Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:35:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083782.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_SRR3083782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:35:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,339,859
Mapped reads	1,277,361 / 38.25%
Unmapped reads	2,062,498 / 61.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,264 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	36,626 / 1.1%
Duplication rate	2.33%
Clipped reads	826,520 / 24.75%

2.2. ACGT Content

Number/percentage of A's	21,758,209 / 28.49%
Number/percentage of C's	14,903,663 / 19.51%
Number/percentage of T's	22,781,571 / 29.83%
Number/percentage of G's	16,937,722 / 22.18%
Number/percentage of N's	821 / 0%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.213

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

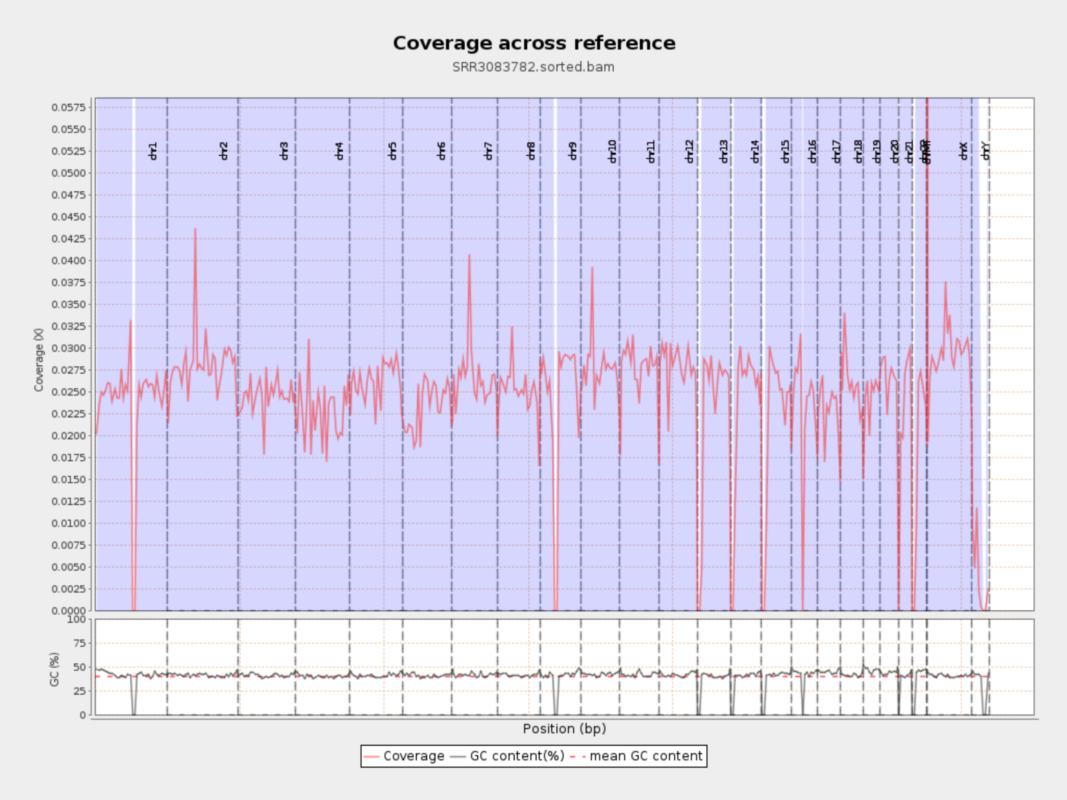
General error rate	0.86%
Mismatches	649,649
Insertions	5,575
Mapped reads with at least one insertion	0.43%
Deletions	15,595
Mapped reads with at least one deletion	1.21%
Homopolymer indels	45.64%

2.6. Chromosome stats

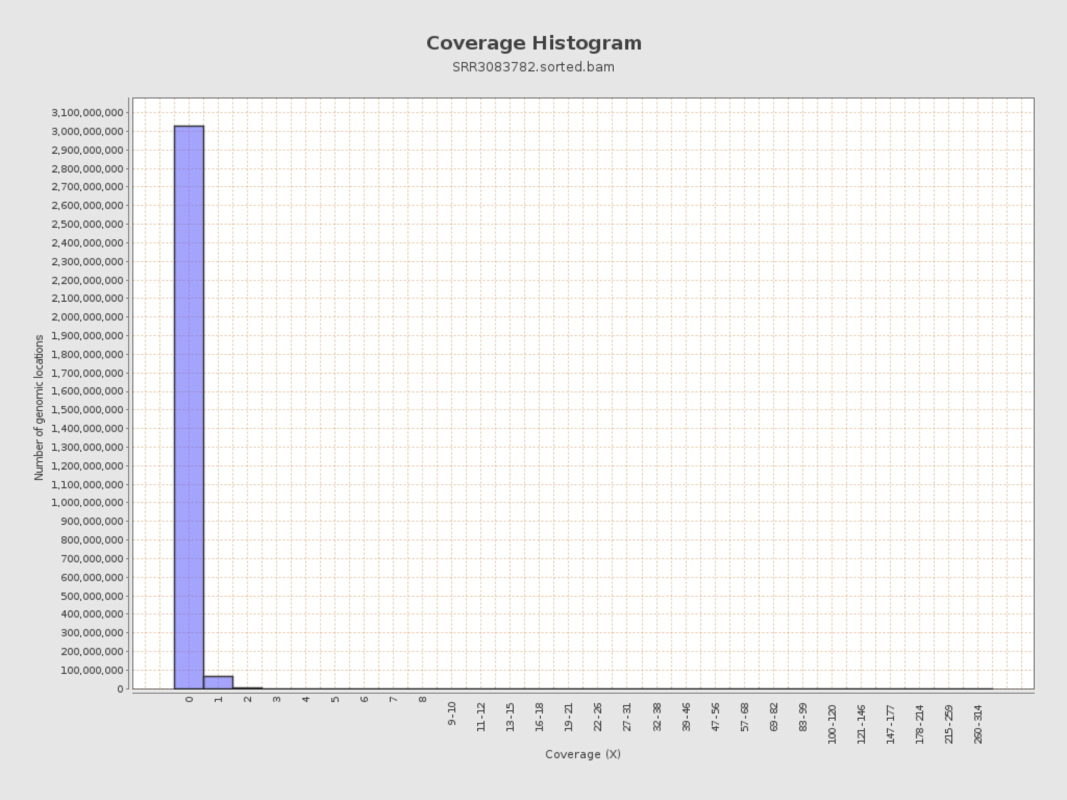
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5907182	0.0237	0.2678
chr2	243199373	6837124	0.0281	0.2618
chr3	198022430	4871132	0.0246	0.1673
chr4	191154276	4324372	0.0226	0.1693
chr5	180915260	4785591	0.0265	0.1739
chr6	171115067	3989290	0.0233	0.1774
chr7	159138663	4267811	0.0268	0.2641

chr8	146364022	3682769	0.0252	0.2208
chr9	141213431	3384975	0.024	0.2211
chr10	135534747	3771359	0.0278	0.228
chr11	135006516	3794833	0.0281	0.2144
chr12	133851895	3749773	0.028	0.1799
chr13	115169878	2572296	0.0223	0.1599
chr14	107349540	2442475	0.0228	0.1661
chr15	102531392	2186406	0.0213	0.1578
chr16	90354753	2051831	0.0227	0.1736
chr17	81195210	1853763	0.0228	0.1778
chr18	78077248	2038456	0.0261	0.4085
chr19	59128983	1439694	0.0243	0.2447
chr20	63025520	1661801	0.0264	0.1768
chr21	48129895	1085391	0.0226	0.1674
chr22	51304566	904760	0.0176	0.1403
chrMT	16571	11599	0.7	0.9017
chrX	155270560	4573750	0.0295	0.1979
chrY	59373566	218407	0.0037	0.0894

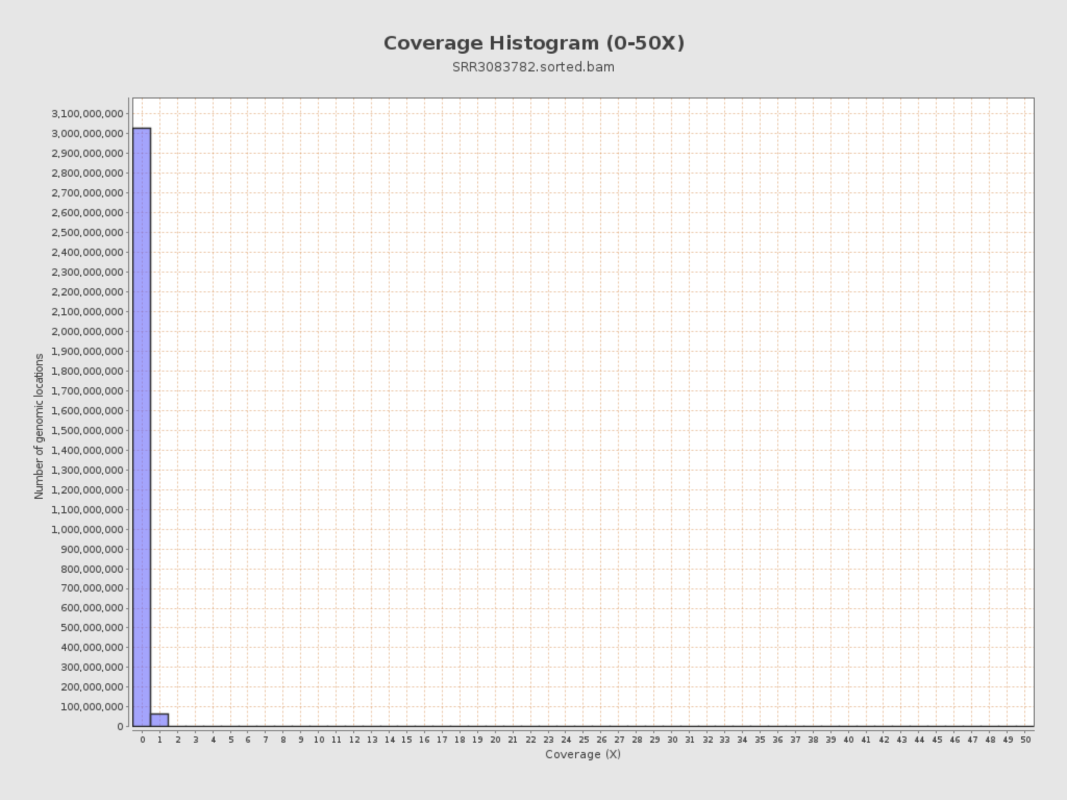
3. Results : Coverage across reference



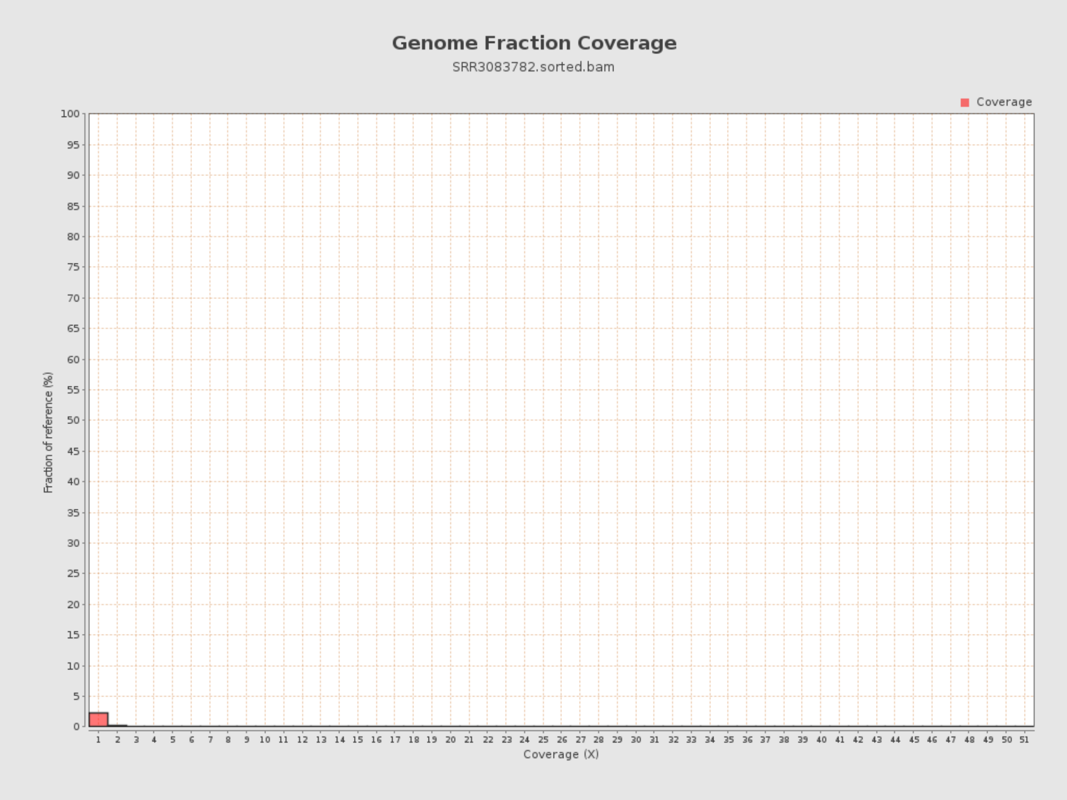
4. Results : Coverage Histogram



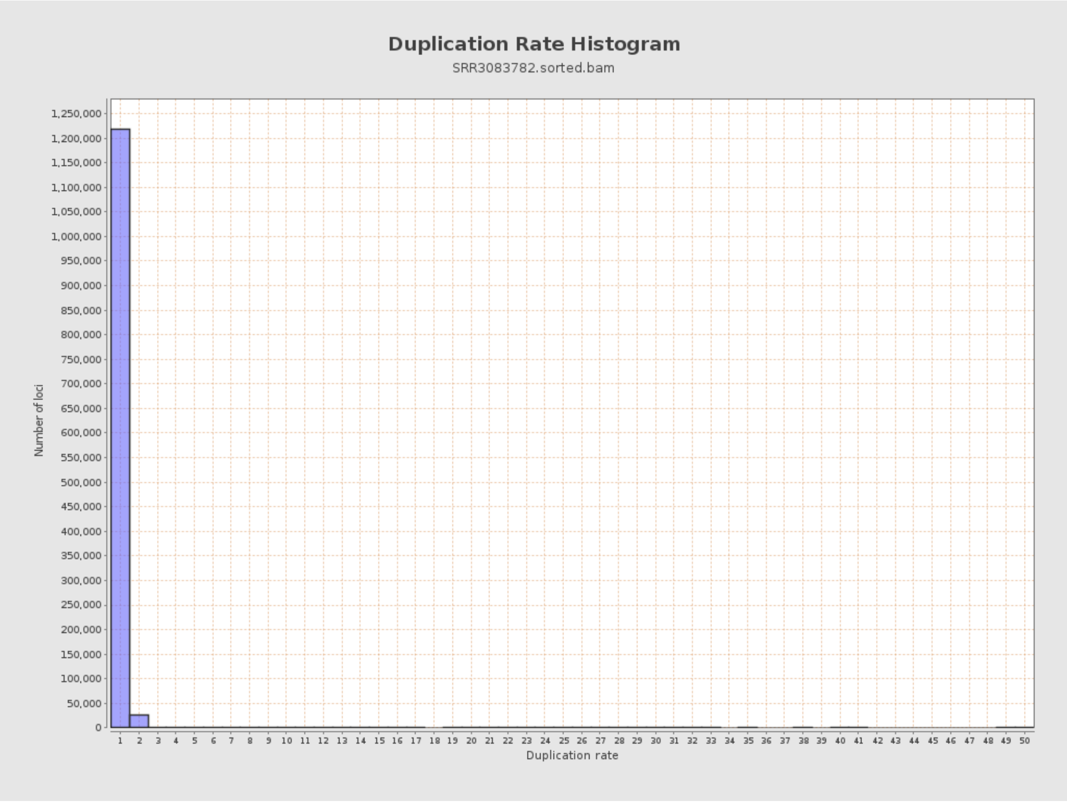
5. Results : Coverage Histogram (0-50X)



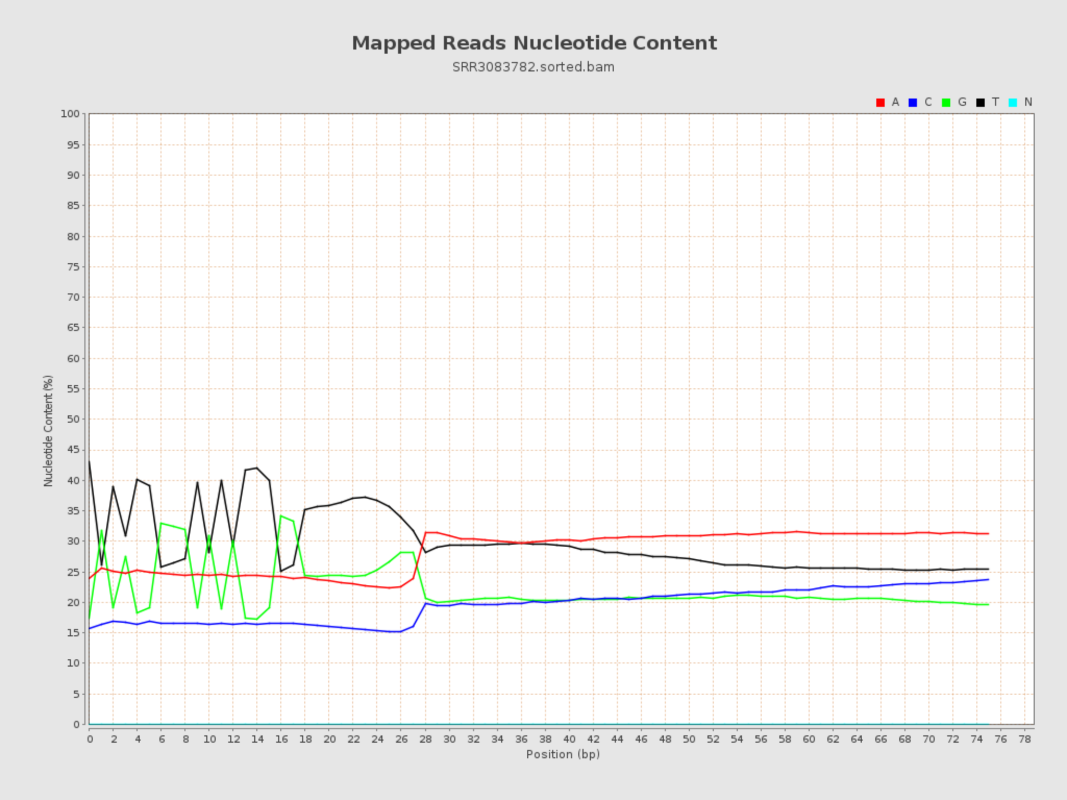
6. Results : Genome Fraction Coverage



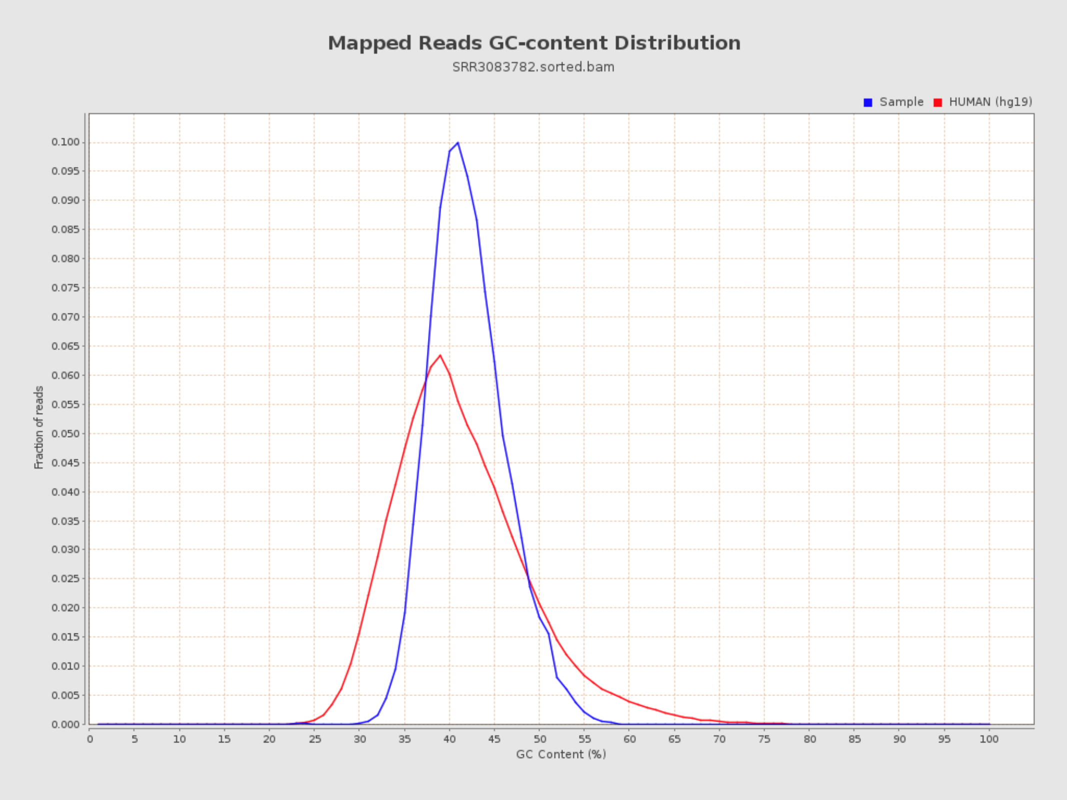
7. Results : Duplication Rate Histogram



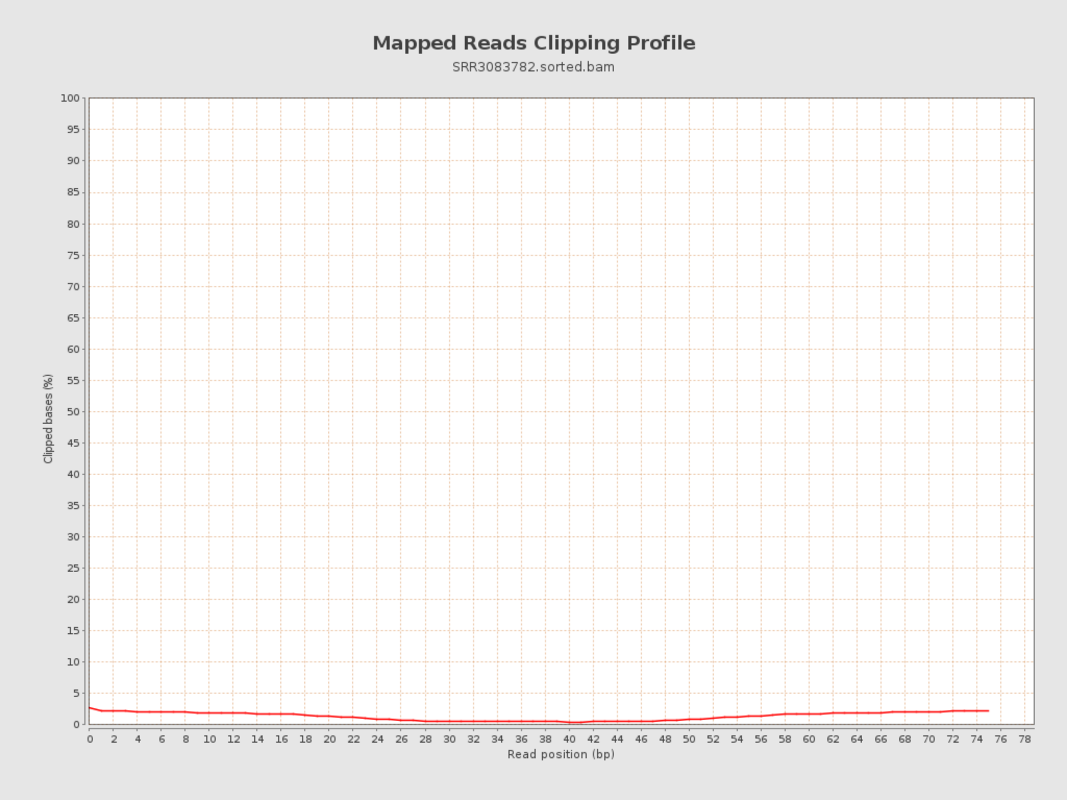
8. Results : Mapped Reads Nucleotide Content



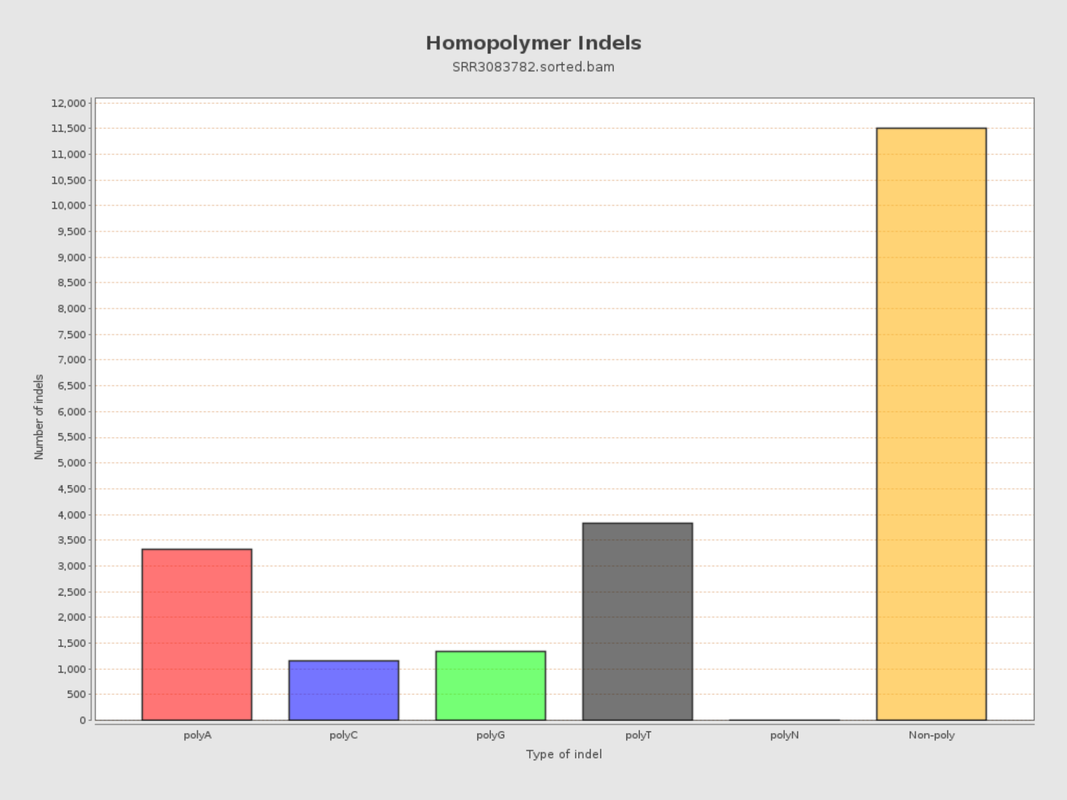
9. Results : Mapped Reads GC-content Distribution



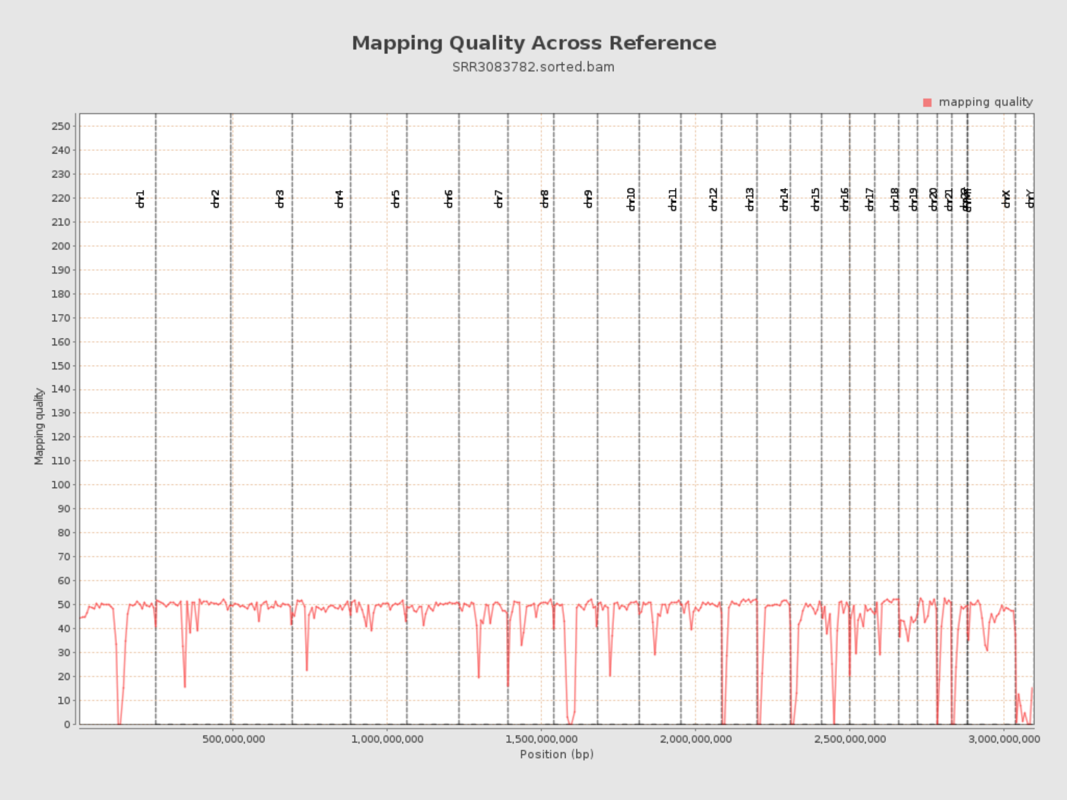
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram