Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525218.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_SRR10525218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:42:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,820,537
Mapped reads	1,406,159 / 77.24%
Unmapped reads	414,378 / 22.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,353 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	40,767 / 2.24%
Duplication rate	2.04%
Clipped reads	1,404,303 / 77.14%

2.2. ACGT Content

Number/percentage of A's	20,827,005 / 25.1%
Number/percentage of C's	17,094,741 / 20.6%
Number/percentage of T's	26,291,352 / 31.68%
Number/percentage of G's	18,773,095 / 22.62%
Number/percentage of N's	2,027 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2619

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

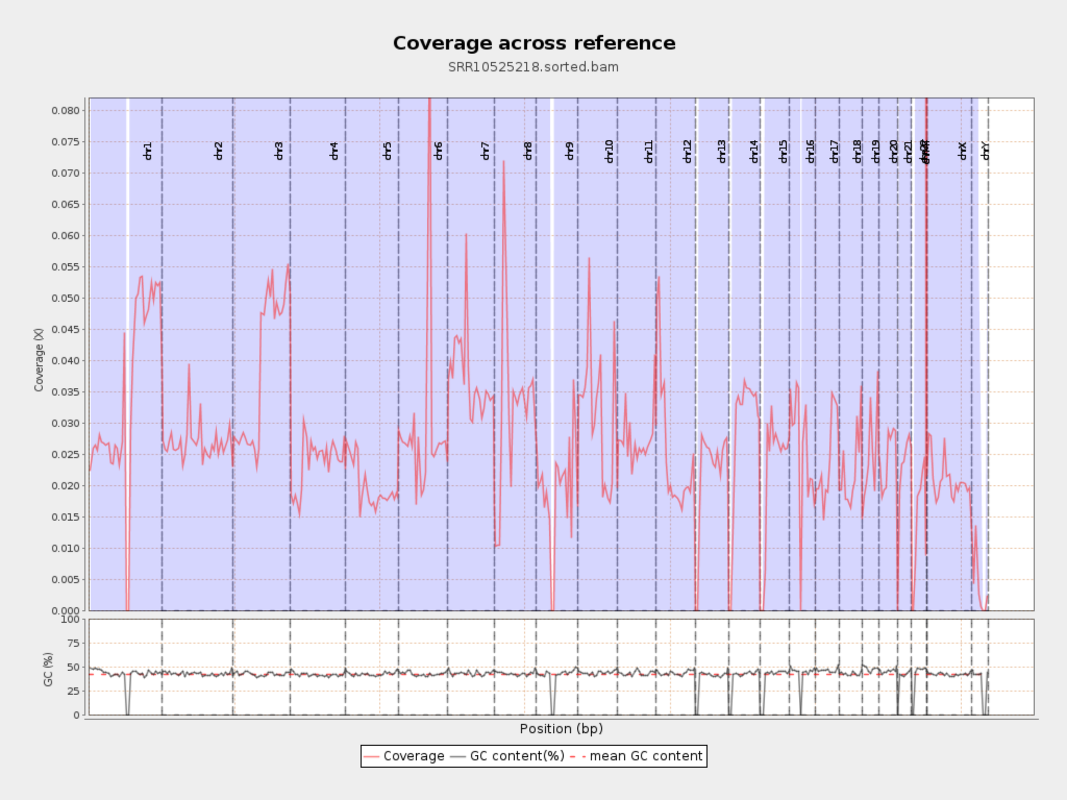
General error rate	0.52%
Mismatches	417,089
Insertions	7,411
Mapped reads with at least one insertion	0.52%
Deletions	17,062
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.4%

2.6. Chromosome stats

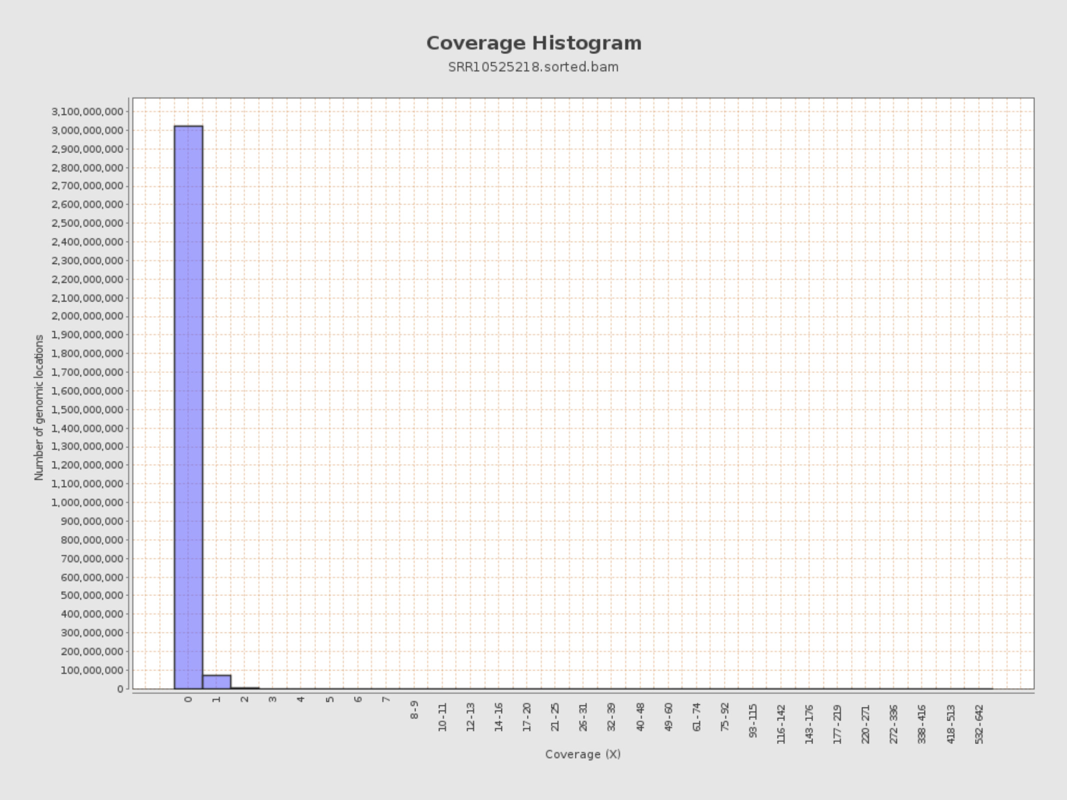
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8635940	0.0346	0.4679
chr2	243199373	6559246	0.027	0.3206
chr3	198022430	7668859	0.0387	0.2134
chr4	191154276	4524200	0.0237	0.1736
chr5	180915260	3611859	0.02	0.1514
chr6	171115067	5133934	0.03	0.2066
chr7	159138663	5983927	0.0376	0.4556

chr8	146364022	4698978	0.0321	0.2453
chr9	141213431	2700671	0.0191	0.1856
chr10	135534747	4323295	0.0319	0.2783
chr11	135006516	3697788	0.0274	0.2066
chr12	133851895	3320425	0.0248	0.1713
chr13	115169878	2541074	0.0221	0.1609
chr14	107349540	3044053	0.0284	0.187
chr15	102531392	2250194	0.0219	0.161
chr16	90354753	2261002	0.025	0.1837
chr17	81195210	1962398	0.0242	0.1713
chr18	78077248	1742392	0.0223	0.3345
chr19	59128983	1477425	0.025	0.3267
chr20	63025520	1520109	0.0241	0.1682
chr21	48129895	1068638	0.0222	0.1704
chr22	51304566	730520	0.0142	0.128
chrMT	16571	62733	3.7857	2.8242
chrX	155270560	3263747	0.021	0.1693
chrY	59373566	232000	0.0039	0.1165

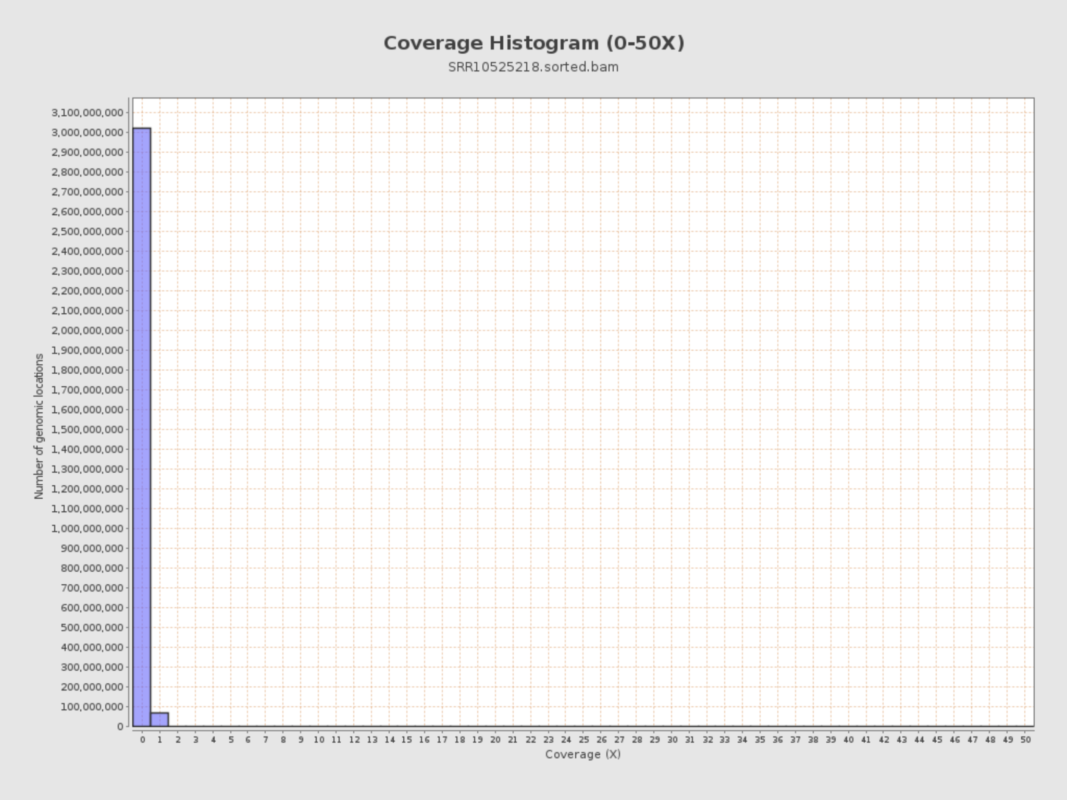
3. Results : Coverage across reference



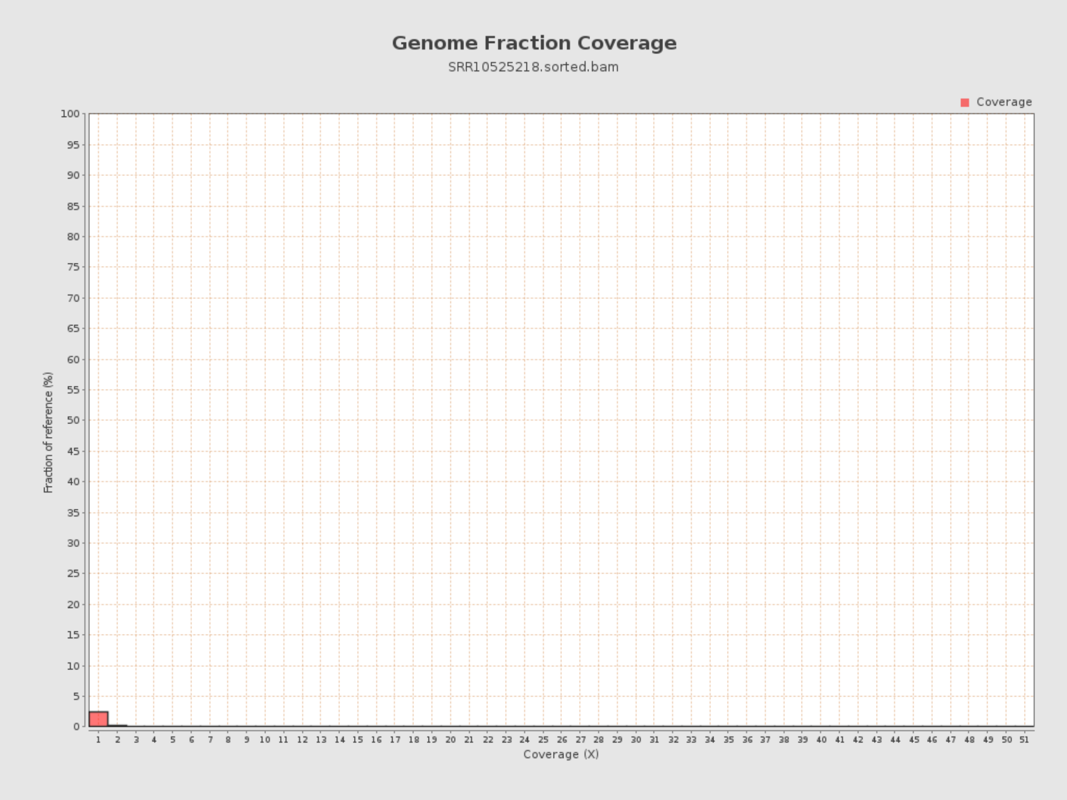
4. Results : Coverage Histogram



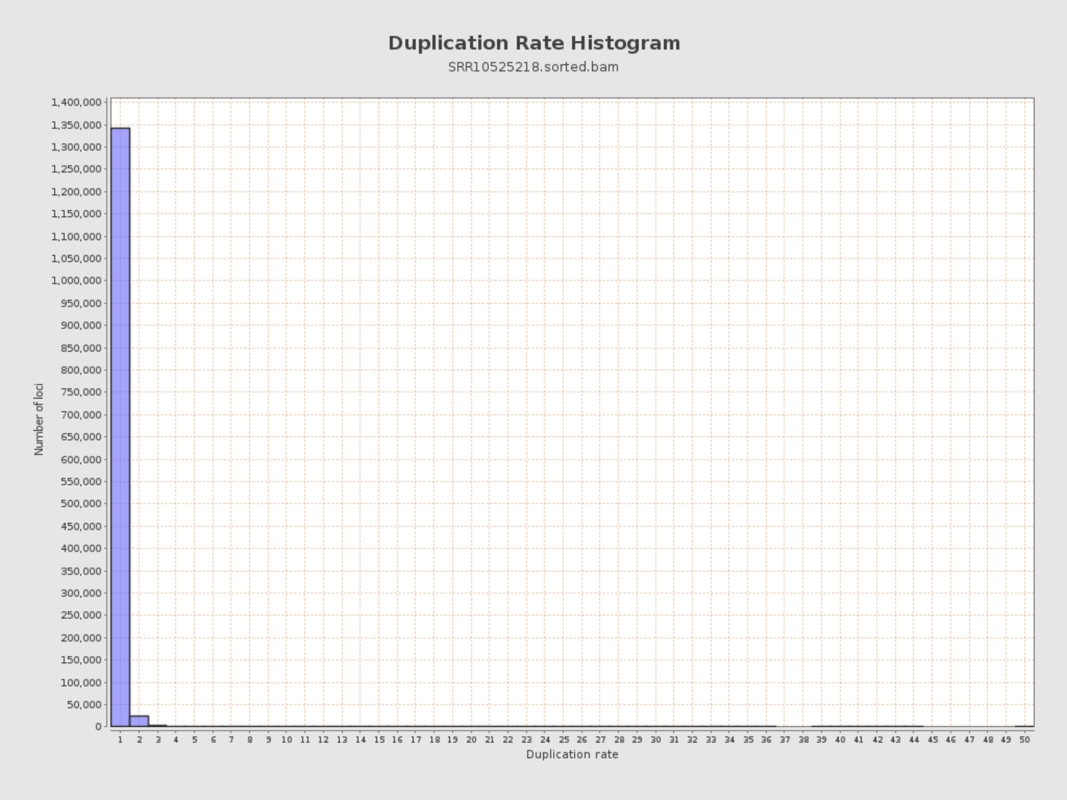
5. Results : Coverage Histogram (0-50X)



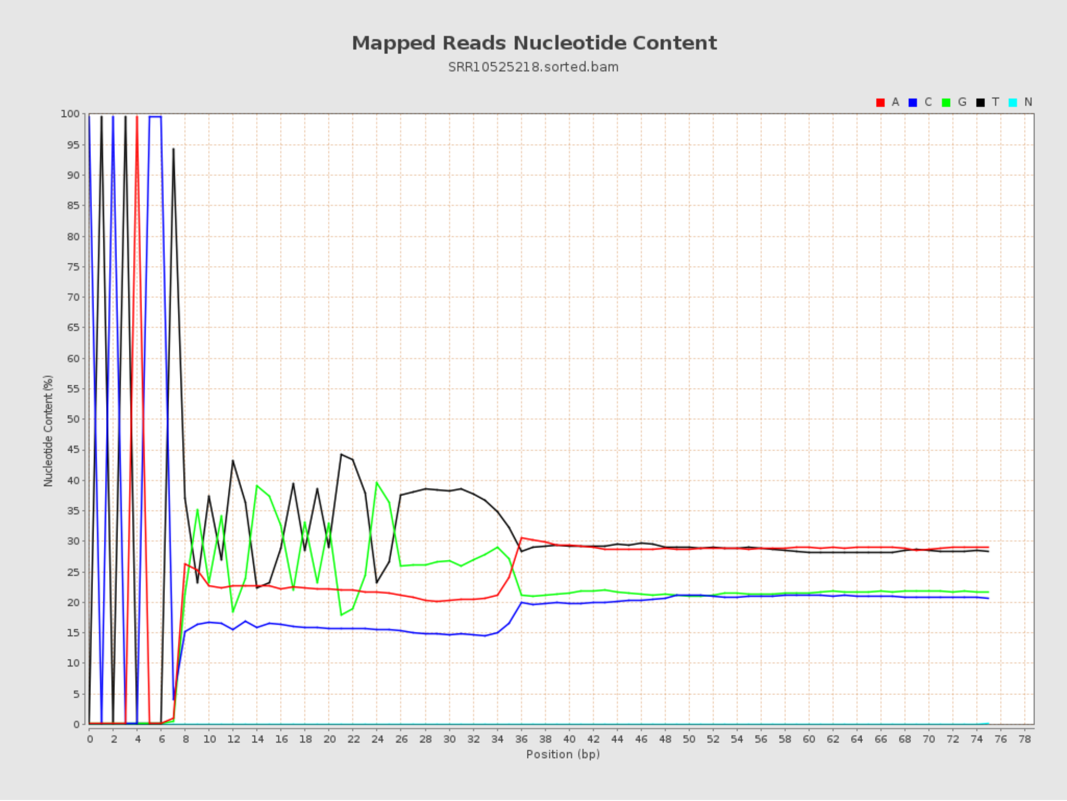
6. Results : Genome Fraction Coverage



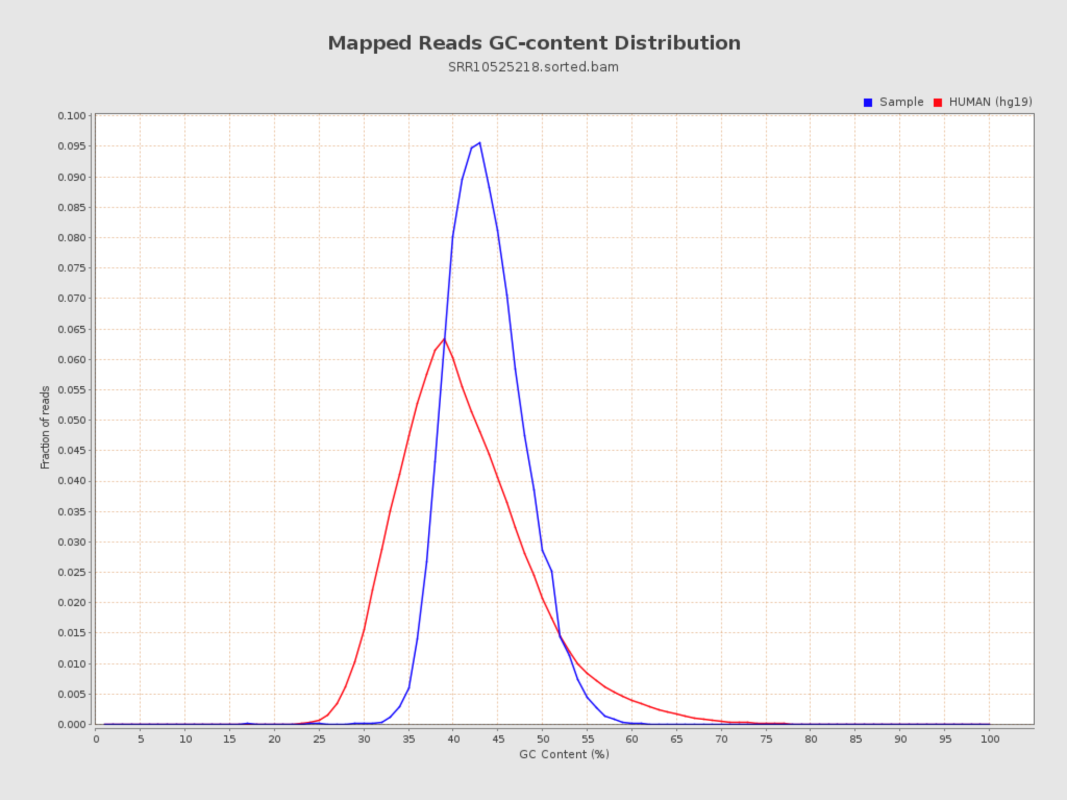
7. Results : Duplication Rate Histogram



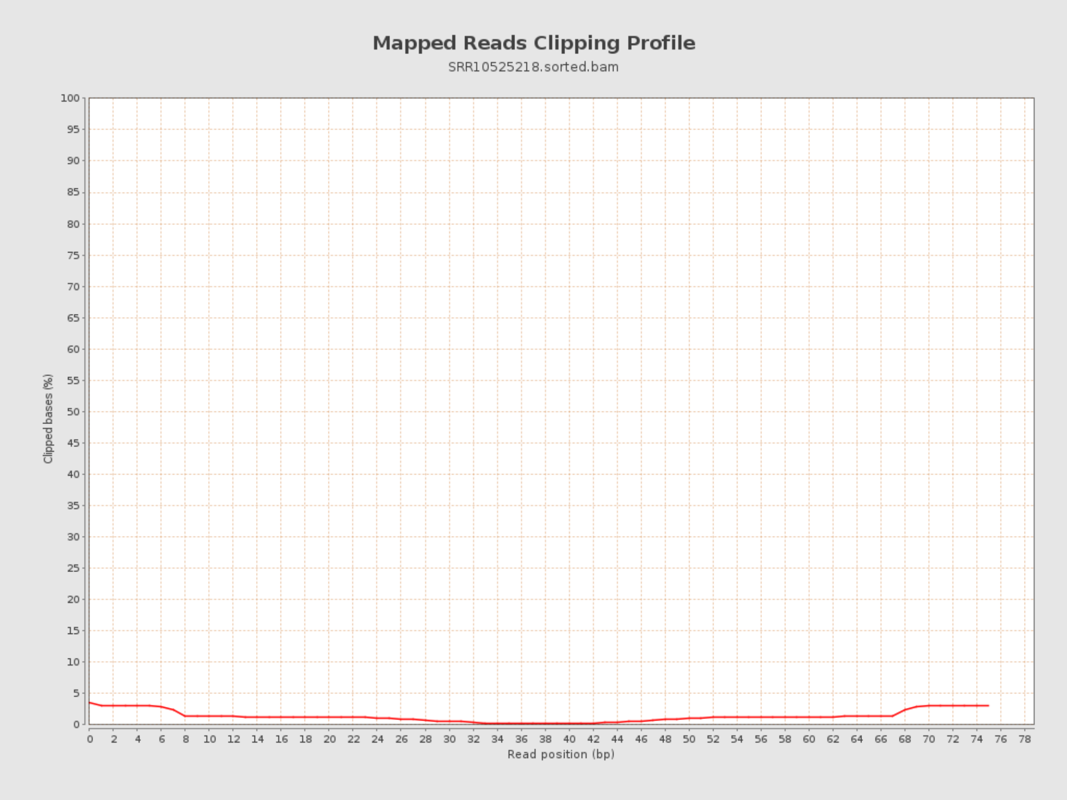
8. Results : Mapped Reads Nucleotide Content



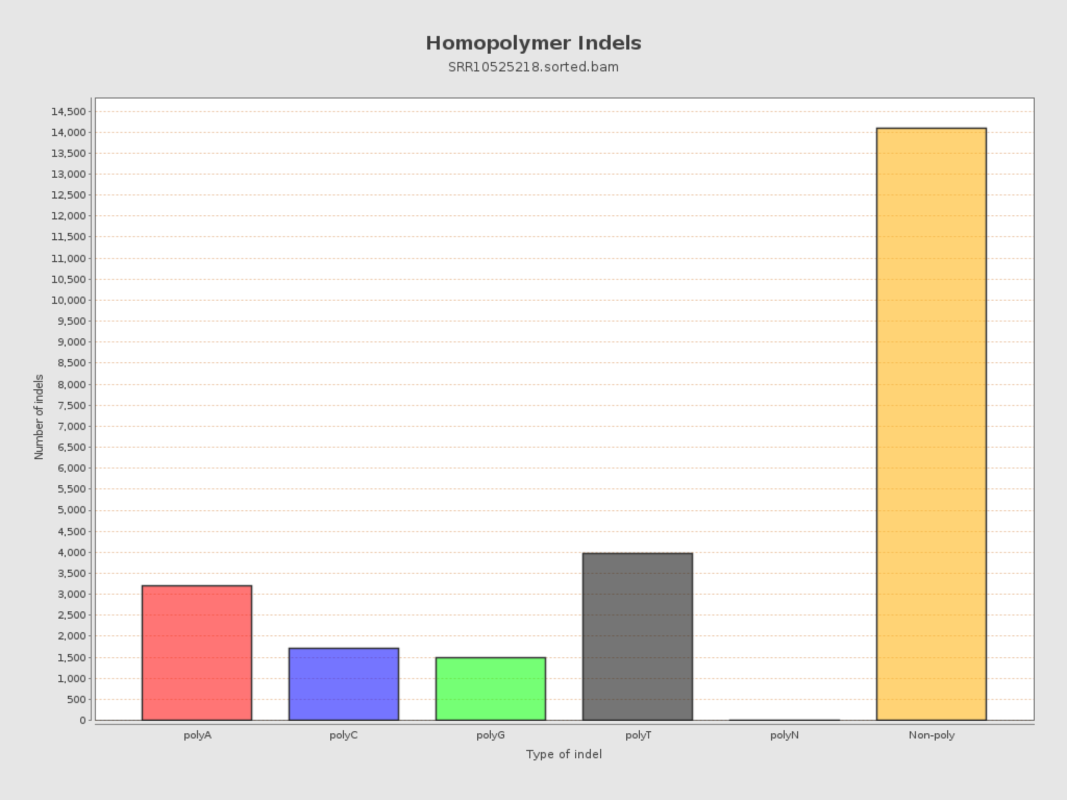
9. Results : Mapped Reads GC-content Distribution



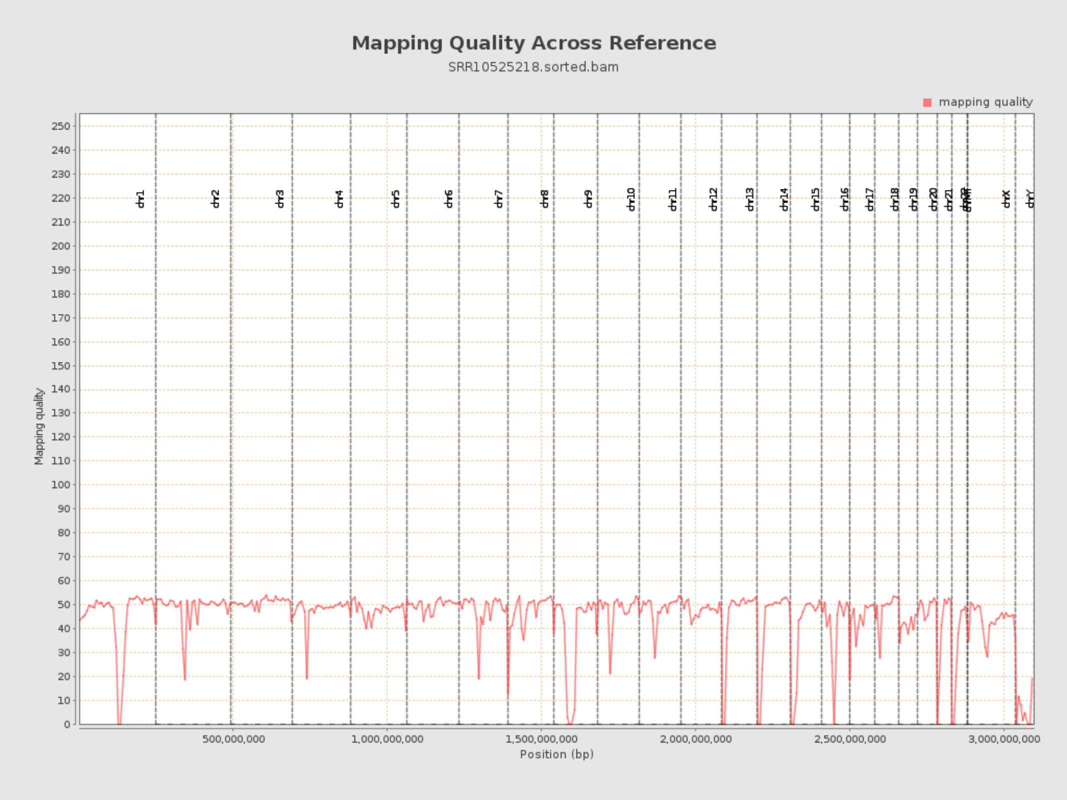
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram