Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:19:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708582.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_SRR1708582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708582.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:19:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,114,344
Mapped reads	5,007,926 / 97.92%
Unmapped reads	106,418 / 2.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	150 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	51,121 / 1%
Duplication rate	1.02%
Clipped reads	69,290 / 1.35%

2.2. ACGT Content

Number/percentage of A's	77,467,621 / 31.02%
Number/percentage of C's	47,222,557 / 18.91%
Number/percentage of T's	77,132,428 / 30.88%
Number/percentage of G's	47,912,148 / 19.18%
Number/percentage of N's	9,525 / 0%
GC Percentage	38.09%

2.3. Coverage

Mean	0.0807

Standard Deviation	0.2975

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

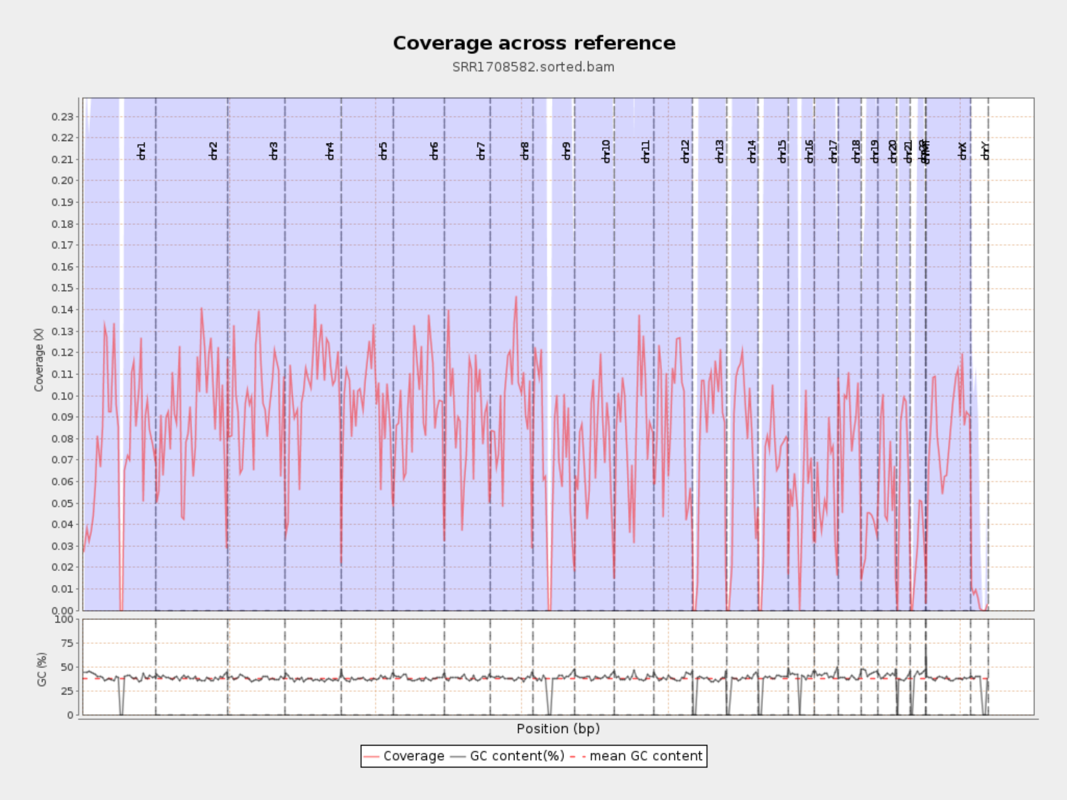
General error rate	0.15%
Mismatches	364,503
Insertions	16,098
Mapped reads with at least one insertion	0.32%
Deletions	12,603
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.74%

2.6. Chromosome stats

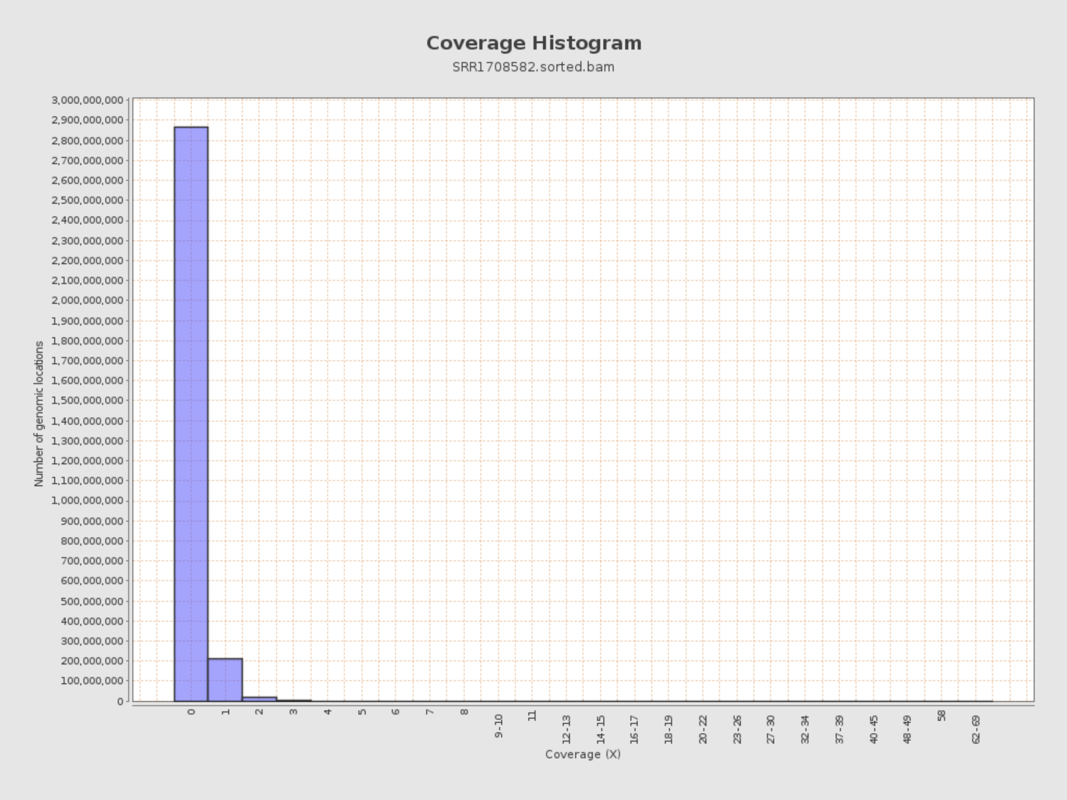
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19104199	0.0766	0.2921
chr2	243199373	21784402	0.0896	0.3117
chr3	198022430	19379647	0.0979	0.3264
chr4	191154276	19803733	0.1036	0.335
chr5	180915260	17362672	0.096	0.3223
chr6	171115067	16545431	0.0967	0.3243
chr7	159138663	14276598	0.0897	0.3136

chr8	146364022	14005506	0.0957	0.3229
chr9	141213431	10092438	0.0715	0.2802
chr10	135534747	10325783	0.0762	0.2879
chr11	135006516	11512591	0.0853	0.307
chr12	133851895	11679992	0.0873	0.3085
chr13	115169878	9434713	0.0819	0.2997
chr14	107349540	7978256	0.0743	0.2866
chr15	102531392	6499608	0.0634	0.2642
chr16	90354753	4639369	0.0513	0.2359
chr17	81195210	4350659	0.0536	0.242
chr18	78077248	6830081	0.0875	0.3077
chr19	59128983	2123827	0.0359	0.1963
chr20	63025520	4022146	0.0638	0.2639
chr21	48129895	3101545	0.0644	0.2688
chr22	51304566	1417870	0.0276	0.1727
chrMT	16571	50	0.003	0.0548
chrX	155270560	13228154	0.0852	0.3046
chrY	59373566	266410	0.0045	0.0714

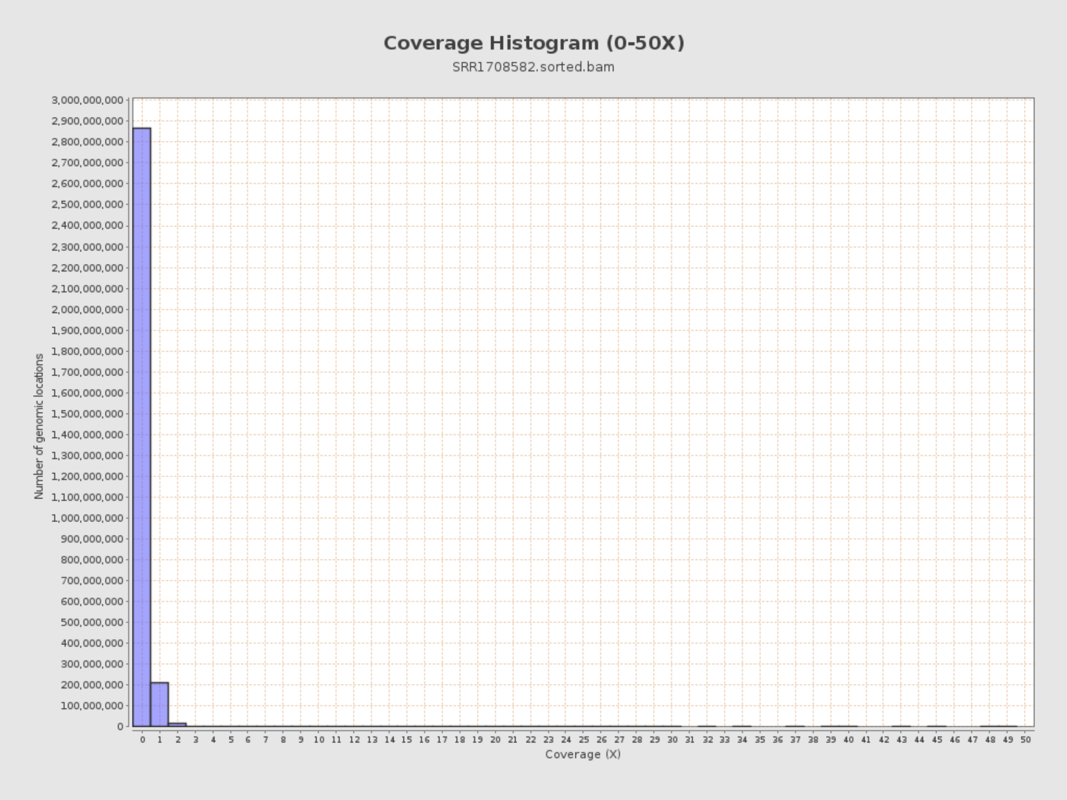
3. Results : Coverage across reference



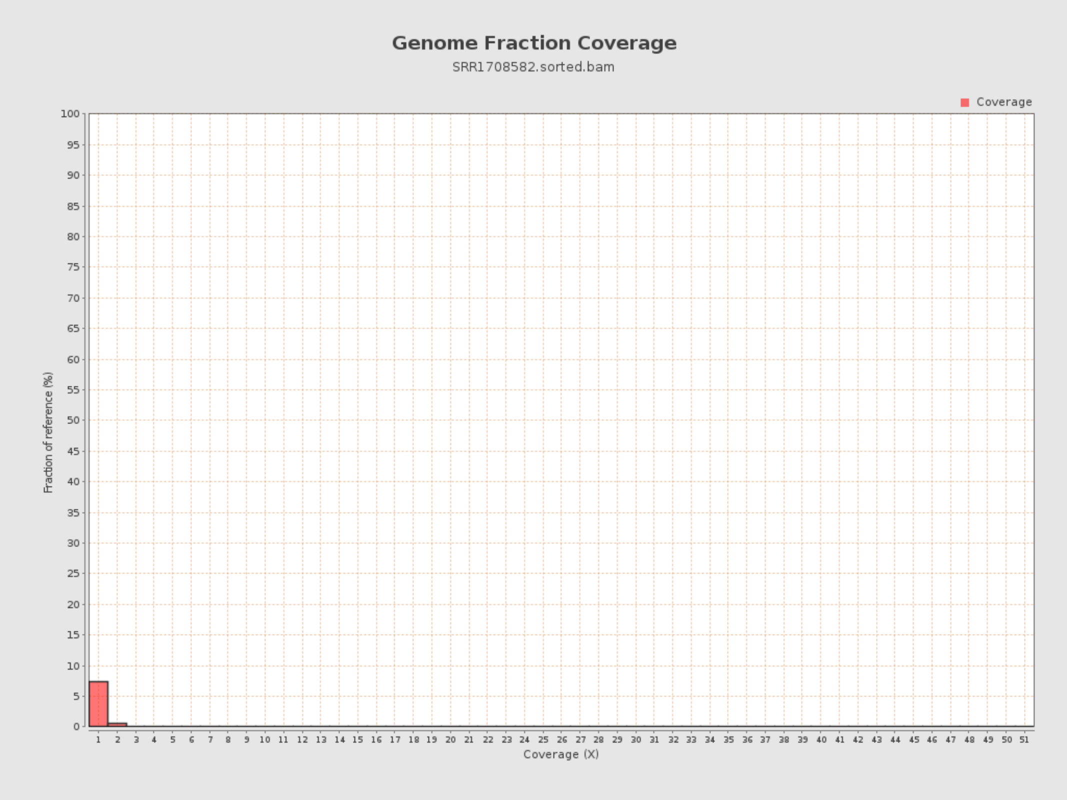
4. Results : Coverage Histogram



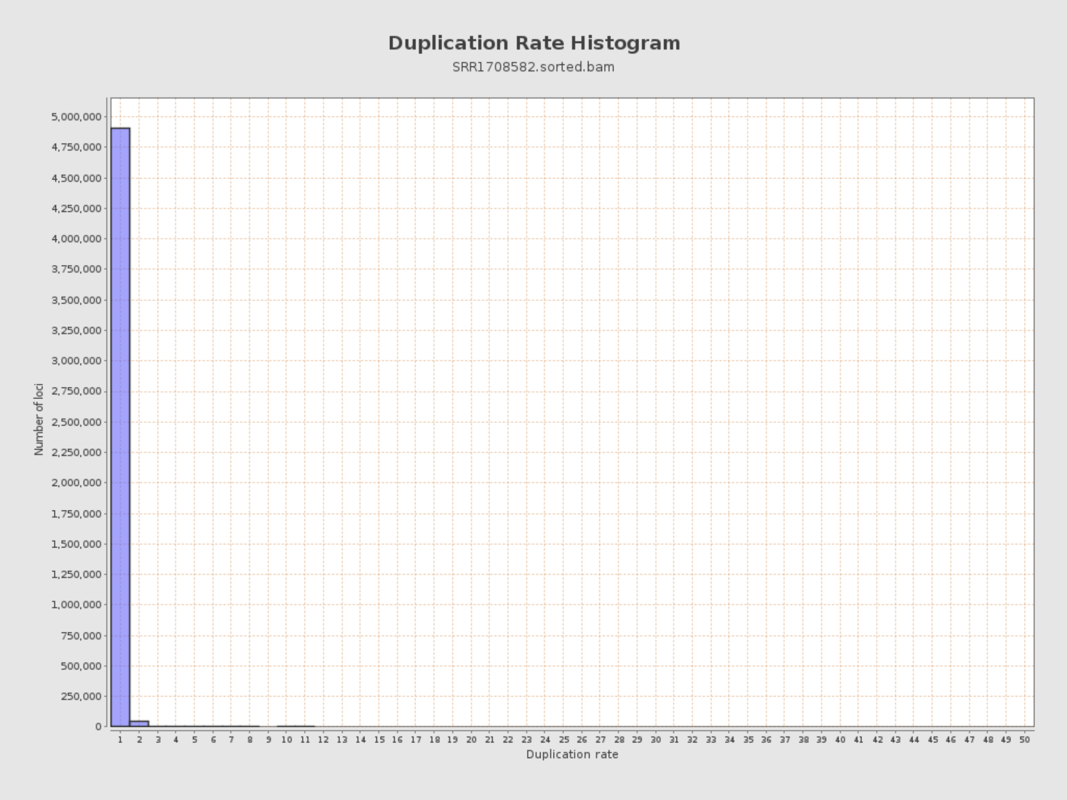
5. Results : Coverage Histogram (0-50X)



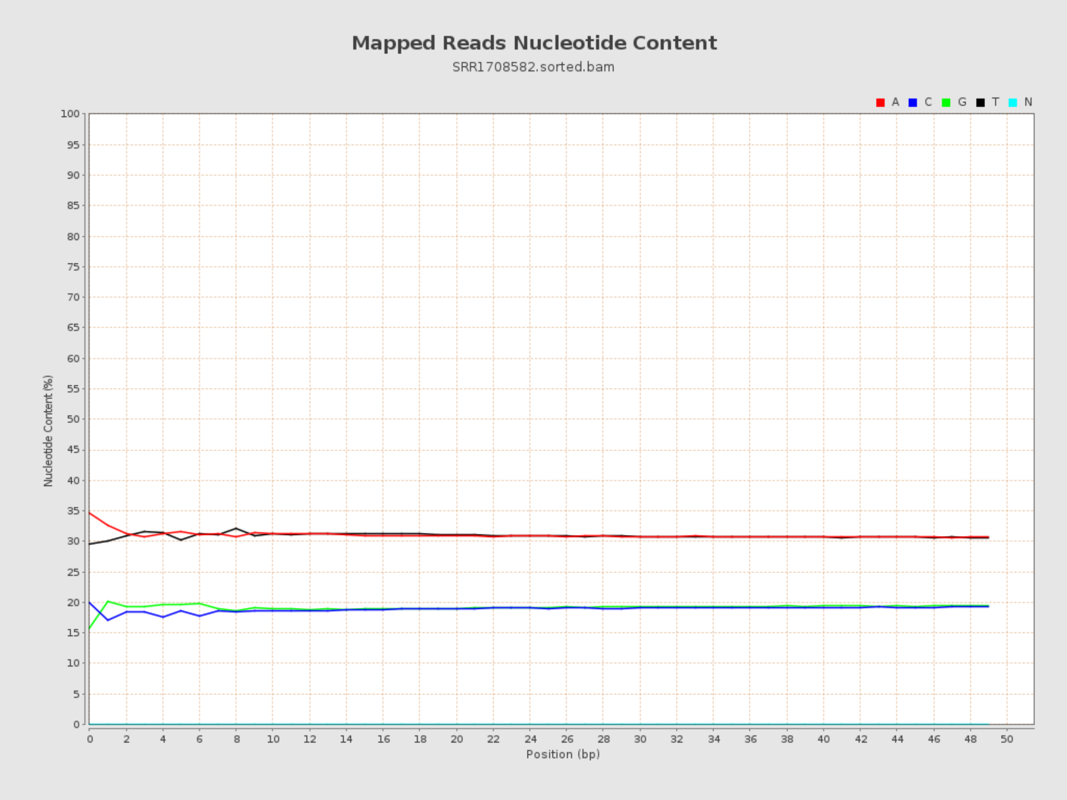
6. Results : Genome Fraction Coverage



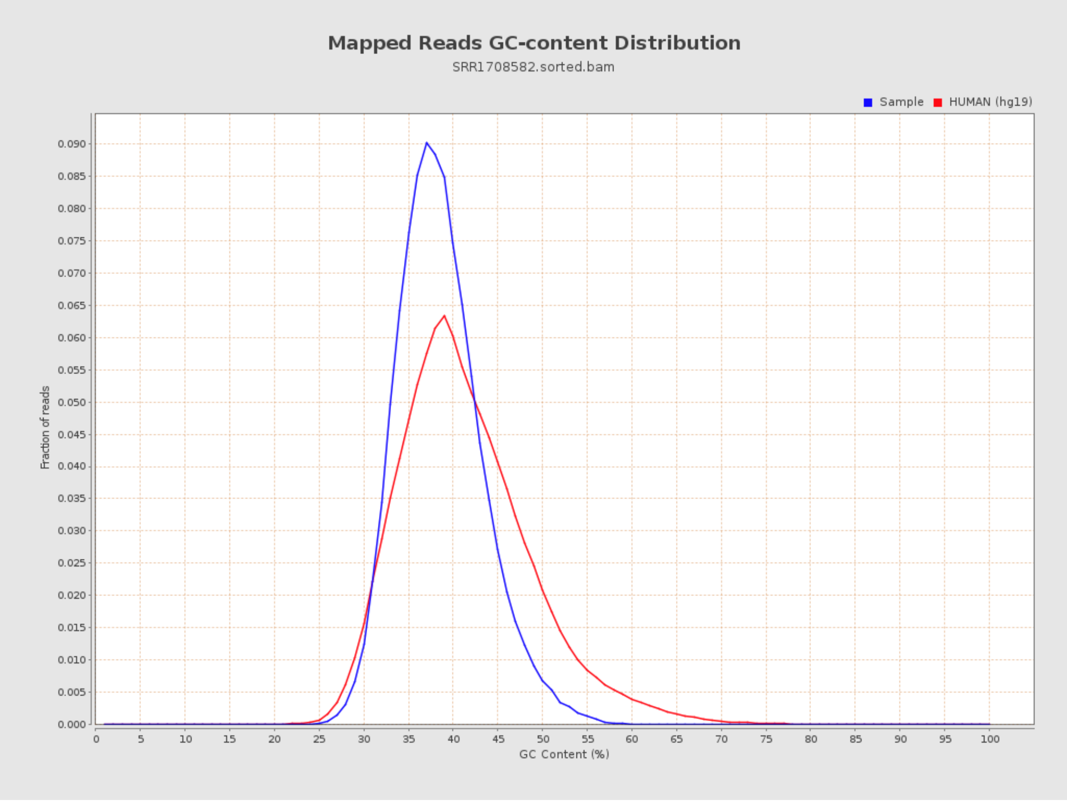
7. Results : Duplication Rate Histogram



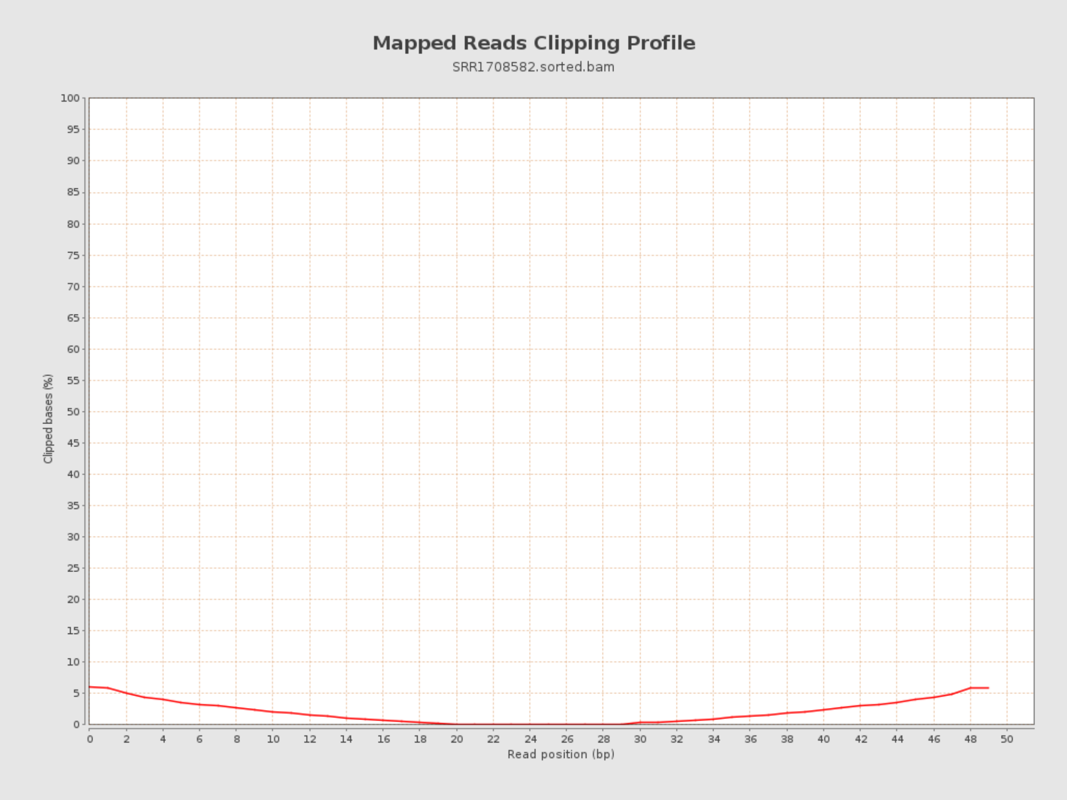
8. Results : Mapped Reads Nucleotide Content



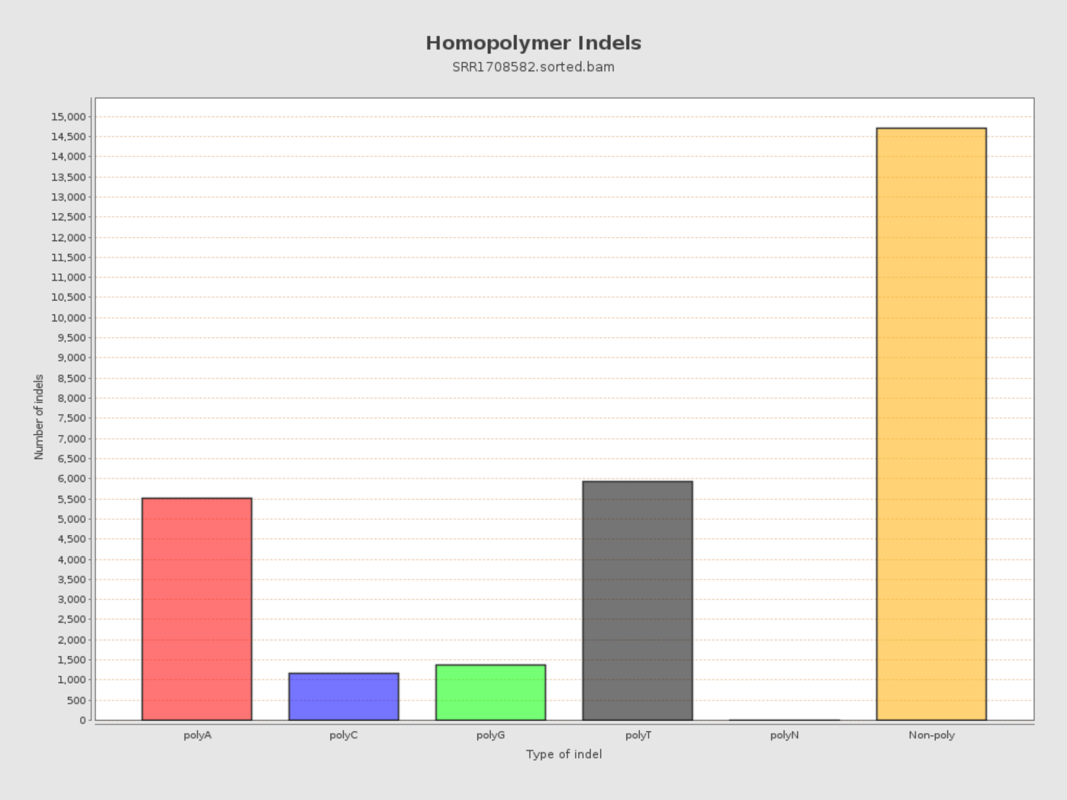
9. Results : Mapped Reads GC-content Distribution



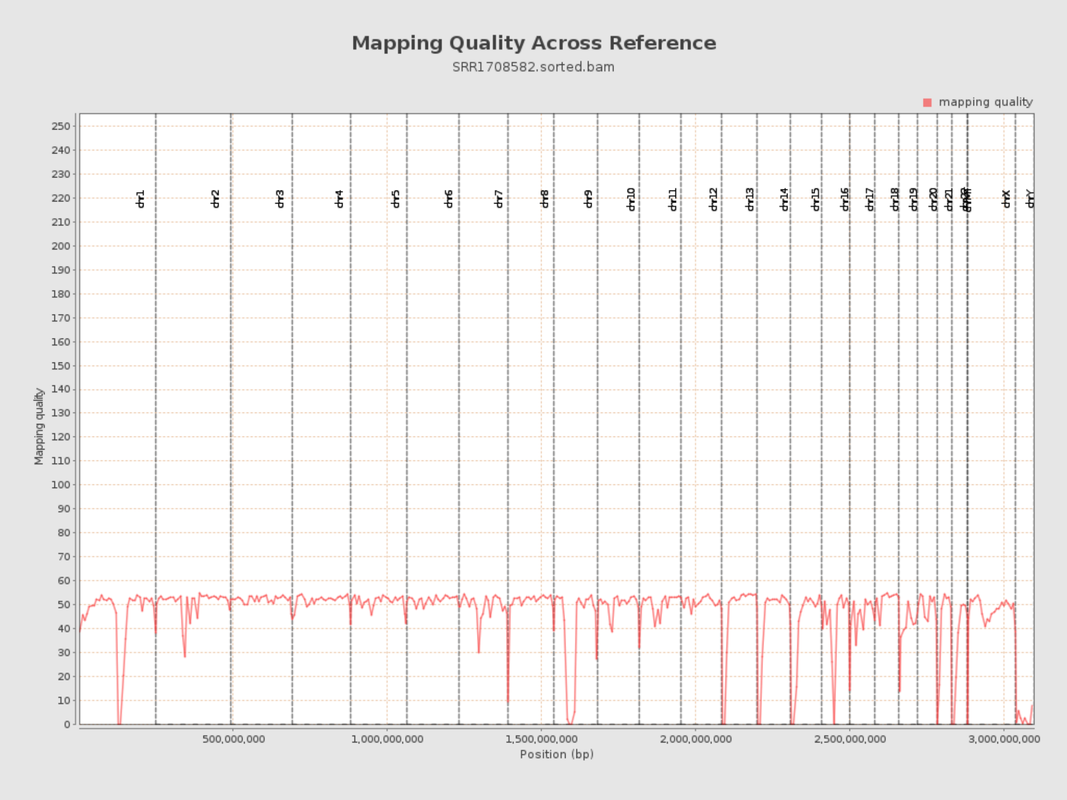
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram