Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:47:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525119.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_SRR10525119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:47:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	488,740
Mapped reads	445,767 / 91.21%
Unmapped reads	42,973 / 8.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,388 / 2.33%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	7,803 / 1.6%
Duplication rate	1.06%
Clipped reads	456,505 / 93.4%

2.2. ACGT Content

Number/percentage of A's	9,164,897 / 26.44%
Number/percentage of C's	6,976,321 / 20.13%
Number/percentage of T's	10,535,502 / 30.4%
Number/percentage of G's	7,979,335 / 23.02%
Number/percentage of N's	1,251 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0112

Standard Deviation	0.1446

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

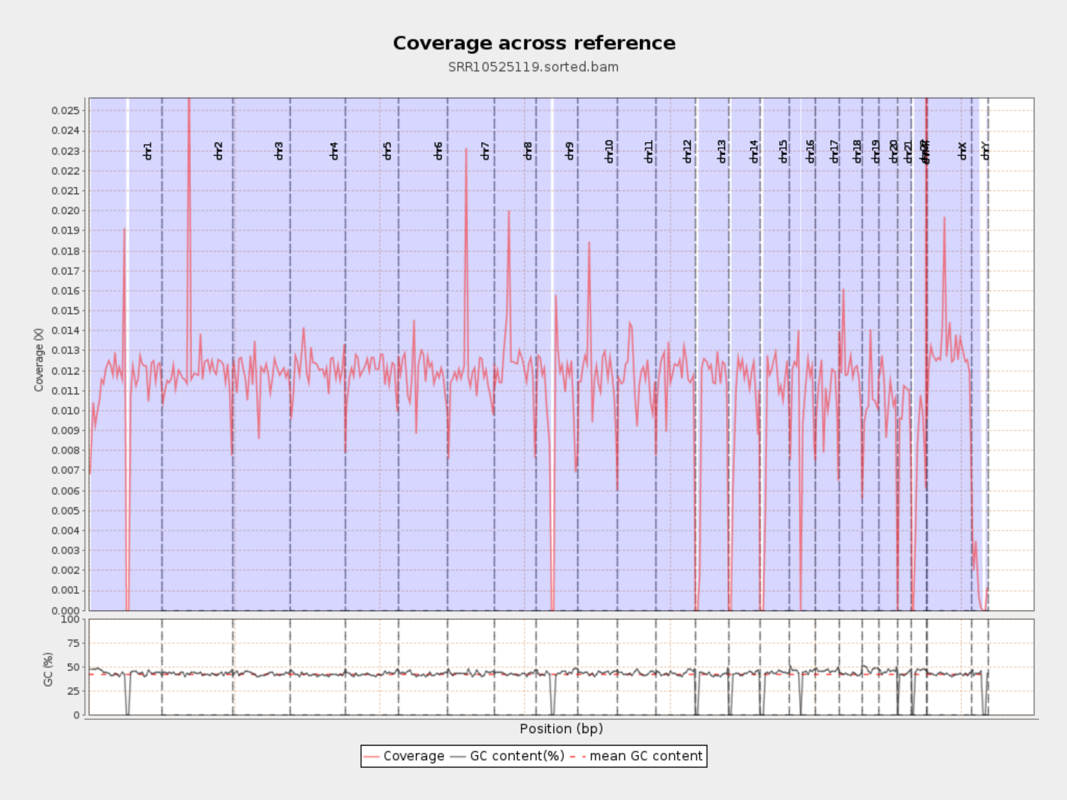
General error rate	0.76%
Mismatches	258,120
Insertions	3,104
Mapped reads with at least one insertion	0.69%
Deletions	7,934
Mapped reads with at least one deletion	1.76%
Homopolymer indels	43.11%

2.6. Chromosome stats

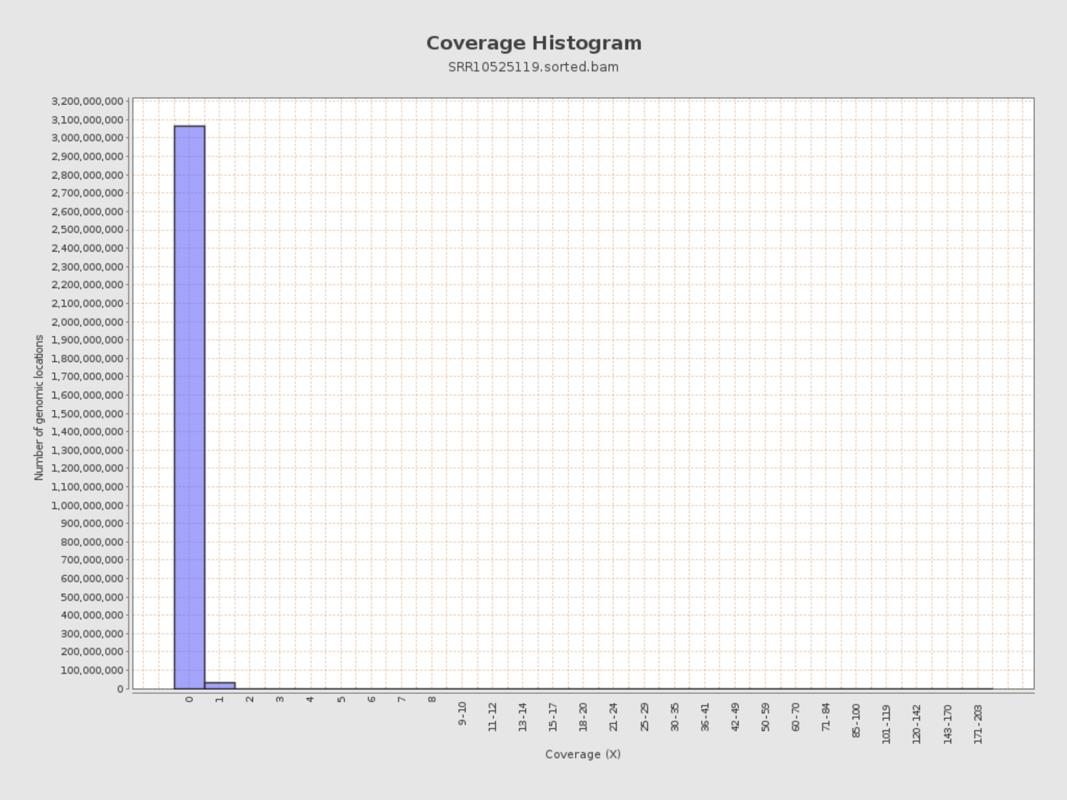
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2749158	0.011	0.1918
chr2	243199373	2996185	0.0123	0.1865
chr3	198022430	2338009	0.0118	0.1115
chr4	191154276	2317197	0.0121	0.1151
chr5	180915260	2169137	0.012	0.1138
chr6	171115067	2035598	0.0119	0.1187
chr7	159138663	1920536	0.0121	0.2019

chr8	146364022	1831487	0.0125	0.189
chr9	141213431	1453017	0.0103	0.1395
chr10	135534747	1629007	0.012	0.1443
chr11	135006516	1562213	0.0116	0.1417
chr12	133851895	1580325	0.0118	0.1128
chr13	115169878	1145300	0.0099	0.1031
chr14	107349540	1043651	0.0097	0.1127
chr15	102531392	983997	0.0096	0.101
chr16	90354753	939433	0.0104	0.1105
chr17	81195210	851835	0.0105	0.117
chr18	78077248	964210	0.0123	0.222
chr19	59128983	621363	0.0105	0.1634
chr20	63025520	669140	0.0106	0.1075
chr21	48129895	441779	0.0092	0.102
chr22	51304566	324875	0.0063	0.082
chrMT	16571	1856	0.112	0.3416
chrX	155270560	2025326	0.013	0.1323
chrY	59373566	76386	0.0013	0.0446

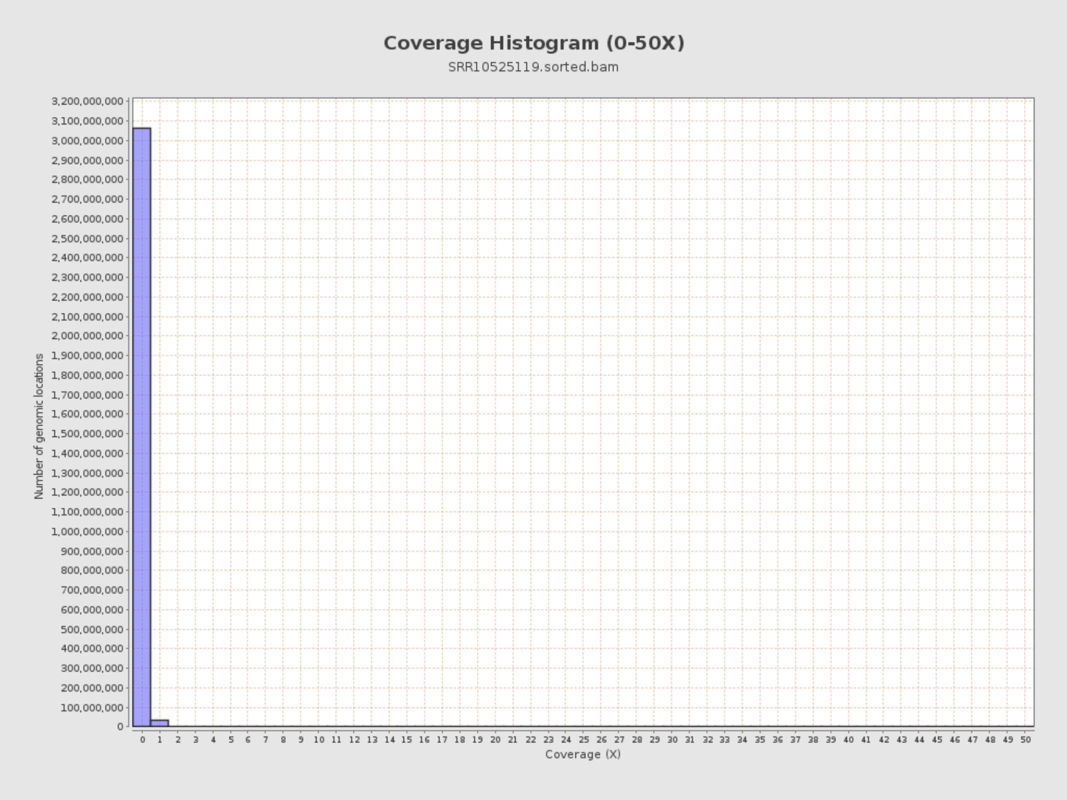
3. Results : Coverage across reference



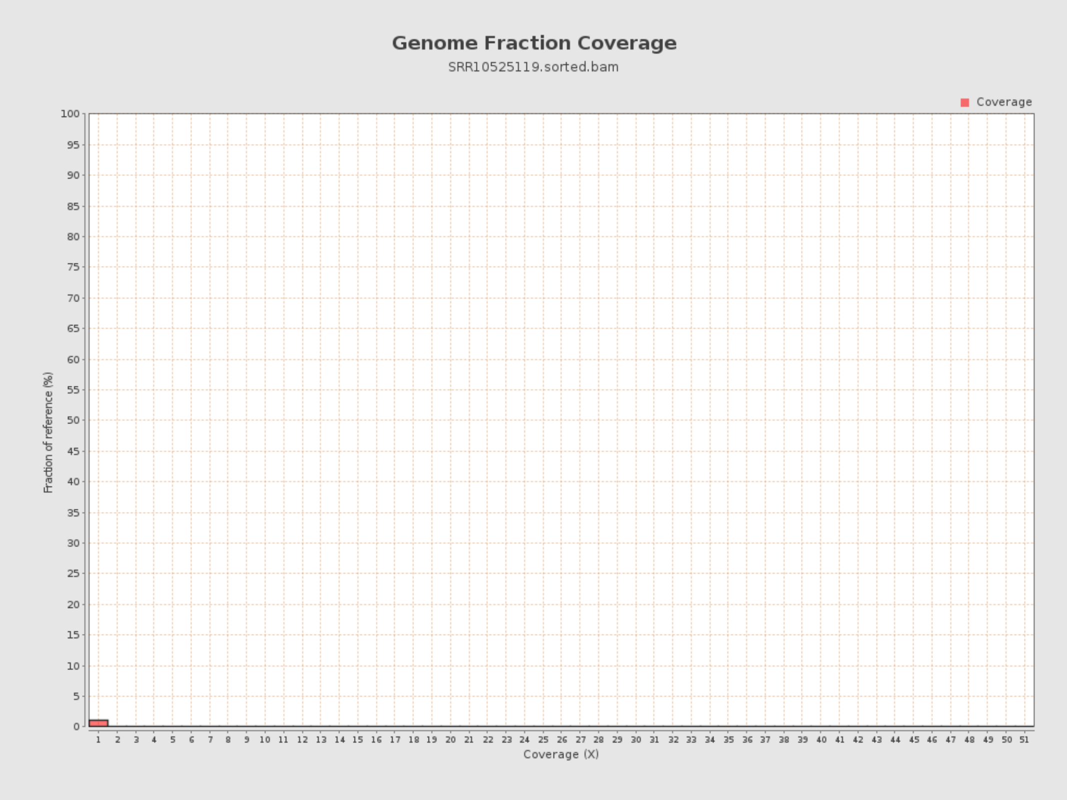
4. Results : Coverage Histogram



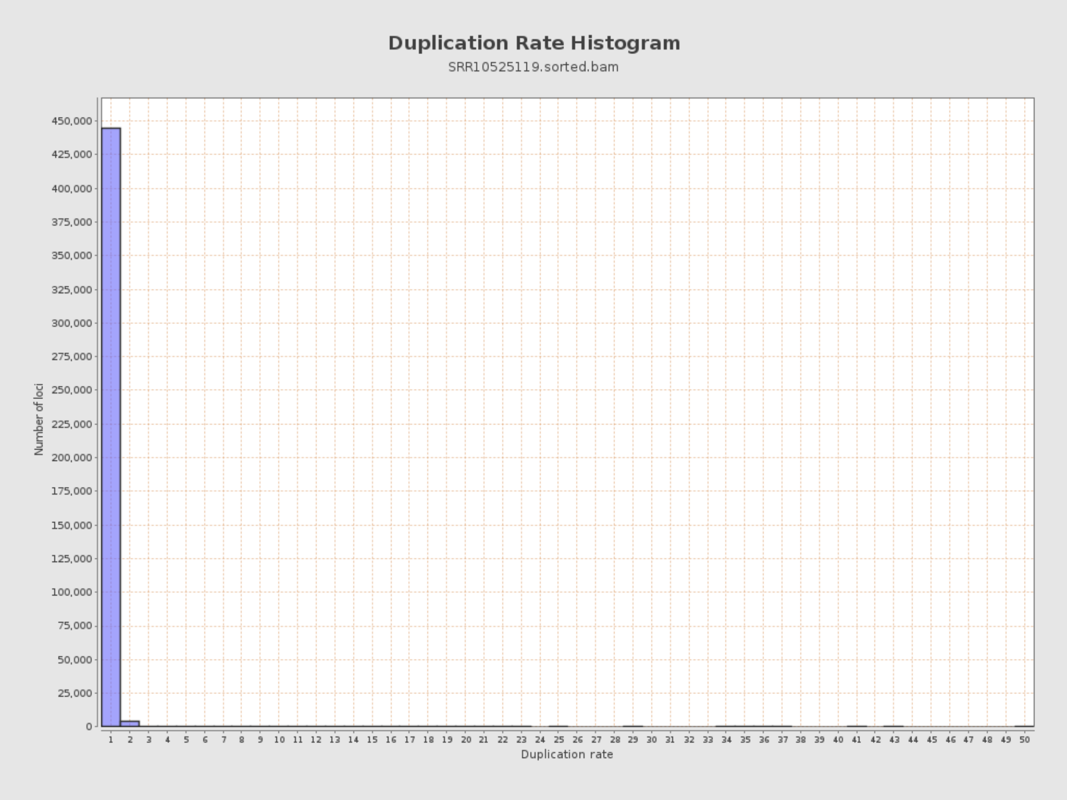
5. Results : Coverage Histogram (0-50X)



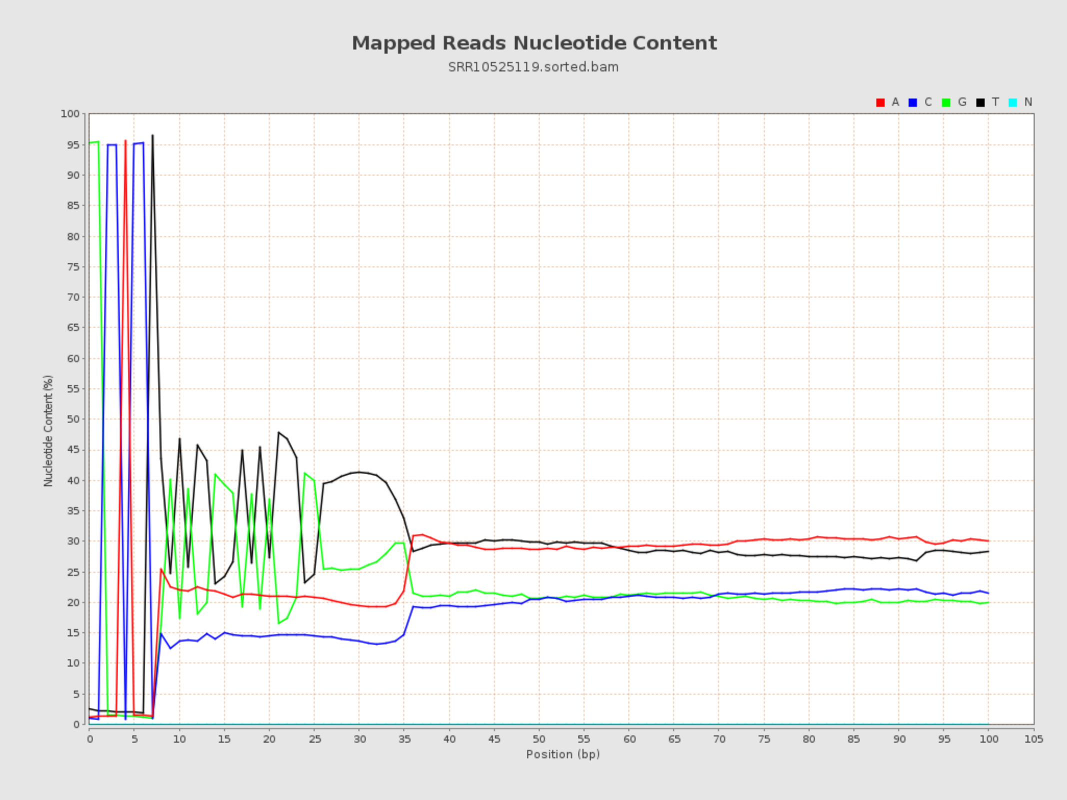
6. Results : Genome Fraction Coverage



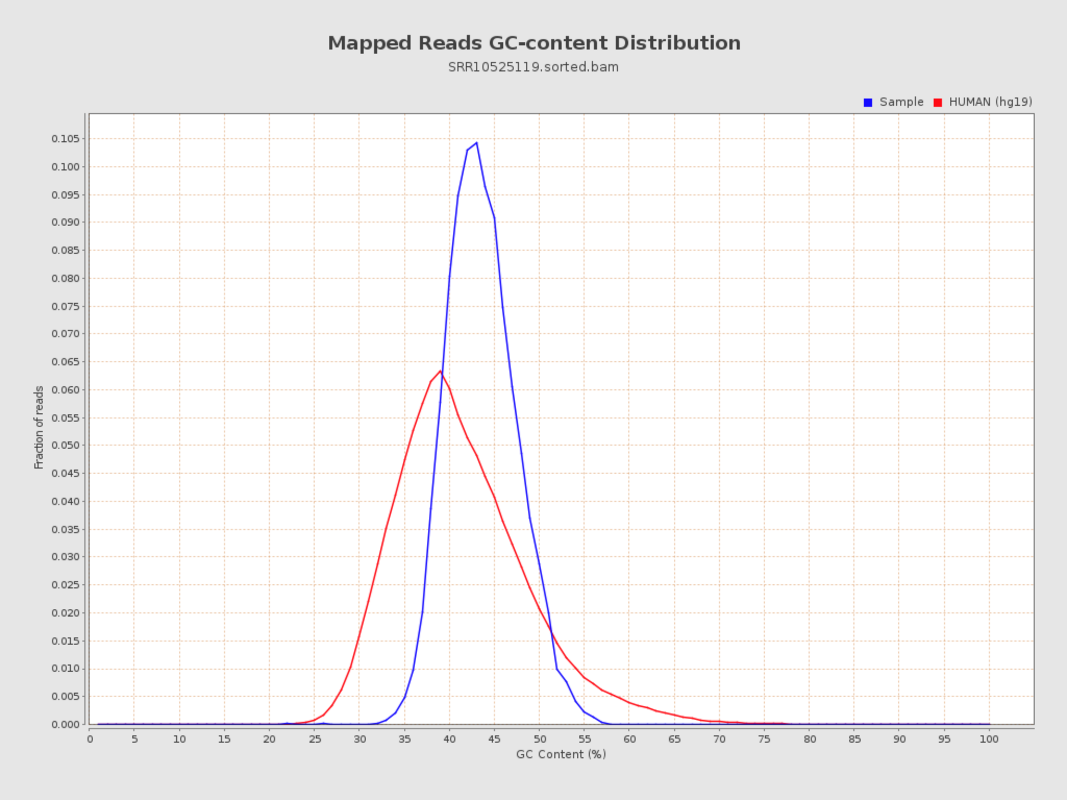
7. Results : Duplication Rate Histogram



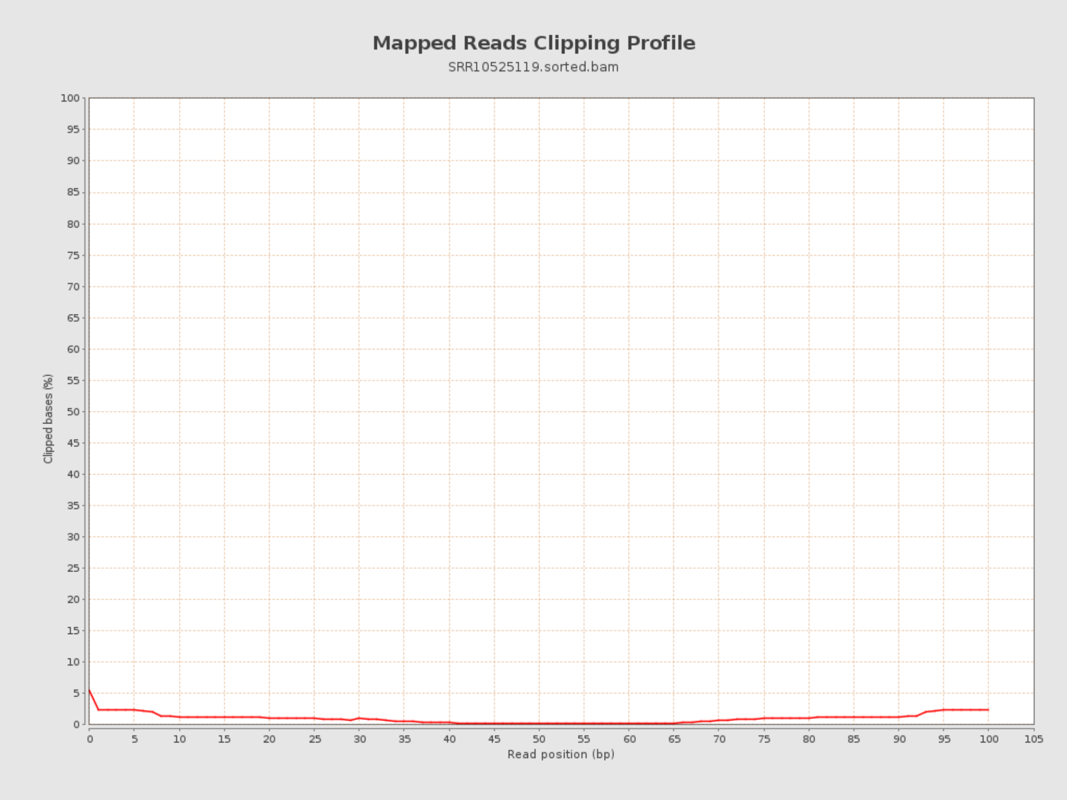
8. Results : Mapped Reads Nucleotide Content



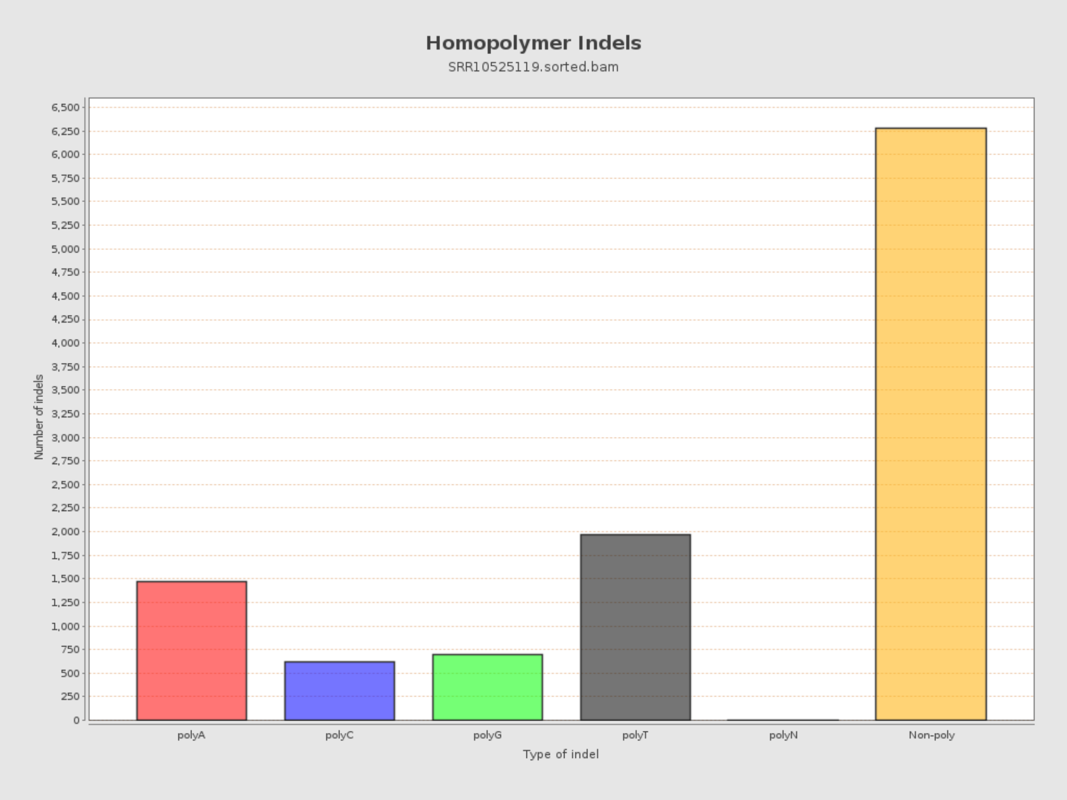
9. Results : Mapped Reads GC-content Distribution



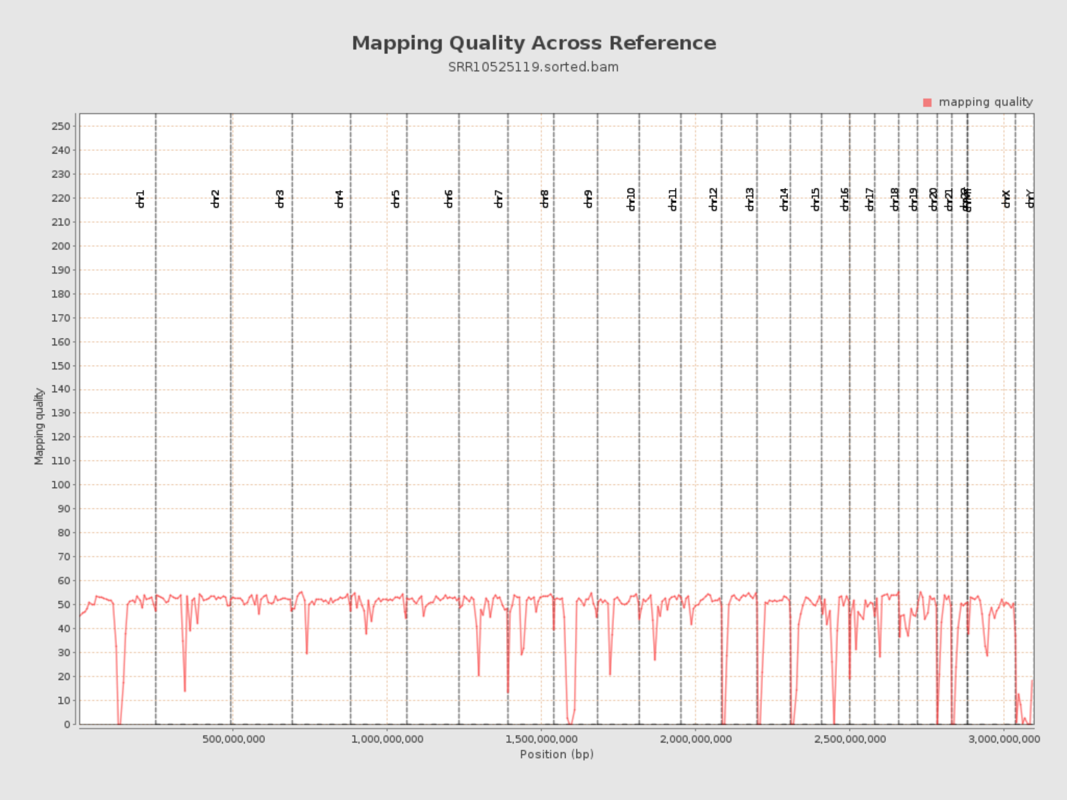
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram