Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:57:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708521.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_SRR1708521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708521.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:57:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,588,772
Mapped reads	2,553,953 / 71.17%
Unmapped reads	1,034,819 / 28.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	585 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	103,593 / 2.89%
Duplication rate	3.21%
Clipped reads	468,295 / 13.05%

2.2. ACGT Content

Number/percentage of A's	35,754,826 / 29.06%
Number/percentage of C's	23,013,274 / 18.71%
Number/percentage of T's	39,178,329 / 31.85%
Number/percentage of G's	25,075,184 / 20.38%
Number/percentage of N's	1,712 / 0%
GC Percentage	39.09%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3375

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

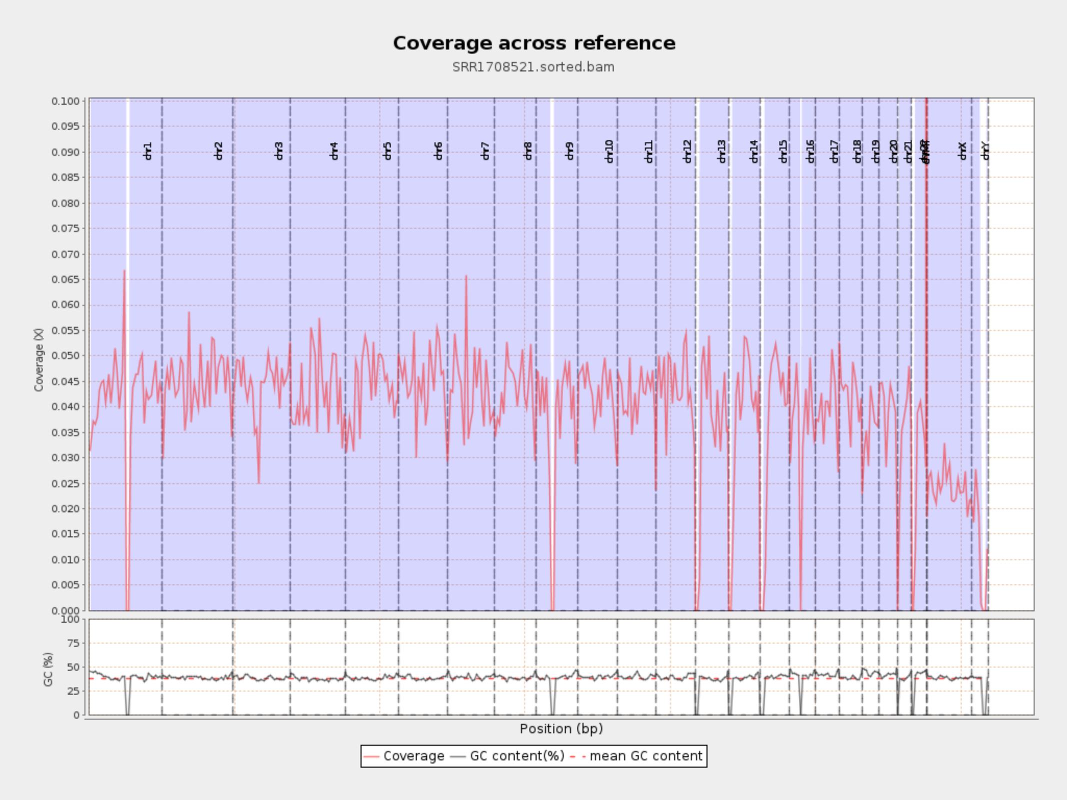
General error rate	0.48%
Mismatches	579,474
Insertions	5,883
Mapped reads with at least one insertion	0.23%
Deletions	14,716
Mapped reads with at least one deletion	0.57%
Homopolymer indels	49.18%

2.6. Chromosome stats

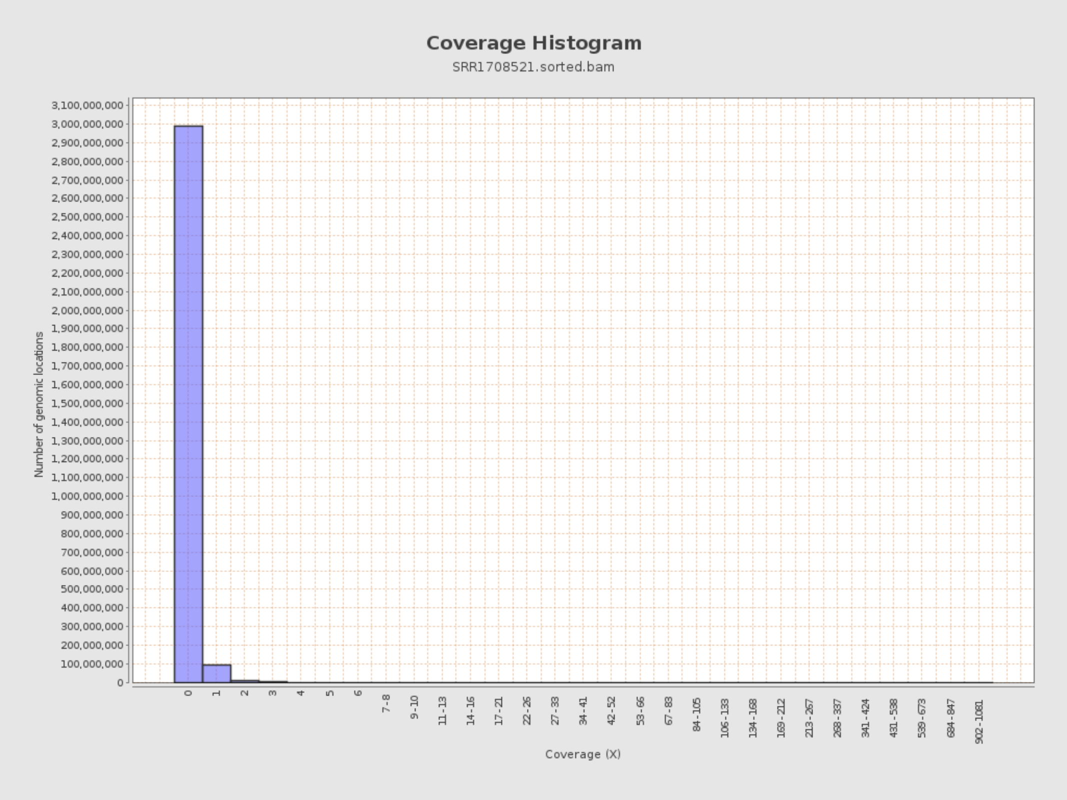
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10242177	0.0411	0.5936
chr2	243199373	10941304	0.045	0.3155
chr3	198022430	8744718	0.0442	0.2365
chr4	191154276	8144138	0.0426	0.2361
chr5	180915260	7923330	0.0438	0.236
chr6	171115067	7748981	0.0453	0.283
chr7	159138663	6974128	0.0438	0.4497

chr8	146364022	6283994	0.0429	0.6299
chr9	141213431	5165338	0.0366	0.2571
chr10	135534747	5858648	0.0432	0.2819
chr11	135006516	5687570	0.0421	0.3012
chr12	133851895	5902042	0.0441	0.2396
chr13	115169878	3974577	0.0345	0.2093
chr14	107349540	3899195	0.0363	0.2178
chr15	102531392	3642315	0.0355	0.2117
chr16	90354753	3247038	0.0359	0.217
chr17	81195210	3180610	0.0392	0.2632
chr18	78077248	3354644	0.043	0.3995
chr19	59128983	2112782	0.0357	0.4295
chr20	63025520	2488743	0.0395	0.2235
chr21	48129895	1604965	0.0333	0.2268
chr22	51304566	1315872	0.0256	0.1904
chrMT	16571	159539	9.6276	7.1035
chrX	155270560	3750785	0.0242	0.1939
chrY	59373566	698359	0.0118	0.1313

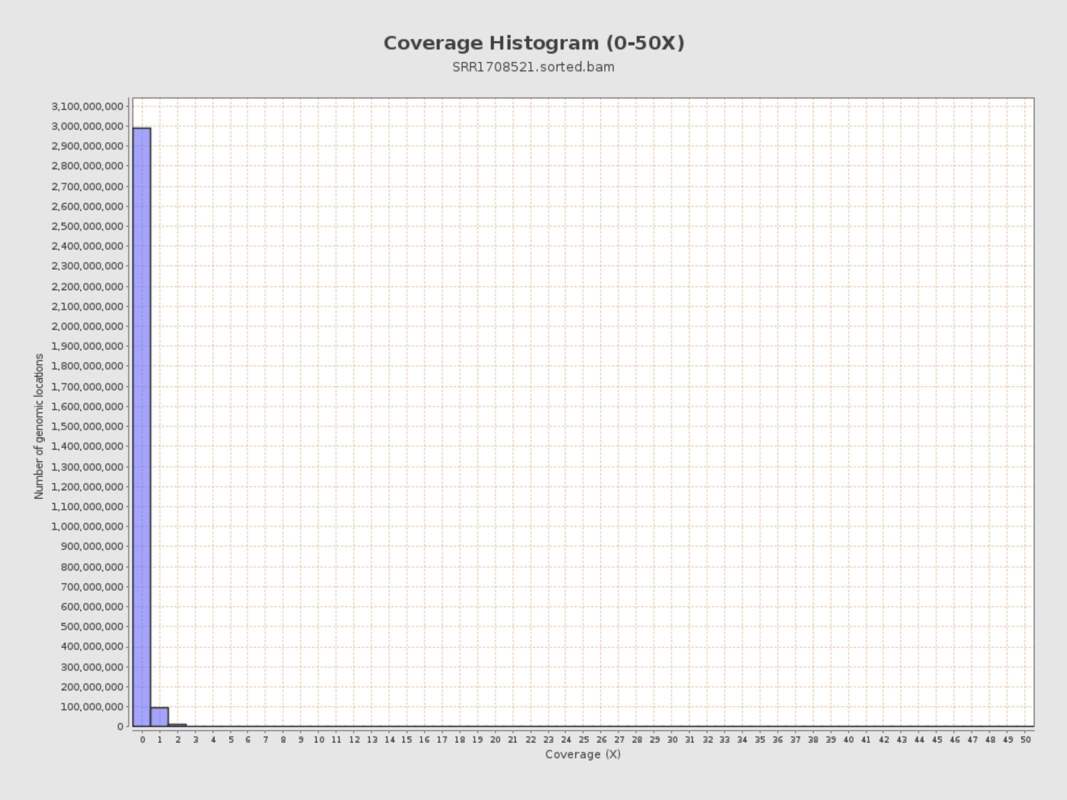
3. Results : Coverage across reference



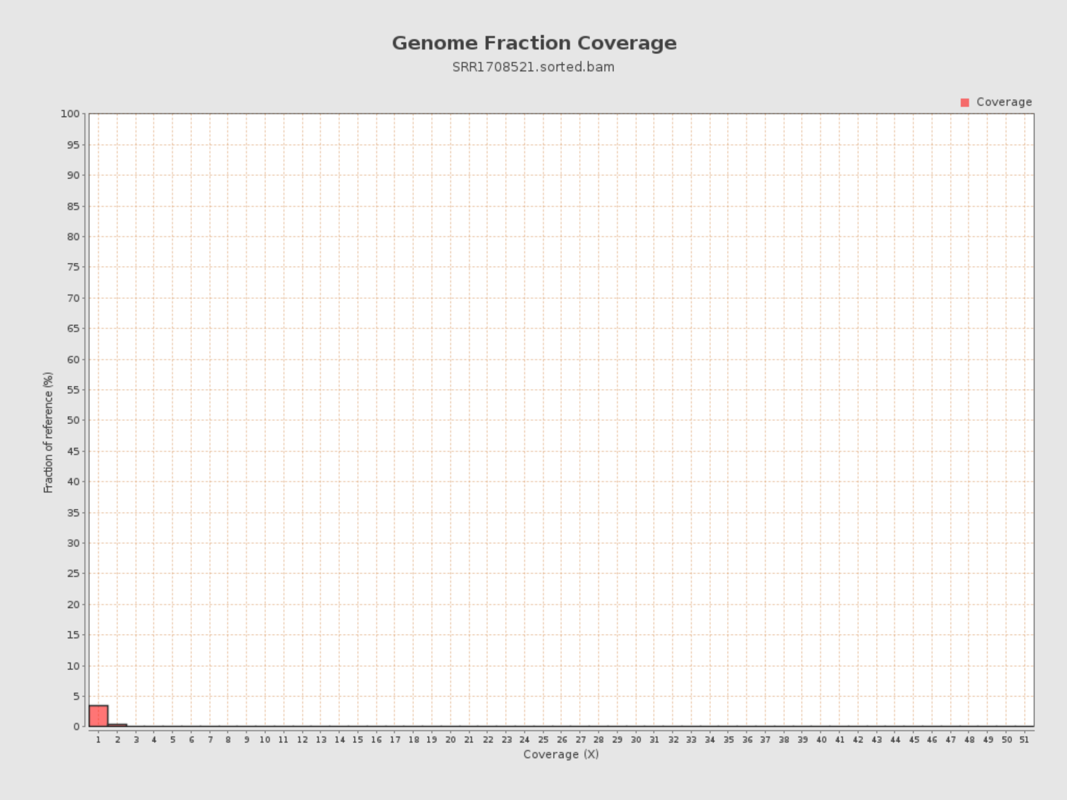
4. Results : Coverage Histogram



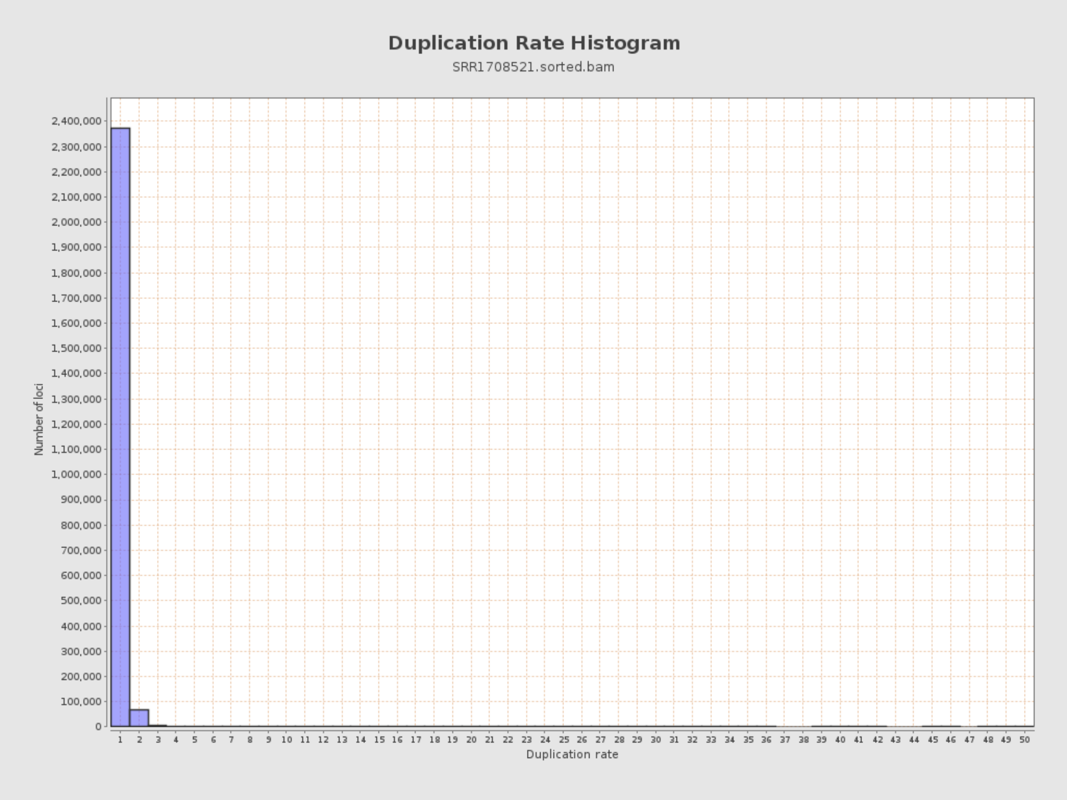
5. Results : Coverage Histogram (0-50X)



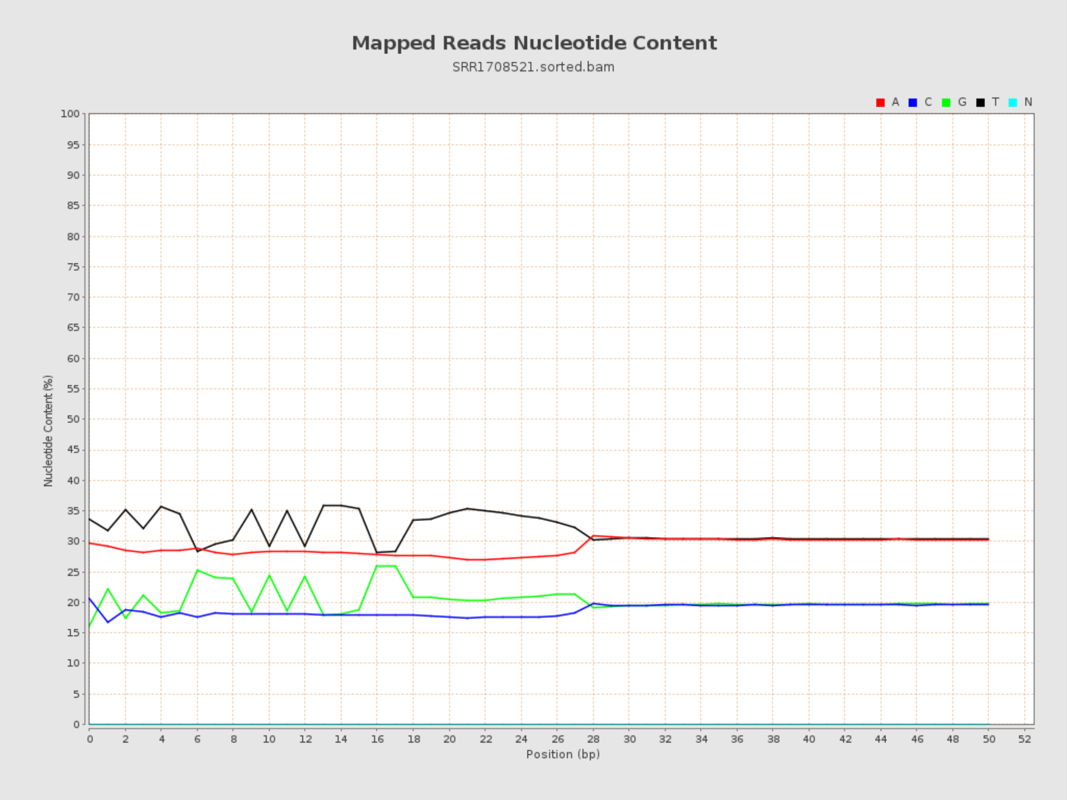
6. Results : Genome Fraction Coverage



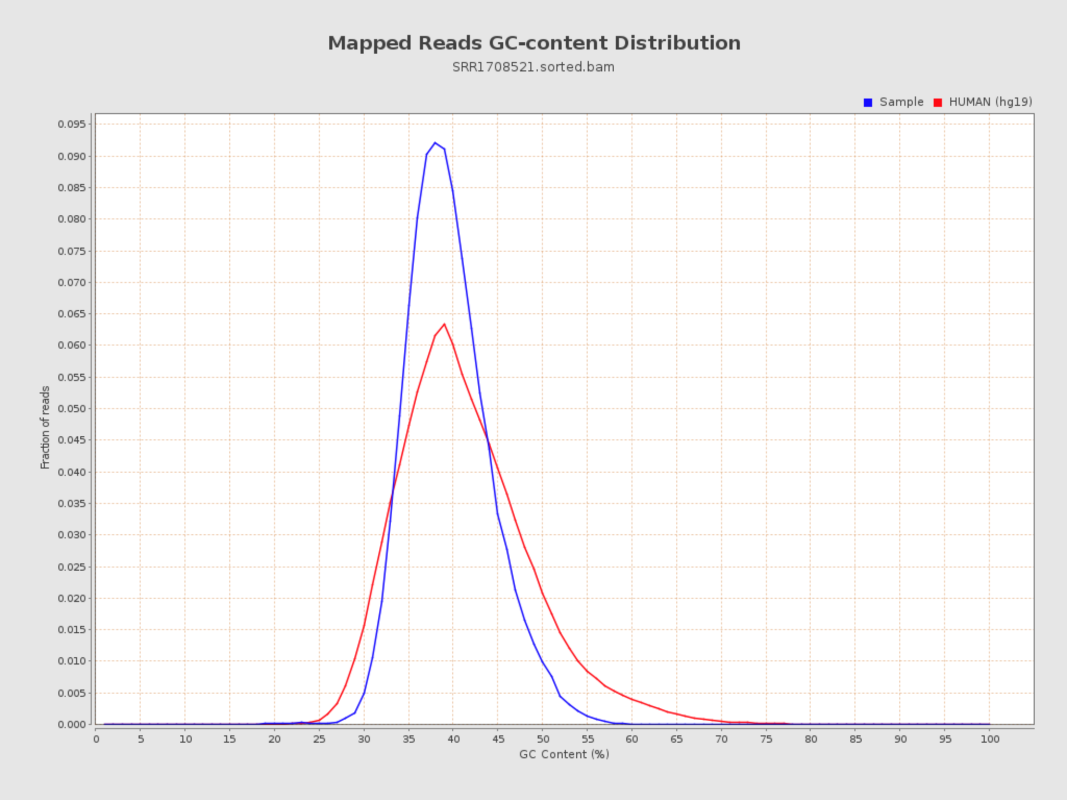
7. Results : Duplication Rate Histogram



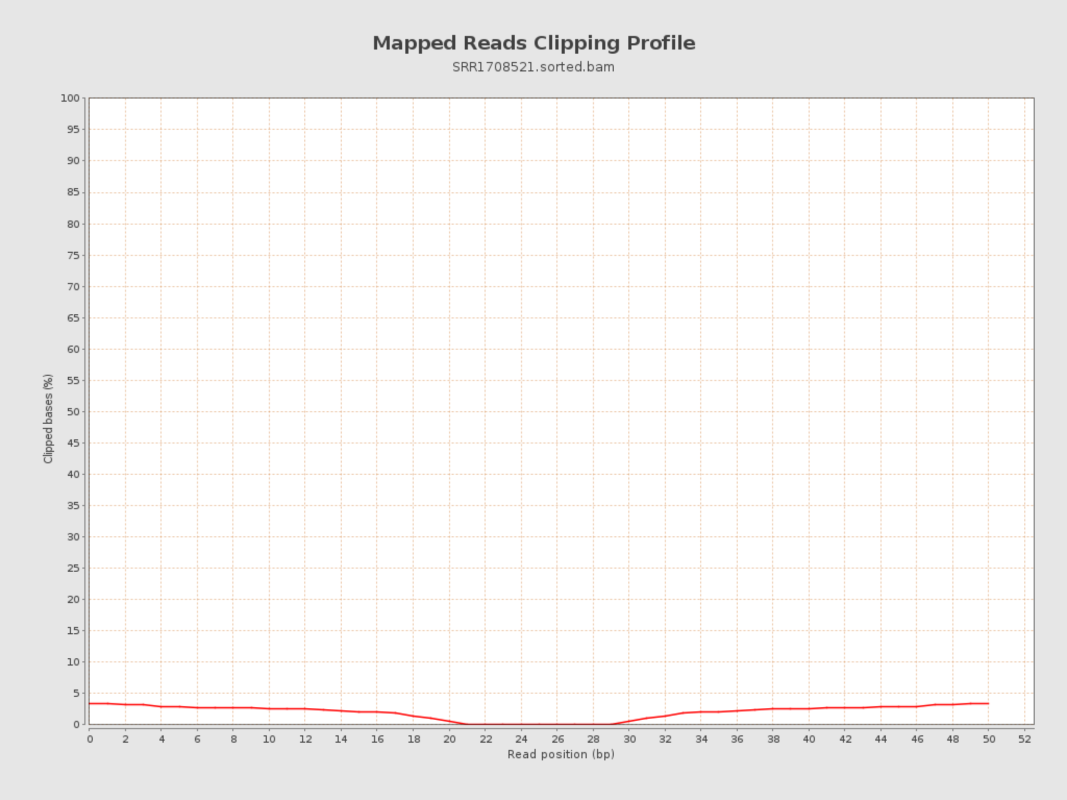
8. Results : Mapped Reads Nucleotide Content



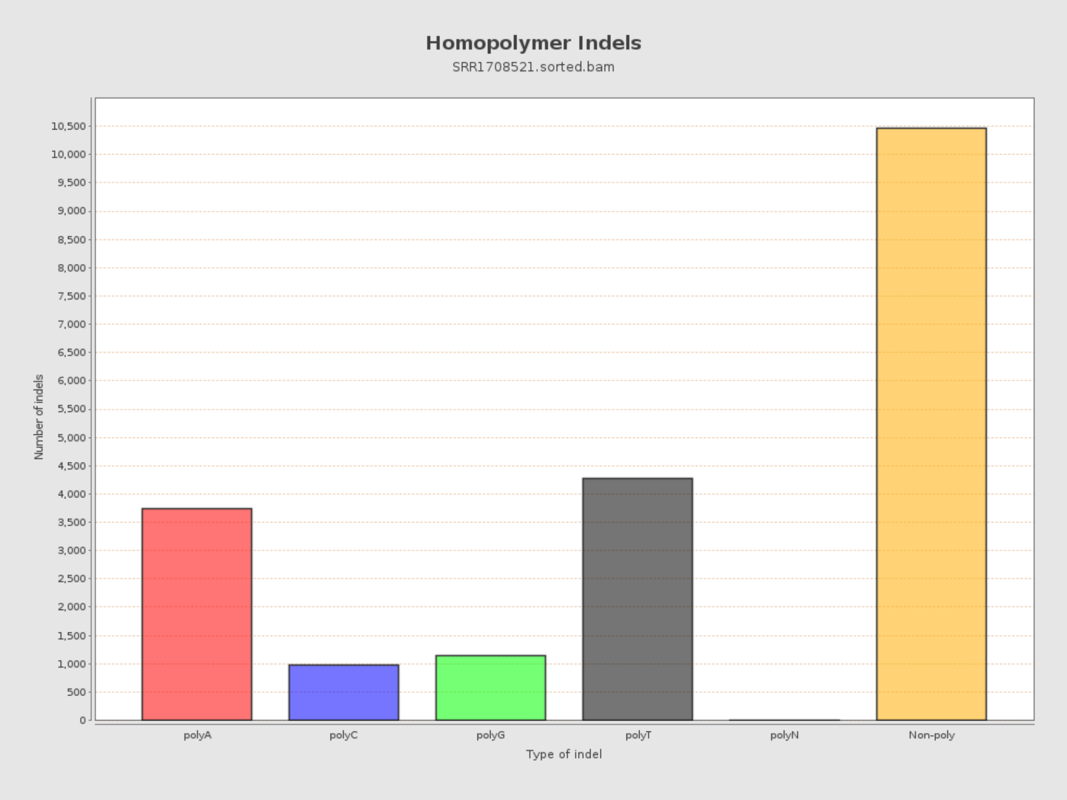
9. Results : Mapped Reads GC-content Distribution



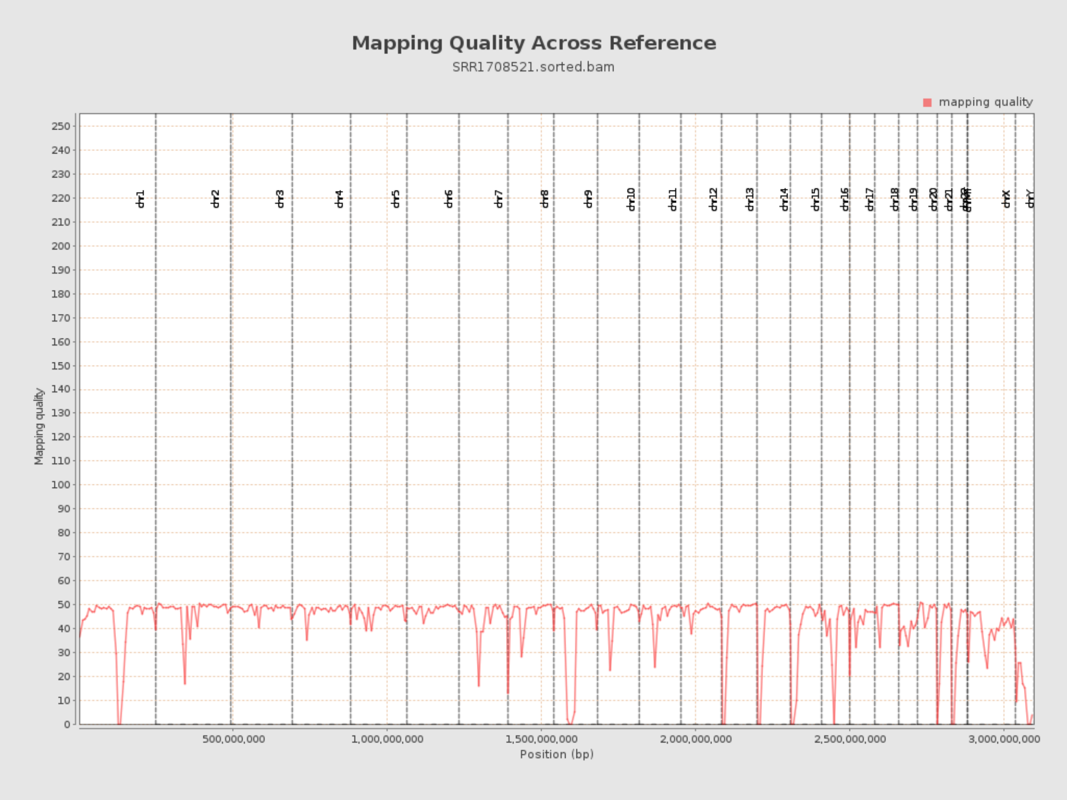
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram