Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:59:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008798.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_SRR6008798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:59:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,682,607
Mapped reads	1,449,688 / 86.16%
Unmapped reads	232,919 / 13.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,400 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	187,301 / 11.13%
Duplication rate	9.61%
Clipped reads	709,412 / 42.16%

2.2. ACGT Content

Number/percentage of A's	26,226,509 / 27.61%
Number/percentage of C's	17,090,227 / 17.99%
Number/percentage of T's	30,714,991 / 32.33%
Number/percentage of G's	20,921,555 / 22.02%
Number/percentage of N's	44,820 / 0.05%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.4023

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

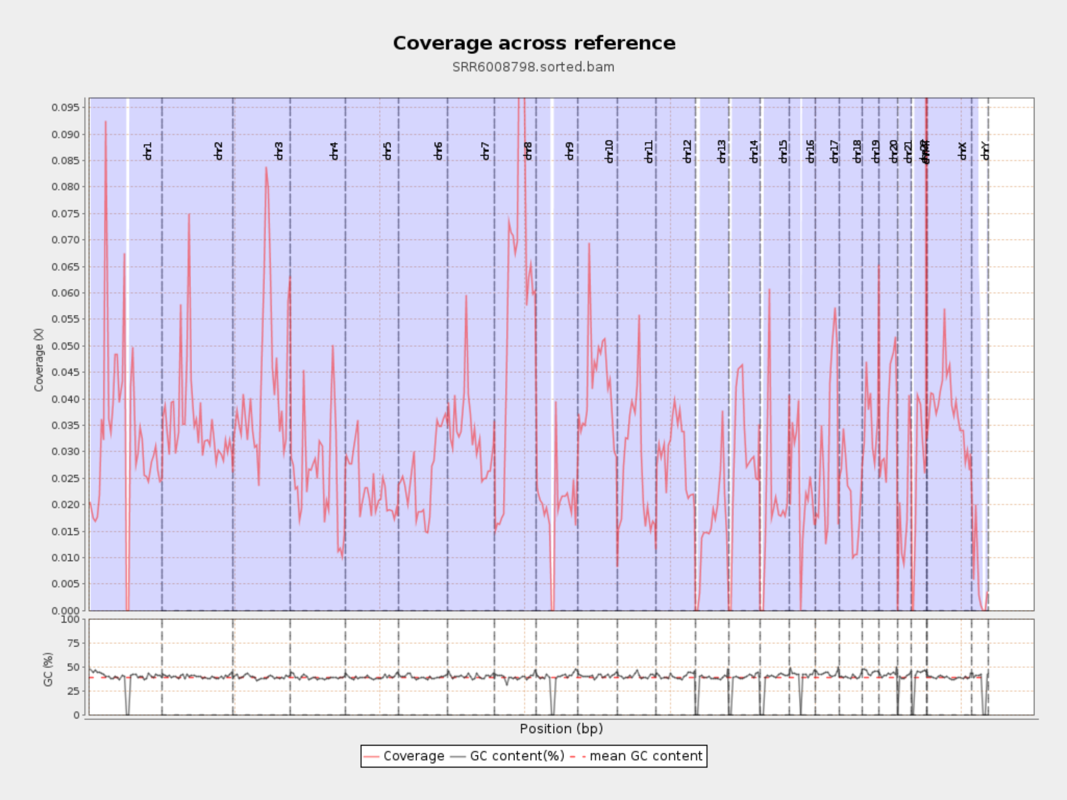
General error rate	0.82%
Mismatches	766,965
Insertions	7,246
Mapped reads with at least one insertion	0.5%
Deletions	20,234
Mapped reads with at least one deletion	1.38%
Homopolymer indels	48.16%

2.6. Chromosome stats

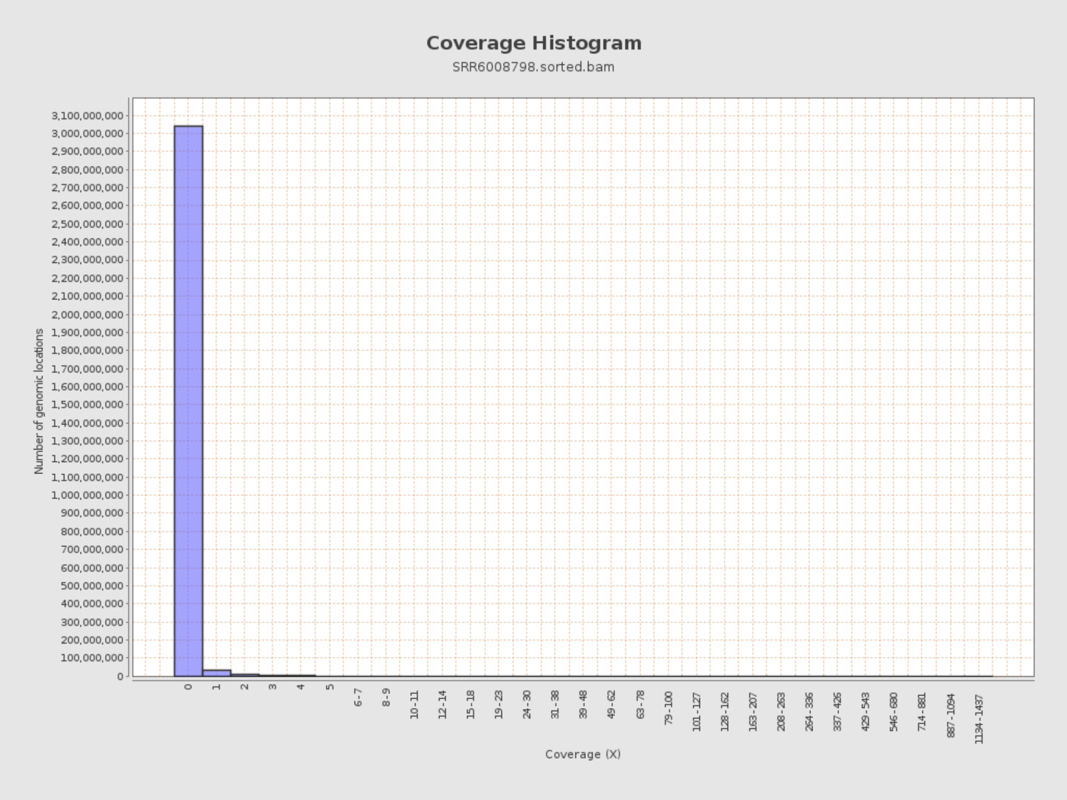
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8103233	0.0325	0.6121
chr2	243199373	8758883	0.036	0.4189
chr3	198022430	8448152	0.0427	0.3287
chr4	191154276	4818787	0.0252	0.2658
chr5	180915260	4213107	0.0233	0.2399
chr6	171115067	4335129	0.0253	0.2618
chr7	159138663	5347940	0.0336	0.4139

chr8	146364022	8547701	0.0584	0.9325
chr9	141213431	2689444	0.019	0.3085
chr10	135534747	5808073	0.0429	0.3927
chr11	135006516	3668100	0.0272	0.3637
chr12	133851895	3988963	0.0298	0.273
chr13	115169878	1814813	0.0158	0.1966
chr14	107349540	3118984	0.0291	0.2739
chr15	102531392	2120087	0.0207	0.2209
chr16	90354753	2124017	0.0235	0.2469
chr17	81195210	2579130	0.0318	0.3224
chr18	78077248	1620147	0.0208	0.479
chr19	59128983	2168858	0.0367	0.4257
chr20	63025520	2337628	0.0371	0.3051
chr21	48129895	910995	0.0189	0.2206
chr22	51304566	1238054	0.0241	0.2373
chrMT	16571	14349	0.8659	1.7677
chrX	155270560	5918174	0.0381	0.3362
chrY	59373566	340106	0.0057	0.1931

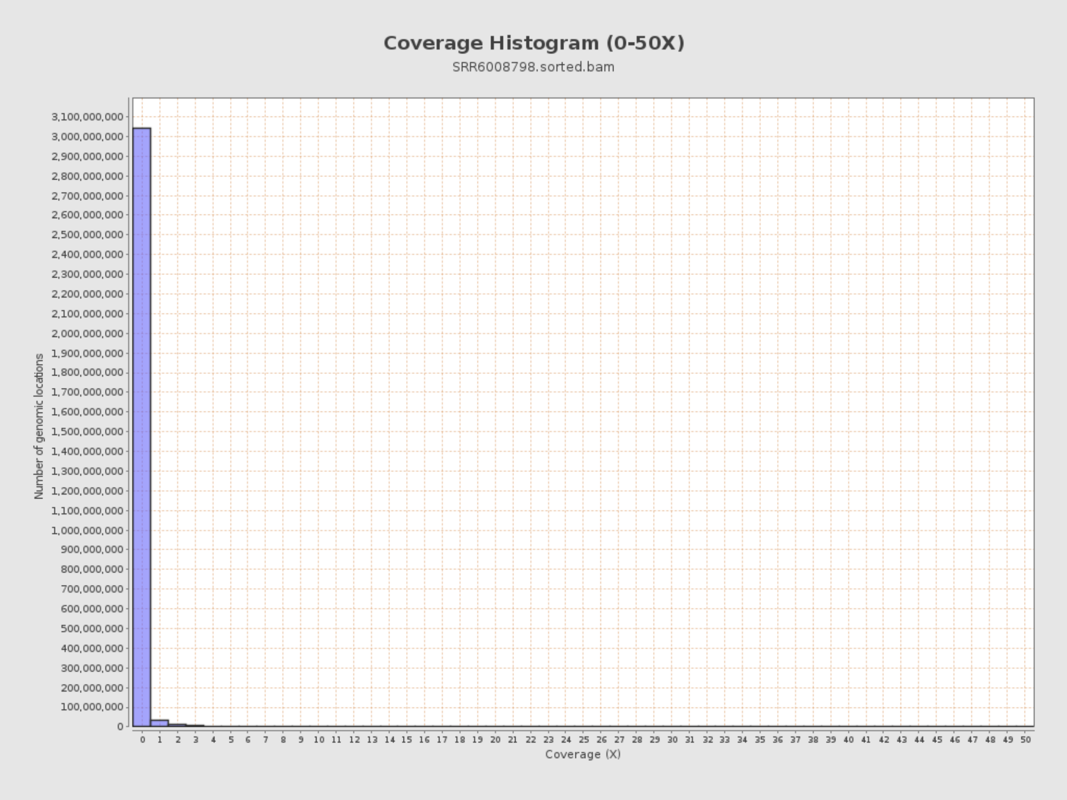
3. Results : Coverage across reference



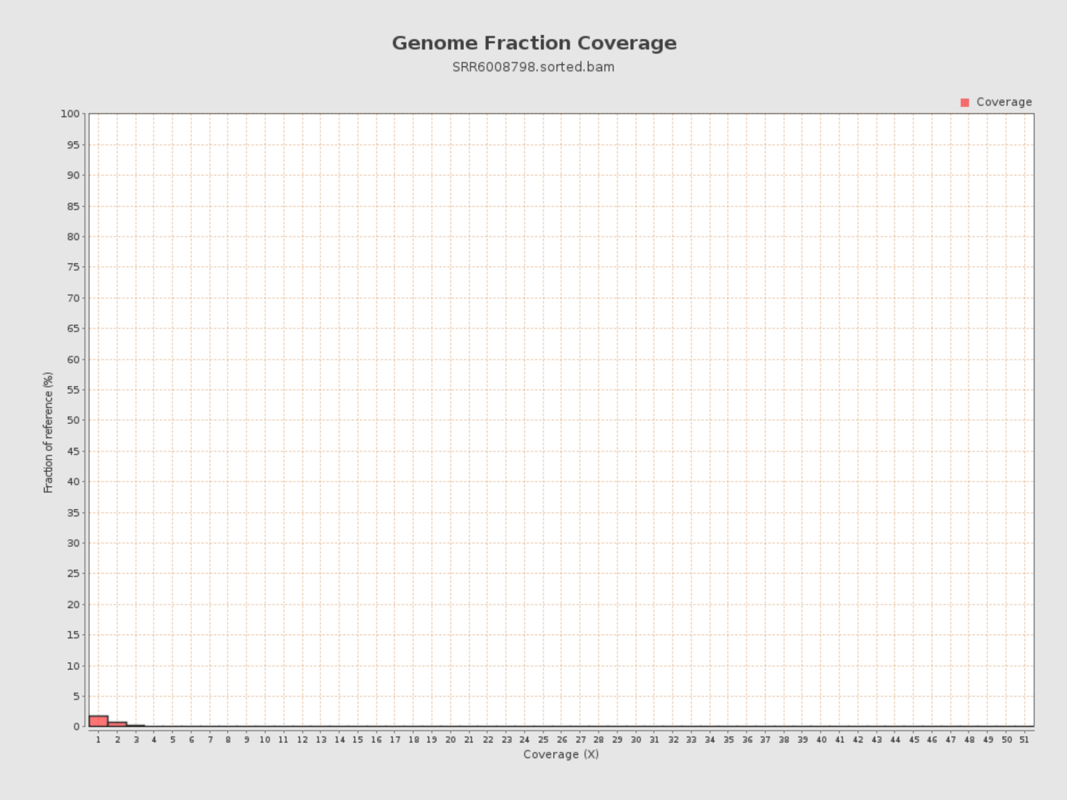
4. Results : Coverage Histogram



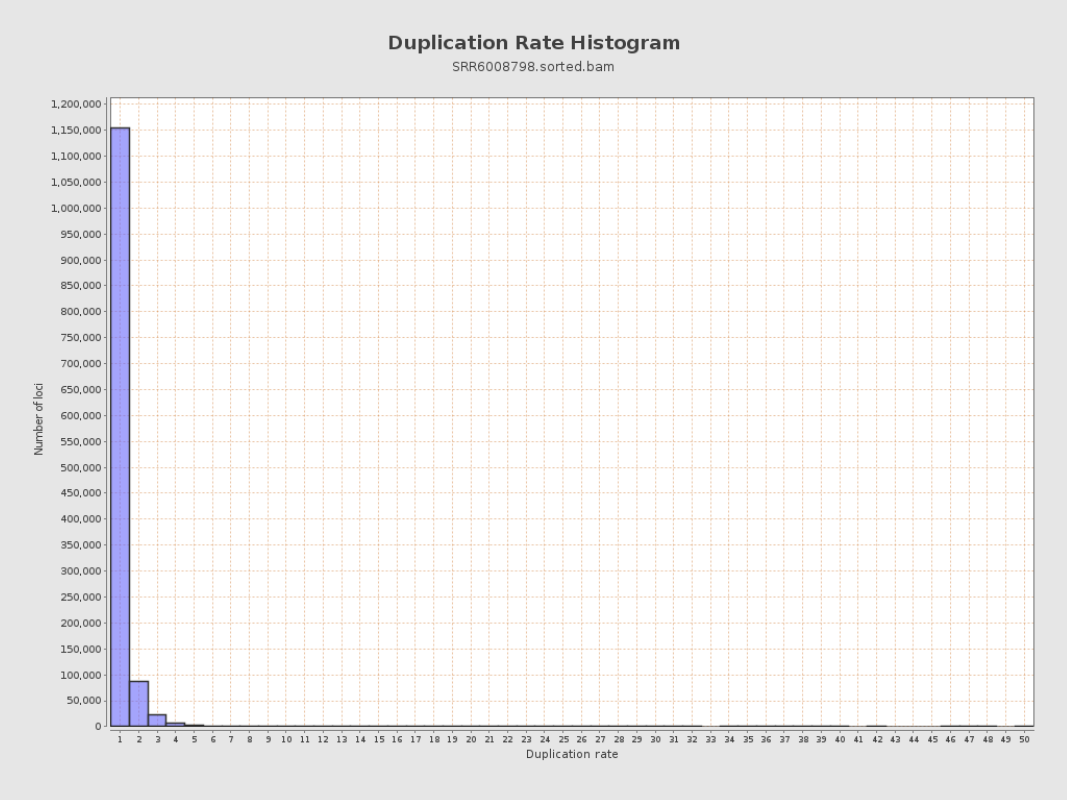
5. Results : Coverage Histogram (0-50X)



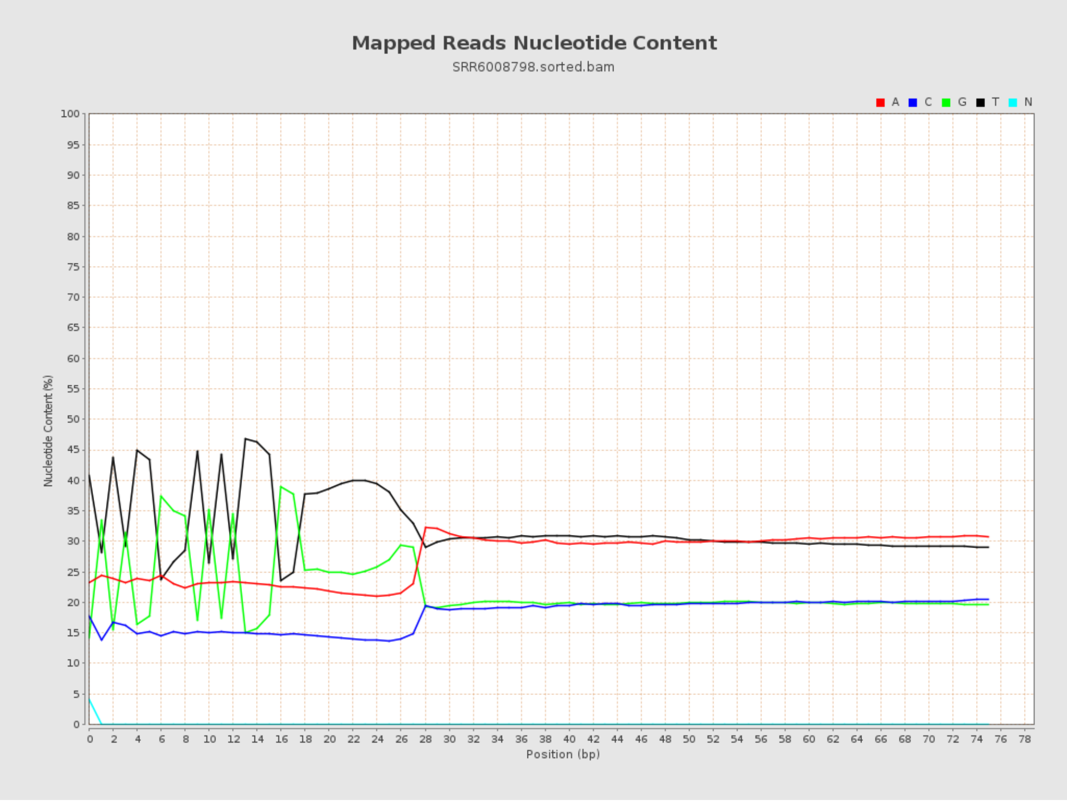
6. Results : Genome Fraction Coverage



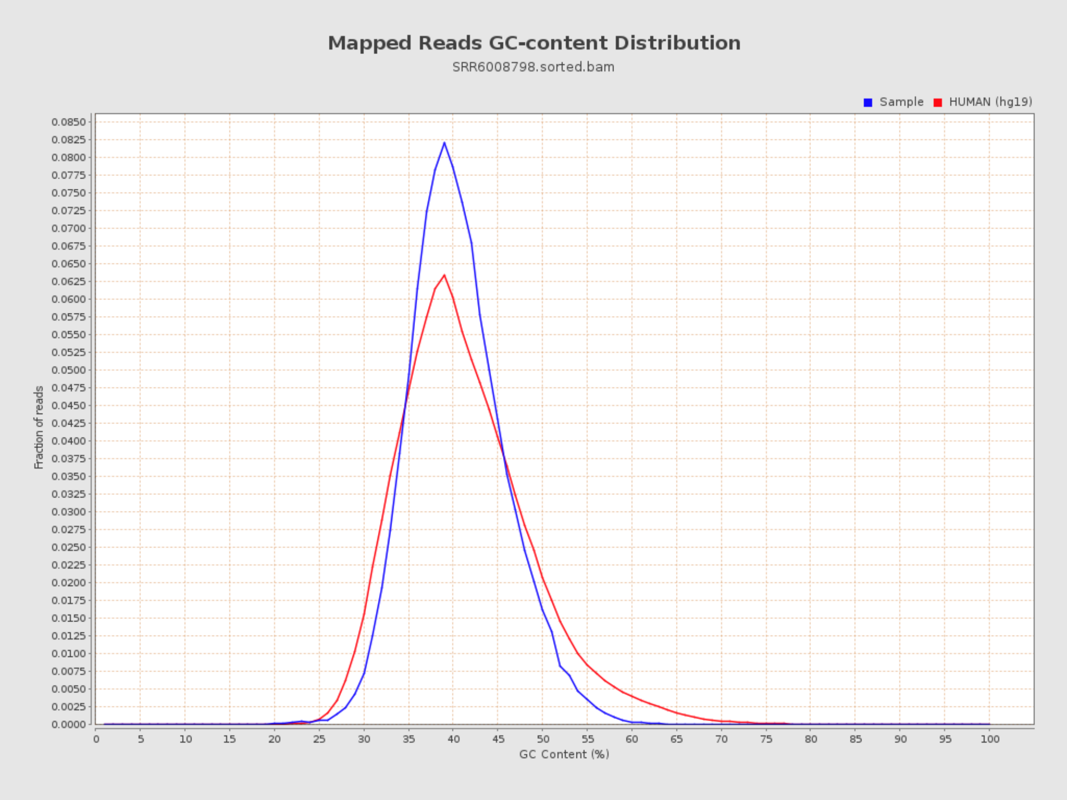
7. Results : Duplication Rate Histogram



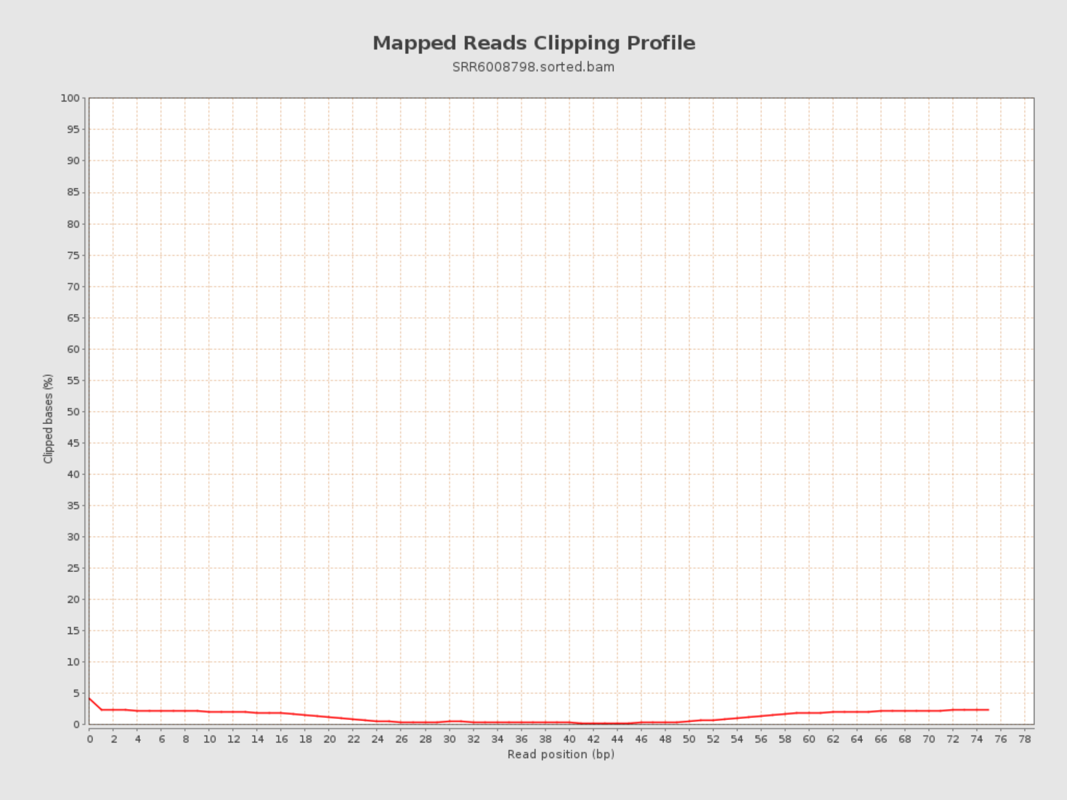
8. Results : Mapped Reads Nucleotide Content



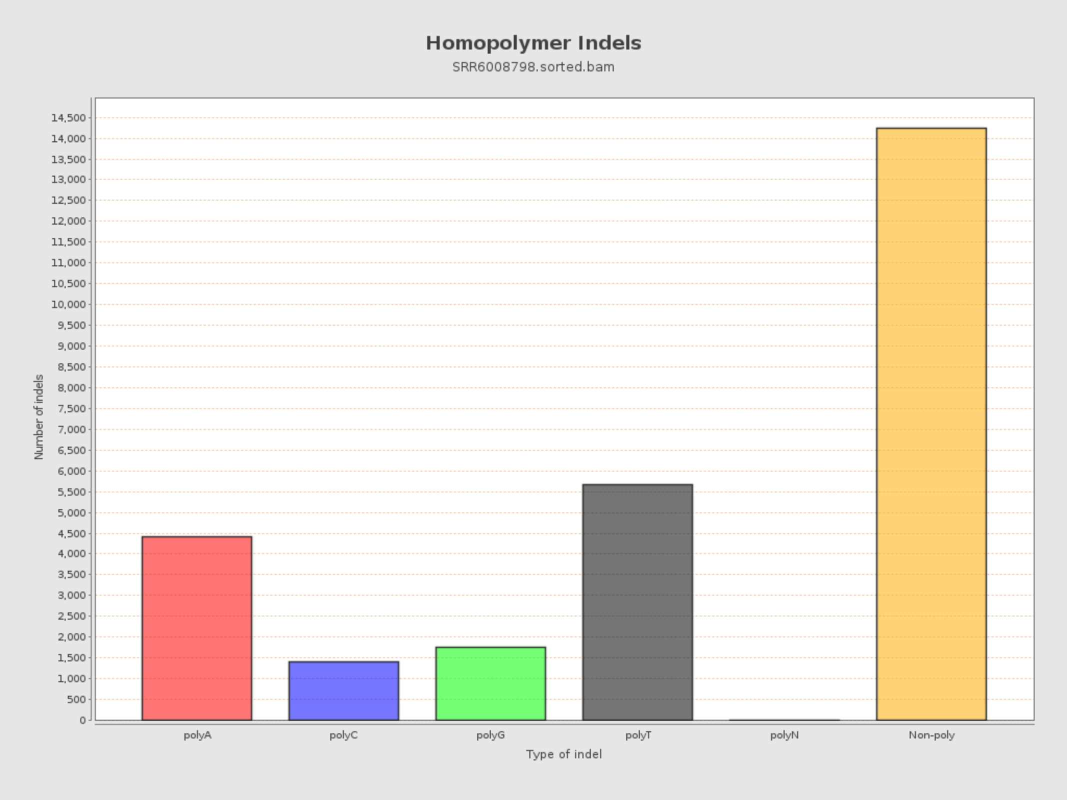
9. Results : Mapped Reads GC-content Distribution



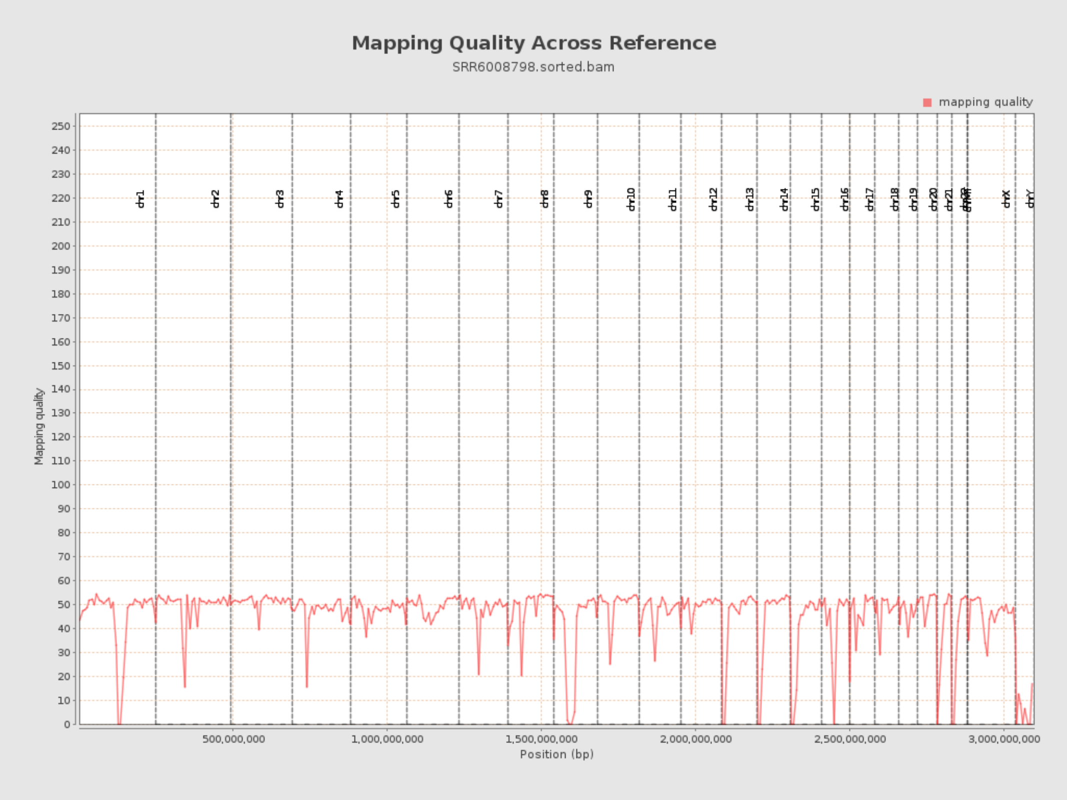
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram