Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:22:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549125.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_SRR1549125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:22:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,903,769
Mapped reads	6,317,459 / 57.94%
Unmapped reads	4,586,310 / 42.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	304,794 / 2.8%
Duplication rate	3.63%
Clipped reads	331,021 / 3.04%

2.2. ACGT Content

Number/percentage of A's	73,923,955 / 29.49%
Number/percentage of C's	51,294,998 / 20.46%
Number/percentage of T's	74,221,843 / 29.6%
Number/percentage of G's	51,264,262 / 20.45%
Number/percentage of N's	10,185 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.081
Standard Deviation	0.9828

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

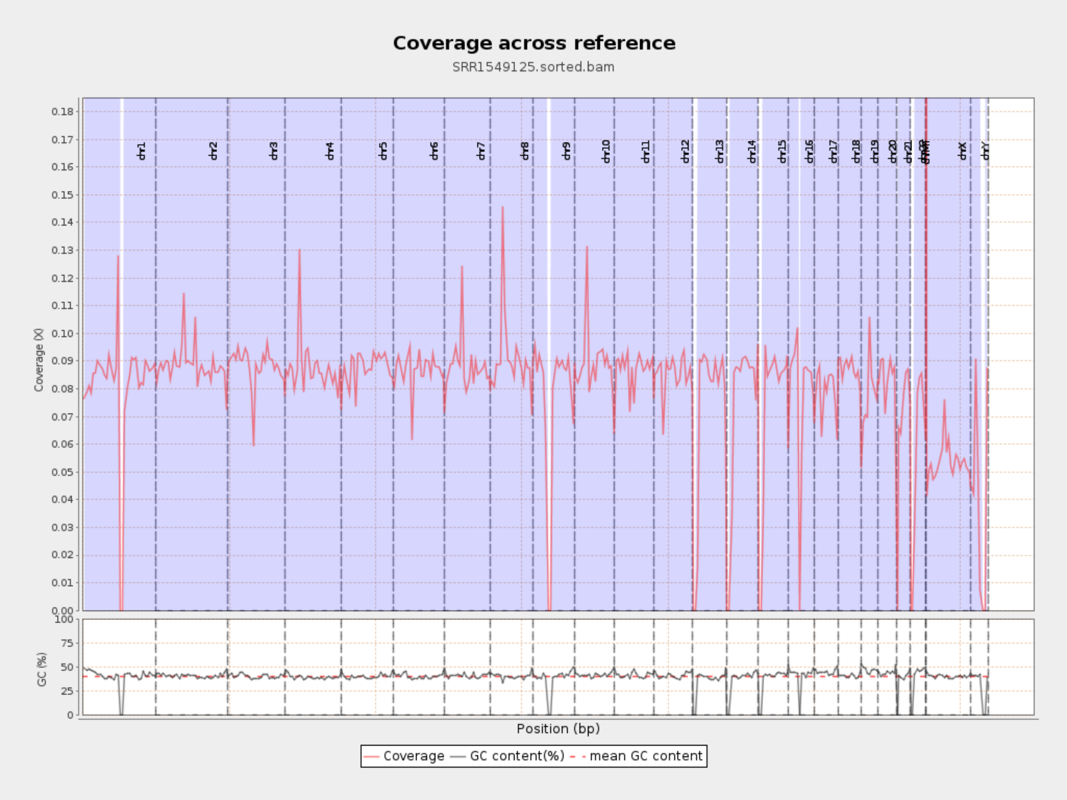
General error rate	0.32%
Mismatches	793,293
Insertions	6,423
Mapped reads with at least one insertion	0.1%
Deletions	21,335
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.92%

2.6. Chromosome stats

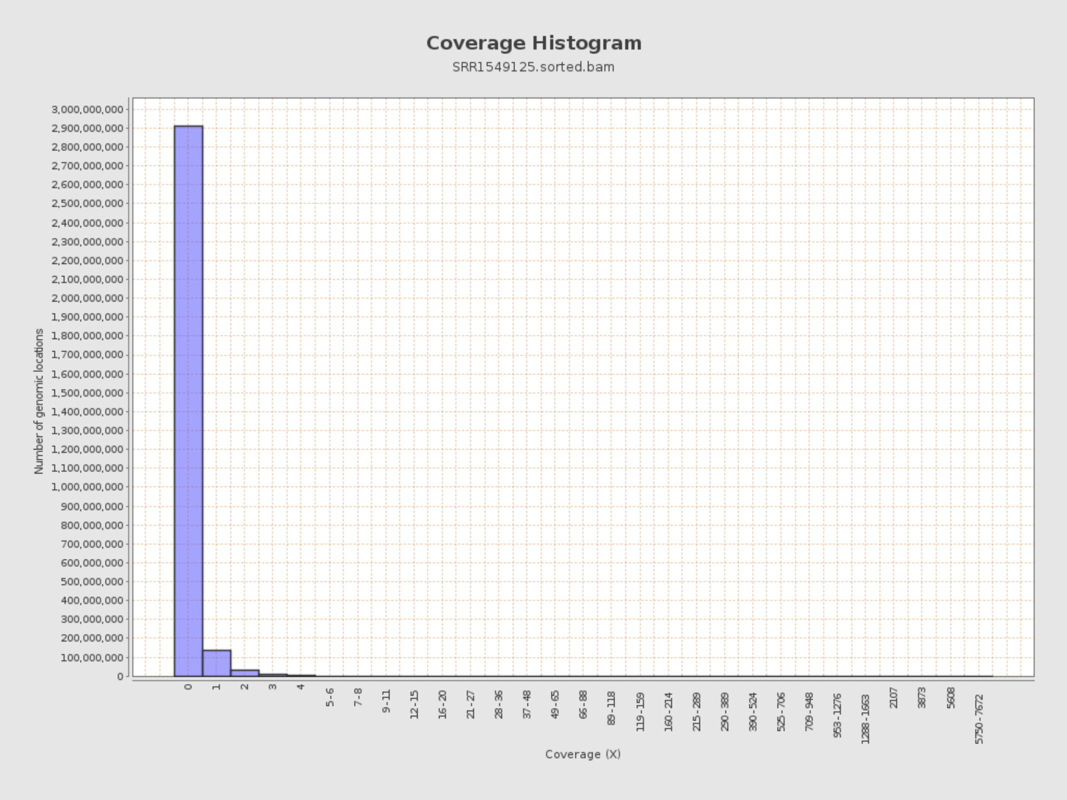
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20223663	0.0811	1.0945
chr2	243199373	21572401	0.0887	0.5231
chr3	198022430	17449380	0.0881	0.3828
chr4	191154276	16771100	0.0877	0.4502
chr5	180915260	15869754	0.0877	0.389
chr6	171115067	14894969	0.087	0.3995
chr7	159138663	14015459	0.0881	0.6851
chr8	146364022	13341624	0.0912	3.7609

chr9	141213431	10736639	0.076	0.4661
chr10	135534747	12134915	0.0895	0.5862
chr11	135006516	11741532	0.087	0.4785
chr12	133851895	11471013	0.0857	0.3886
chr13	115169878	8326754	0.0723	0.3456
chr14	107349540	7784429	0.0725	0.4174
chr15	102531392	7322931	0.0714	0.3393
chr16	90354753	6931373	0.0767	0.3845
chr17	81195210	6447709	0.0794	0.3805
chr18	78077248	6817507	0.0873	0.8836
chr19	59128983	4620784	0.0781	0.8275
chr20	63025520	5291140	0.084	0.4003
chr21	48129895	3326533	0.0691	0.4159
chr22	51304566	2819425	0.055	0.313
chrMT	16571	91798	5.5397	6.7861
chrX	155270560	8330274	0.0537	0.3524
chrY	59373566	2409377	0.0406	0.4909

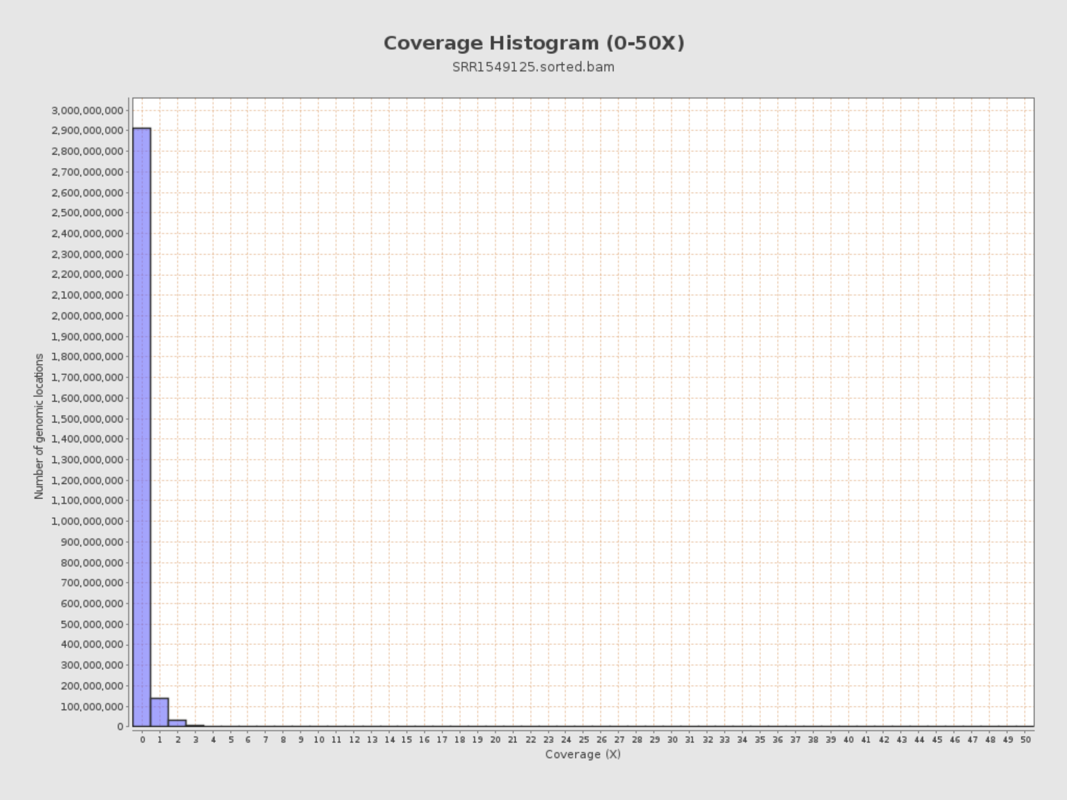
3. Results : Coverage across reference



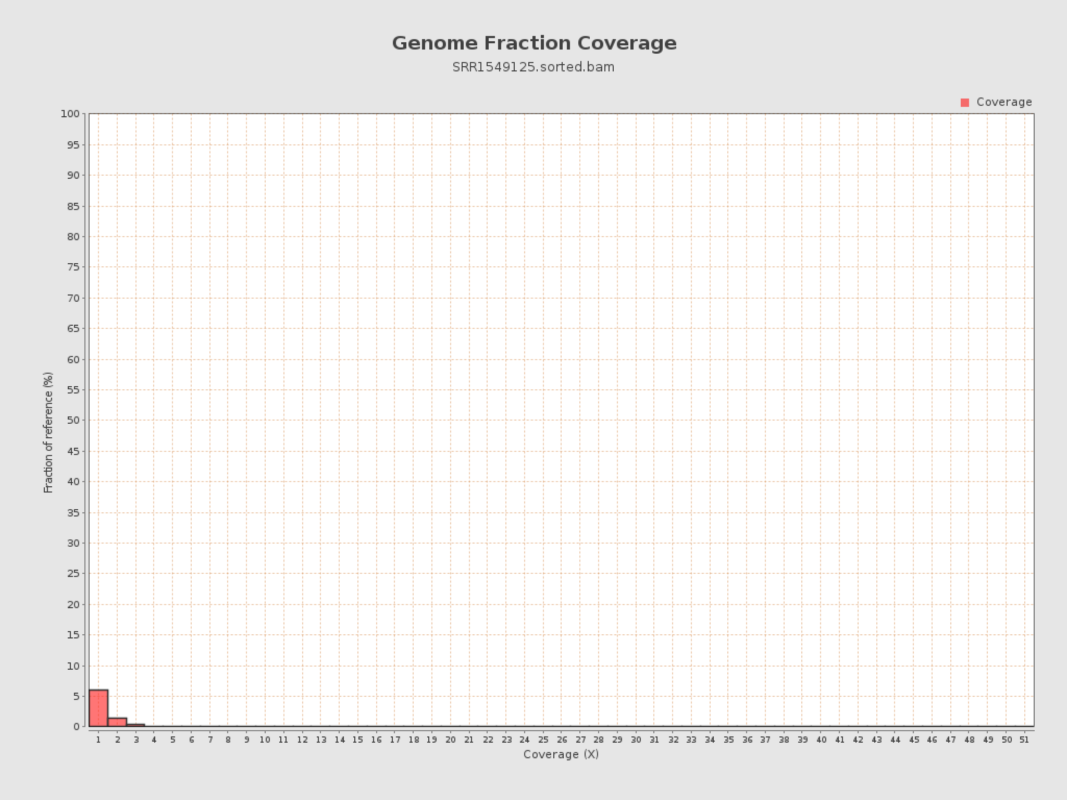
4. Results : Coverage Histogram



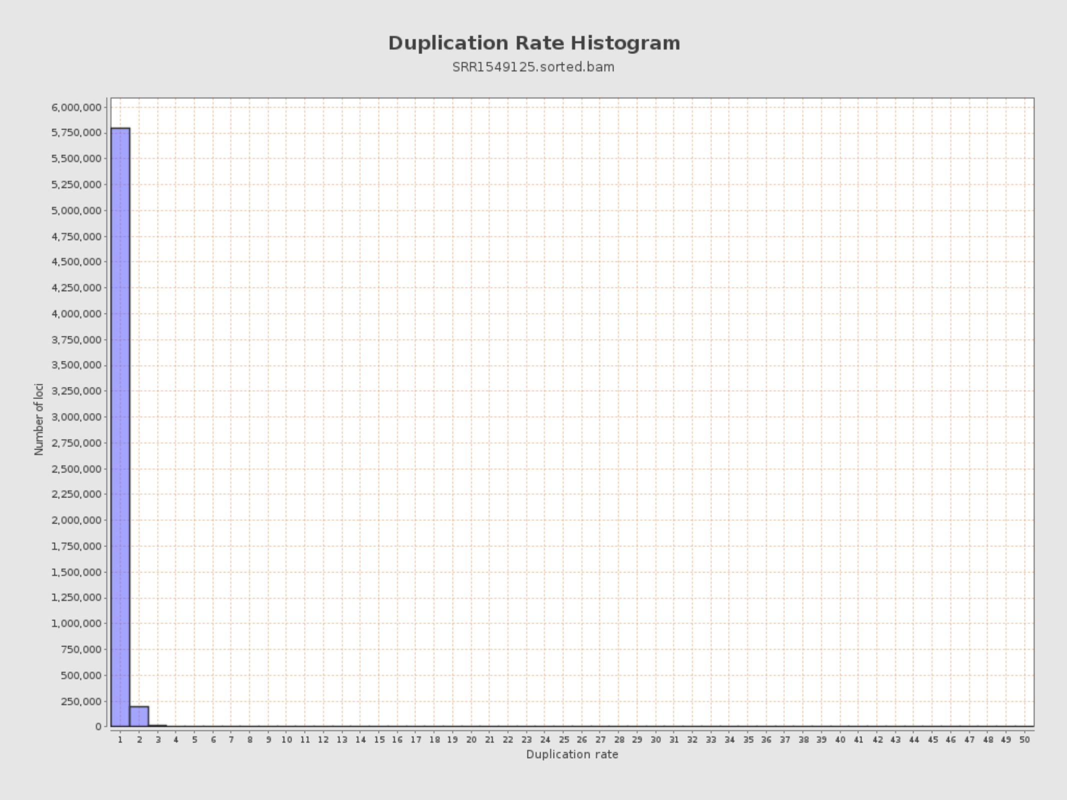
5. Results : Coverage Histogram (0-50X)



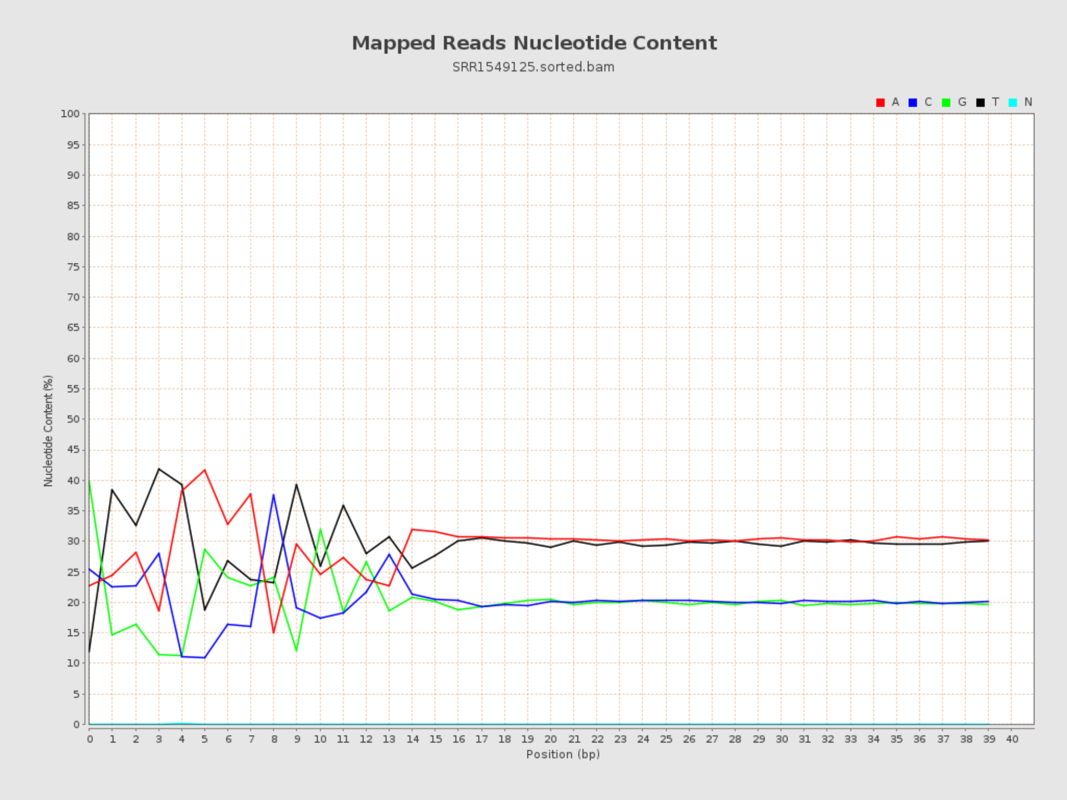
6. Results : Genome Fraction Coverage



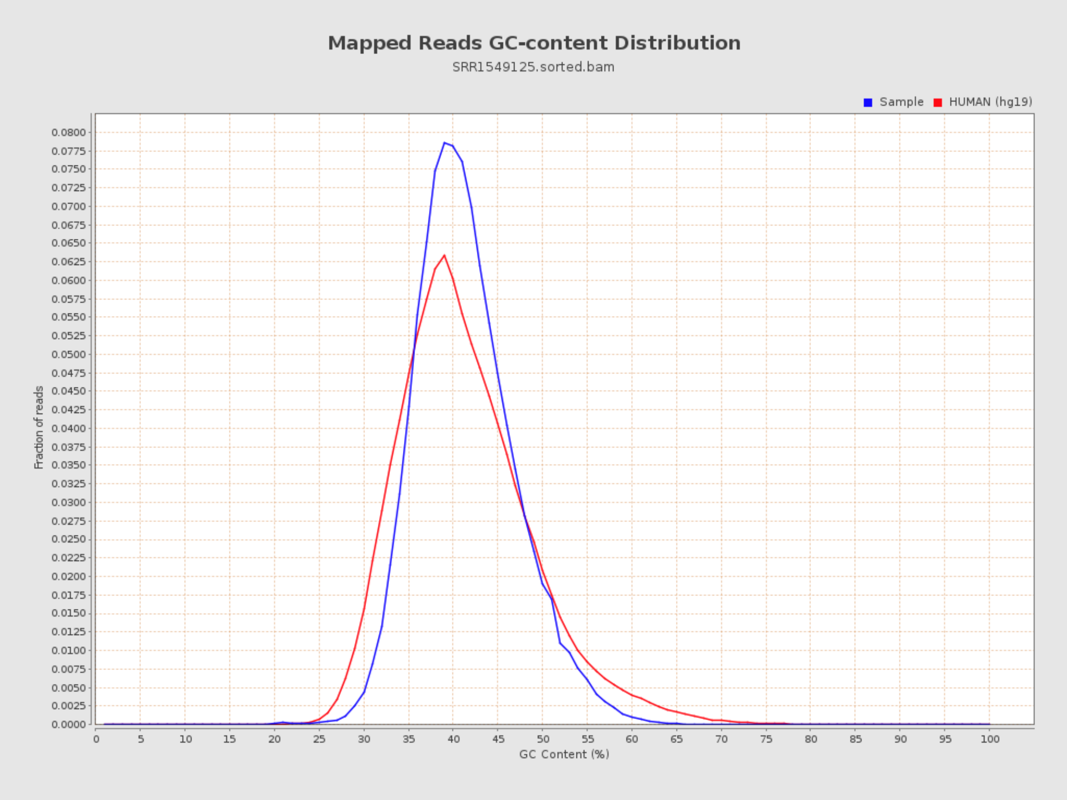
7. Results : Duplication Rate Histogram



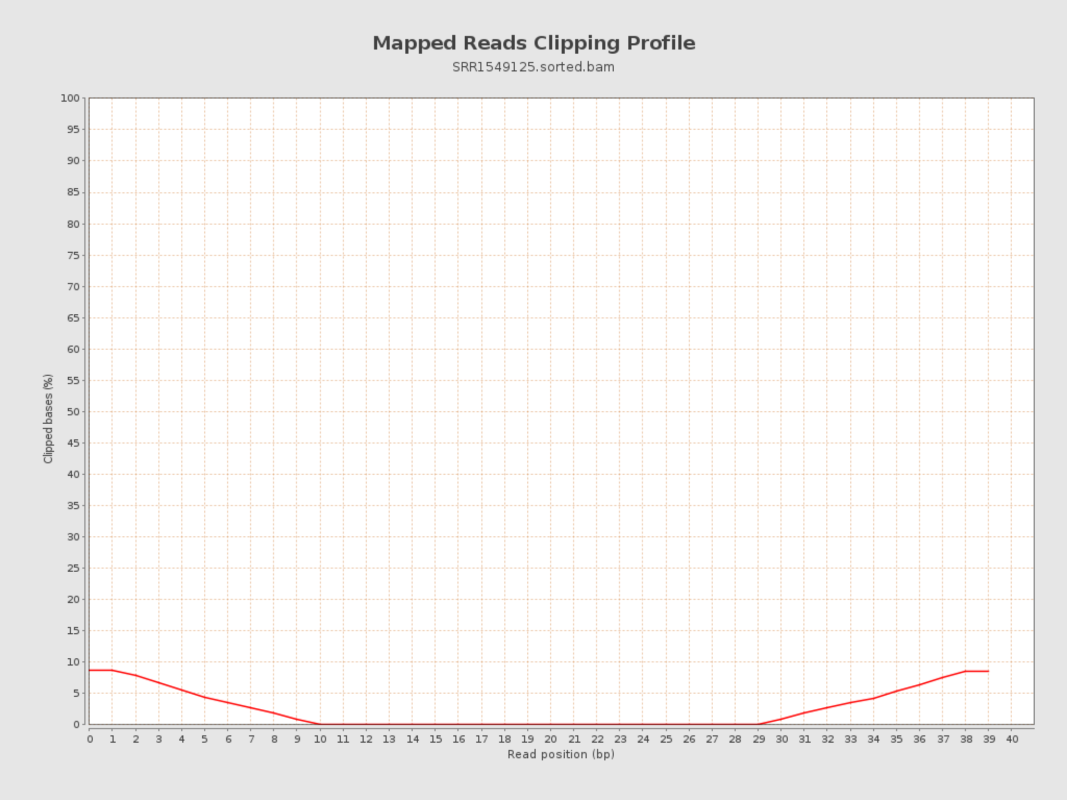
8. Results : Mapped Reads Nucleotide Content



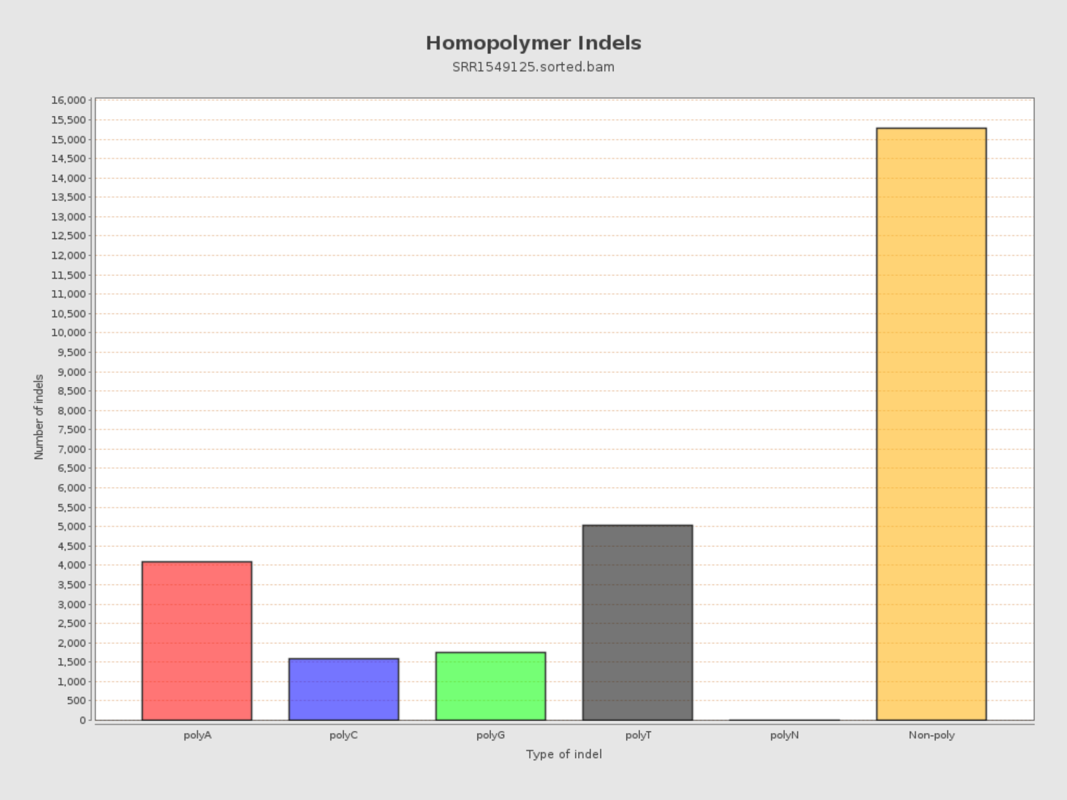
9. Results : Mapped Reads GC-content Distribution



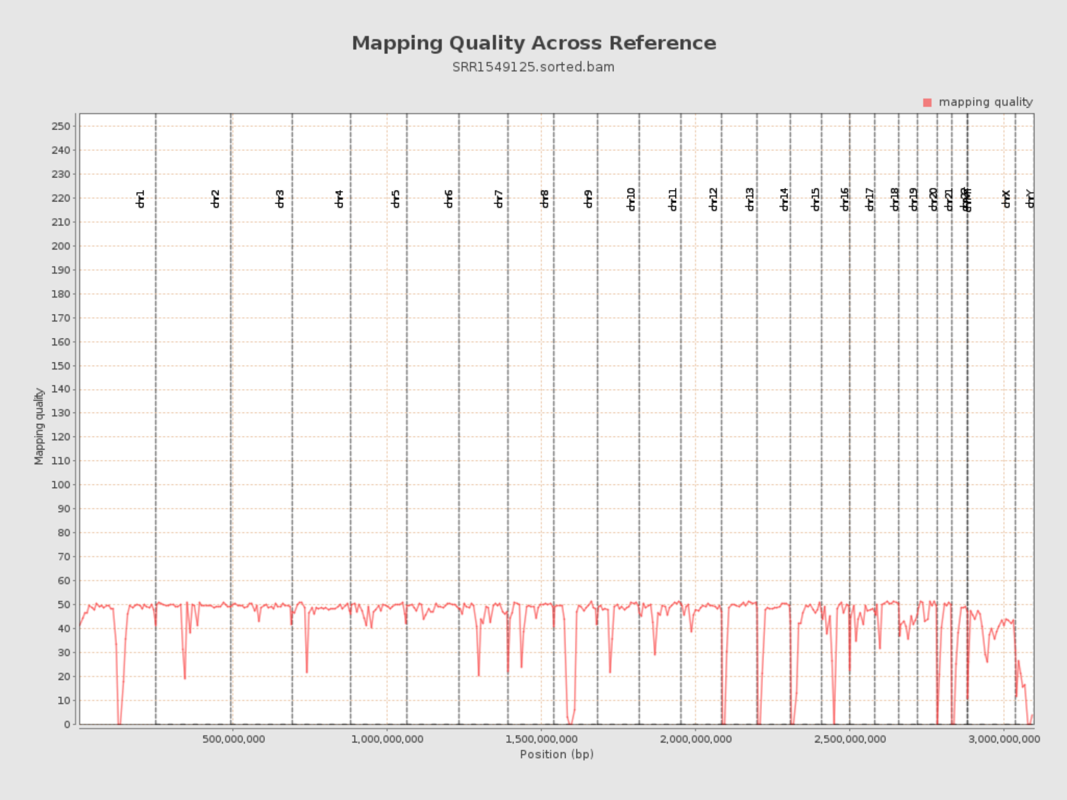
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram