Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:24:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084782.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_SRR3084782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:24:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,429,467
Mapped reads	2,198,259 / 90.48%
Unmapped reads	231,208 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,205 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	99,231 / 4.08%
Duplication rate	3.47%
Clipped reads	958,427 / 39.45%

2.2. ACGT Content

Number/percentage of A's	41,386,541 / 28.04%
Number/percentage of C's	27,600,306 / 18.7%
Number/percentage of T's	46,398,094 / 31.43%
Number/percentage of G's	32,180,547 / 21.8%
Number/percentage of N's	48,473 / 0.03%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.4049

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

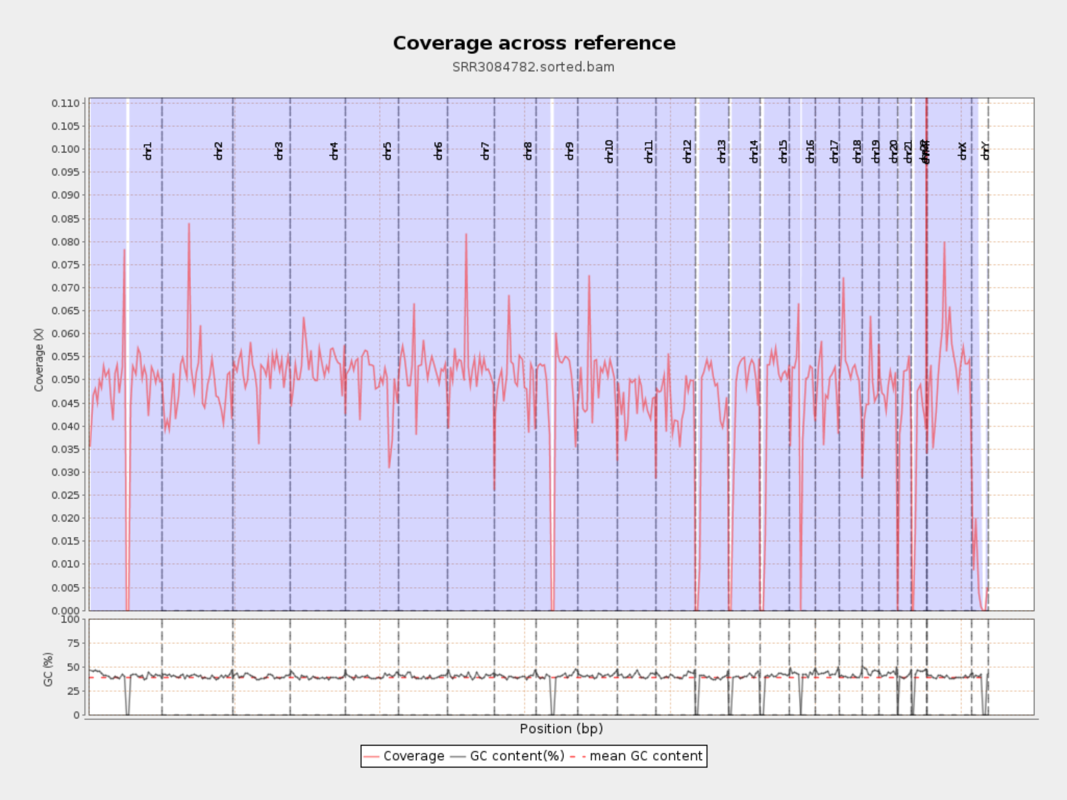
General error rate	0.9%
Mismatches	1,307,860
Insertions	11,962
Mapped reads with at least one insertion	0.54%
Deletions	38,198
Mapped reads with at least one deletion	1.72%
Homopolymer indels	46.63%

2.6. Chromosome stats

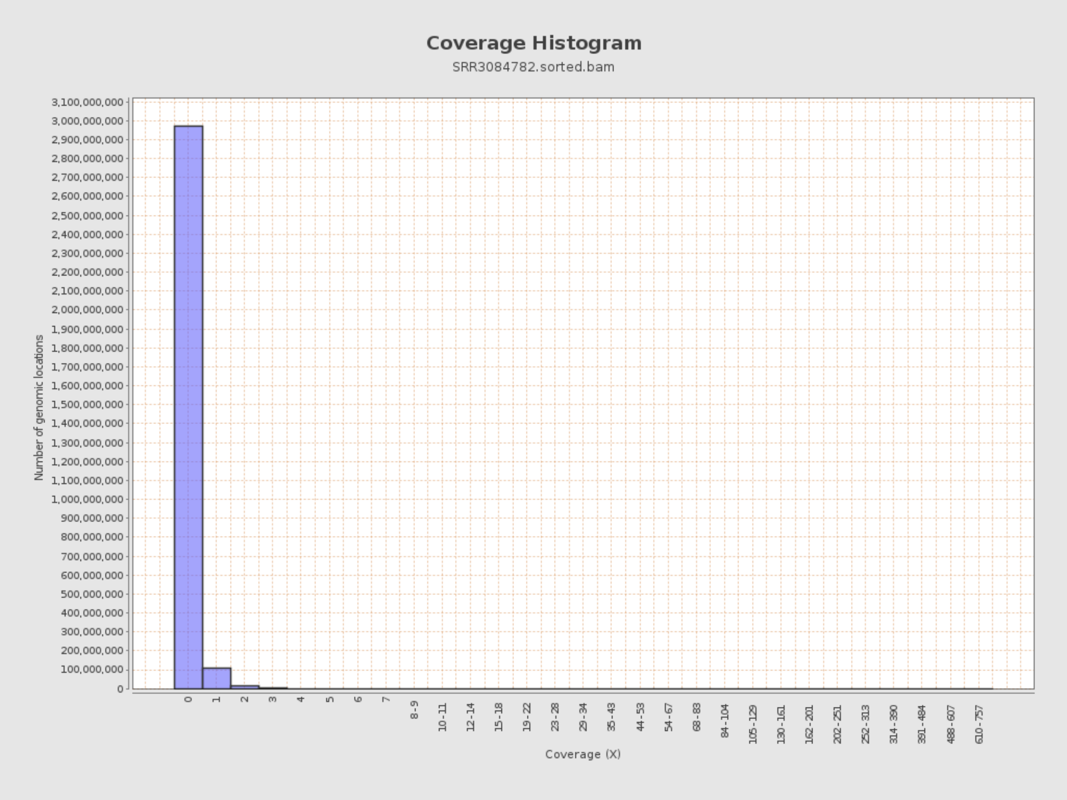
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11794025	0.0473	0.6964
chr2	243199373	11997875	0.0493	0.4766
chr3	198022430	10282163	0.0519	0.2569
chr4	191154276	10135356	0.053	0.278
chr5	180915260	9040624	0.05	0.2548
chr6	171115067	9016126	0.0527	0.3242
chr7	159138663	8492645	0.0534	0.5001

chr8	146364022	7351545	0.0502	0.4865
chr9	141213431	6444837	0.0456	0.3929
chr10	135534747	6841891	0.0505	0.3821
chr11	135006516	6105194	0.0452	0.3675
chr12	133851895	6076895	0.0454	0.2465
chr13	115169878	4645318	0.0403	0.2284
chr14	107349540	4642025	0.0432	0.2574
chr15	102531392	4366104	0.0426	0.2369
chr16	90354753	4159688	0.046	0.2853
chr17	81195210	3887271	0.0479	0.292
chr18	78077248	4184005	0.0536	0.8701
chr19	59128983	2810049	0.0475	0.4744
chr20	63025520	3000157	0.0476	0.2698
chr21	48129895	2055404	0.0427	0.2505
chr22	51304566	1630757	0.0318	0.1978
chrMT	16571	3744	0.2259	0.5536
chrX	155270560	8322652	0.0536	0.3097
chrY	59373566	389155	0.0066	0.1468

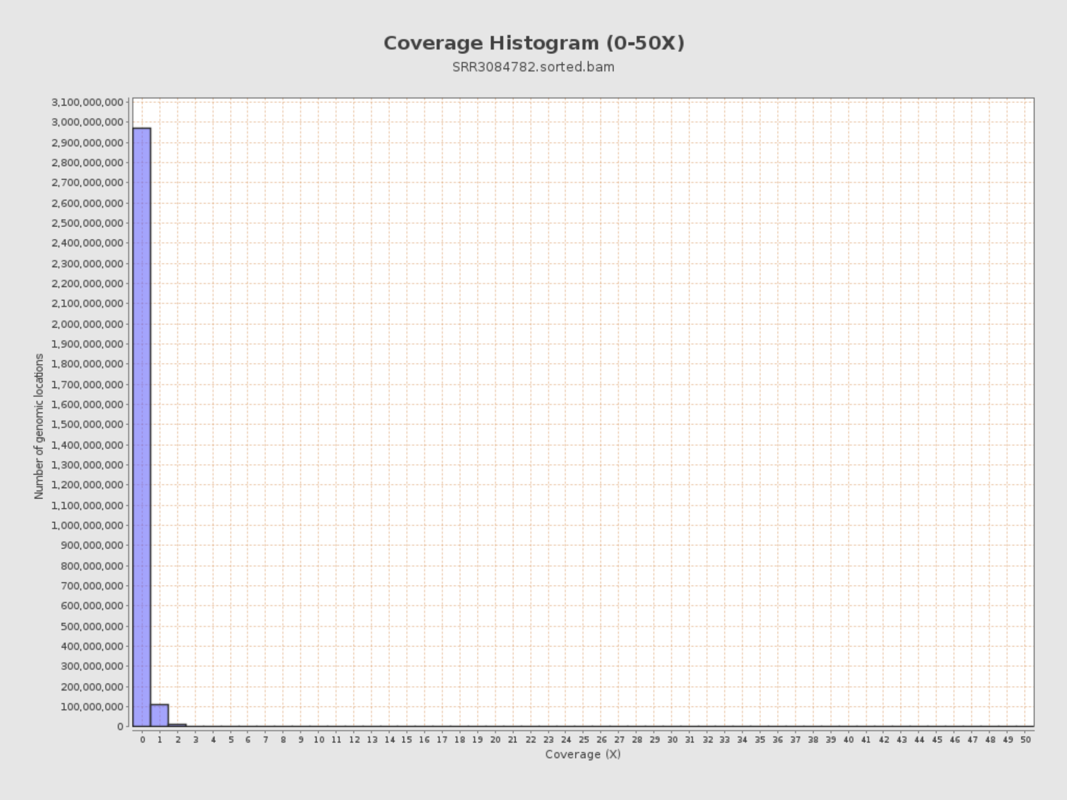
3. Results : Coverage across reference



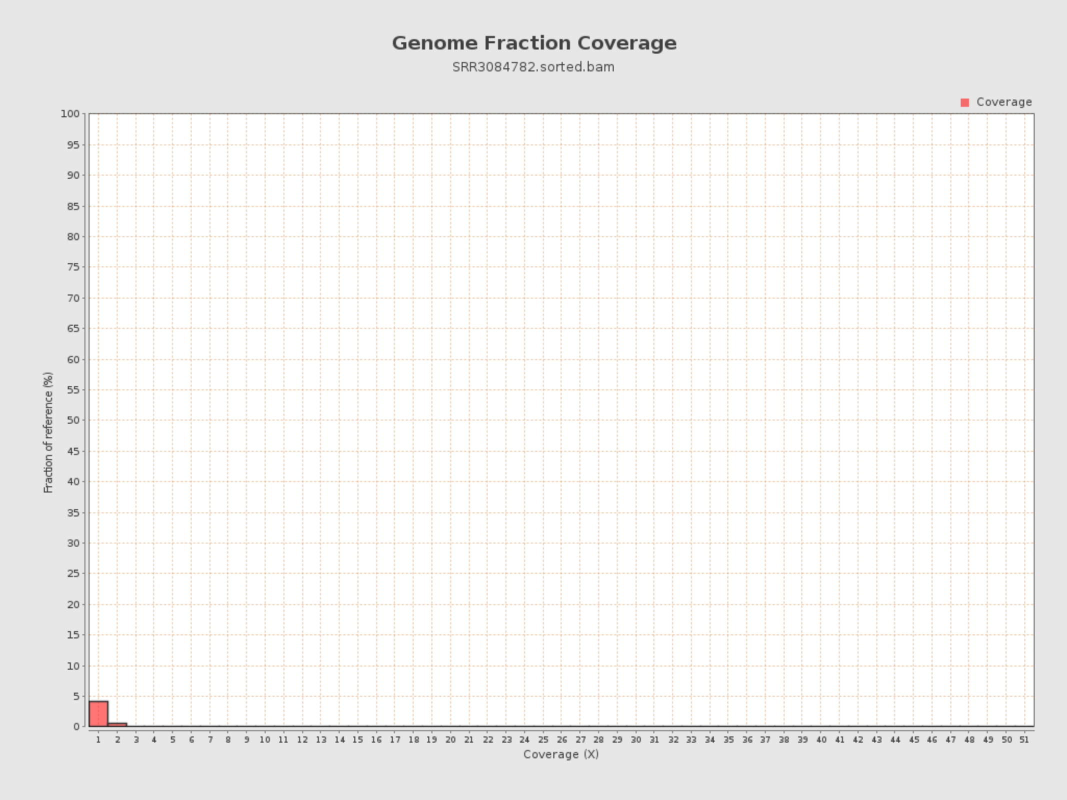
4. Results : Coverage Histogram



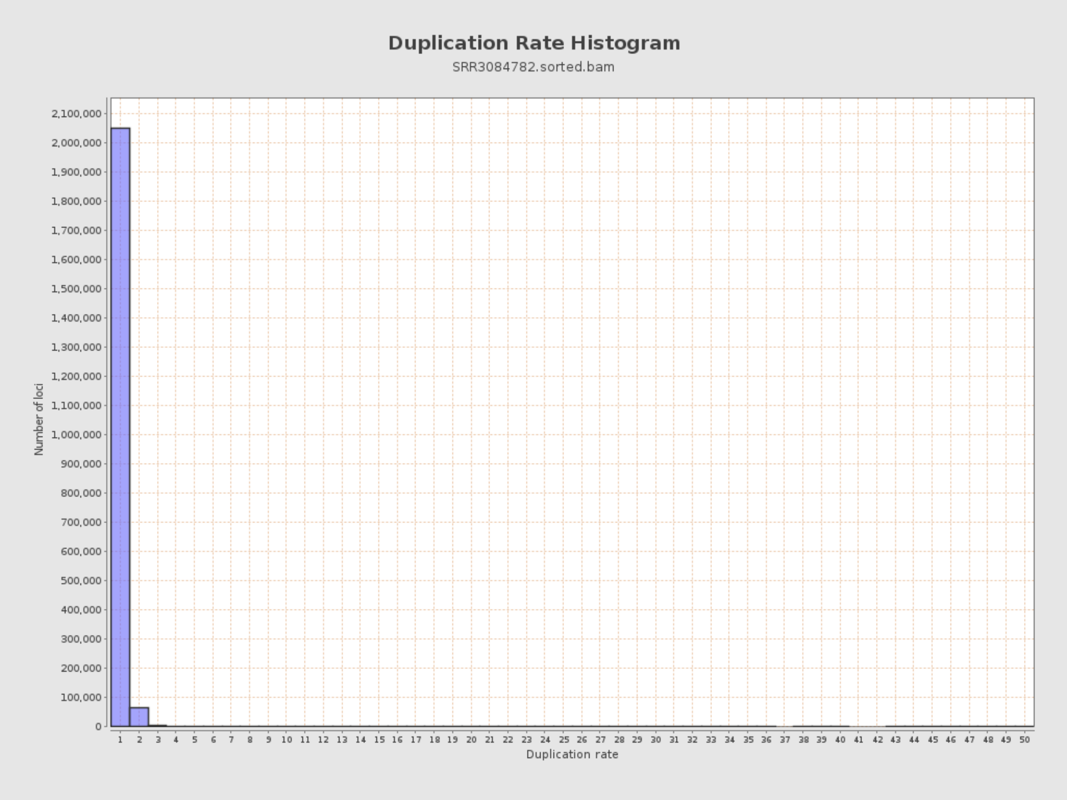
5. Results : Coverage Histogram (0-50X)



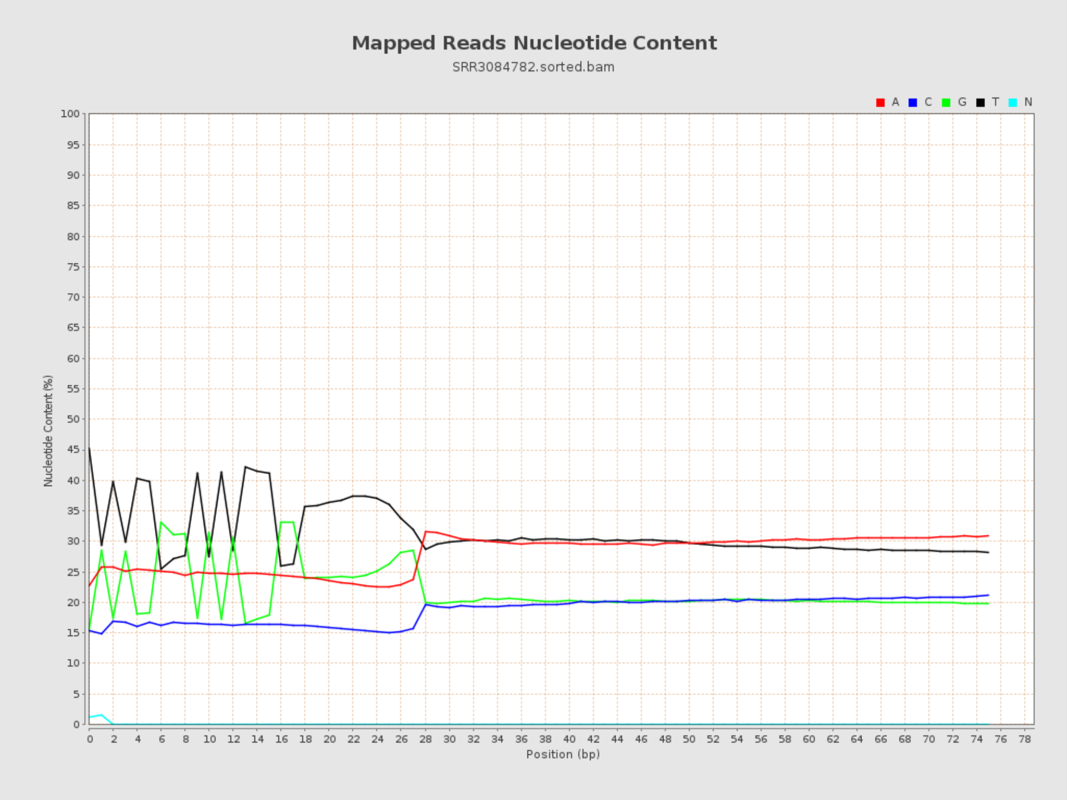
6. Results : Genome Fraction Coverage



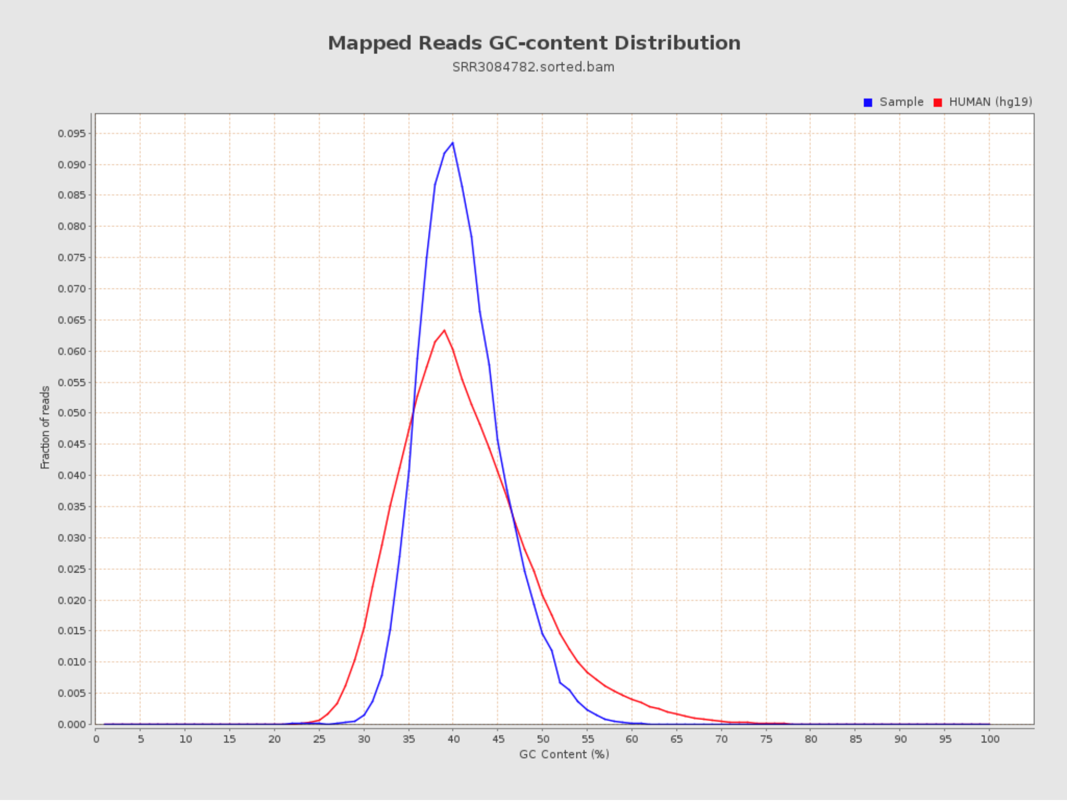
7. Results : Duplication Rate Histogram



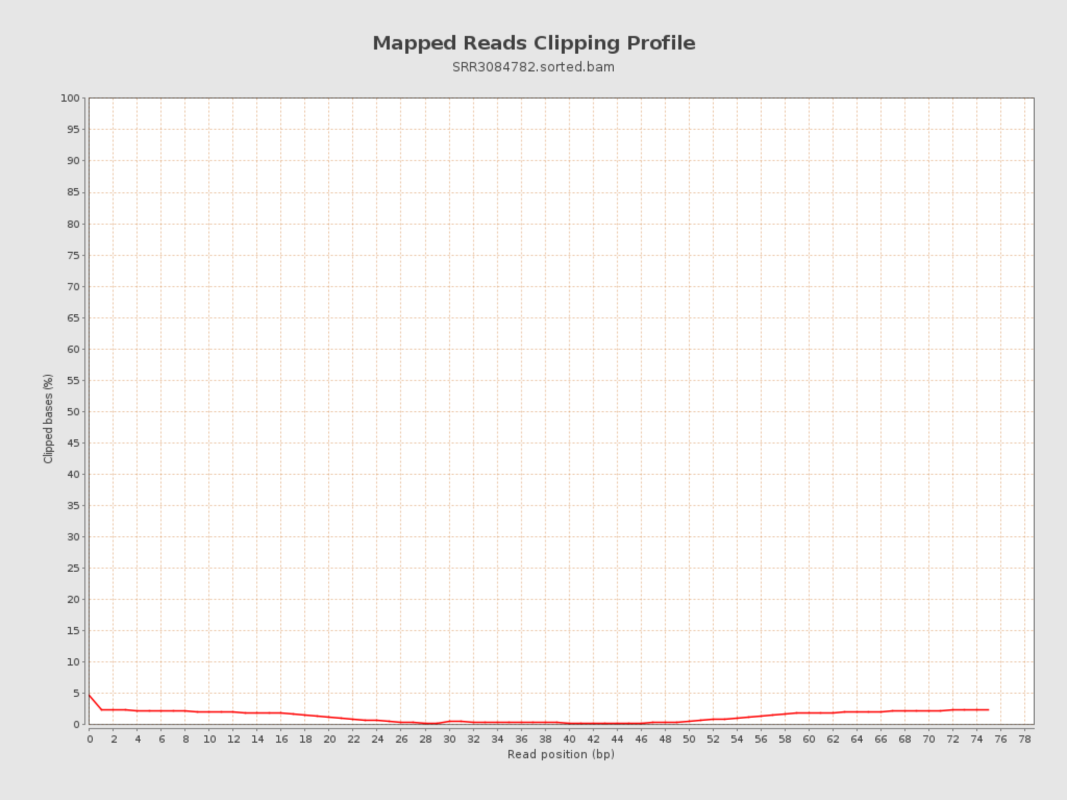
8. Results : Mapped Reads Nucleotide Content



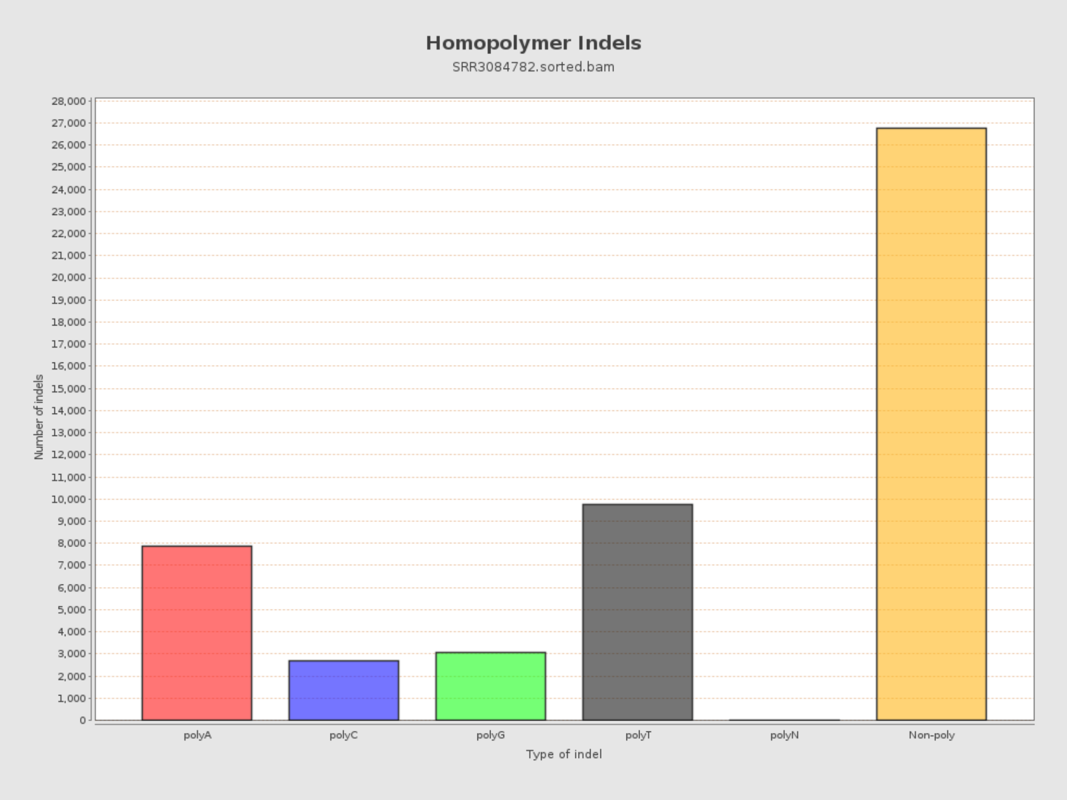
9. Results : Mapped Reads GC-content Distribution



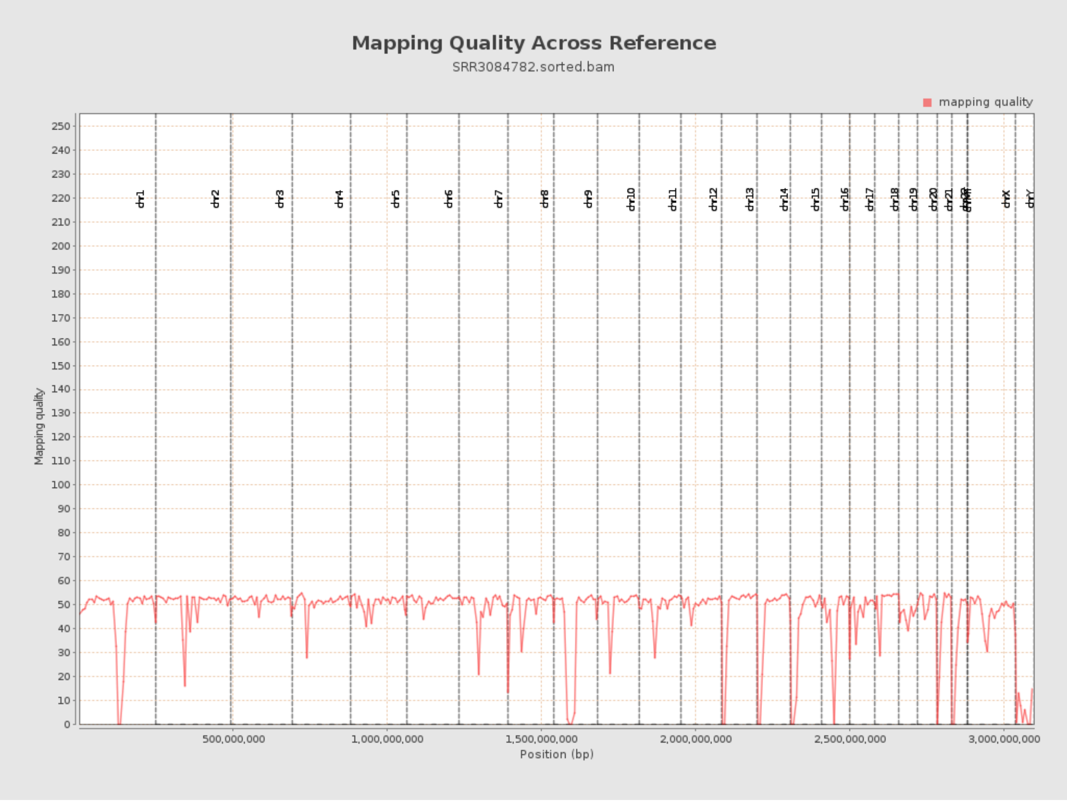
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram