Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:40:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525066.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_SRR10525066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:40:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,379,693
Mapped reads	4,097,047 / 93.55%
Unmapped reads	282,646 / 6.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,916 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	280,317 / 6.4%
Duplication rate	5.17%
Clipped reads	4,101,237 / 93.64%

2.2. ACGT Content

Number/percentage of A's	65,815,516 / 26.6%
Number/percentage of C's	48,301,219 / 19.52%
Number/percentage of T's	75,906,035 / 30.68%
Number/percentage of G's	57,340,960 / 23.18%
Number/percentage of N's	29,201 / 0.01%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0799

Standard Deviation	0.6599

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

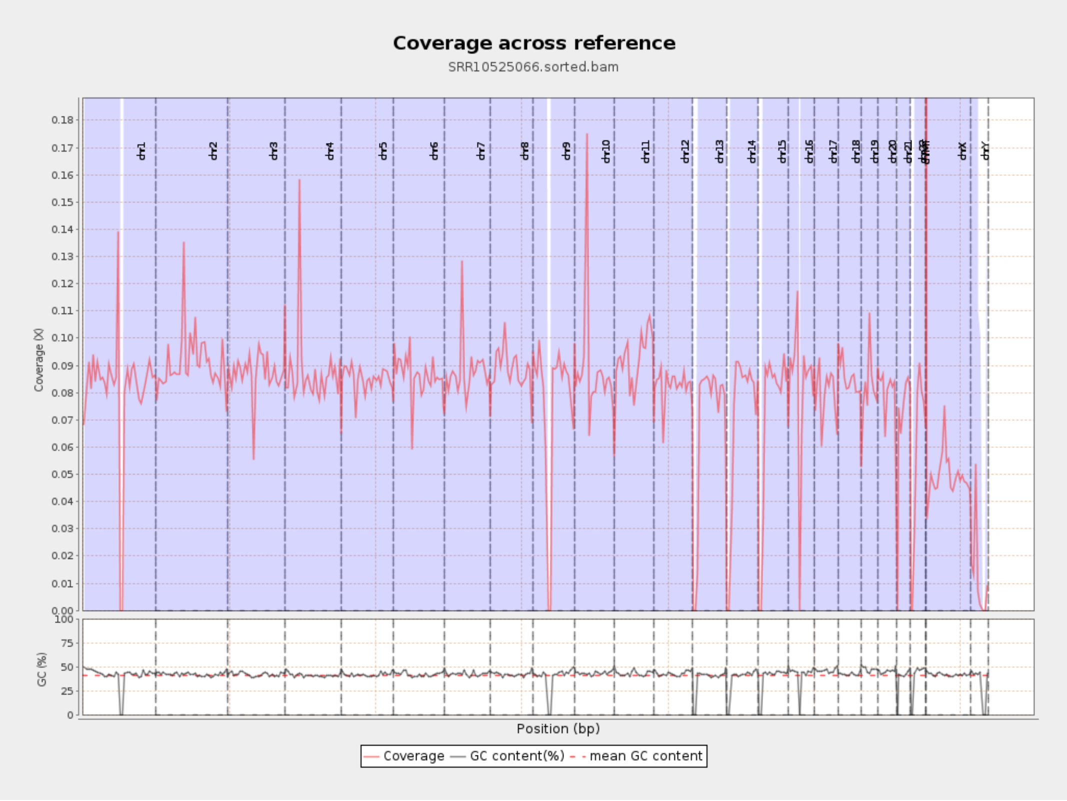
General error rate	0.49%
Mismatches	1,177,501
Insertions	21,911
Mapped reads with at least one insertion	0.53%
Deletions	52,390
Mapped reads with at least one deletion	1.27%
Homopolymer indels	41.75%

2.6. Chromosome stats

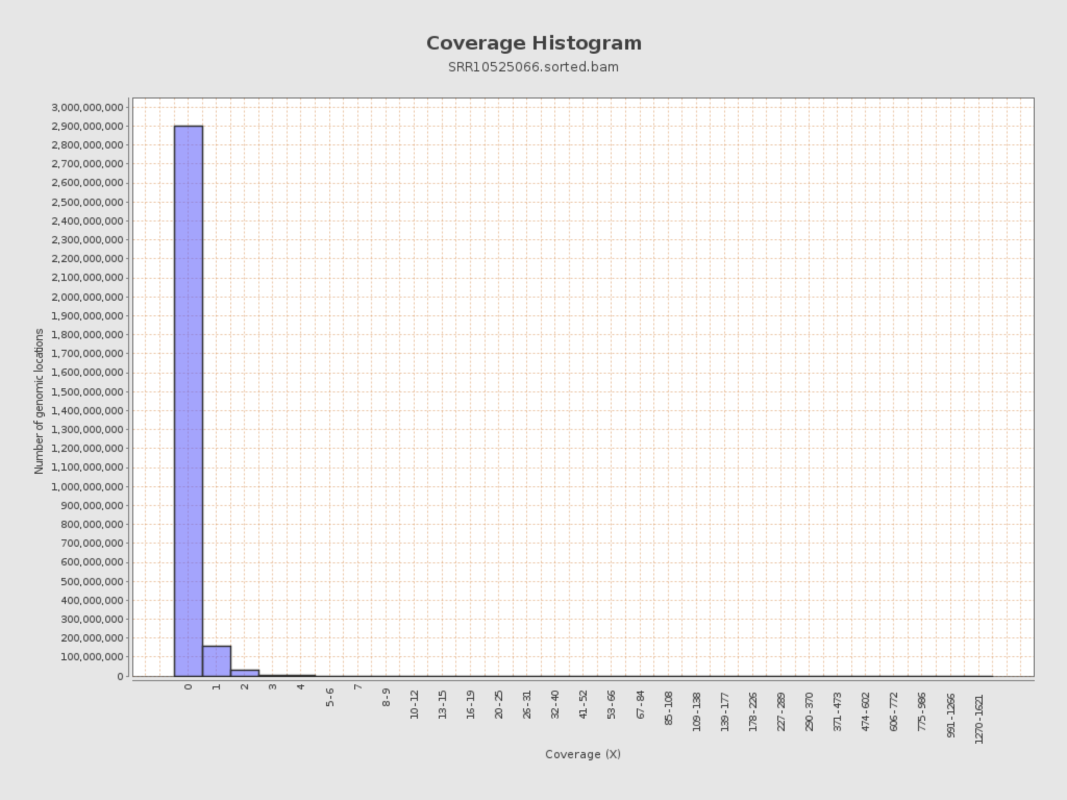
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20226434	0.0811	1.3566
chr2	243199373	22140095	0.091	0.7979
chr3	198022430	17251877	0.0871	0.3613
chr4	191154276	16771748	0.0877	0.4723
chr5	180915260	15372196	0.085	0.3575
chr6	171115067	14778899	0.0864	0.4166
chr7	159138663	13958265	0.0877	0.7558

chr8	146364022	12952018	0.0885	0.8957
chr9	141213431	10744513	0.0761	0.5043
chr10	135534747	11948939	0.0882	0.757
chr11	135006516	12429919	0.0921	0.4794
chr12	133851895	11093969	0.0829	0.3673
chr13	115169878	7893281	0.0685	0.3188
chr14	107349540	7592429	0.0707	0.3474
chr15	102531392	7205083	0.0703	0.3217
chr16	90354753	7271836	0.0805	0.4111
chr17	81195210	6488001	0.0799	0.3923
chr18	78077248	6692612	0.0857	0.9486
chr19	59128983	4891716	0.0827	0.9815
chr20	63025520	5059591	0.0803	0.3689
chr21	48129895	3389591	0.0704	0.4237
chr22	51304566	2892287	0.0564	0.2868
chrMT	16571	42906	2.5892	2.1779
chrX	155270560	7638601	0.0492	0.3361
chrY	59373566	751317	0.0127	0.4554

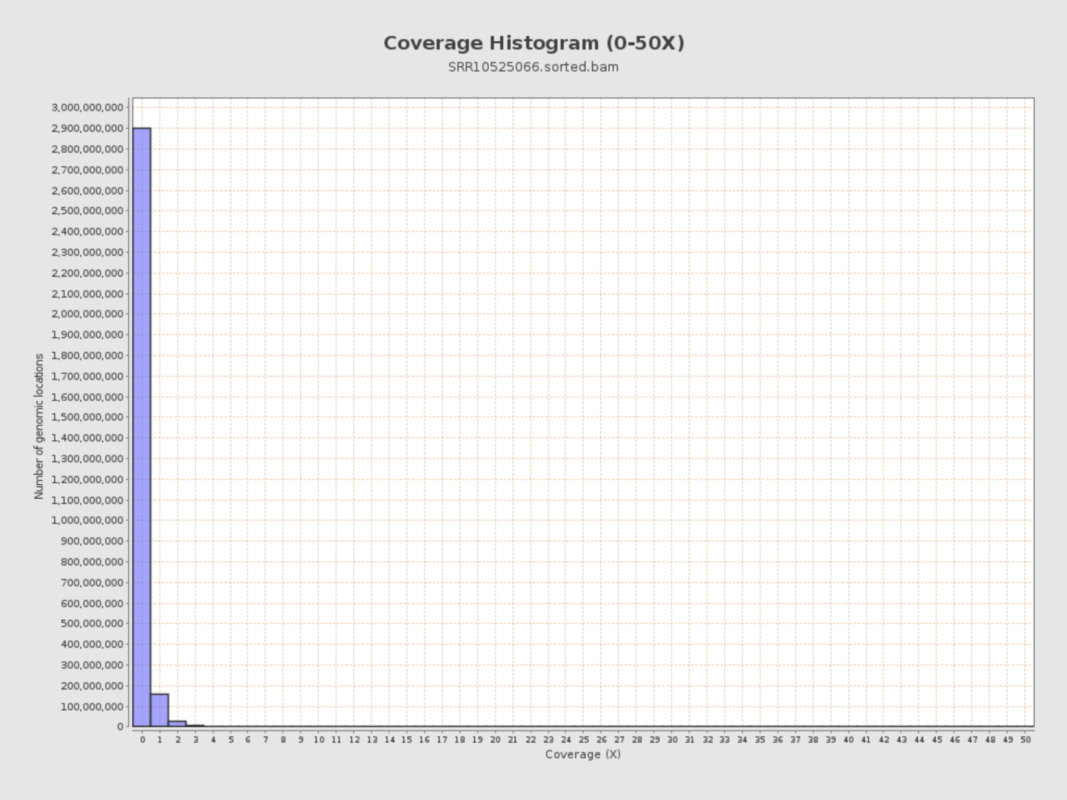
3. Results : Coverage across reference



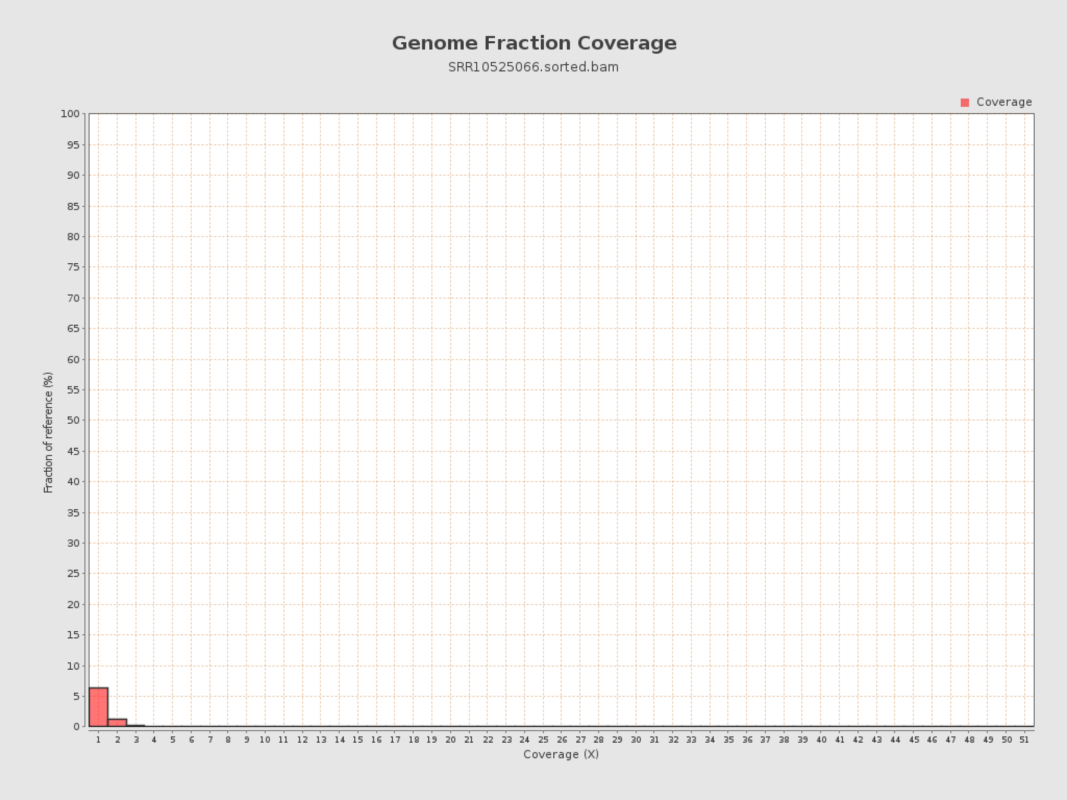
4. Results : Coverage Histogram



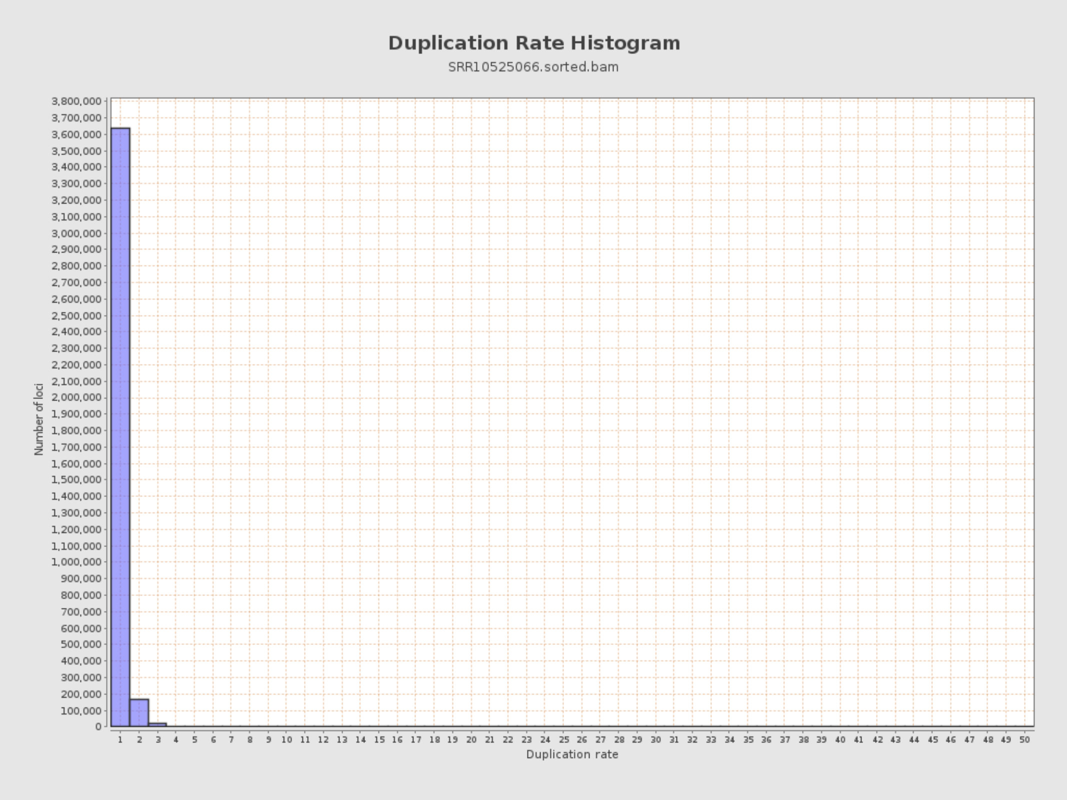
5. Results : Coverage Histogram (0-50X)



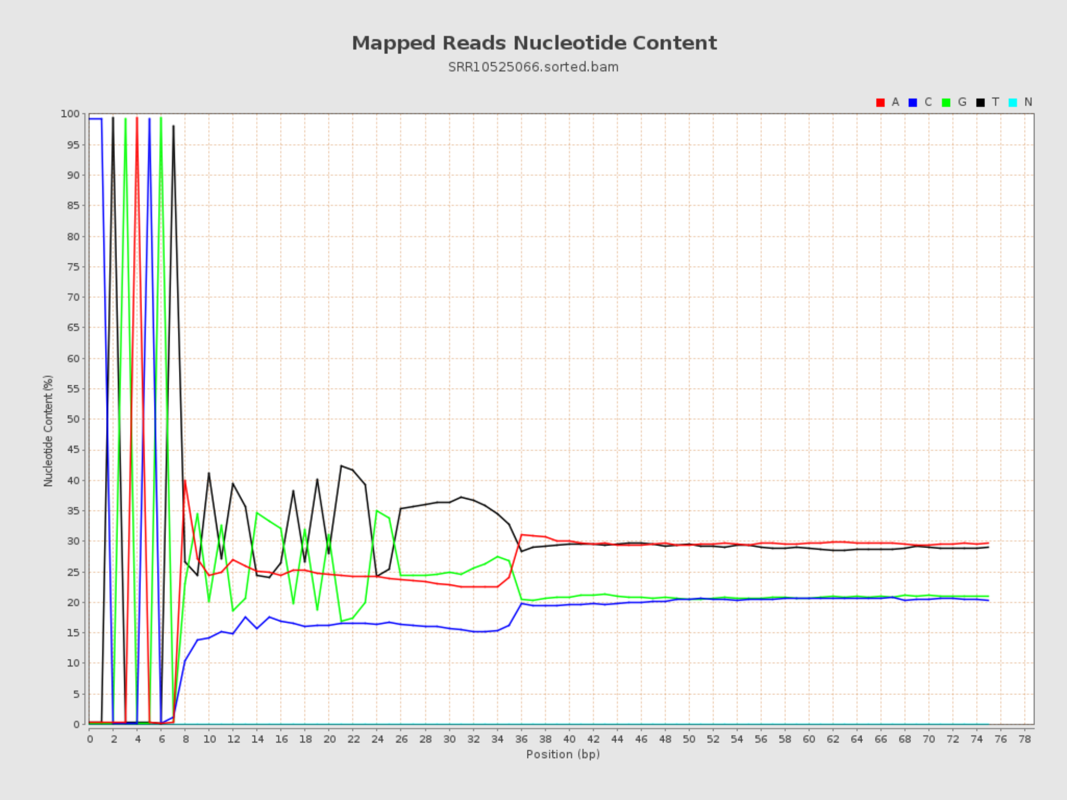
6. Results : Genome Fraction Coverage



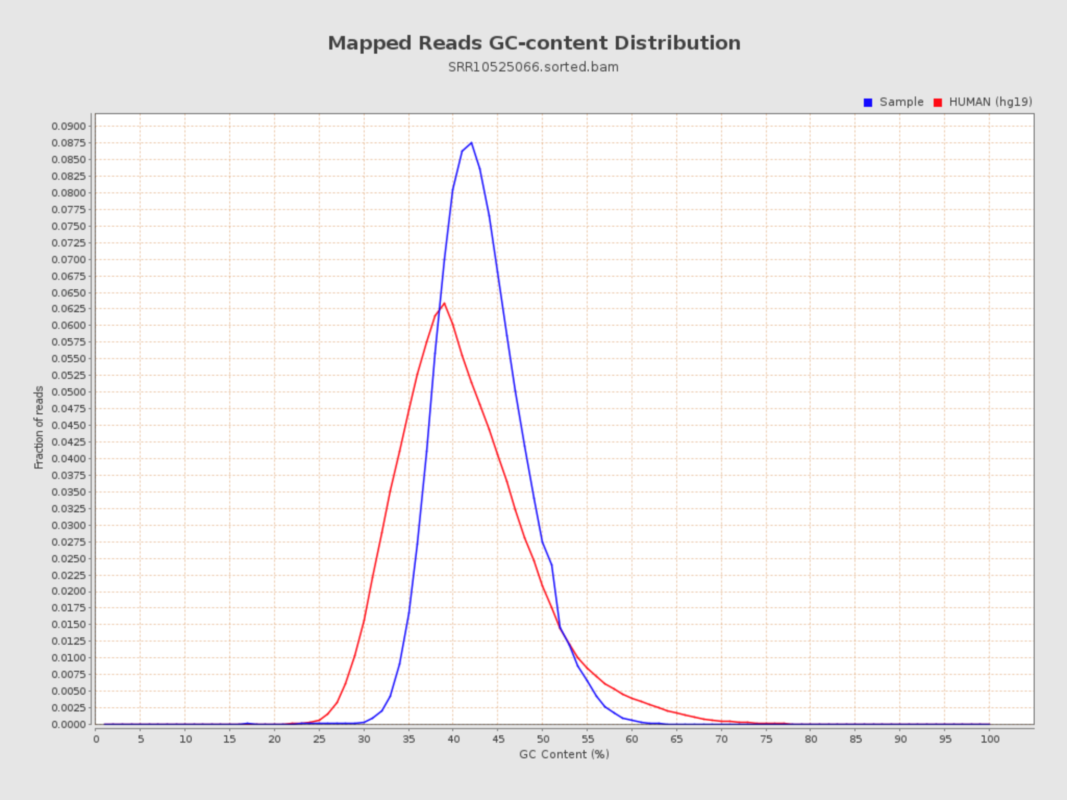
7. Results : Duplication Rate Histogram



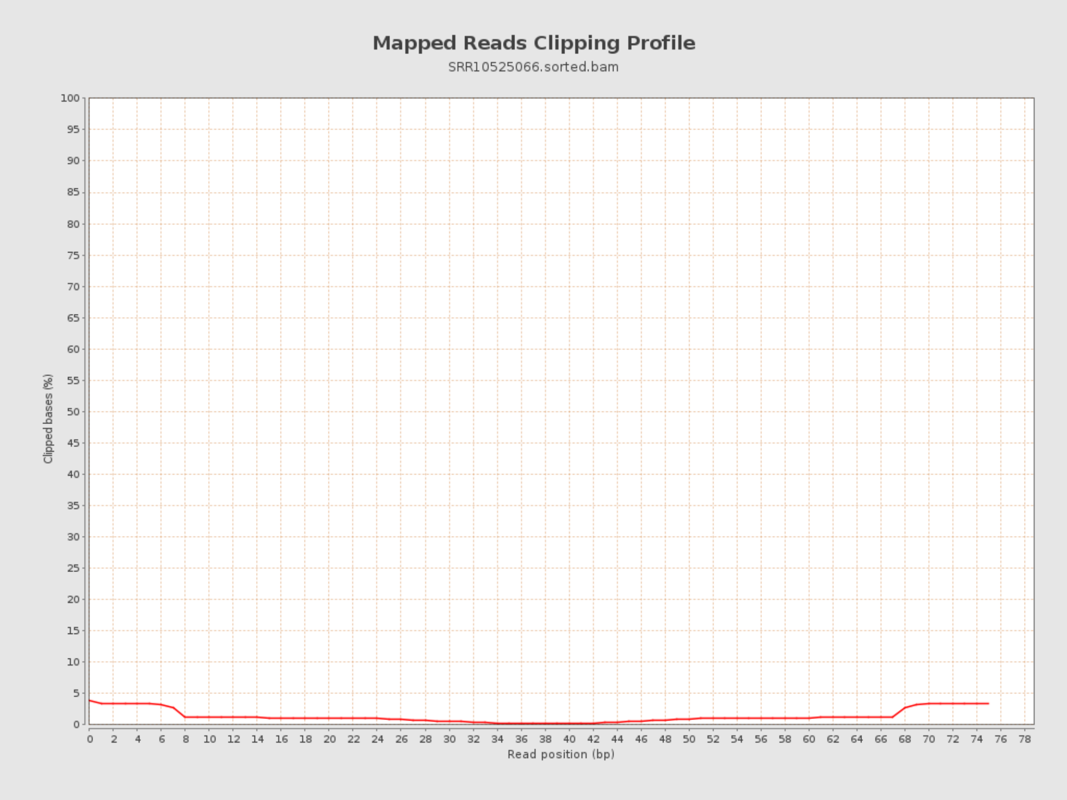
8. Results : Mapped Reads Nucleotide Content



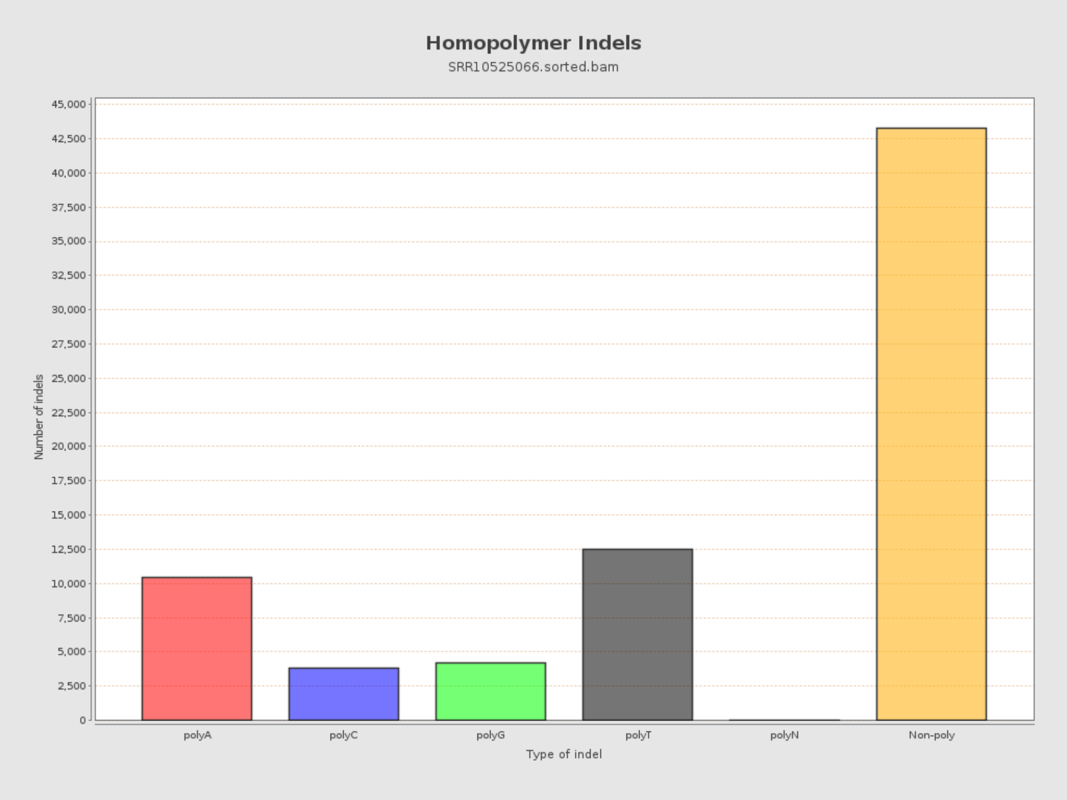
9. Results : Mapped Reads GC-content Distribution



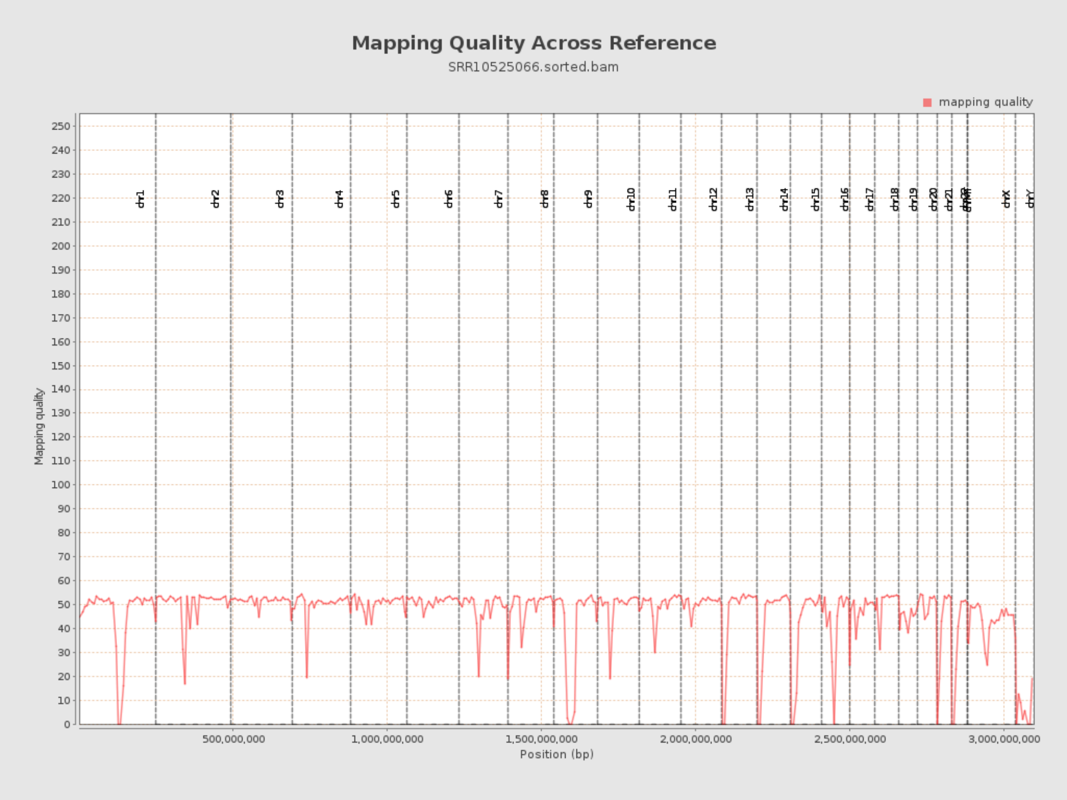
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram