Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:54:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525182.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_SRR10525182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:54:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,869,803
Mapped reads	1,657,319 / 88.64%
Unmapped reads	212,484 / 11.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,952 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	54,071 / 2.89%
Duplication rate	2.43%
Clipped reads	1,660,391 / 88.8%

2.2. ACGT Content

Number/percentage of A's	25,223,868 / 26.65%
Number/percentage of C's	17,136,368 / 18.1%
Number/percentage of T's	29,338,636 / 30.99%
Number/percentage of G's	22,956,549 / 24.25%
Number/percentage of N's	2,693 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.2646

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

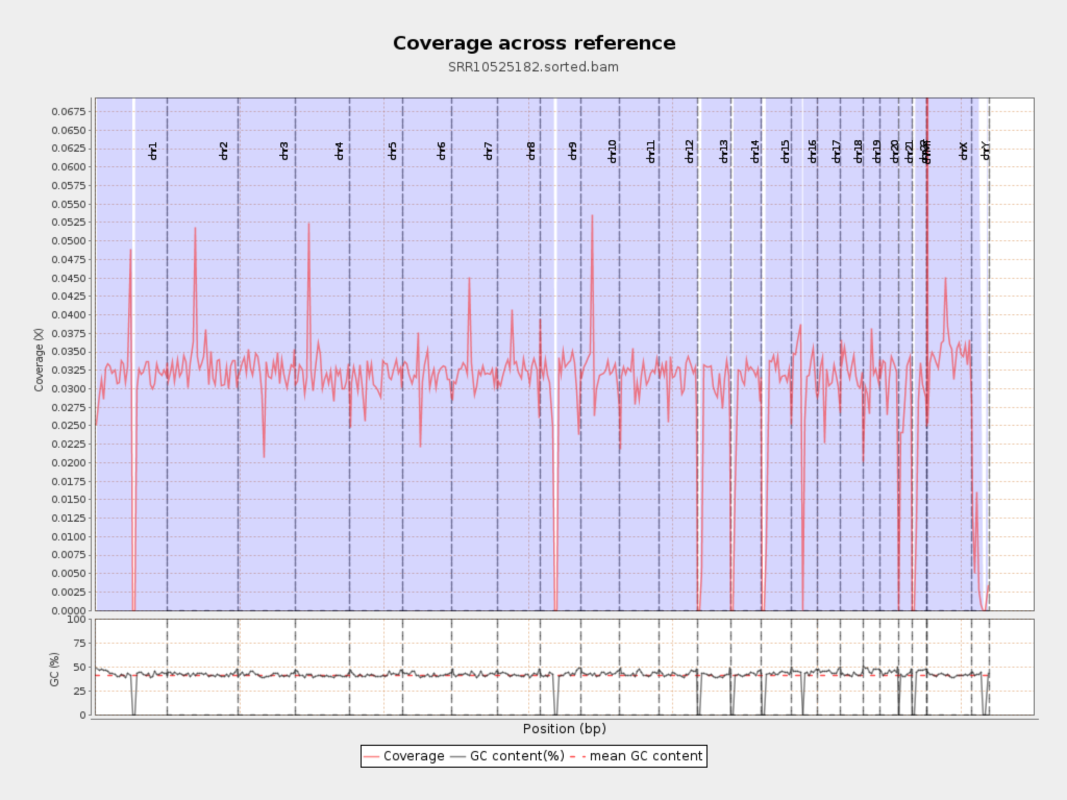
General error rate	0.49%
Mismatches	454,032
Insertions	6,021
Mapped reads with at least one insertion	0.36%
Deletions	14,737
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.46%

2.6. Chromosome stats

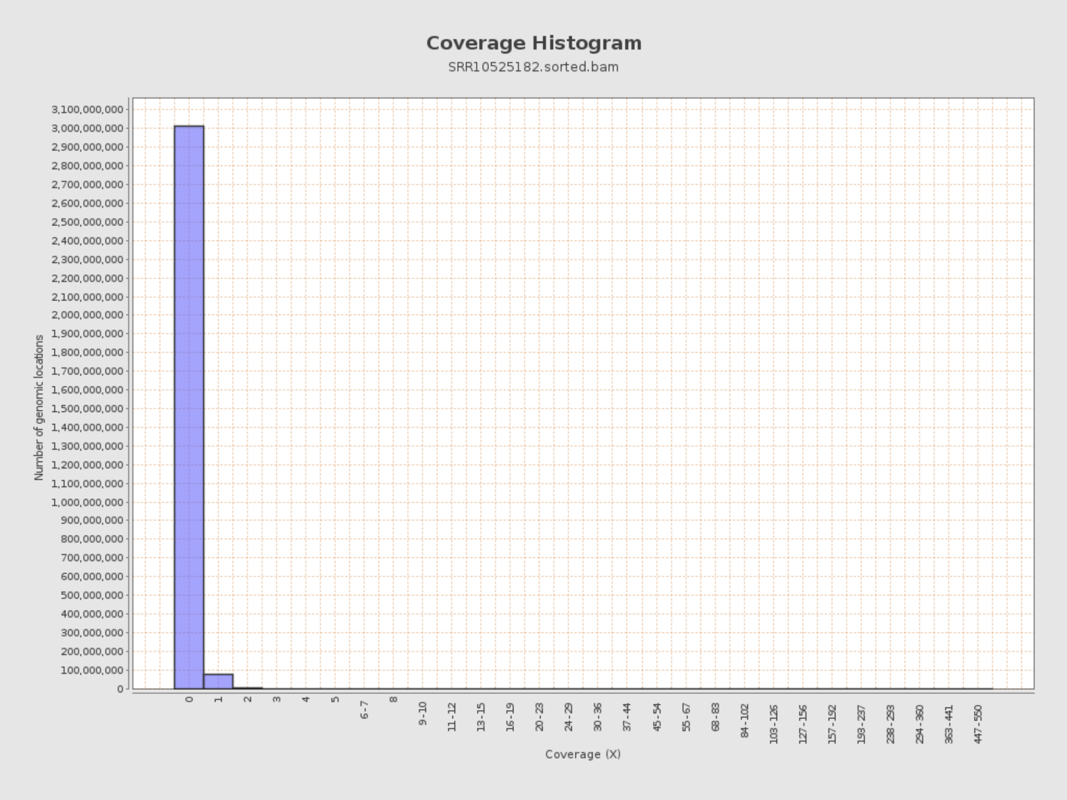
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7537243	0.0302	0.4535
chr2	243199373	8134632	0.0334	0.2904
chr3	198022430	6390402	0.0323	0.1958
chr4	191154276	6214863	0.0325	0.2185
chr5	180915260	5714334	0.0316	0.1953
chr6	171115067	5456687	0.0319	0.2129
chr7	159138663	5178205	0.0325	0.2984

chr8	146364022	4779677	0.0327	0.2773
chr9	141213431	4013831	0.0284	0.2573
chr10	135534747	4495775	0.0332	0.275
chr11	135006516	4279042	0.0317	0.2584
chr12	133851895	4270272	0.0319	0.2007
chr13	115169878	3011580	0.0261	0.1751
chr14	107349540	2874760	0.0268	0.1958
chr15	102531392	2690278	0.0262	0.1773
chr16	90354753	2711165	0.03	0.2014
chr17	81195210	2489851	0.0307	0.2035
chr18	78077248	2556933	0.0327	0.4374
chr19	59128983	1827896	0.0309	0.3298
chr20	63025520	1989634	0.0316	0.2
chr21	48129895	1252531	0.026	0.1968
chr22	51304566	1076807	0.021	0.1577
chrMT	16571	13657	0.8242	1.0876
chrX	155270560	5438651	0.035	0.2303
chrY	59373566	283912	0.0048	0.1212

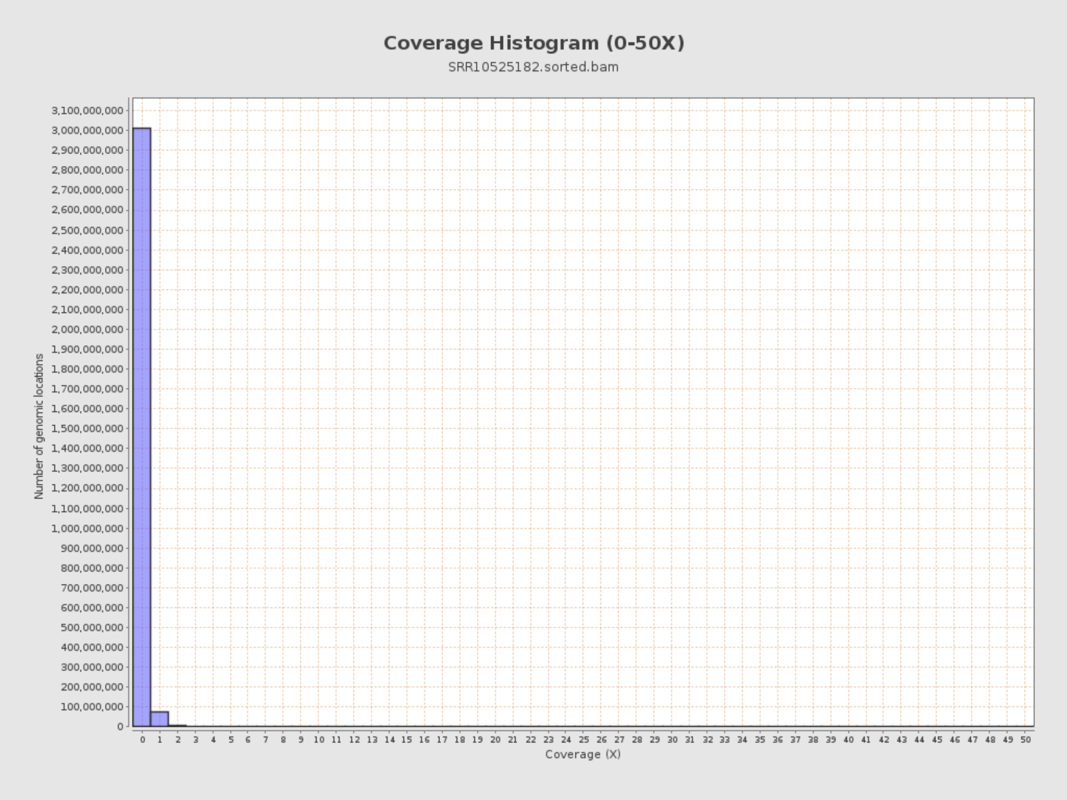
3. Results : Coverage across reference



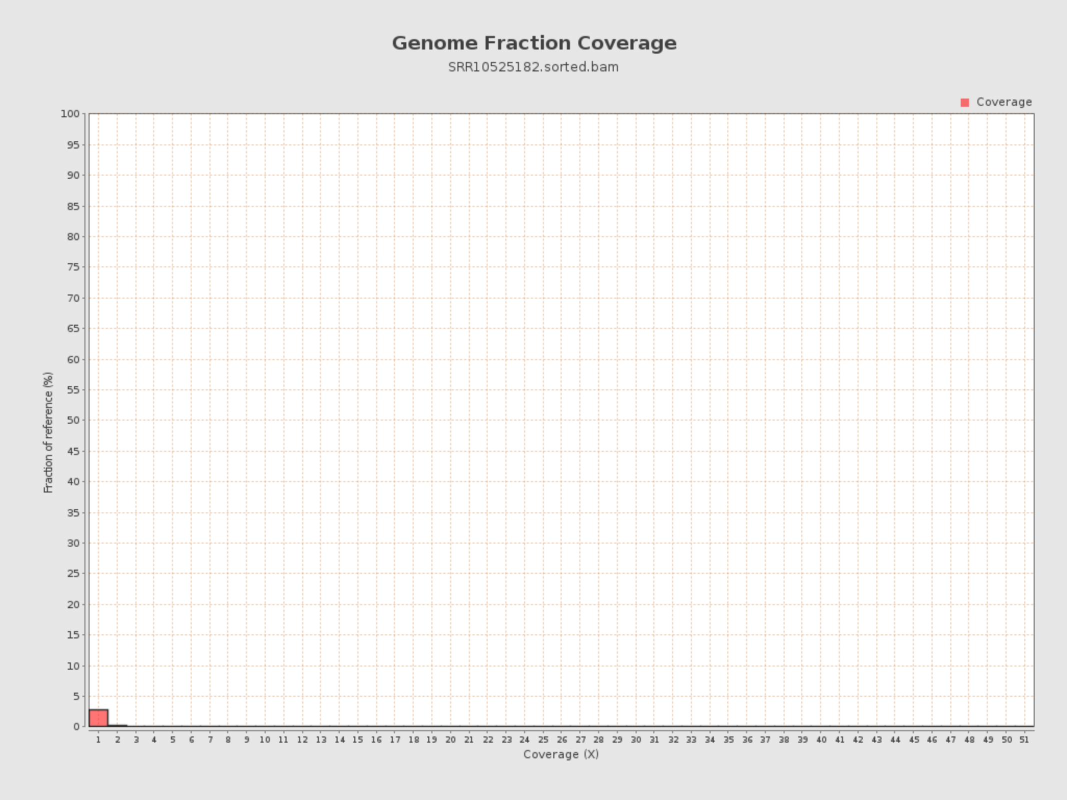
4. Results : Coverage Histogram



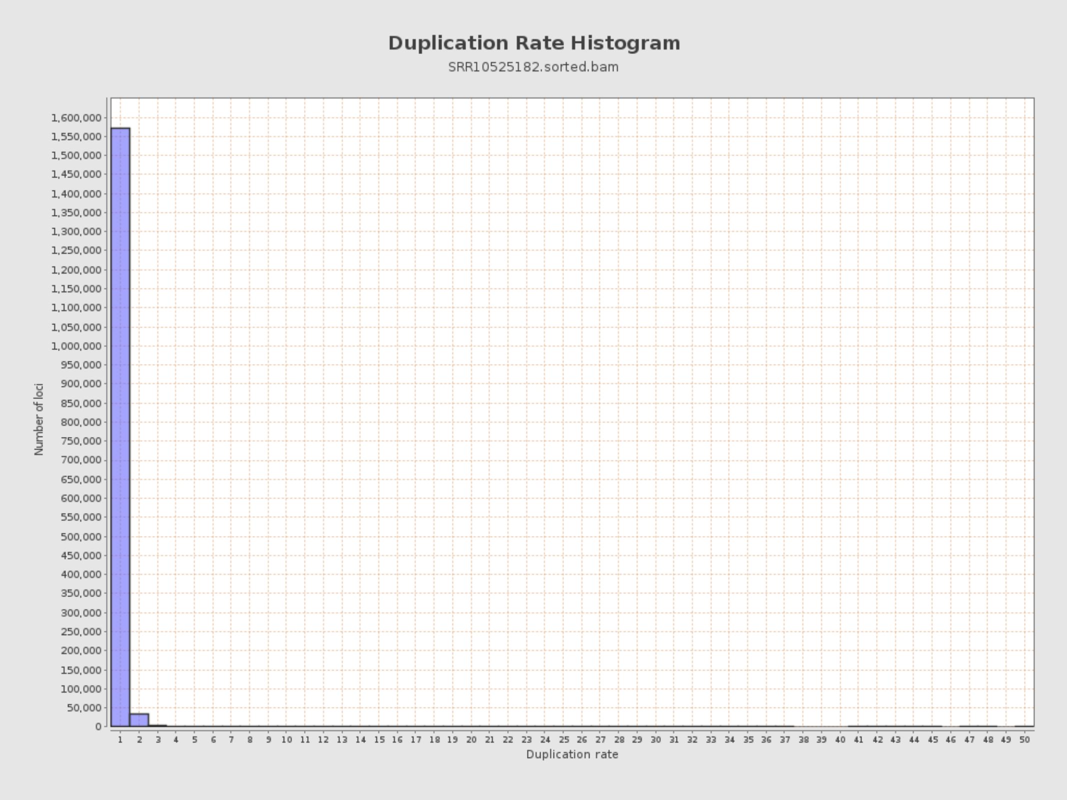
5. Results : Coverage Histogram (0-50X)



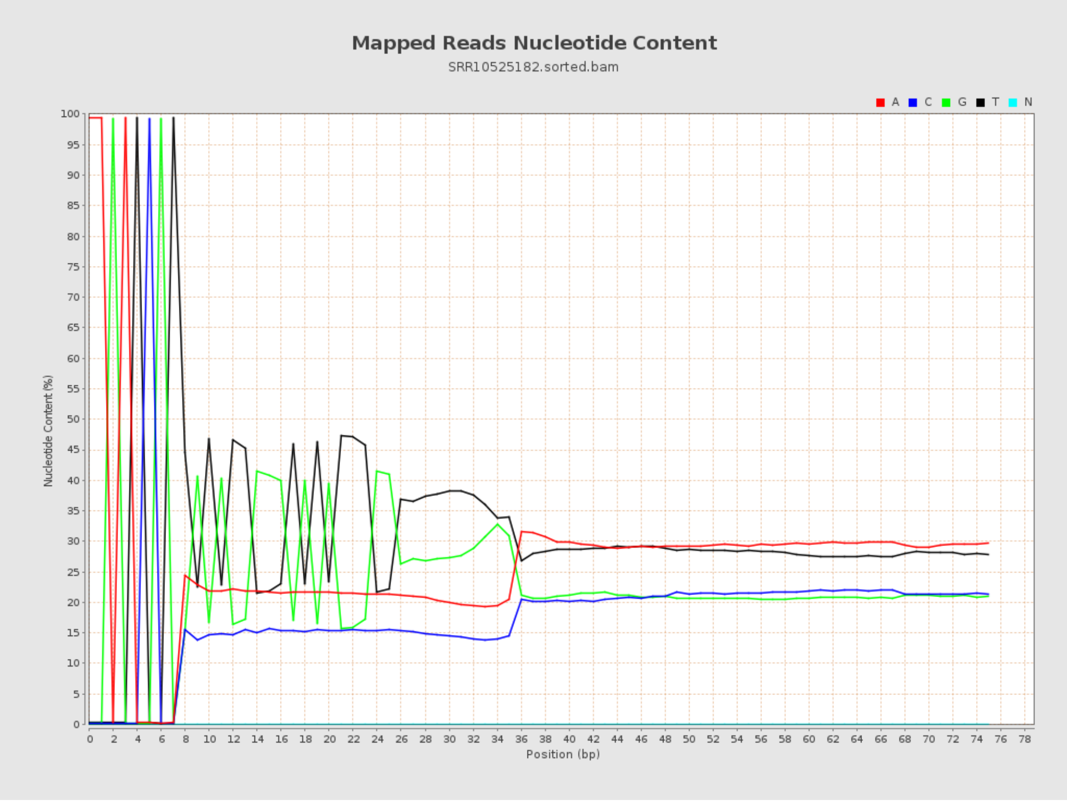
6. Results : Genome Fraction Coverage



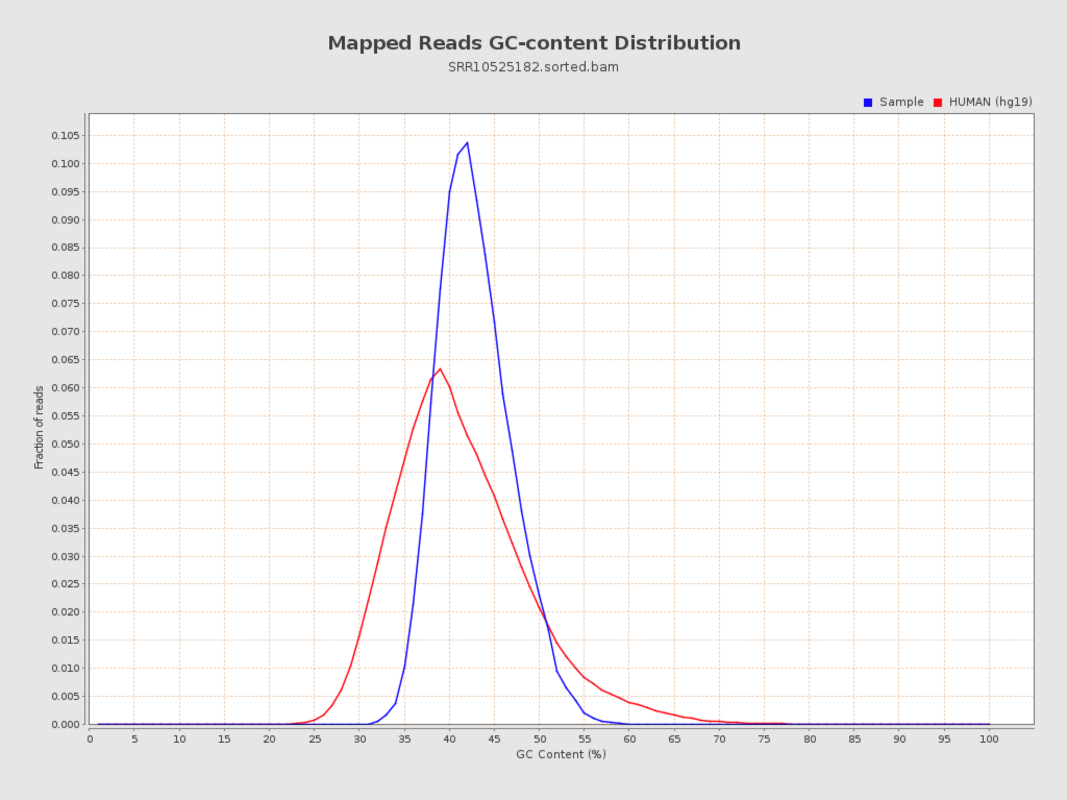
7. Results : Duplication Rate Histogram



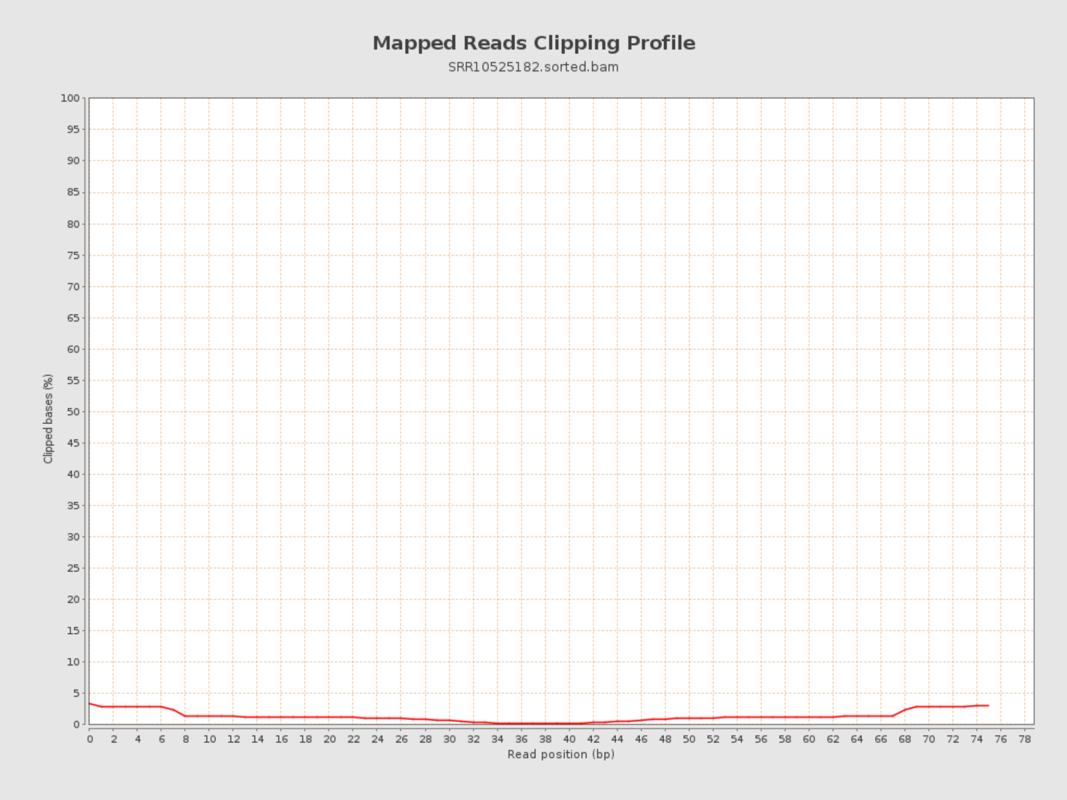
8. Results : Mapped Reads Nucleotide Content



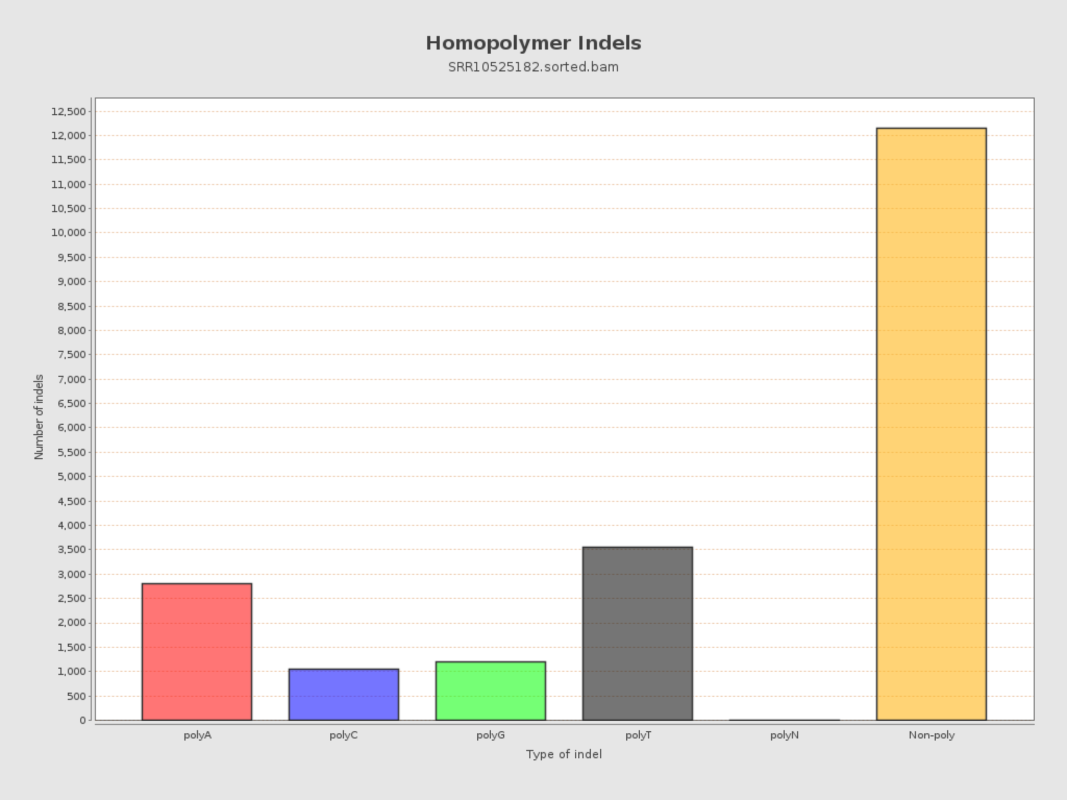
9. Results : Mapped Reads GC-content Distribution



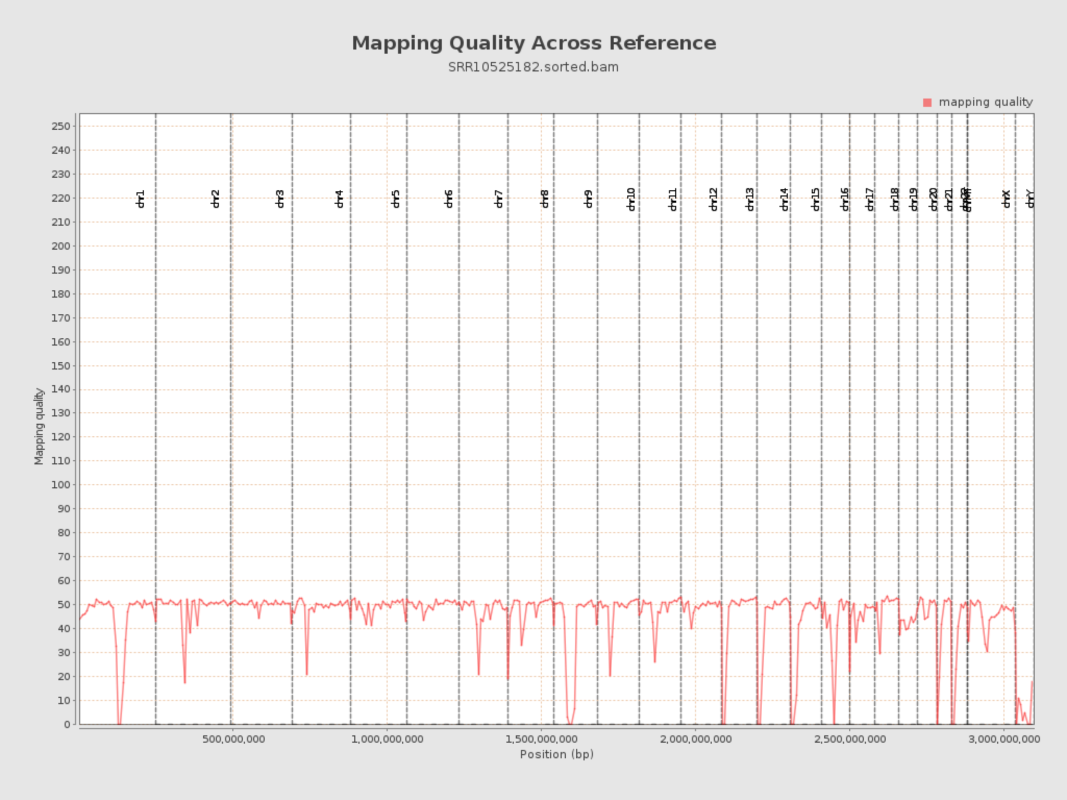
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram