Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:42:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081882.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_SRR3081882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081882.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:42:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,073,590
Mapped reads	2,804,255 / 91.24%
Unmapped reads	269,335 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,164 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	120,233 / 3.91%
Duplication rate	3.25%
Clipped reads	1,193,532 / 38.83%

2.2. ACGT Content

Number/percentage of A's	51,775,483 / 27.46%
Number/percentage of C's	36,273,878 / 19.24%
Number/percentage of T's	57,754,181 / 30.63%
Number/percentage of G's	42,721,493 / 22.66%
Number/percentage of N's	2,159 / 0%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0609

Standard Deviation	0.4712

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

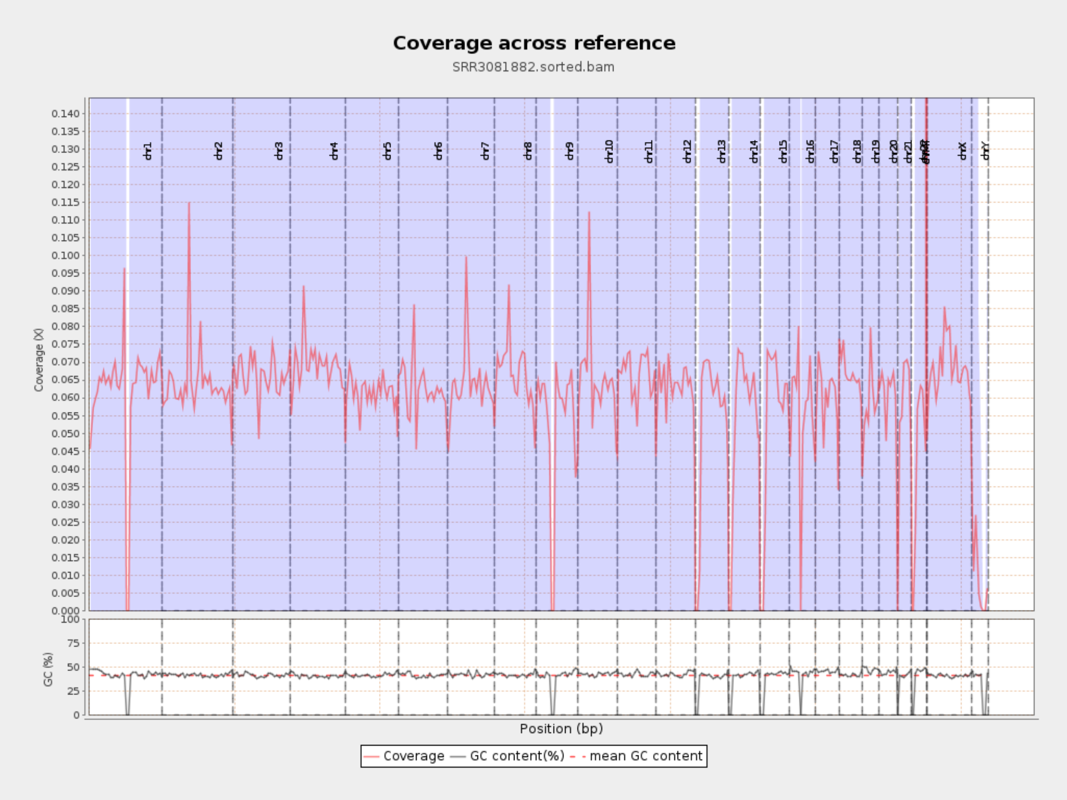
General error rate	0.84%
Mismatches	1,556,710
Insertions	13,602
Mapped reads with at least one insertion	0.48%
Deletions	38,617
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.12%

2.6. Chromosome stats

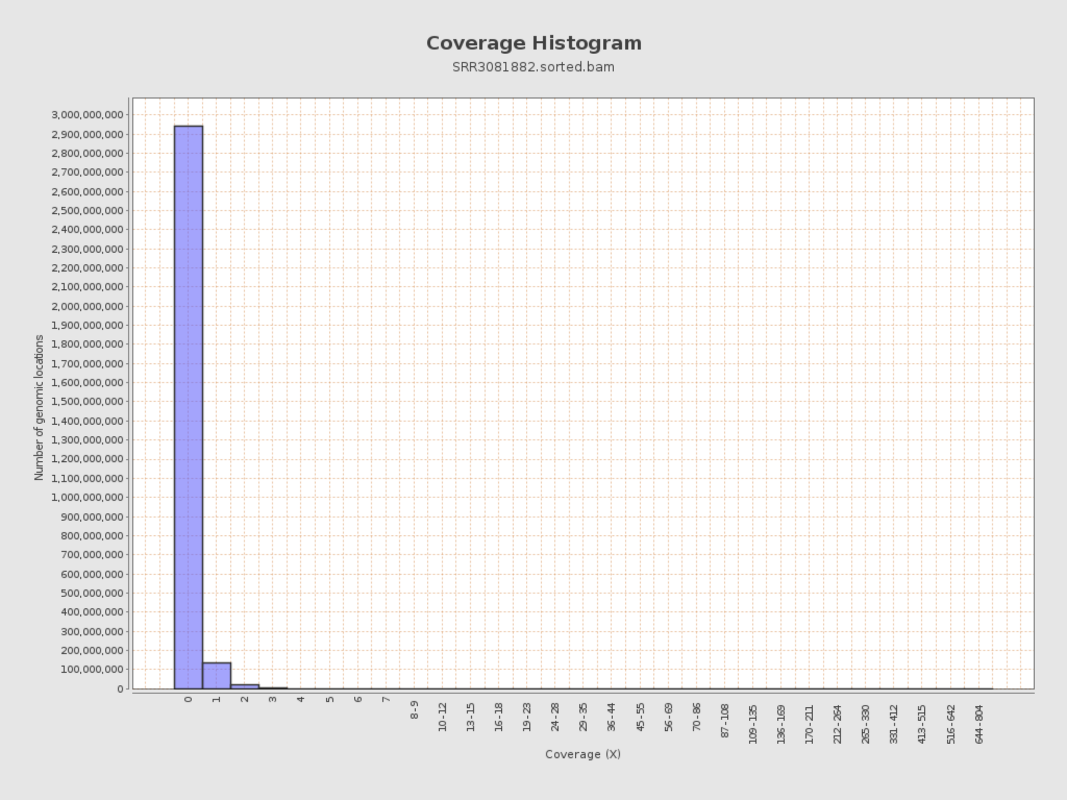
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15376228	0.0617	0.7752
chr2	243199373	15632201	0.0643	0.6
chr3	198022430	13124861	0.0663	0.3028
chr4	191154276	13185818	0.069	0.3414
chr5	180915260	11129759	0.0615	0.2899
chr6	171115067	10744304	0.0628	0.3603
chr7	159138663	10266106	0.0645	0.6749

chr8	146364022	9753151	0.0666	0.5756
chr9	141213431	7503318	0.0531	0.4324
chr10	135534747	8911608	0.0658	0.5477
chr11	135006516	8962551	0.0664	0.4033
chr12	133851895	8483051	0.0634	0.2976
chr13	115169878	6054956	0.0526	0.2668
chr14	107349540	5769855	0.0537	0.2961
chr15	102531392	5476494	0.0534	0.2748
chr16	90354753	4995416	0.0553	0.3311
chr17	81195210	4818712	0.0593	0.3192
chr18	78077248	5244723	0.0672	0.8092
chr19	59128983	3497452	0.0591	0.6012
chr20	63025520	3842636	0.061	0.3001
chr21	48129895	2661638	0.0553	0.3111
chr22	51304566	2064722	0.0402	0.2329
chrMT	16571	28995	1.7497	1.7311
chrX	155270560	10566473	0.0681	0.3442
chrY	59373566	500836	0.0084	0.2058

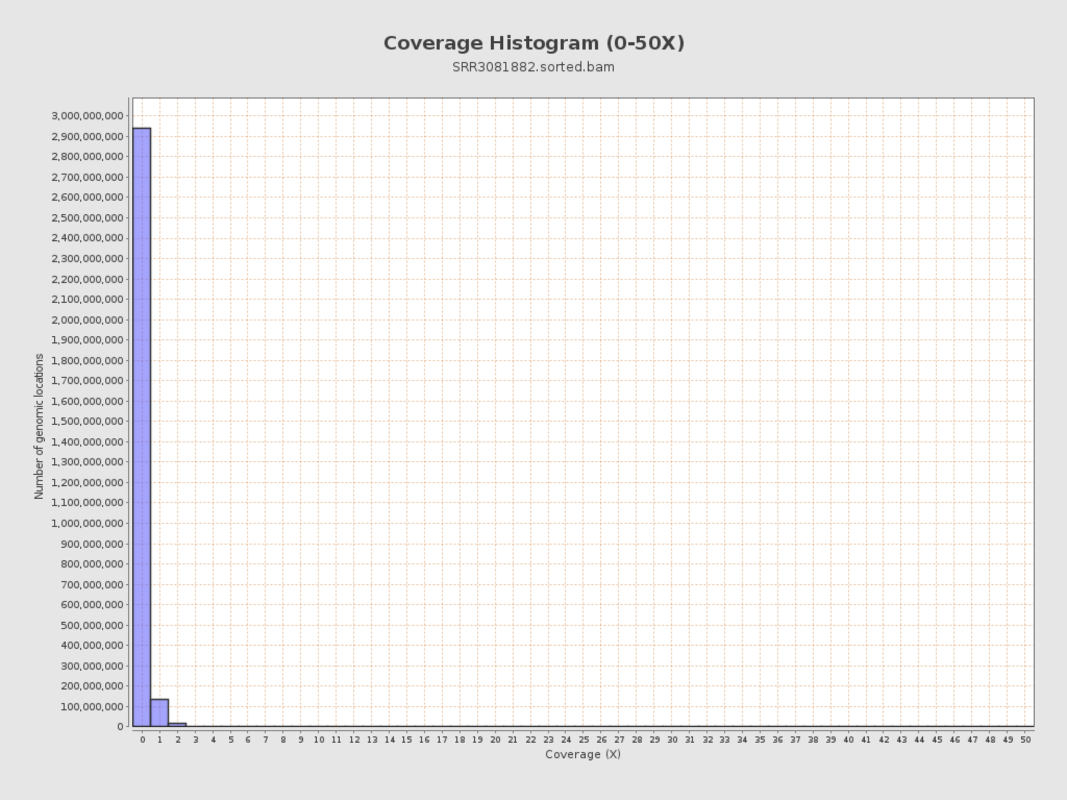
3. Results : Coverage across reference



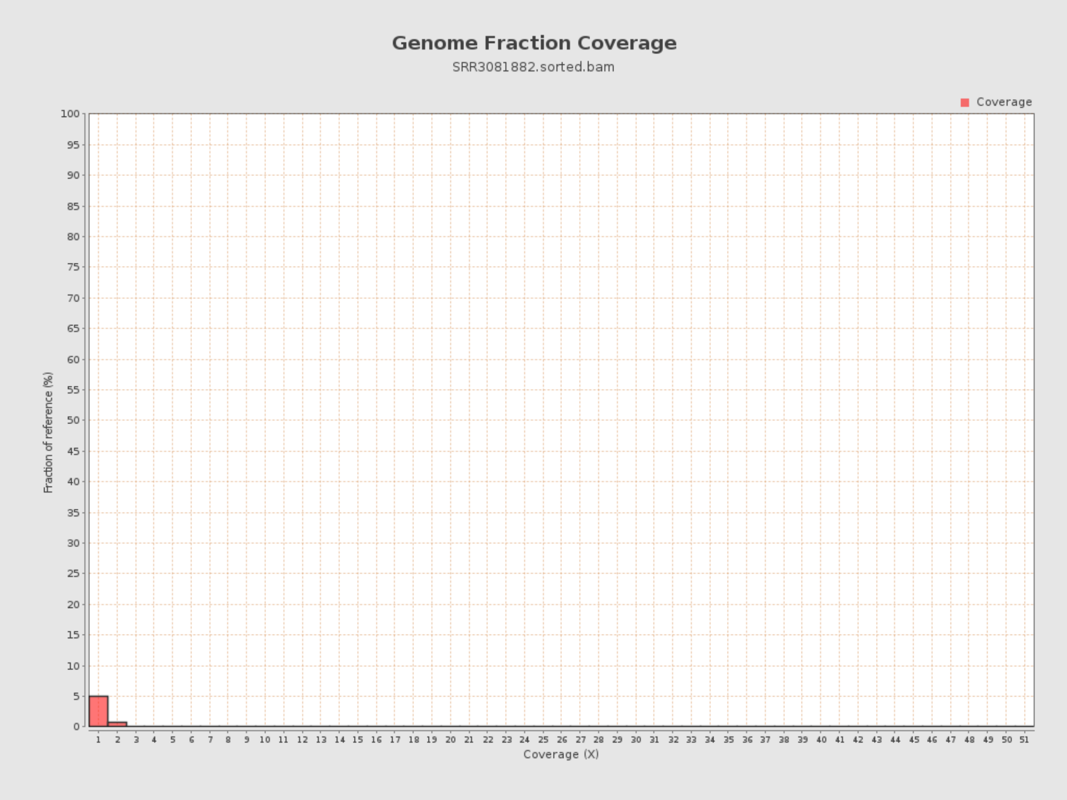
4. Results : Coverage Histogram



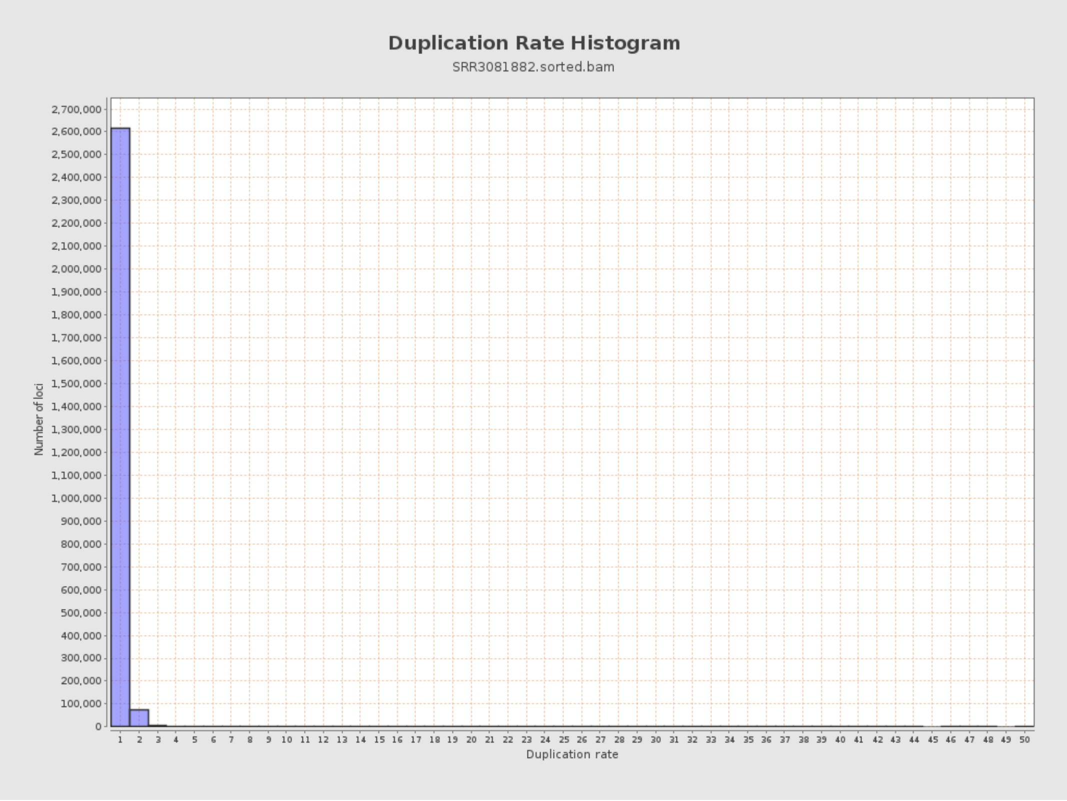
5. Results : Coverage Histogram (0-50X)



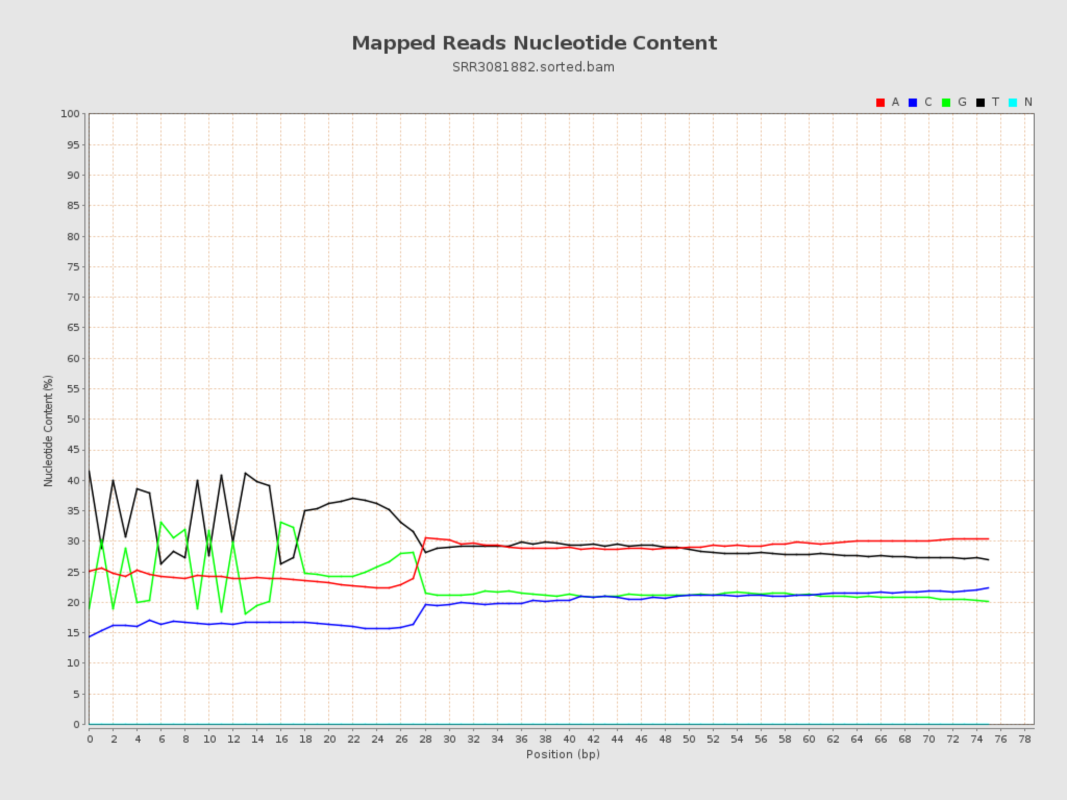
6. Results : Genome Fraction Coverage



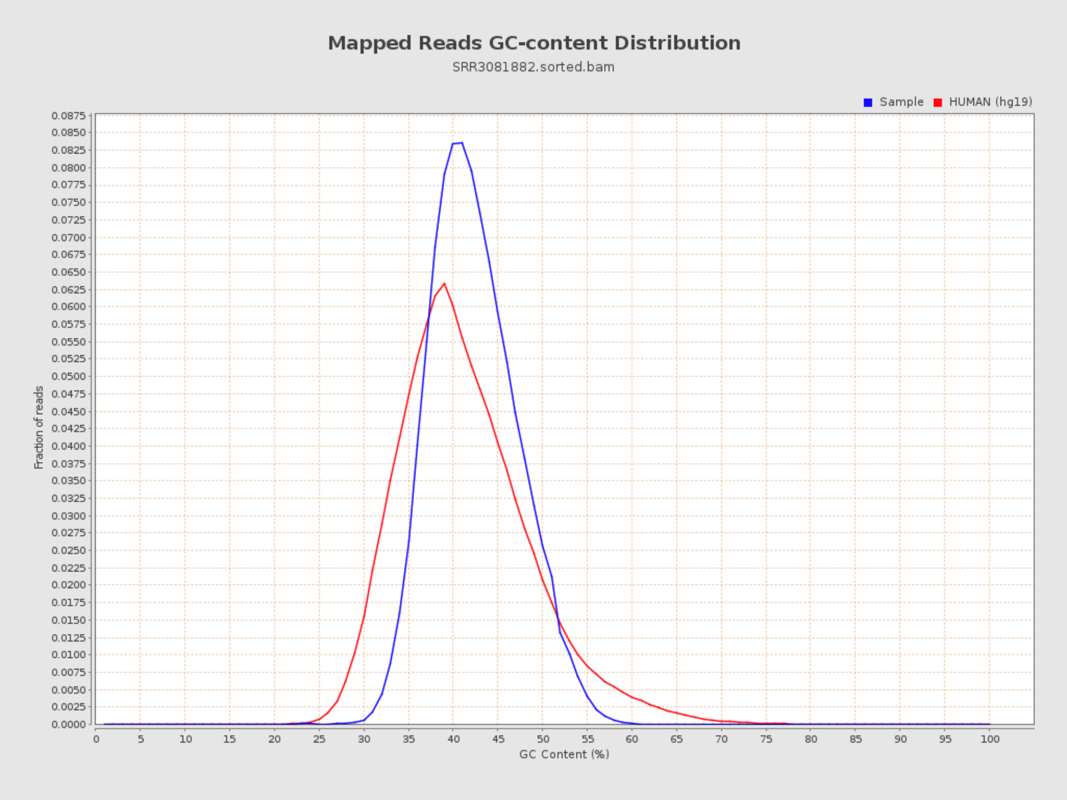
7. Results : Duplication Rate Histogram



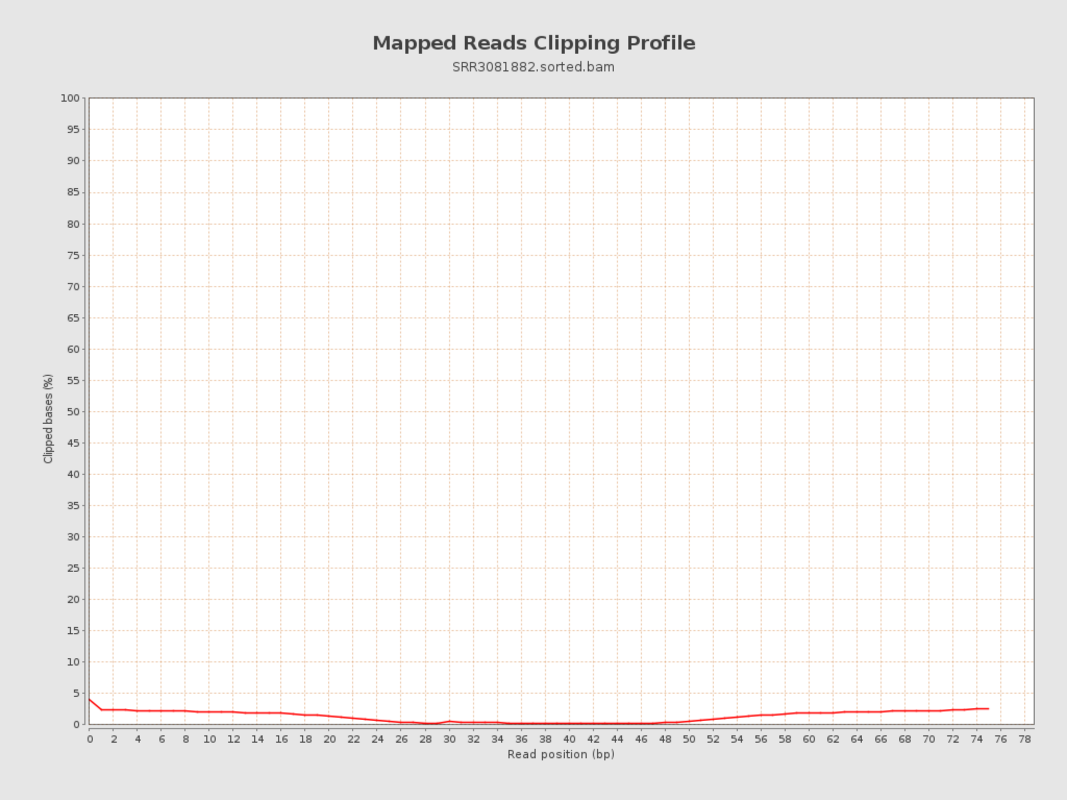
8. Results : Mapped Reads Nucleotide Content



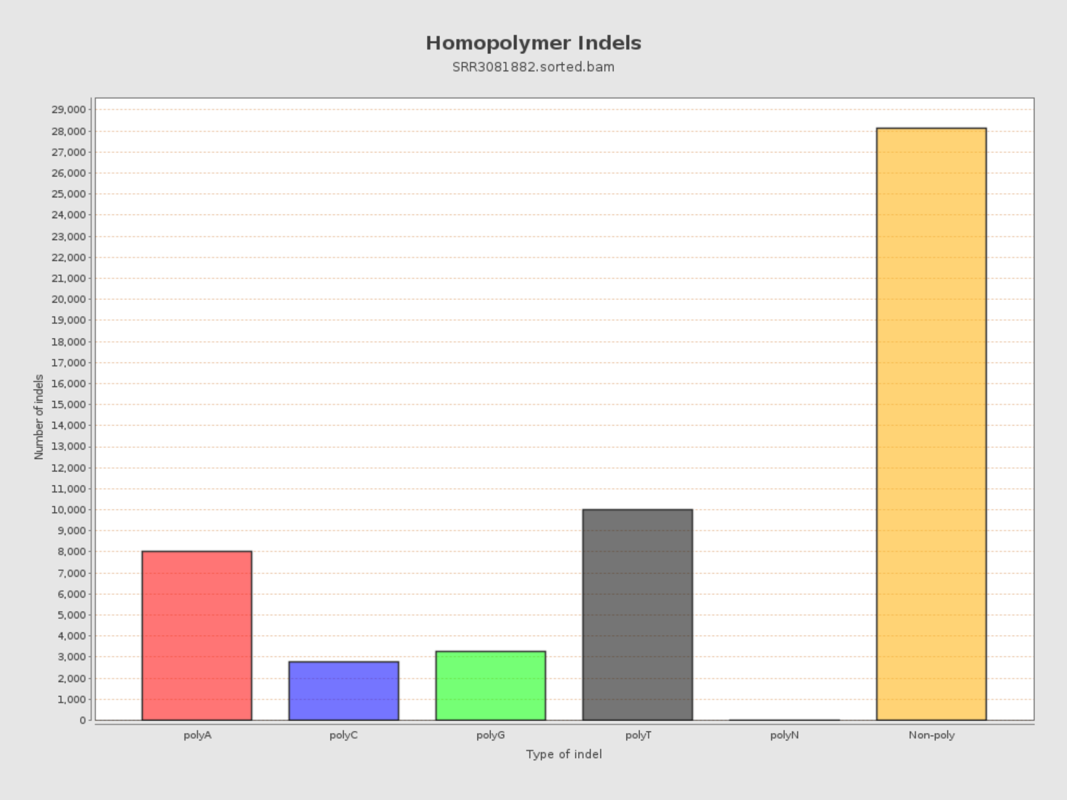
9. Results : Mapped Reads GC-content Distribution



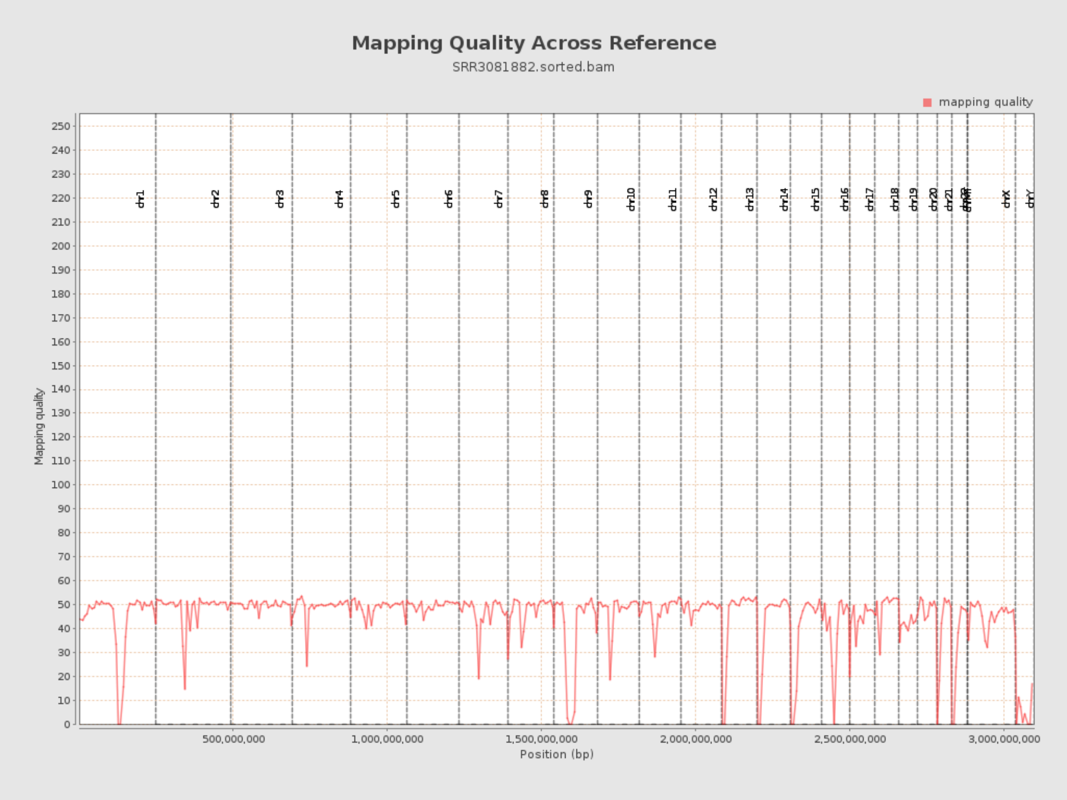
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram