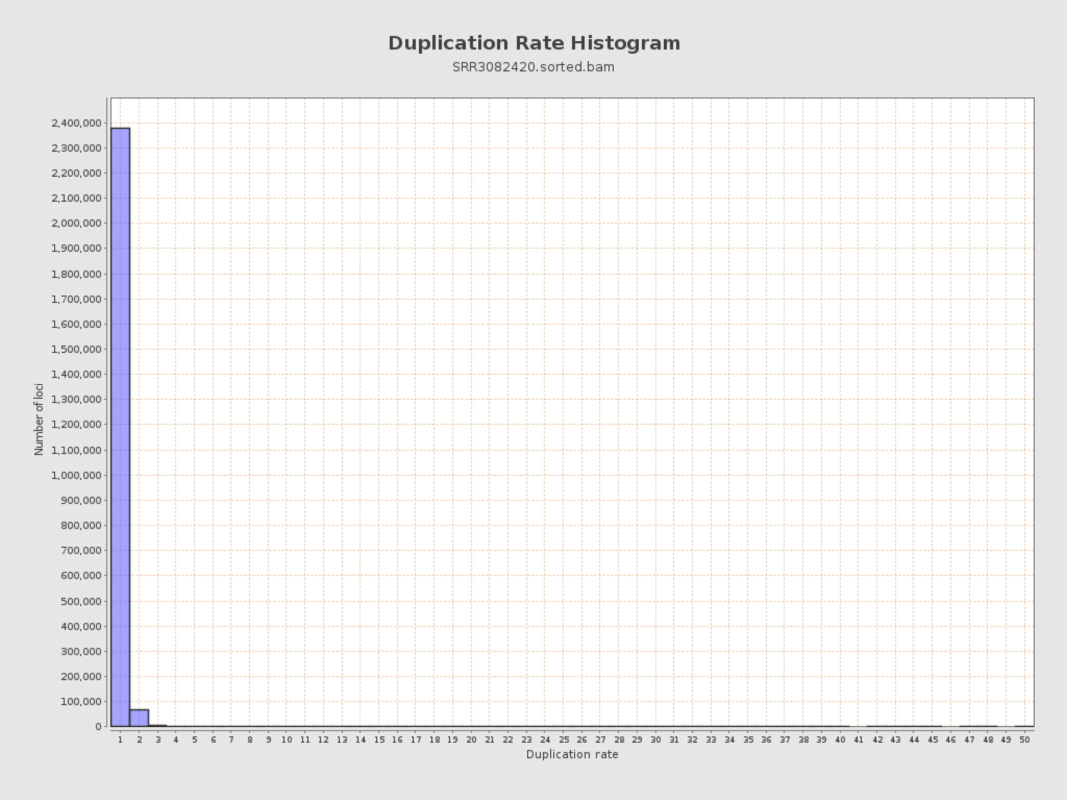
5. Results : Coverage Histogram (0-50X)



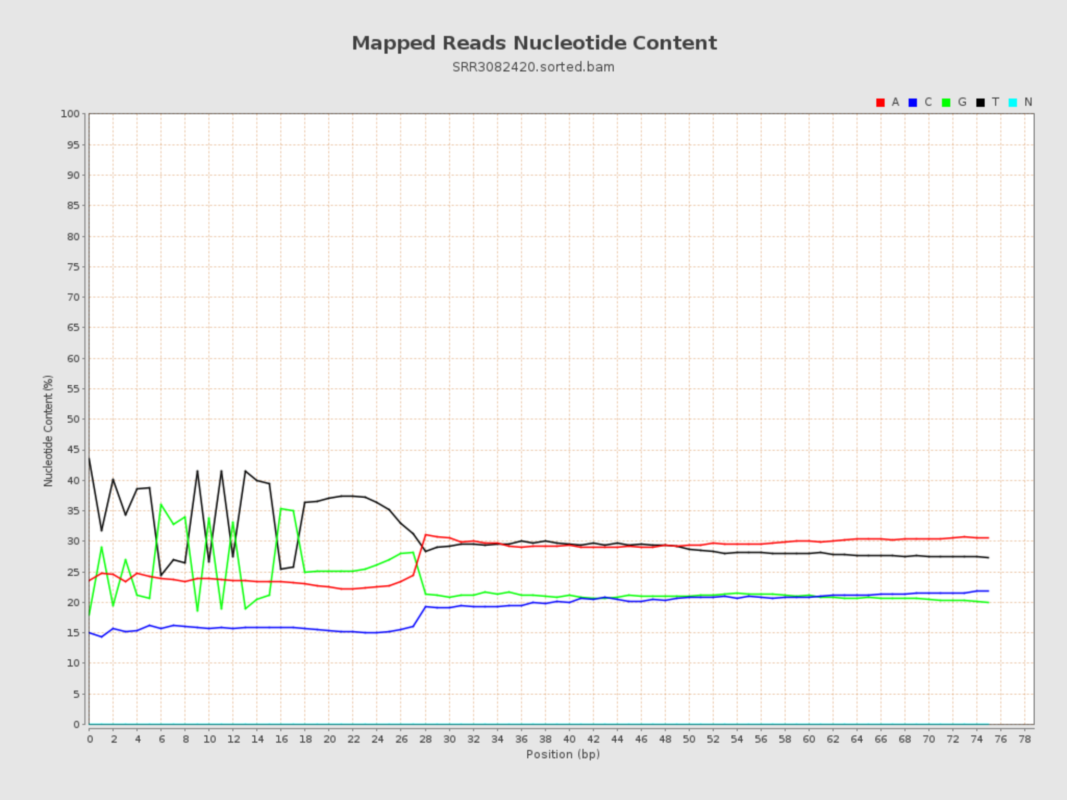
6. Results : Genome Fraction Coverage



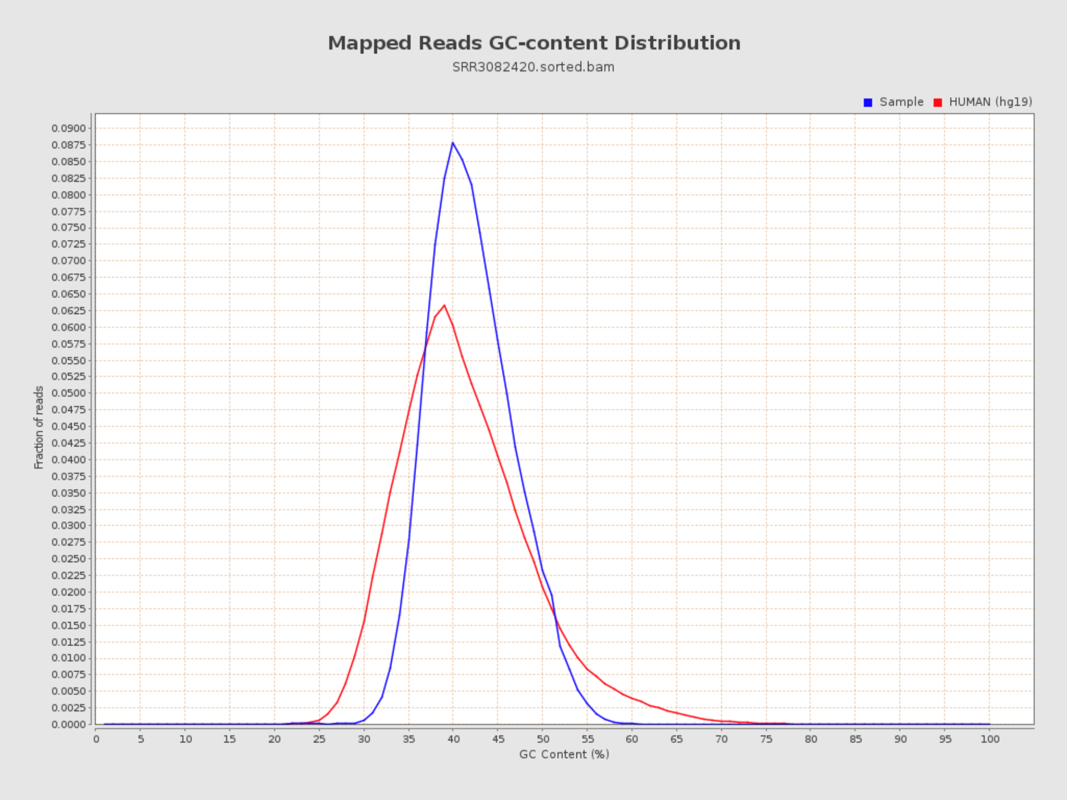
7. Results : Duplication Rate Histogram



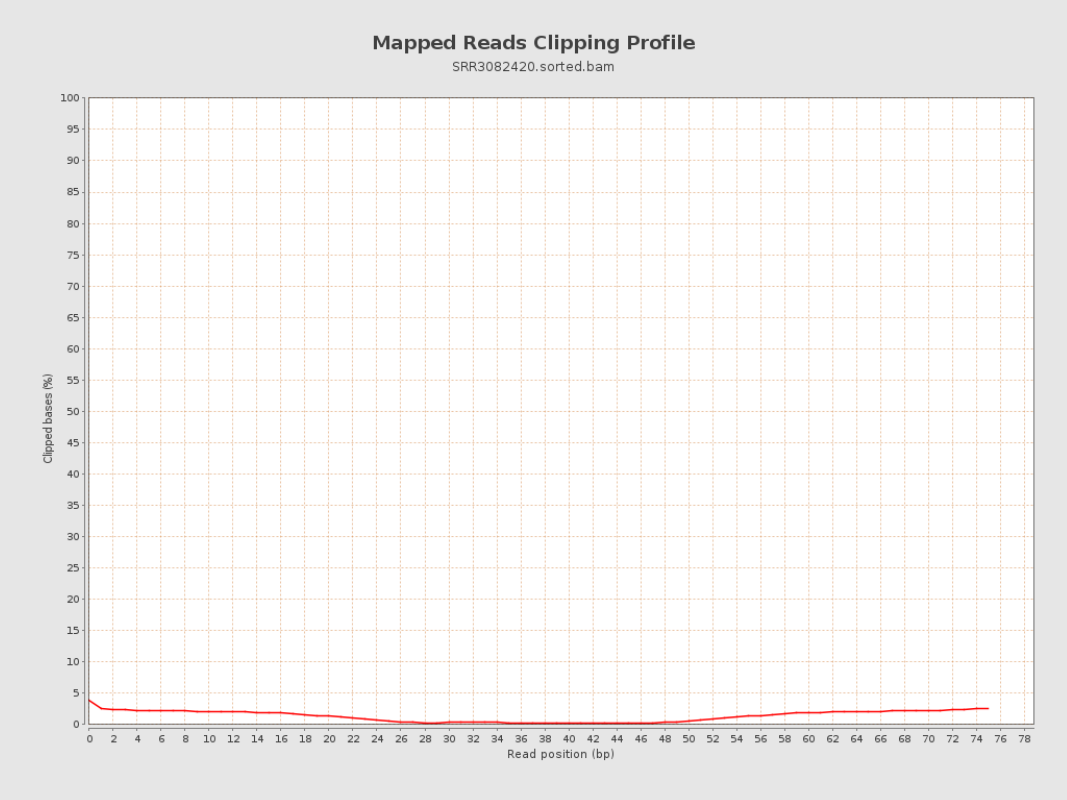
8. Results : Mapped Reads Nucleotide Content



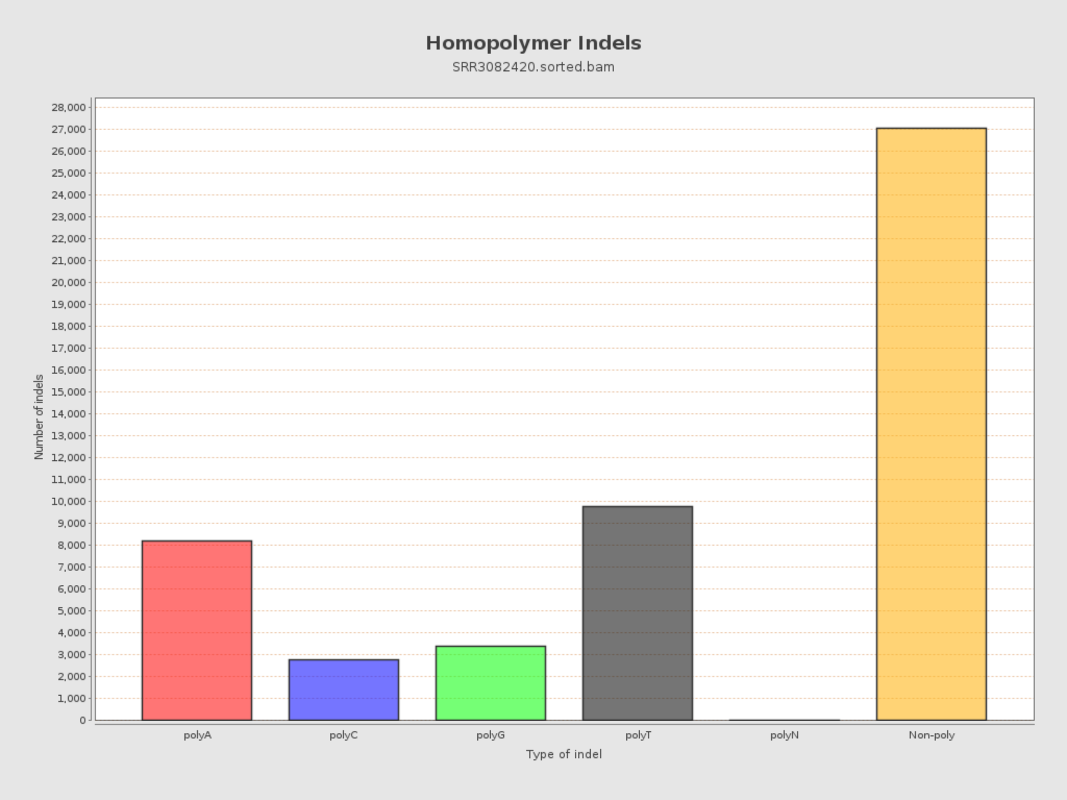
9. Results : Mapped Reads GC-content Distribution



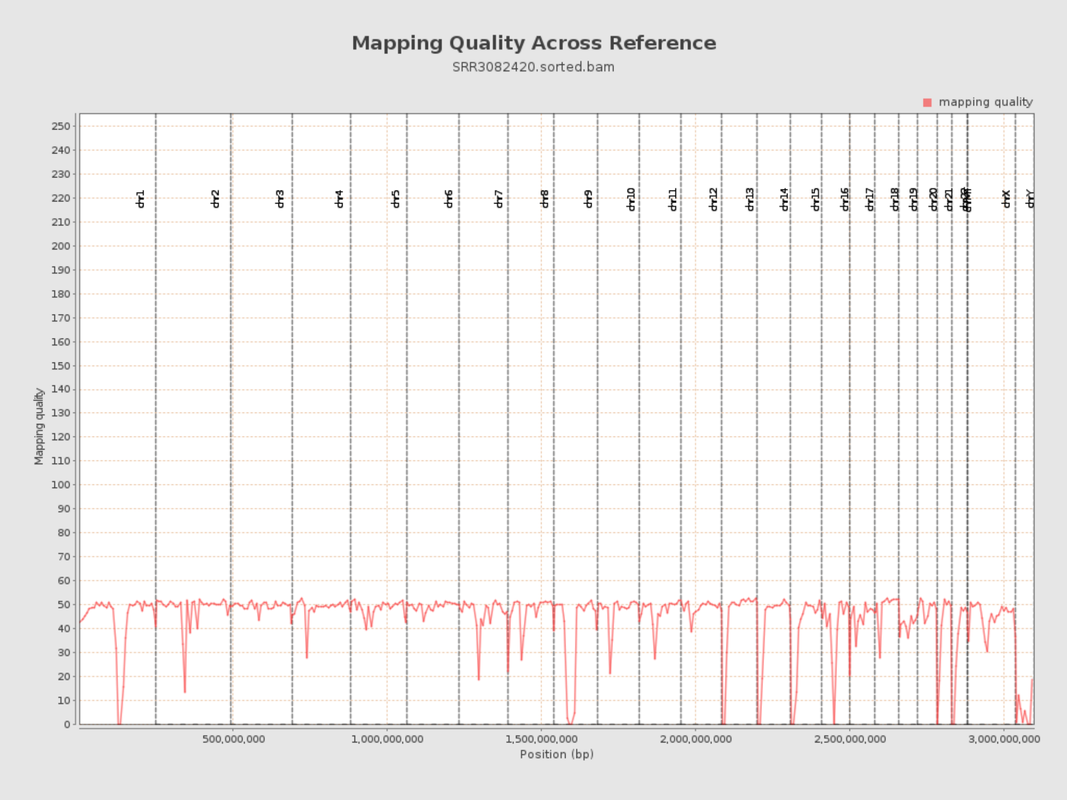
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram