Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:52:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708562.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_SRR1708562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708562.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:52:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,494,671
Mapped reads	3,703,583 / 82.4%
Unmapped reads	791,088 / 17.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	81 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,249 / 0.38%
Duplication rate	0.46%
Clipped reads	50,153 / 1.12%

2.2. ACGT Content

Number/percentage of A's	57,312,343 / 31.03%
Number/percentage of C's	34,965,830 / 18.93%
Number/percentage of T's	57,074,072 / 30.9%
Number/percentage of G's	35,323,906 / 19.13%
Number/percentage of N's	6,647 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	0.0597

Standard Deviation	0.2526

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

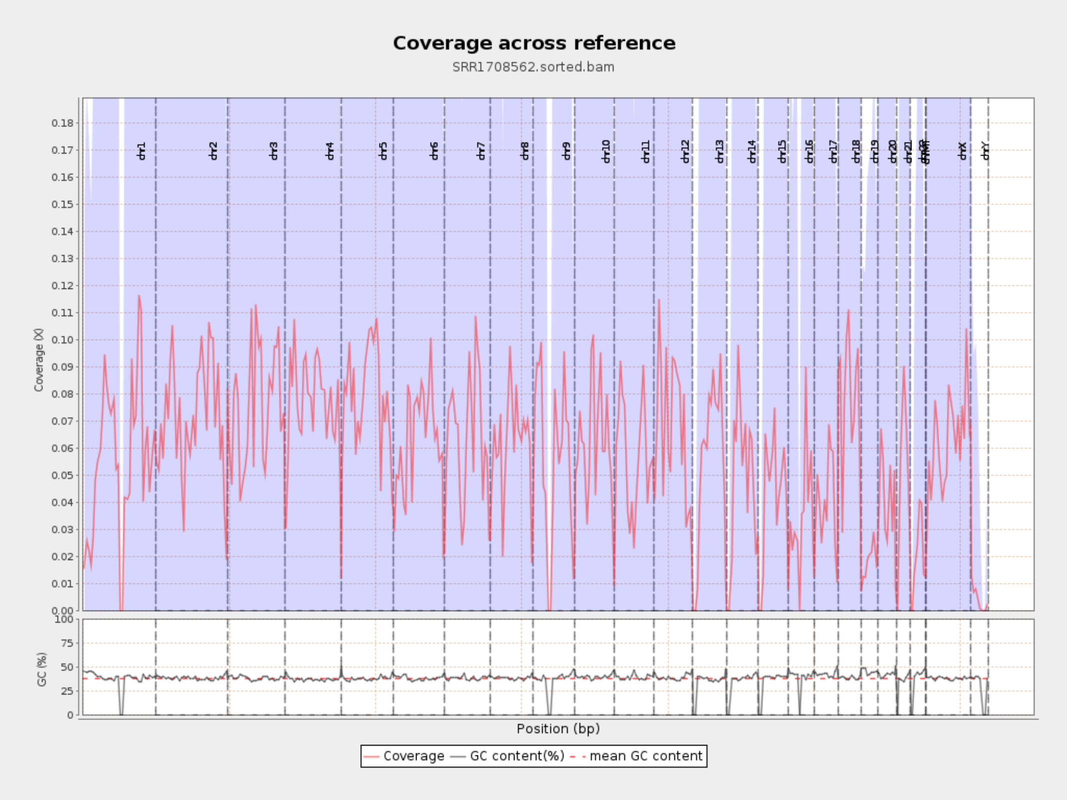
General error rate	0.17%
Mismatches	293,561
Insertions	12,227
Mapped reads with at least one insertion	0.33%
Deletions	10,076
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.91%

2.6. Chromosome stats

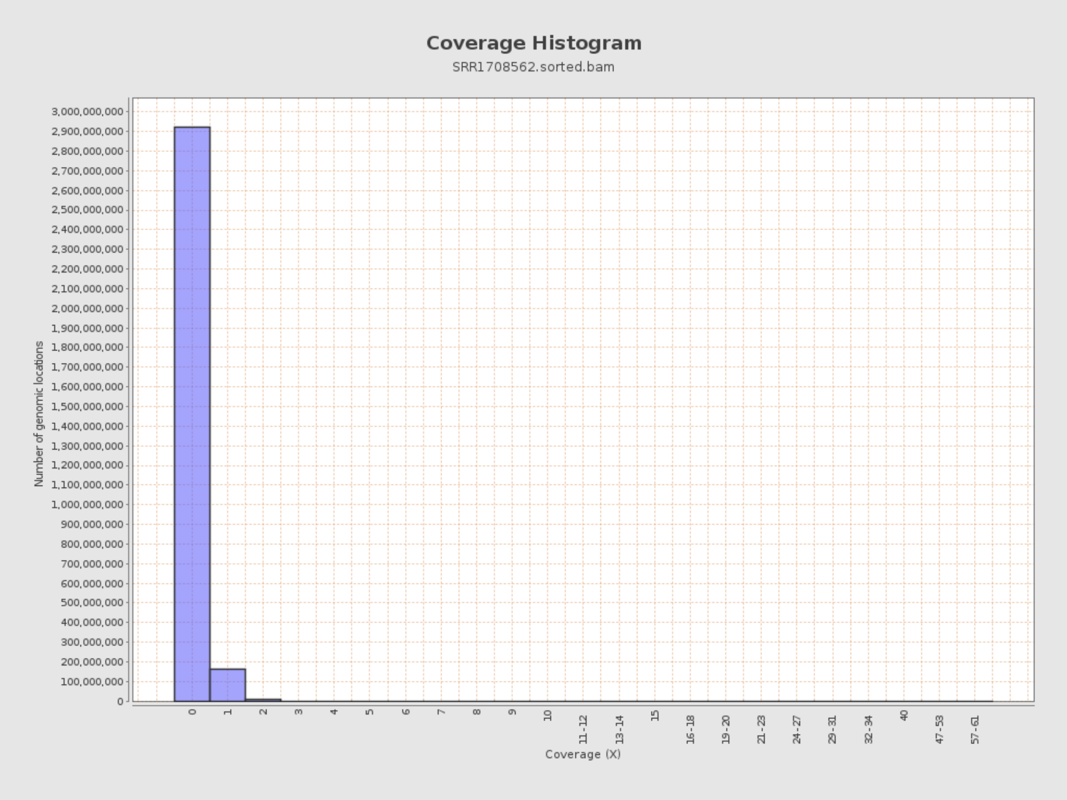
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13854646	0.0556	0.2453
chr2	243199373	17484785	0.0719	0.2763
chr3	198022430	14970617	0.0756	0.2833
chr4	191154276	14790631	0.0774	0.2861
chr5	180915260	14237842	0.0787	0.2886
chr6	171115067	11010837	0.0643	0.2612
chr7	159138663	10081250	0.0633	0.2602

chr8	146364022	9092036	0.0621	0.2563
chr9	141213431	8103946	0.0574	0.2484
chr10	135534747	8572980	0.0633	0.2584
chr11	135006516	7724316	0.0572	0.2472
chr12	133851895	8977717	0.0671	0.2675
chr13	115169878	6444217	0.056	0.2444
chr14	107349540	5274646	0.0491	0.2295
chr15	102531392	4282880	0.0418	0.2118
chr16	90354753	3084118	0.0341	0.1909
chr17	81195210	3355984	0.0413	0.2098
chr18	78077248	6190194	0.0793	0.2905
chr19	59128983	1088887	0.0184	0.1382
chr20	63025520	2661184	0.0422	0.2118
chr21	48129895	2389154	0.0496	0.2318
chr22	51304566	1048217	0.0204	0.1479
chrMT	16571	300	0.0181	0.1333
chrX	155270560	9742709	0.0627	0.2587
chrY	59373566	236266	0.004	0.0656

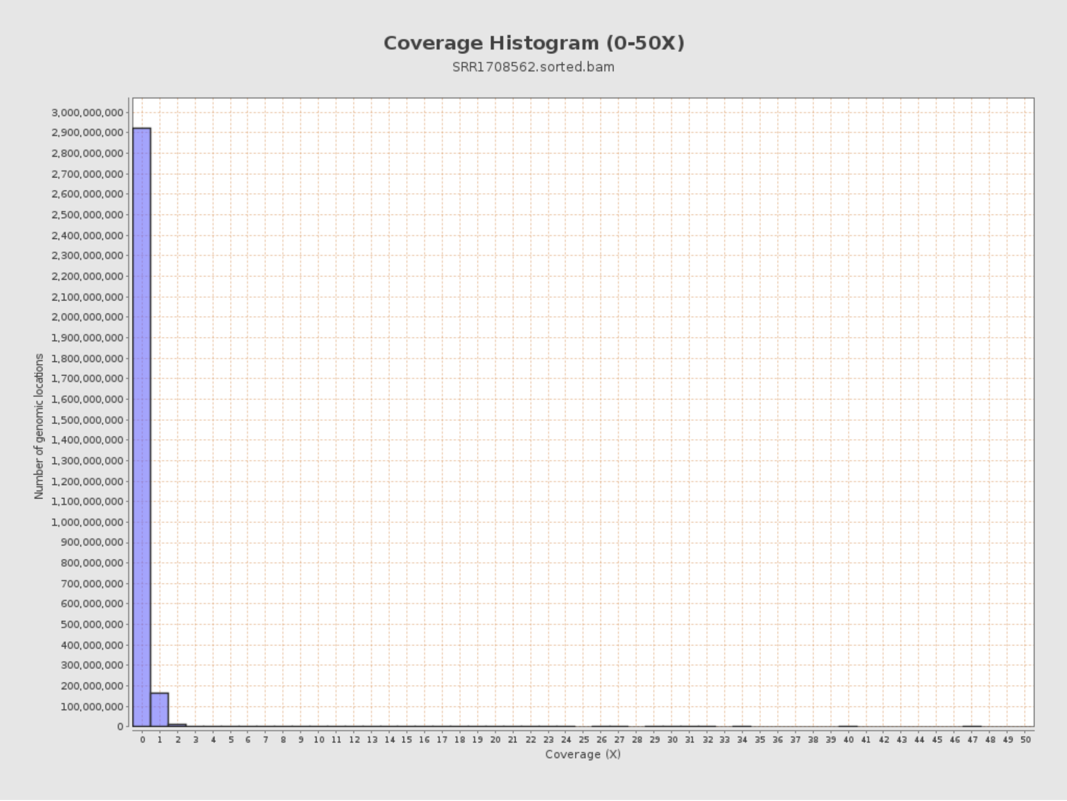
3. Results : Coverage across reference



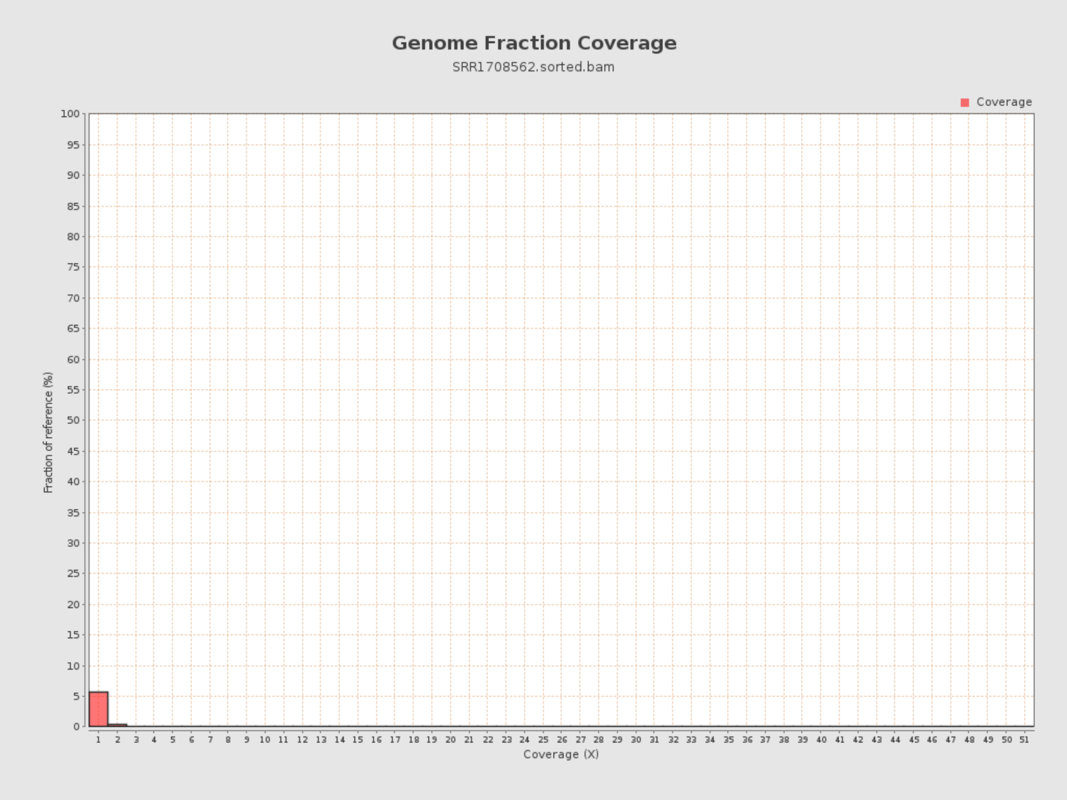
4. Results : Coverage Histogram



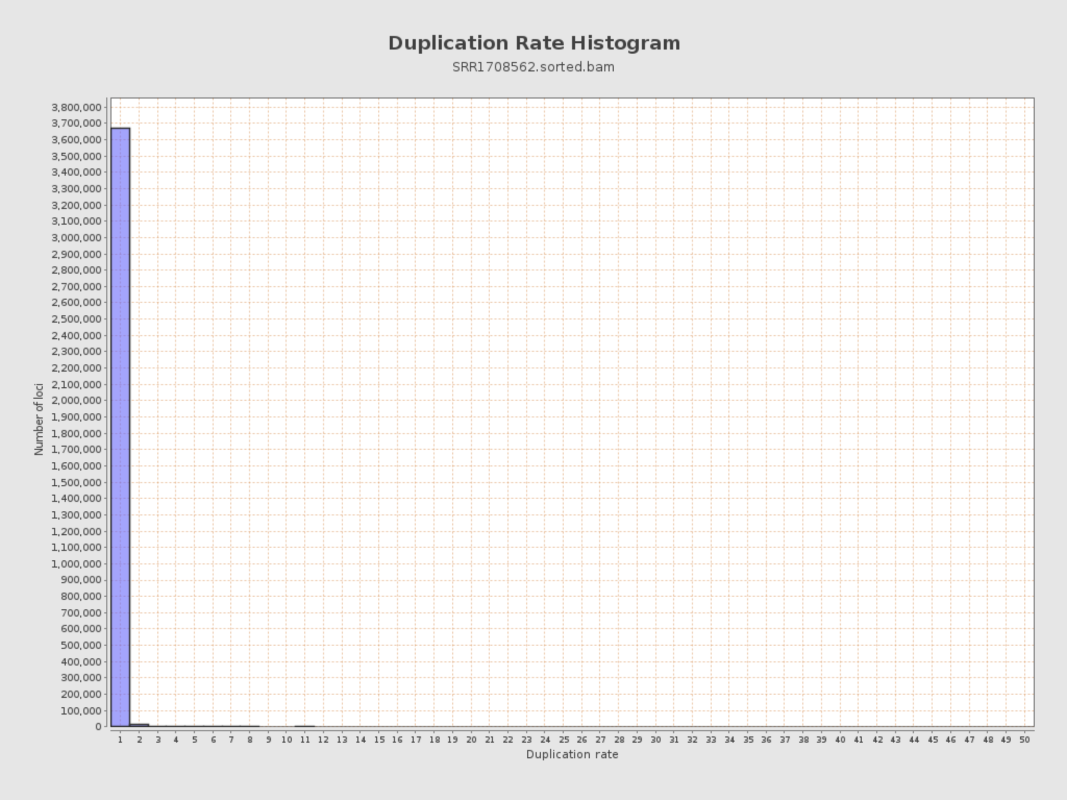
5. Results : Coverage Histogram (0-50X)



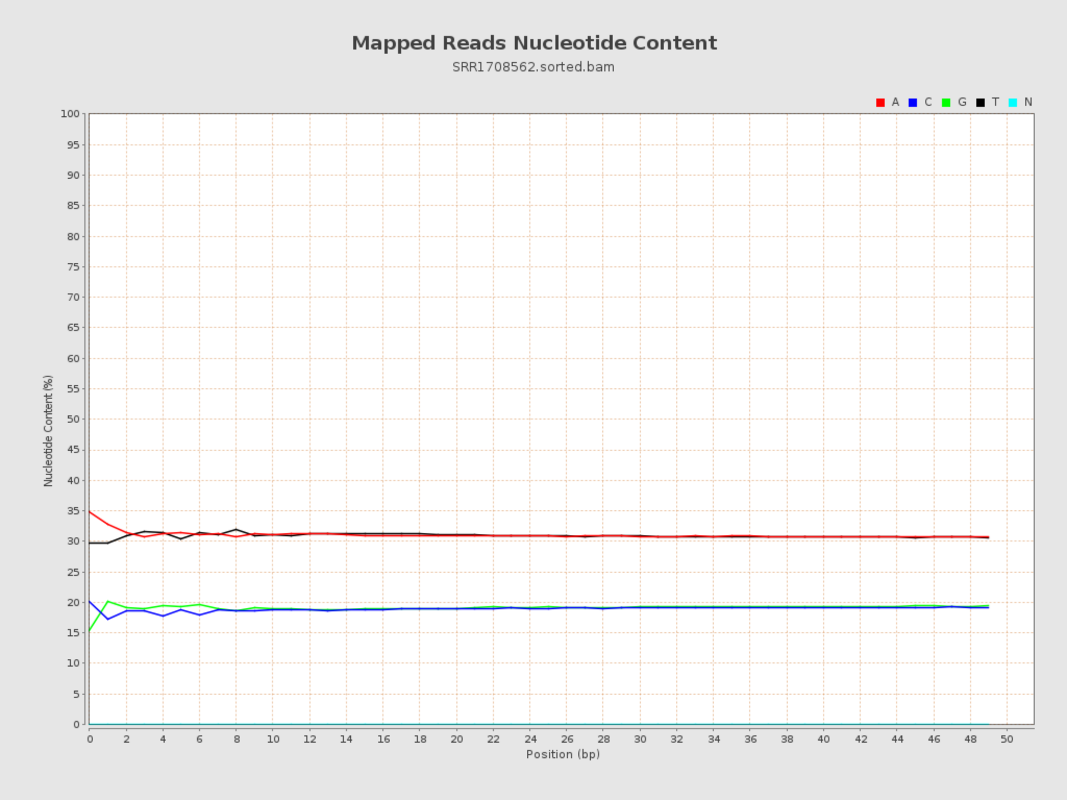
6. Results : Genome Fraction Coverage



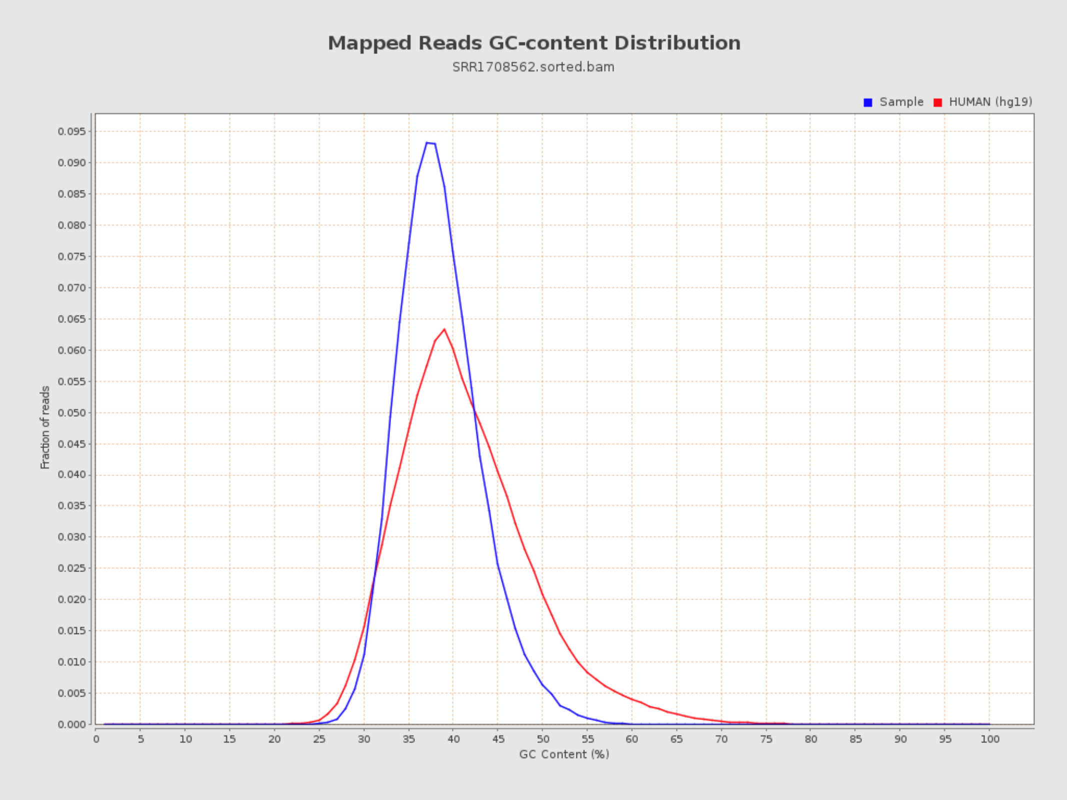
7. Results : Duplication Rate Histogram



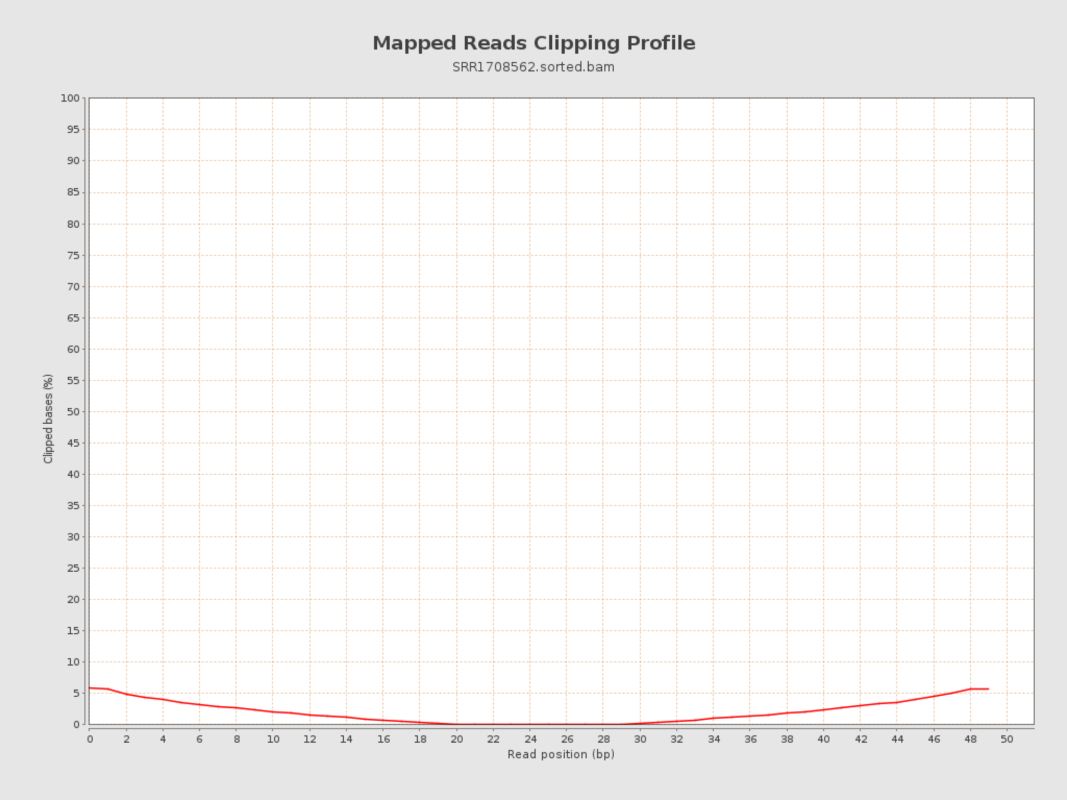
8. Results : Mapped Reads Nucleotide Content



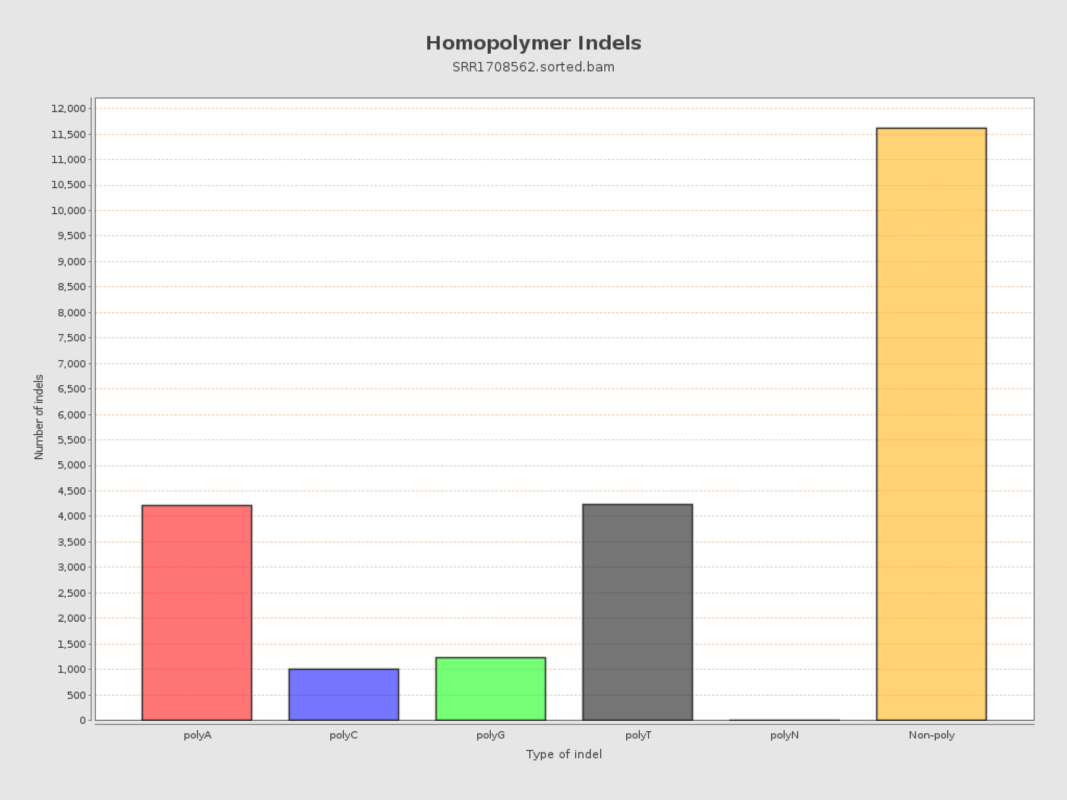
9. Results : Mapped Reads GC-content Distribution



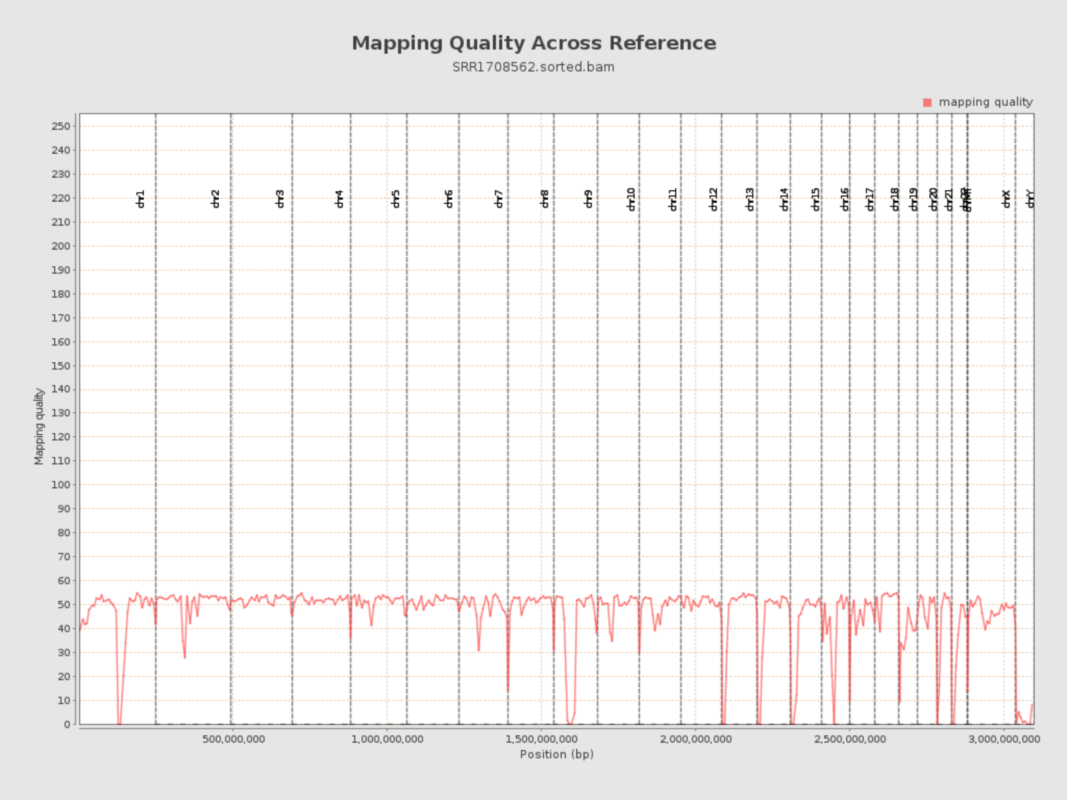
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram