Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:58:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525124.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_SRR10525124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:58:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,104,158
Mapped reads	1,021,914 / 92.55%
Unmapped reads	82,244 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,795 / 2.25%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	25,123 / 2.28%
Duplication rate	1.52%
Clipped reads	1,045,809 / 94.72%

2.2. ACGT Content

Number/percentage of A's	20,546,749 / 25.72%
Number/percentage of C's	15,477,572 / 19.38%
Number/percentage of T's	24,858,184 / 31.12%
Number/percentage of G's	18,998,210 / 23.78%
Number/percentage of N's	3,228 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.2681

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Mismatches and indels

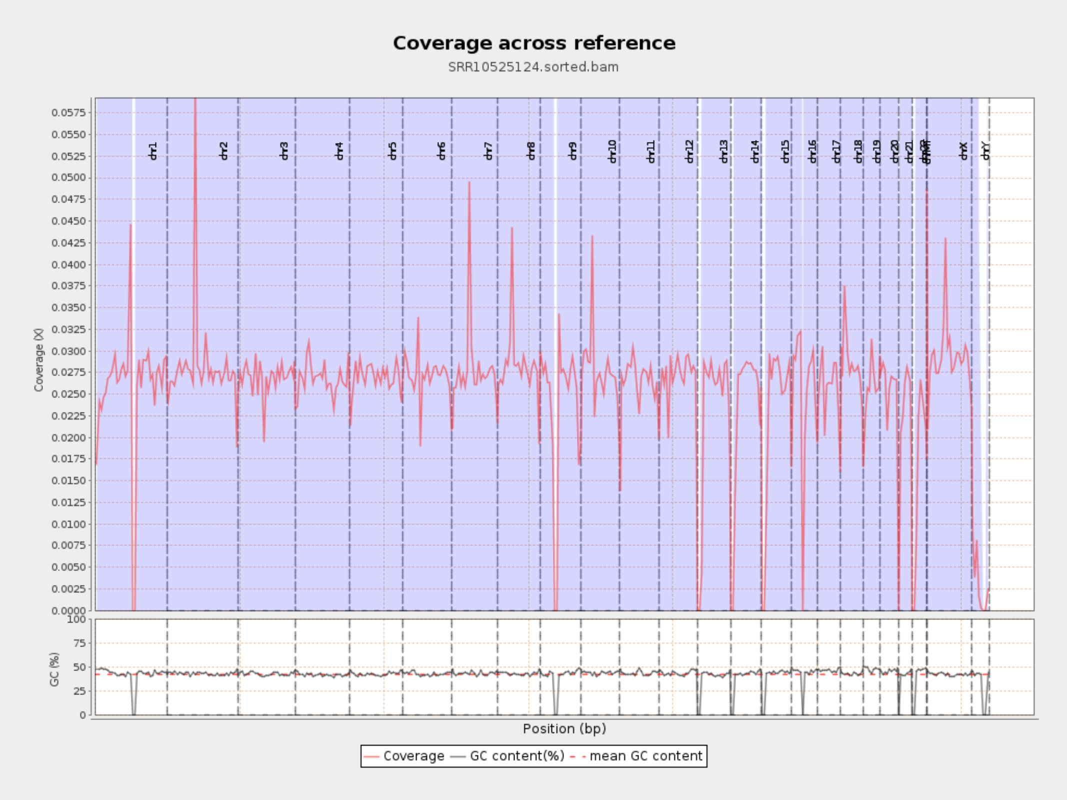
General error rate	0.75%
Mismatches	590,574
Insertions	6,498
Mapped reads with at least one insertion	0.63%
Deletions	18,318
Mapped reads with at least one deletion	1.77%
Homopolymer indels	43.44%

2.6. Chromosome stats

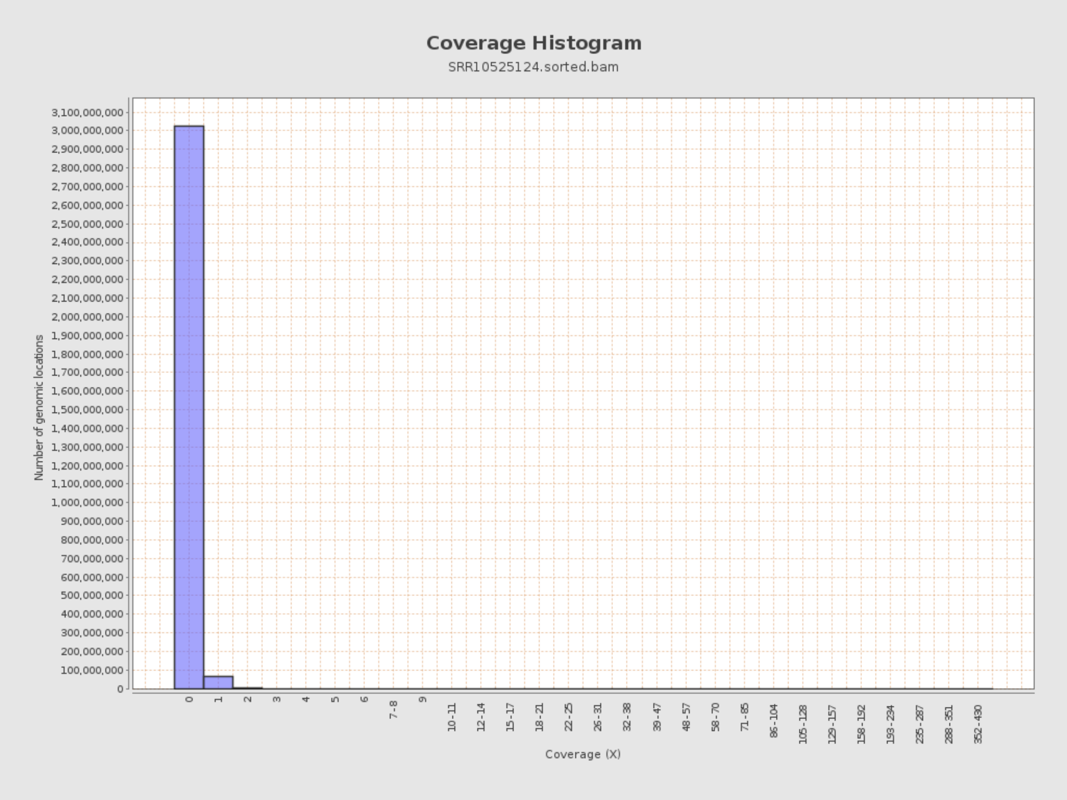
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6386789	0.0256	0.3871
chr2	243199373	6898529	0.0284	0.3801
chr3	198022430	5326948	0.0269	0.1749
chr4	191154276	5120278	0.0268	0.1802
chr5	180915260	4893957	0.0271	0.1778
chr6	171115067	4651077	0.0272	0.1936
chr7	159138663	4451479	0.028	0.4075

chr8	146364022	4159688	0.0284	0.3664
chr9	141213431	3352929	0.0237	0.2621
chr10	135534747	3772258	0.0278	0.2649
chr11	135006516	3593963	0.0266	0.2585
chr12	133851895	3617108	0.027	0.1769
chr13	115169878	2587465	0.0225	0.1591
chr14	107349540	2451911	0.0228	0.1802
chr15	102531392	2310884	0.0225	0.1603
chr16	90354753	2227273	0.0247	0.1781
chr17	81195210	2087343	0.0257	0.2003
chr18	78077248	2238958	0.0287	0.437
chr19	59128983	1527218	0.0258	0.288
chr20	63025520	1618210	0.0257	0.1739
chr21	48129895	1054095	0.0219	0.167
chr22	51304566	831993	0.0162	0.1377
chrMT	16571	808	0.0488	0.2154
chrX	155270560	4578977	0.0295	0.2207
chrY	59373566	175495	0.003	0.0778

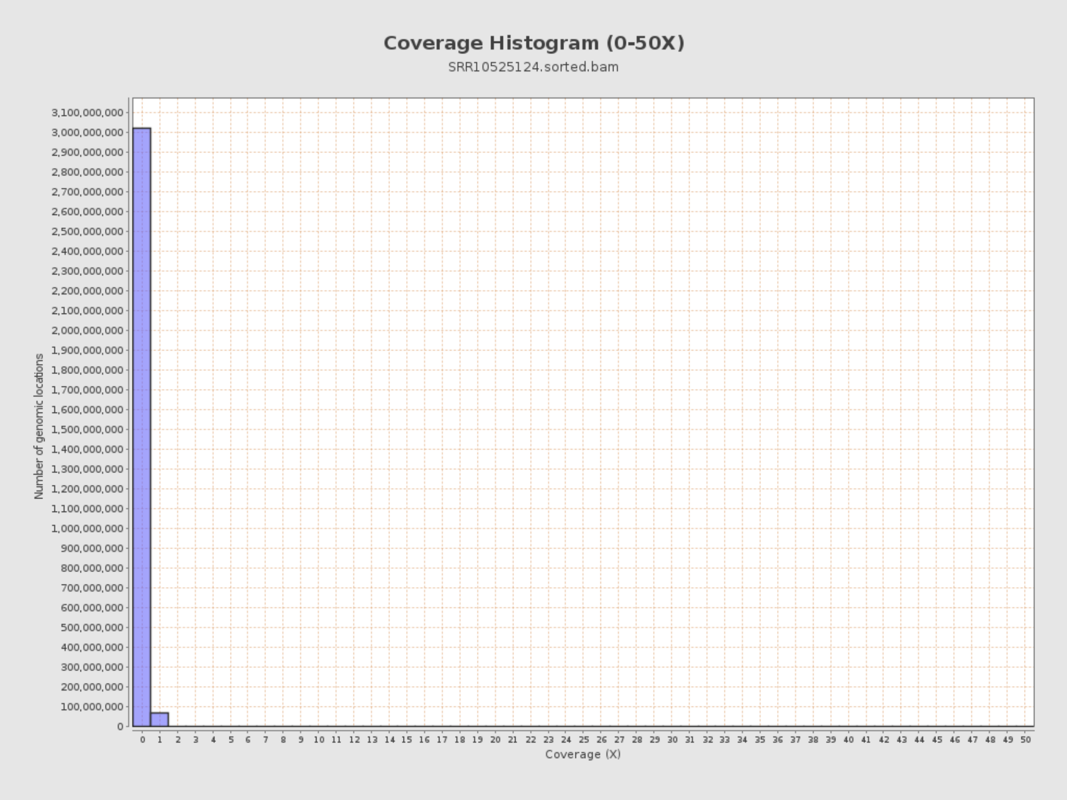
3. Results : Coverage across reference



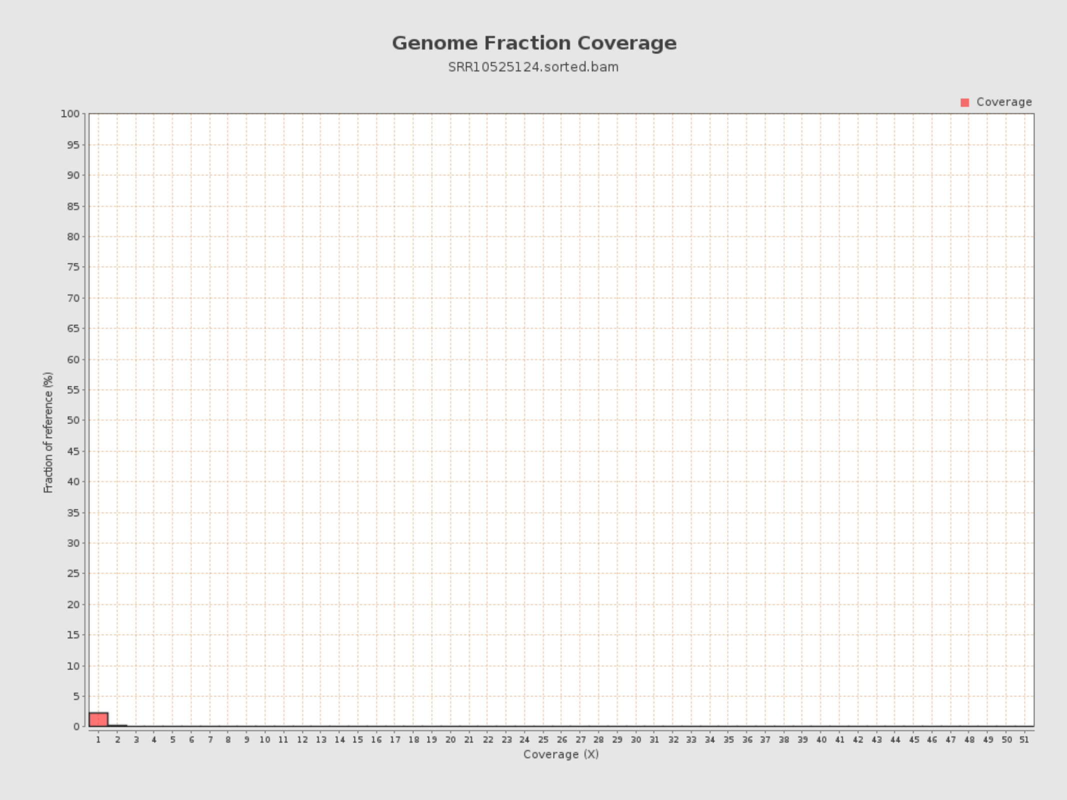
4. Results : Coverage Histogram



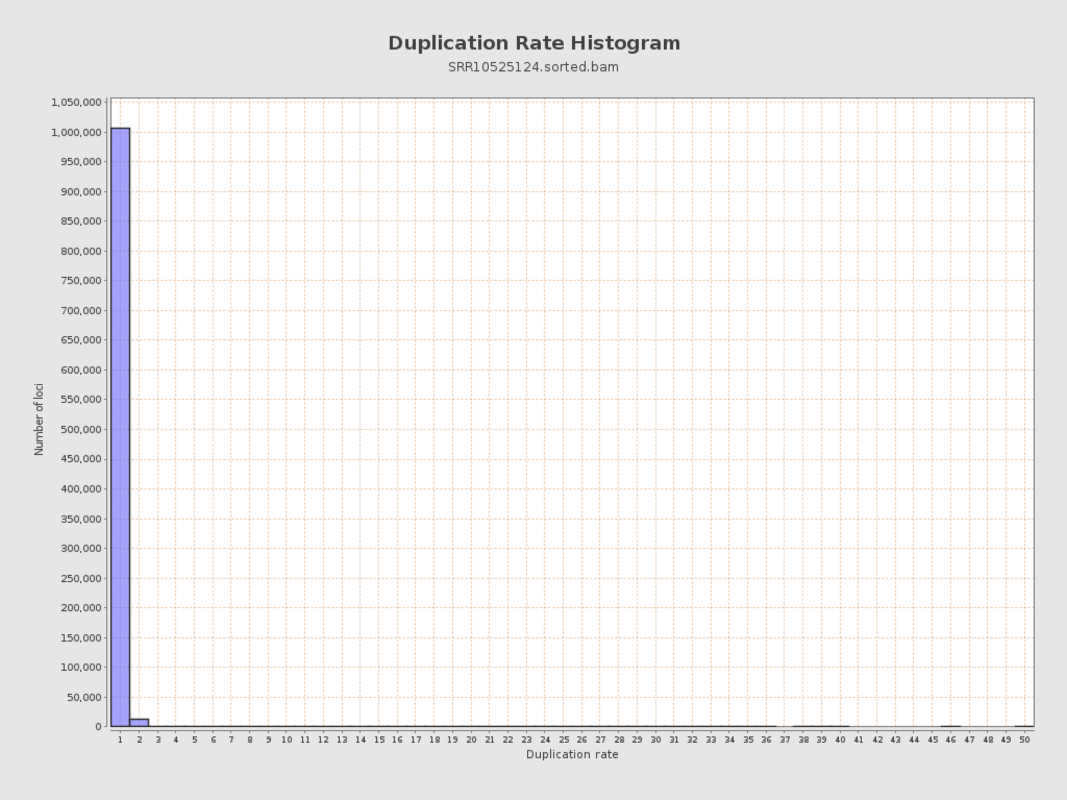
5. Results : Coverage Histogram (0-50X)



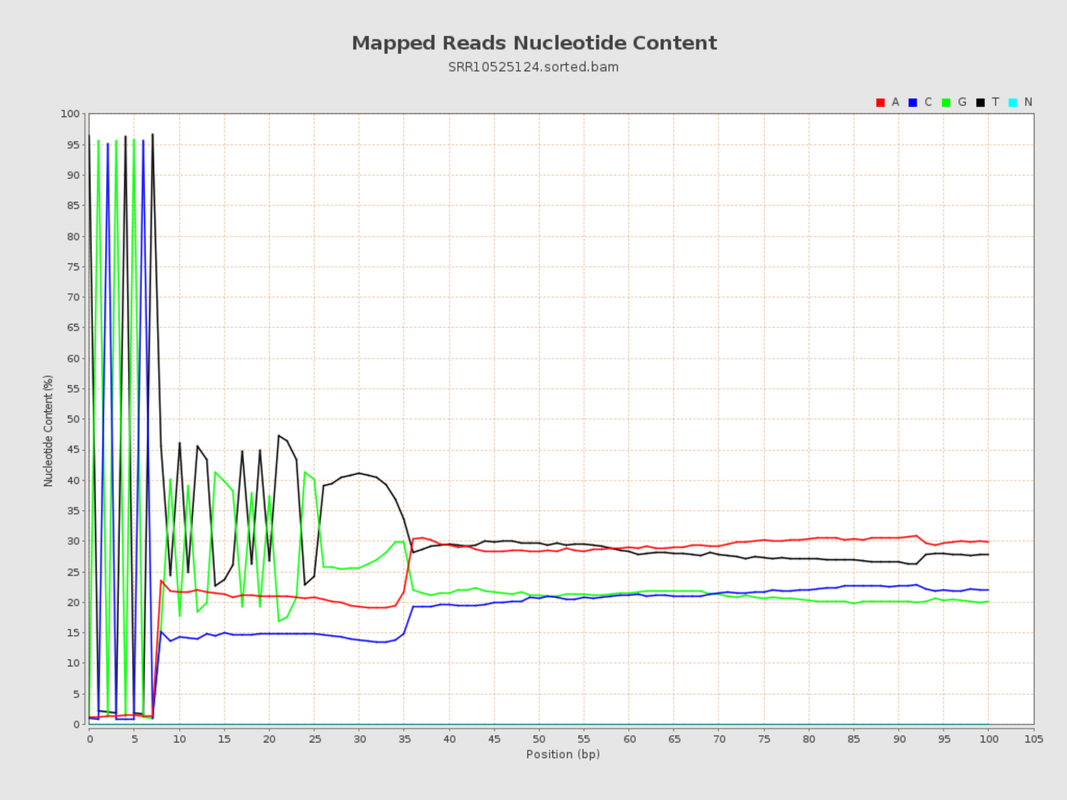
6. Results : Genome Fraction Coverage



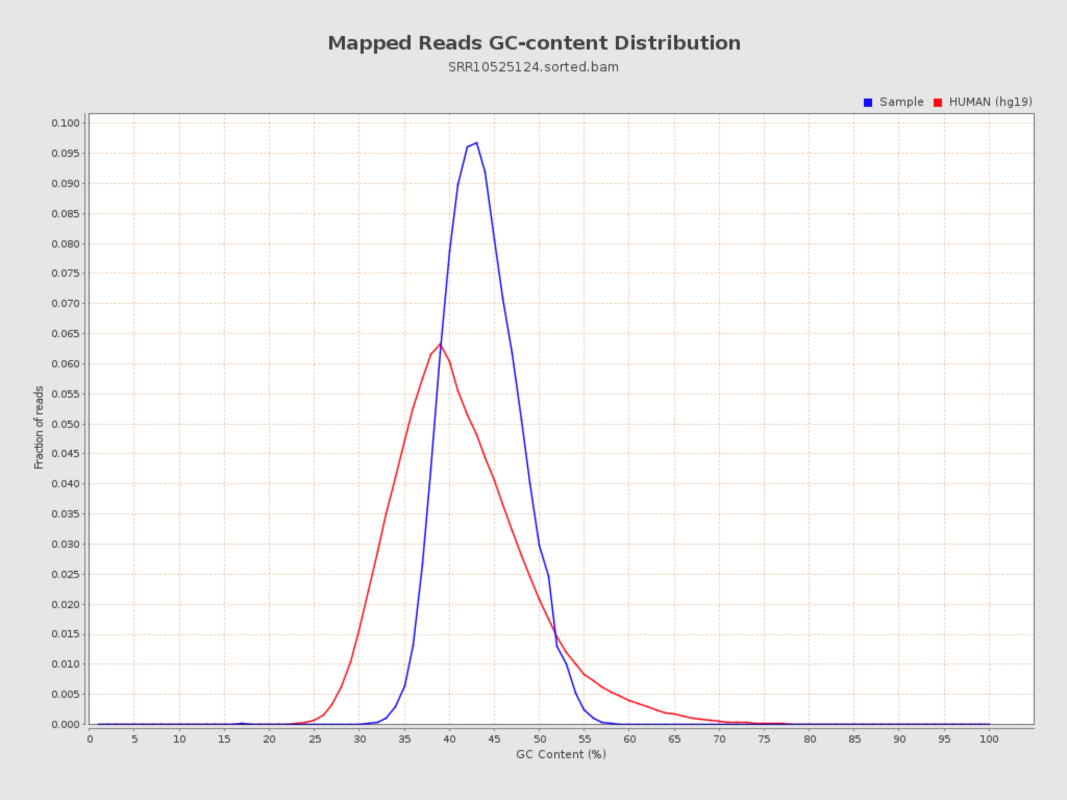
7. Results : Duplication Rate Histogram



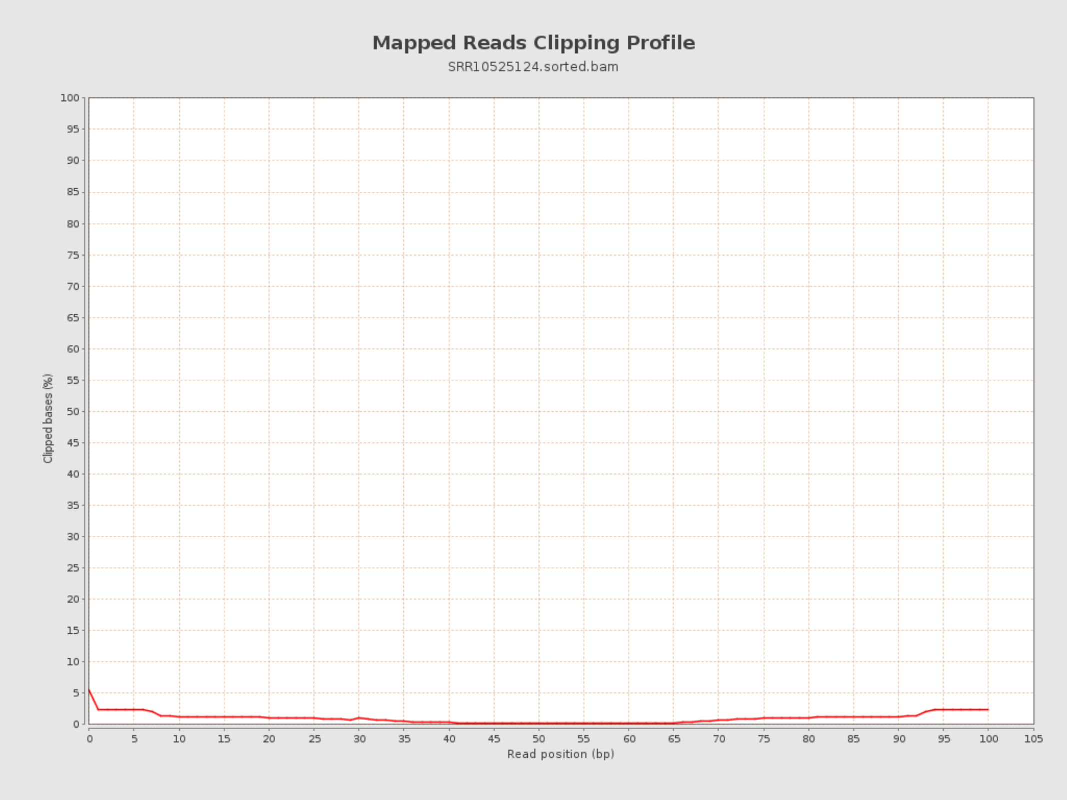
8. Results : Mapped Reads Nucleotide Content



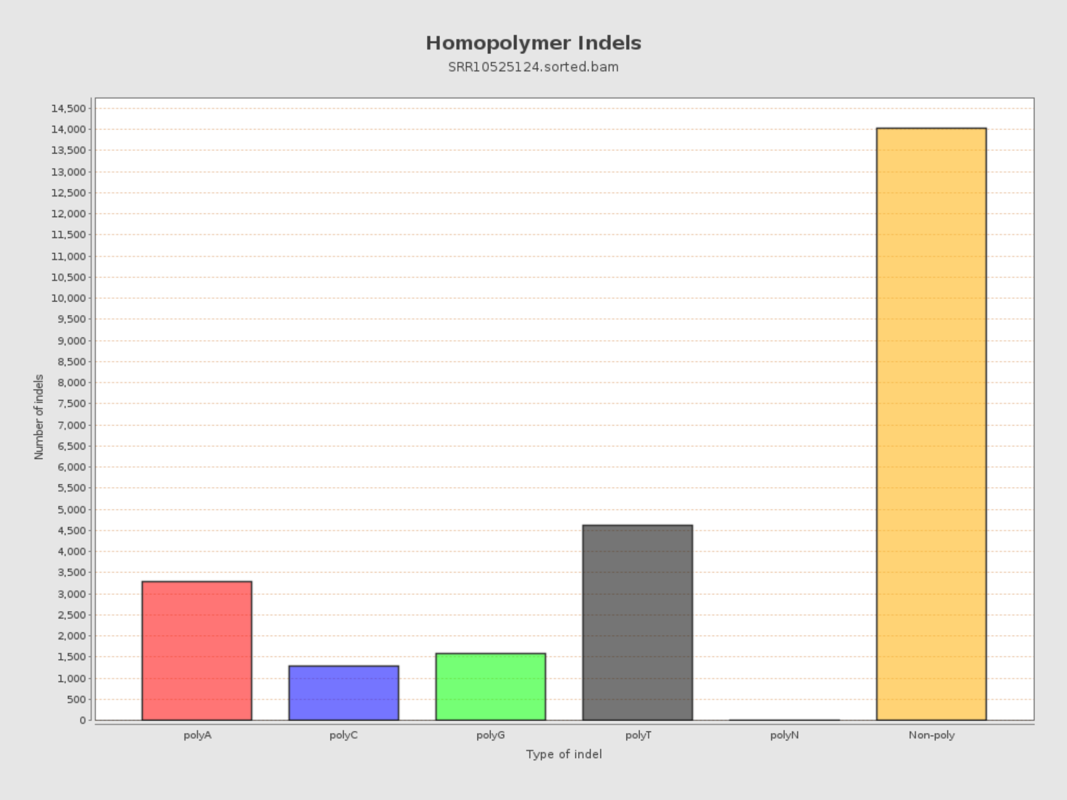
9. Results : Mapped Reads GC-content Distribution



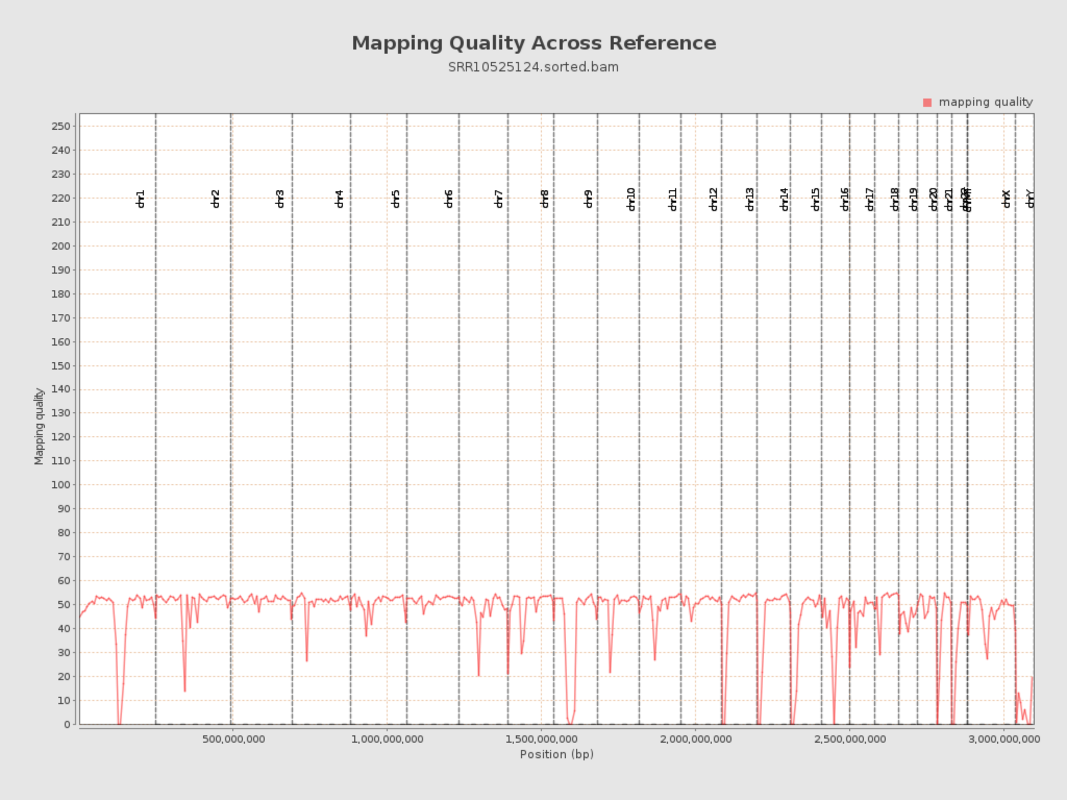
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram