Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:44:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708642.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_SRR1708642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708642.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:44:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,326,904
Mapped reads	5,141,904 / 96.53%
Unmapped reads	185,000 / 3.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	124 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	26,057 / 0.49%
Duplication rate	0.5%
Clipped reads	67,645 / 1.27%

2.2. ACGT Content

Number/percentage of A's	79,289,926 / 30.92%
Number/percentage of C's	48,748,243 / 19.01%
Number/percentage of T's	79,077,820 / 30.84%
Number/percentage of G's	49,324,567 / 19.23%
Number/percentage of N's	8,844 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	0.0828

Standard Deviation	0.3015

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

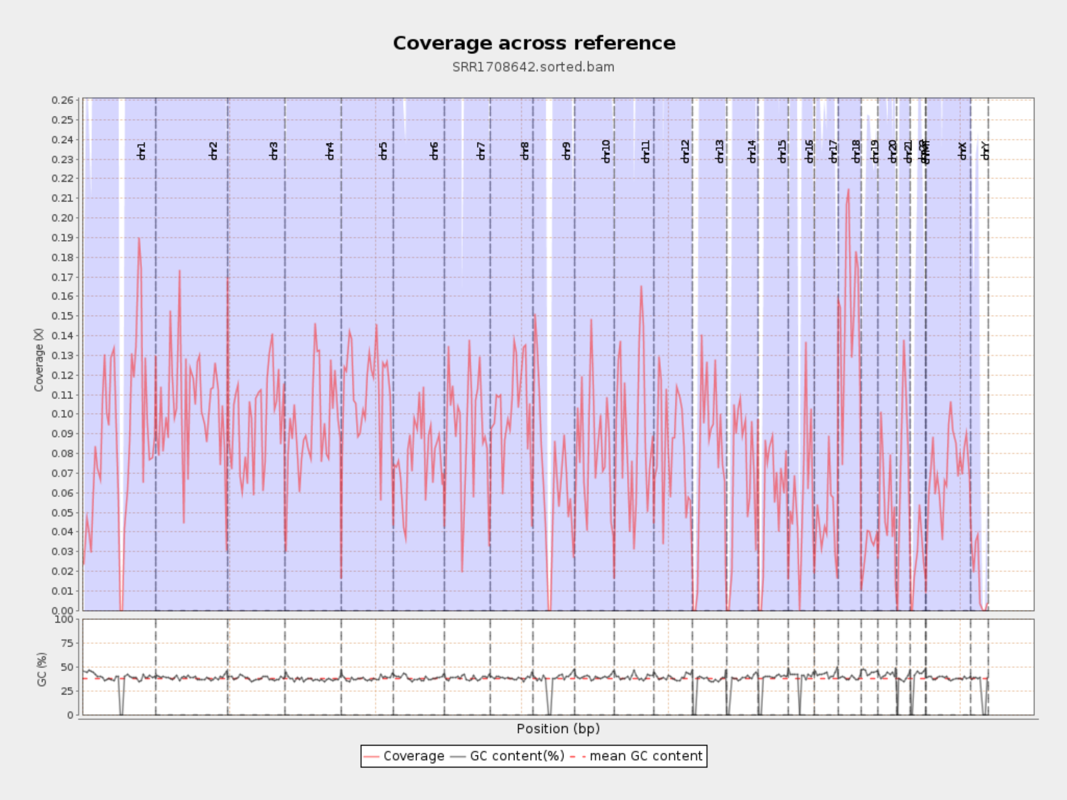
General error rate	0.17%
Mismatches	417,855
Insertions	17,337
Mapped reads with at least one insertion	0.34%
Deletions	14,583
Mapped reads with at least one deletion	0.28%
Homopolymer indels	49.04%

2.6. Chromosome stats

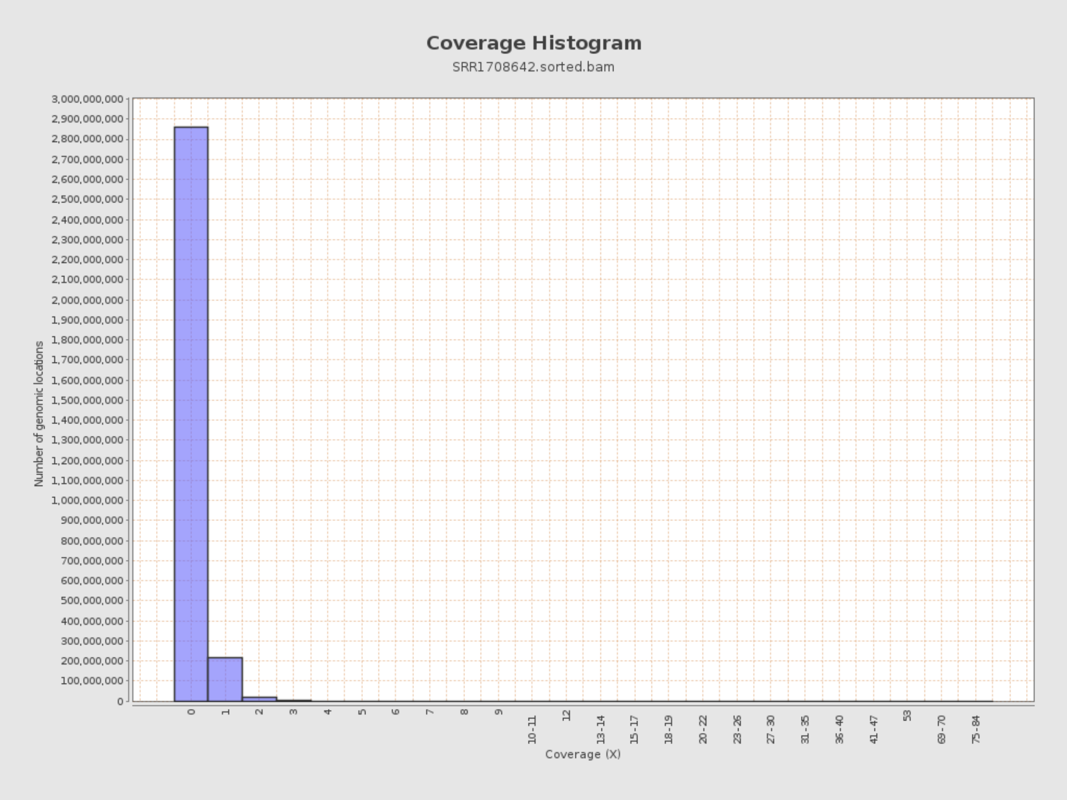
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21462073	0.0861	0.3103
chr2	243199373	25140630	0.1034	0.335
chr3	198022430	19277089	0.0973	0.3246
chr4	191154276	18070385	0.0945	0.3189
chr5	180915260	19931637	0.1102	0.3457
chr6	171115067	13547796	0.0792	0.2919
chr7	159138663	14352760	0.0902	0.3143

chr8	146364022	15091713	0.1031	0.3346
chr9	141213431	9488135	0.0672	0.2711
chr10	135534747	11457619	0.0845	0.3029
chr11	135006516	12175828	0.0902	0.3159
chr12	133851895	10991312	0.0821	0.2983
chr13	115169878	9001705	0.0782	0.2927
chr14	107349540	7187401	0.067	0.2703
chr15	102531392	5799071	0.0566	0.2479
chr16	90354753	5158572	0.0571	0.2501
chr17	81195210	3747958	0.0462	0.2251
chr18	78077248	12096782	0.1549	0.4159
chr19	59128983	1918546	0.0324	0.1854
chr20	63025520	3580753	0.0568	0.2471
chr21	48129895	3503953	0.0728	0.2863
chr22	51304566	1309825	0.0255	0.1657
chrMT	16571	150	0.0091	0.0947
chrX	155270560	11225713	0.0723	0.2787
chrY	59373566	957278	0.0161	0.1314

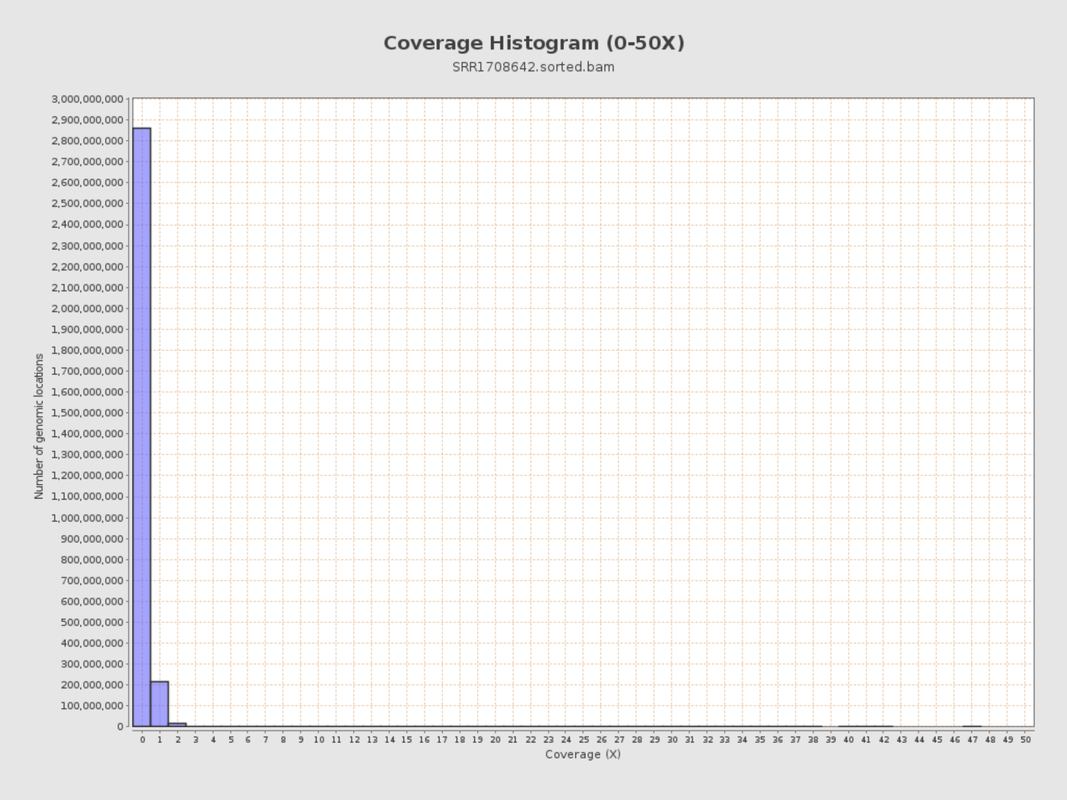
3. Results : Coverage across reference



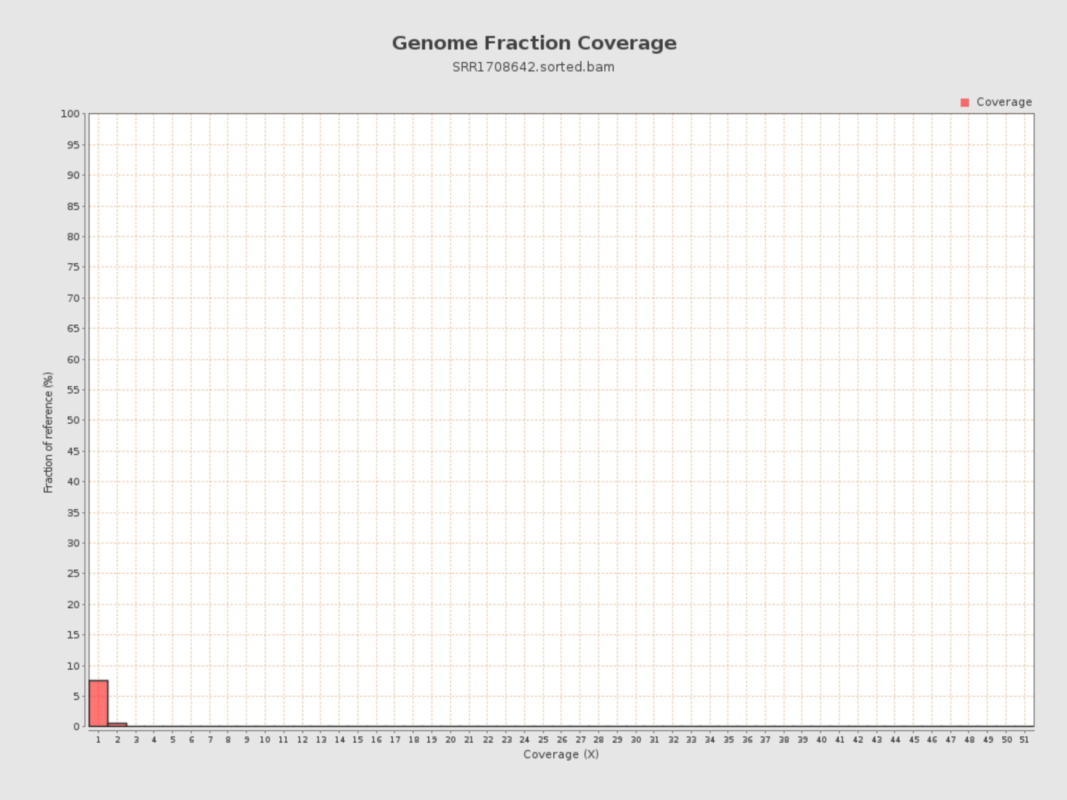
4. Results : Coverage Histogram



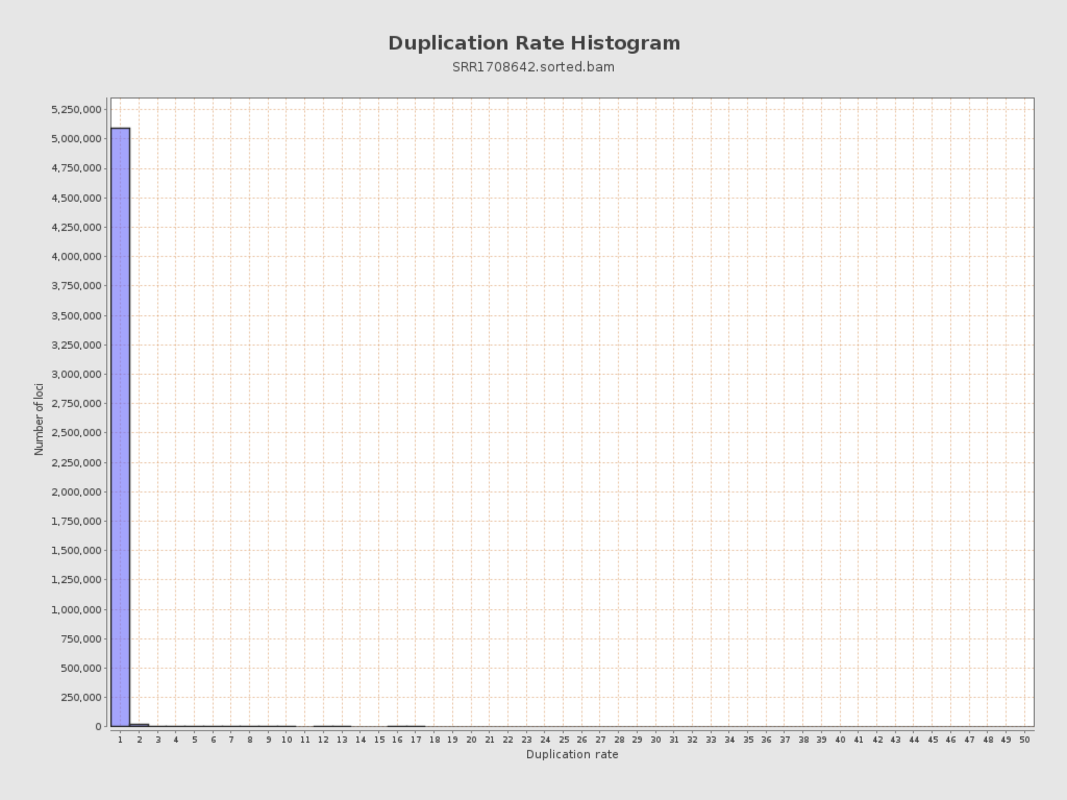
5. Results : Coverage Histogram (0-50X)



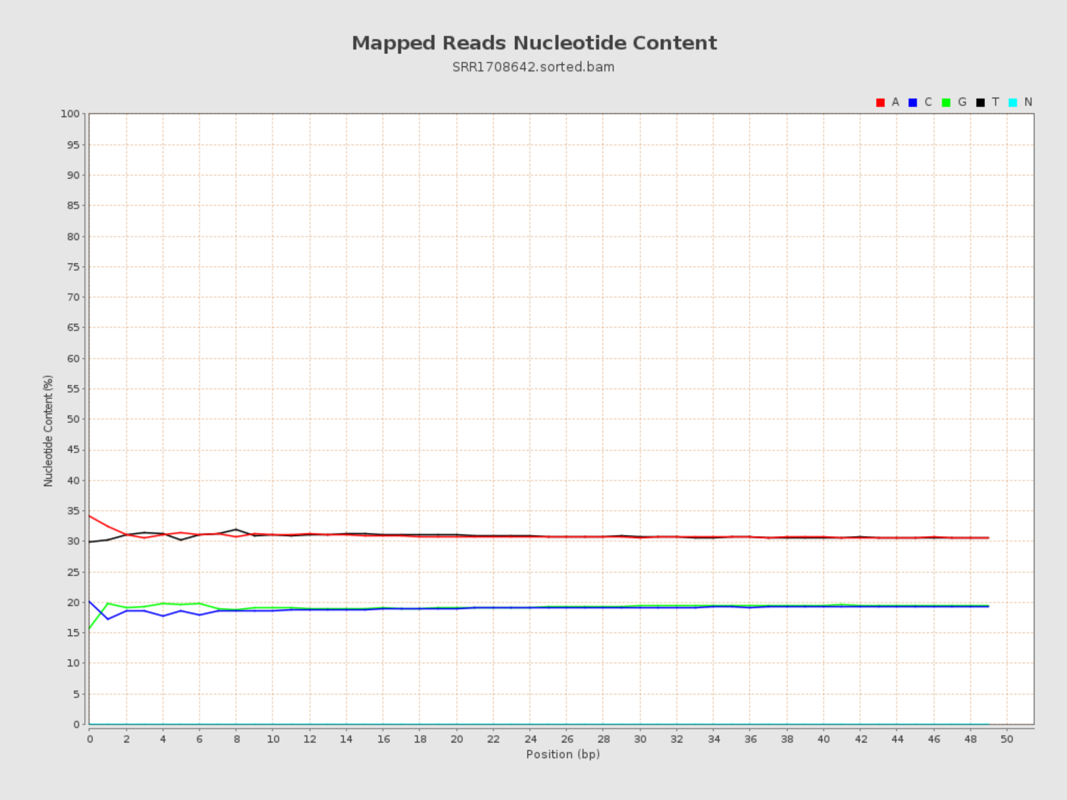
6. Results : Genome Fraction Coverage



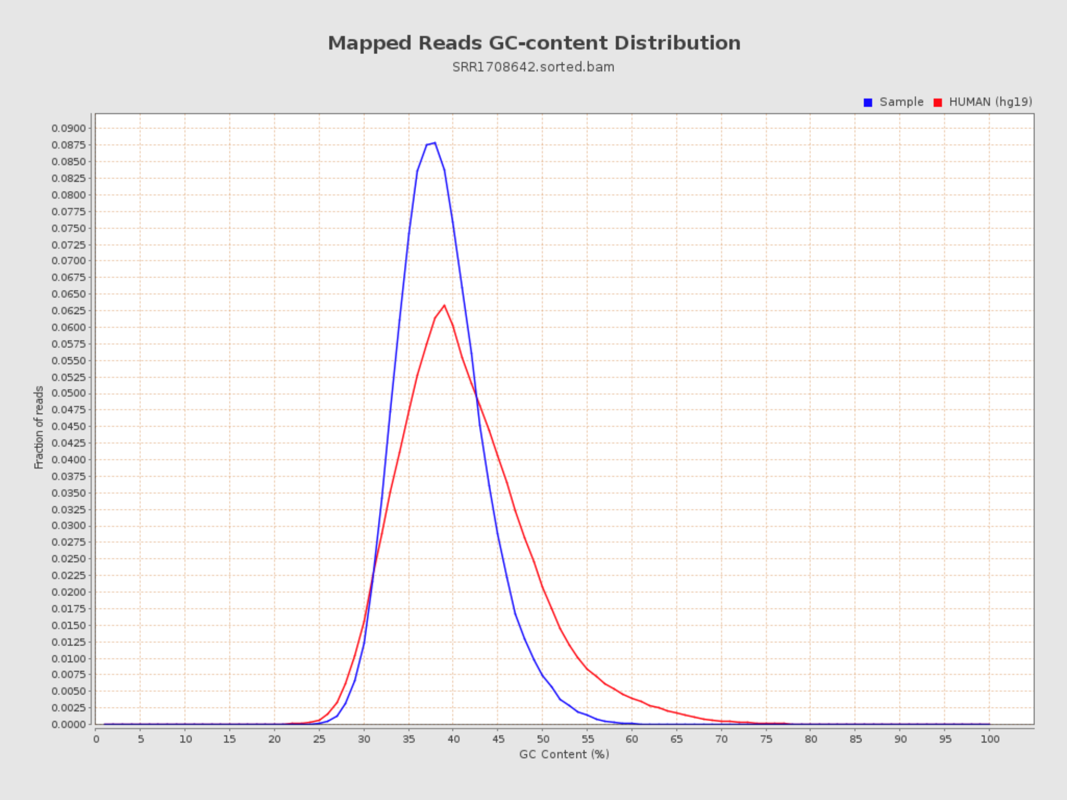
7. Results : Duplication Rate Histogram



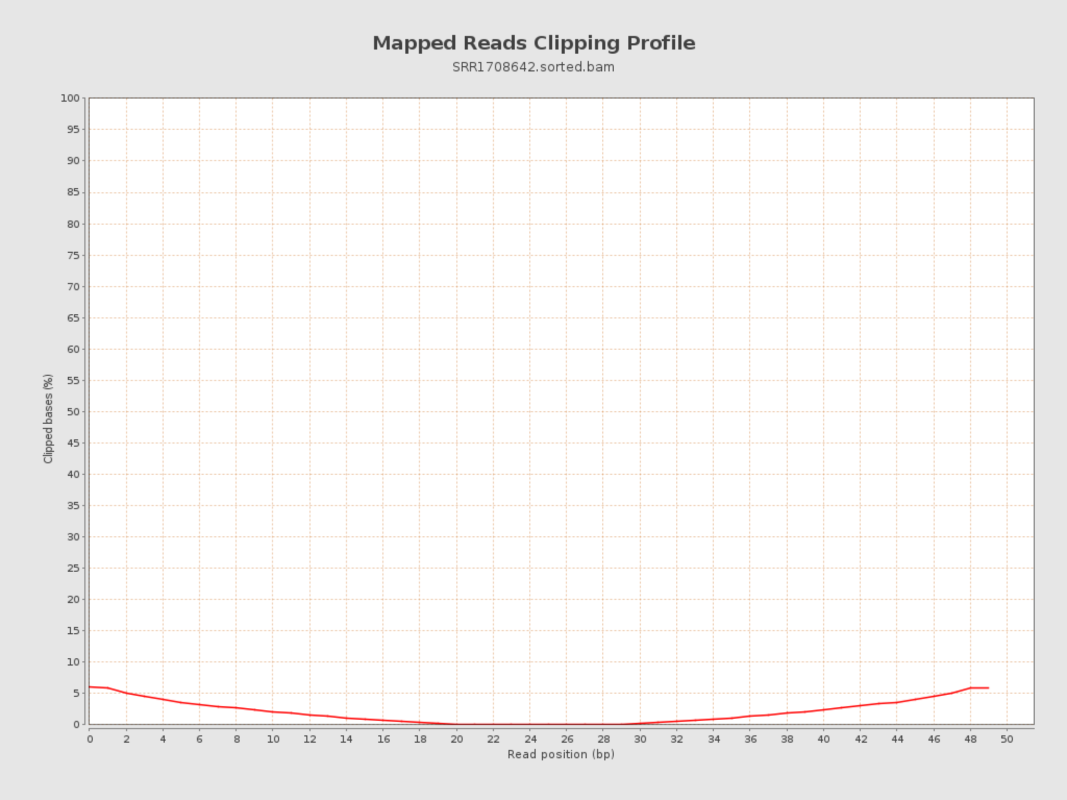
8. Results : Mapped Reads Nucleotide Content



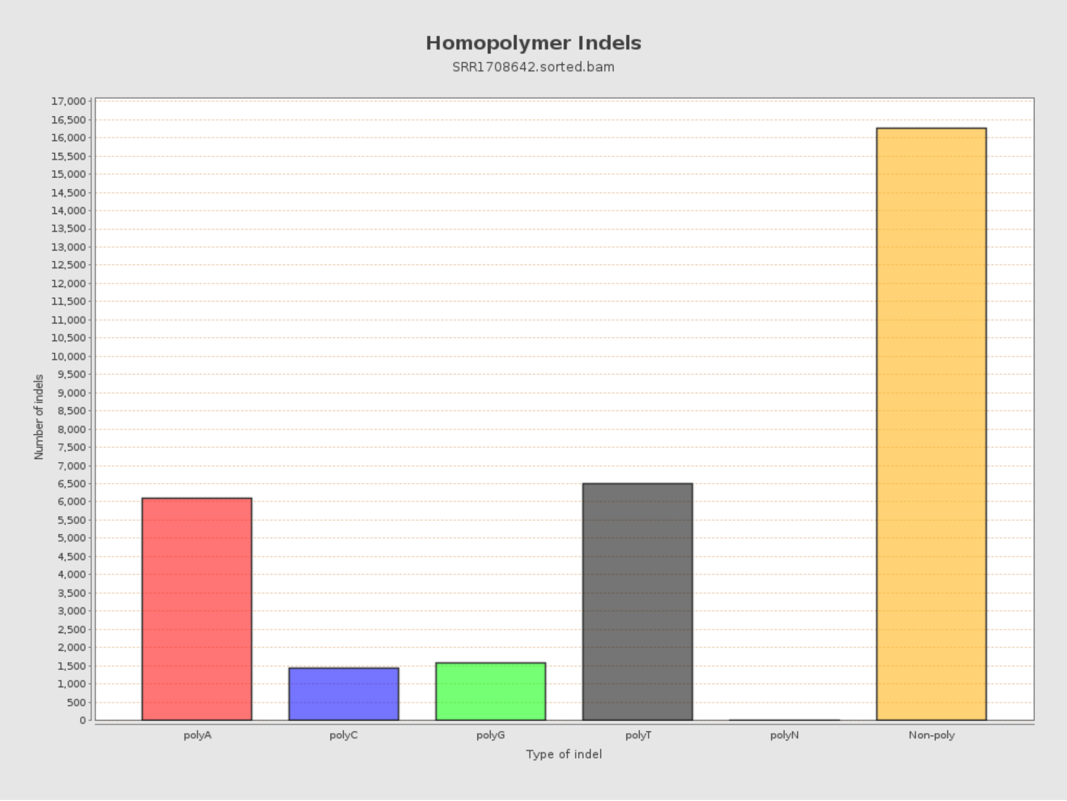
9. Results : Mapped Reads GC-content Distribution



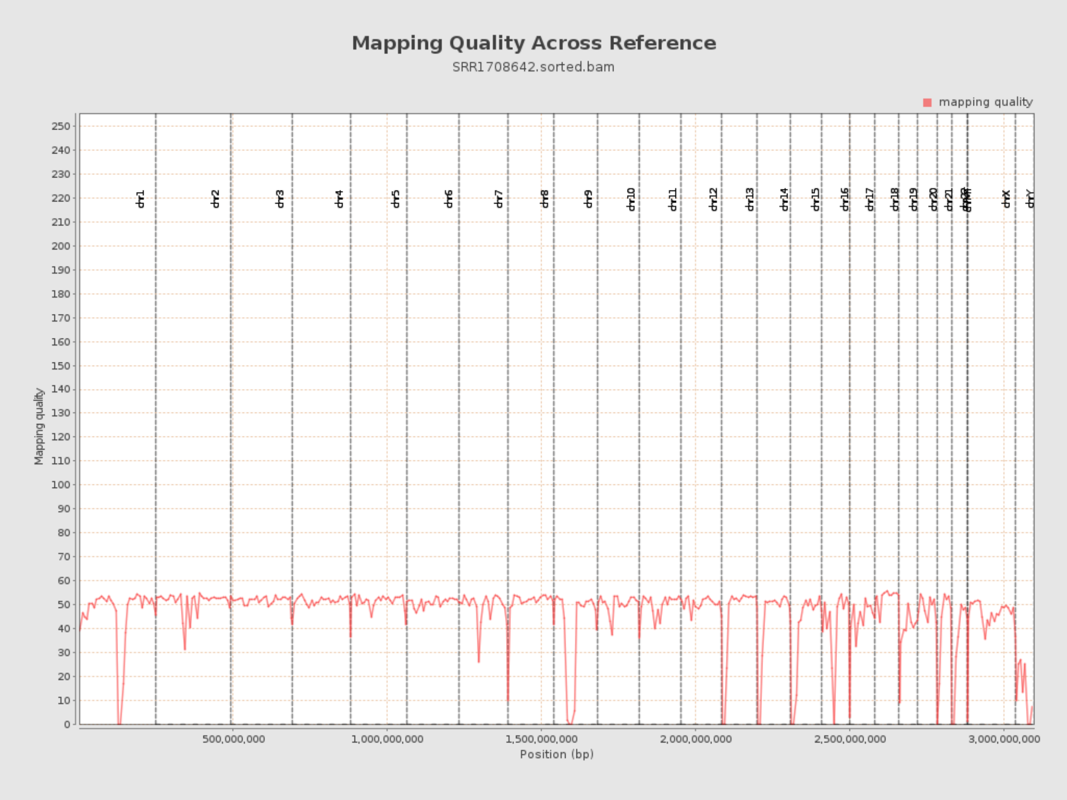
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram