Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:12:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549029.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_SRR1549029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549029.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:12:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,753,173
Mapped reads	6,827,953 / 88.07%
Unmapped reads	925,220 / 11.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	385,420 / 4.97%
Duplication rate	2.99%
Clipped reads	709,406 / 9.15%

2.2. ACGT Content

Number/percentage of A's	74,635,871 / 27.73%
Number/percentage of C's	59,179,932 / 21.99%
Number/percentage of T's	75,885,684 / 28.2%
Number/percentage of G's	59,421,846 / 22.08%
Number/percentage of N's	2,670 / 0%
GC Percentage	44.07%

2.3. Coverage

Mean	0.0869
Standard Deviation	1.2089

2.4. Mapping Quality

Mean Mapping Quality	32.21

2.5. Mismatches and indels

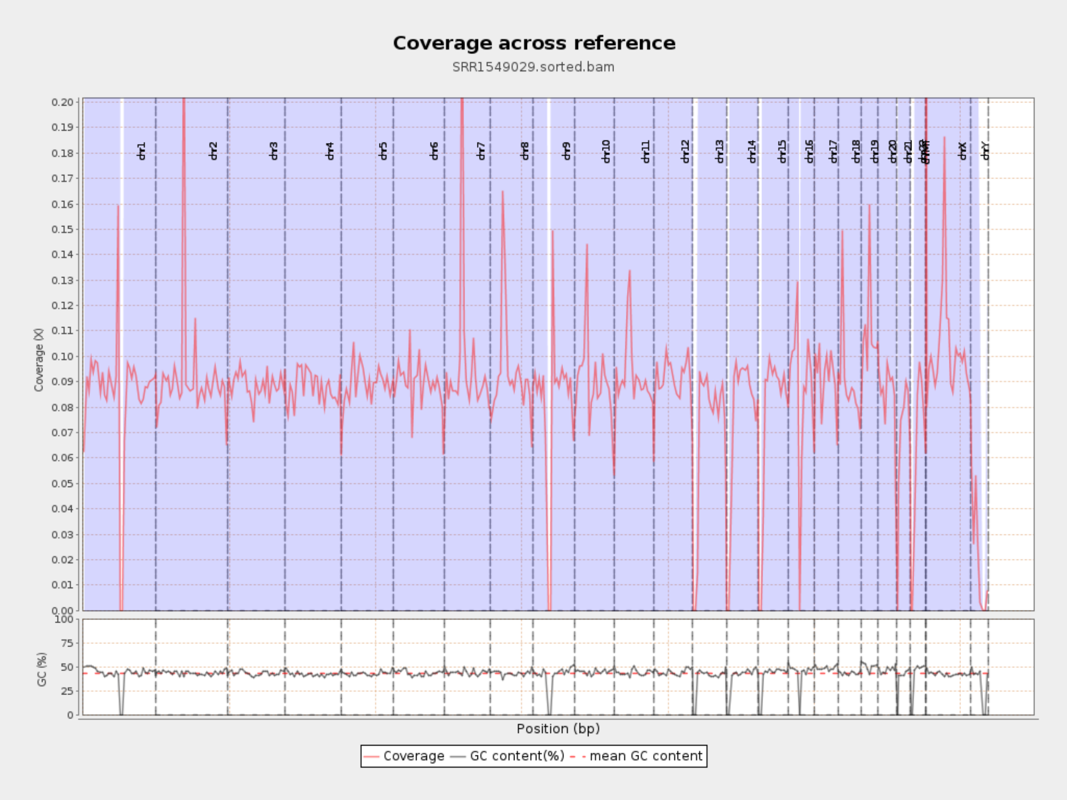
General error rate	0.39%
Mismatches	1,037,990
Insertions	11,213
Mapped reads with at least one insertion	0.16%
Deletions	20,863
Mapped reads with at least one deletion	0.31%
Homopolymer indels	36.3%

2.6. Chromosome stats

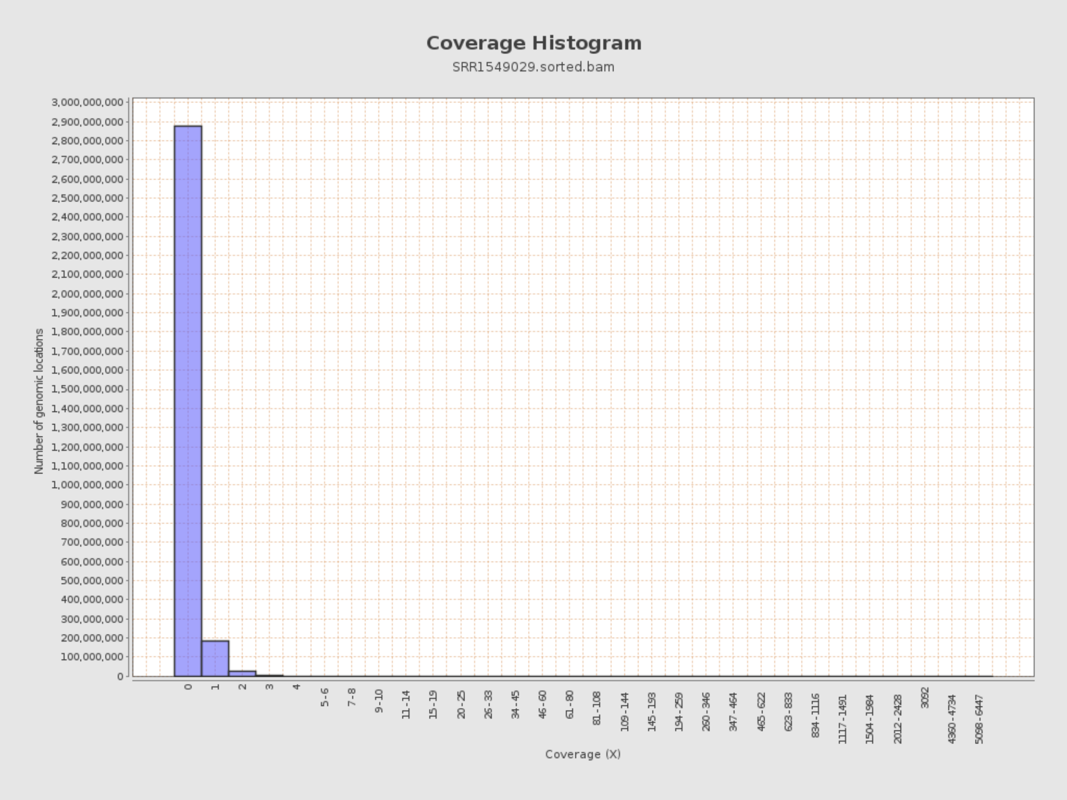
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21291965	0.0854	1.5754
chr2	243199373	22526249	0.0926	1.2109
chr3	198022430	17538291	0.0886	0.3692
chr4	191154276	16777275	0.0878	0.3814
chr5	180915260	16148157	0.0893	0.4113
chr6	171115067	15311695	0.0895	0.465
chr7	159138663	15538255	0.0976	1.6576
chr8	146364022	13754935	0.094	3.1788

chr9	141213431	11434835	0.081	1.3164
chr10	135534747	12294212	0.0907	0.7486
chr11	135006516	12475175	0.0924	1.3683
chr12	133851895	12319753	0.092	0.451
chr13	115169878	8107395	0.0704	0.3046
chr14	107349540	8181926	0.0762	0.6412
chr15	102531392	7611018	0.0742	0.3339
chr16	90354753	7660099	0.0848	0.5604
chr17	81195210	7541852	0.0929	0.5008
chr18	78077248	7121473	0.0912	2.5618
chr19	59128983	6517439	0.1102	1.6871
chr20	63025520	5409795	0.0858	0.4171
chr21	48129895	3275283	0.0681	0.5212
chr22	51304566	3087956	0.0602	0.3499
chrMT	16571	26462	1.5969	2.1417
chrX	155270560	16016422	0.1032	0.7159
chrY	59373566	1183882	0.0199	0.2328

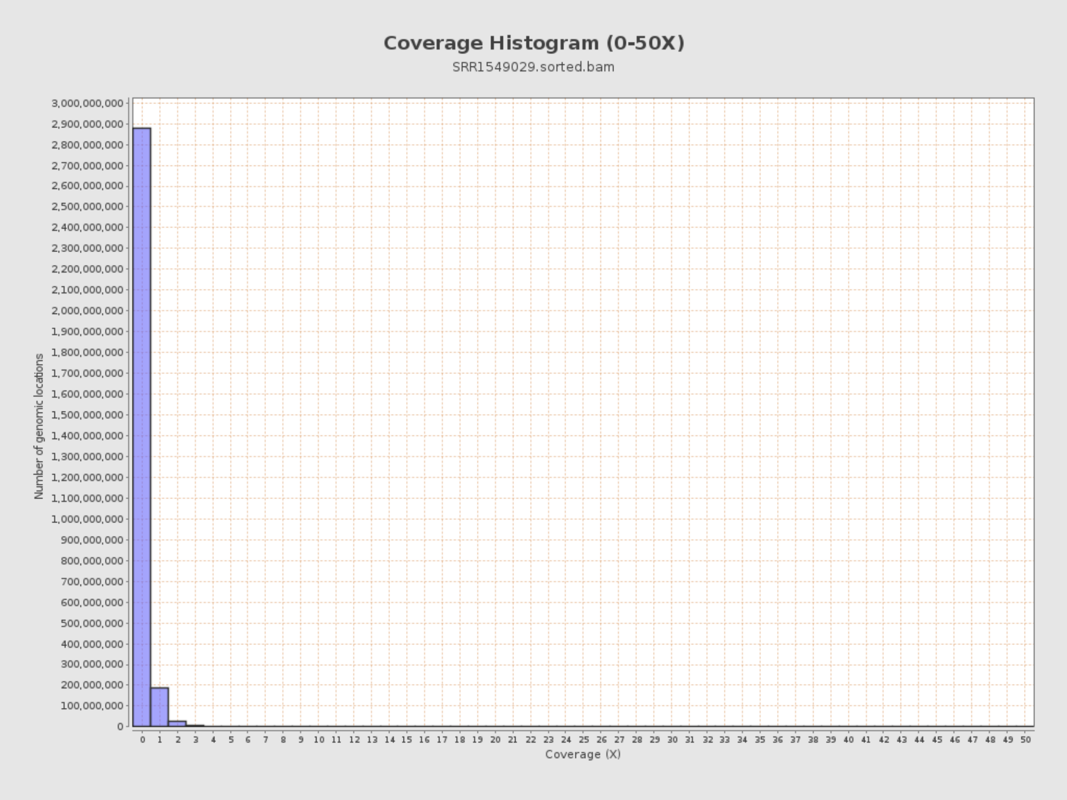
3. Results : Coverage across reference



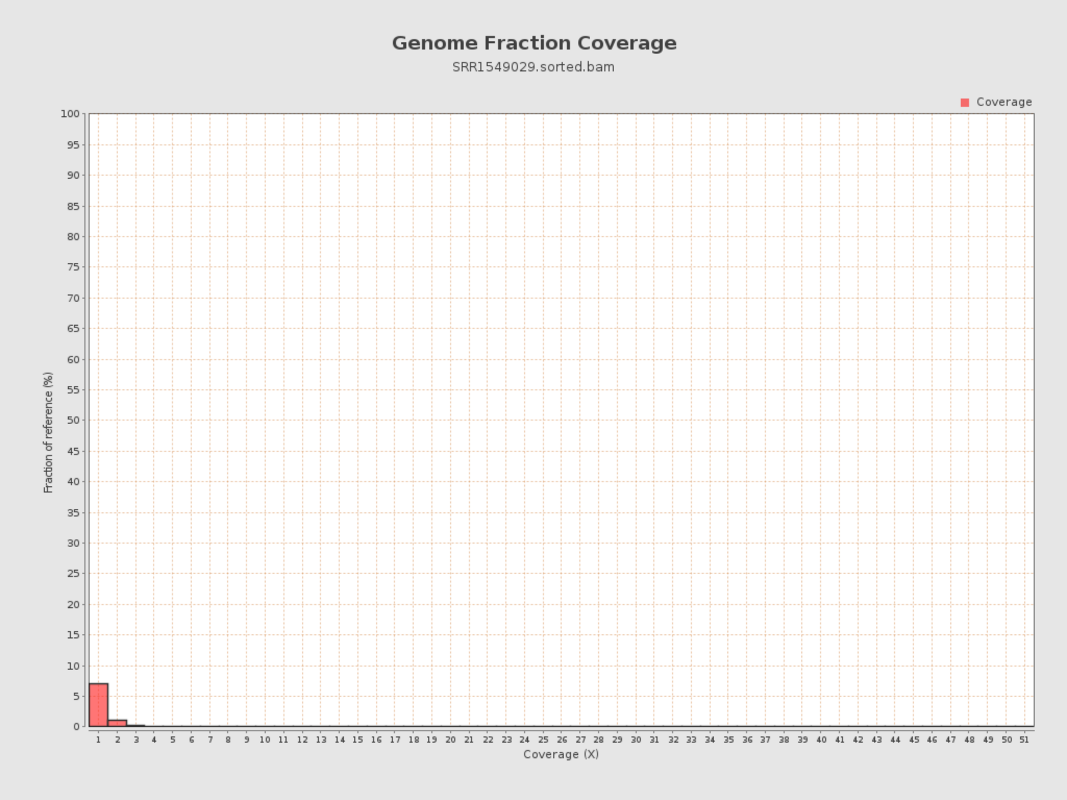
4. Results : Coverage Histogram



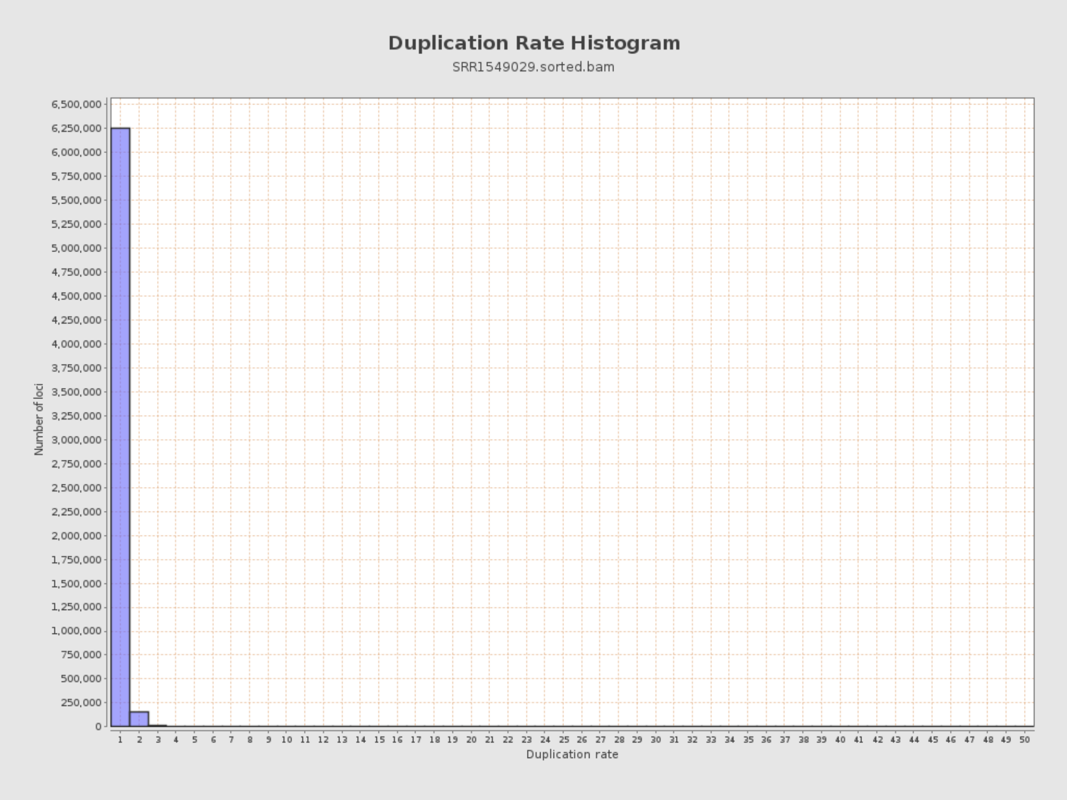
5. Results : Coverage Histogram (0-50X)



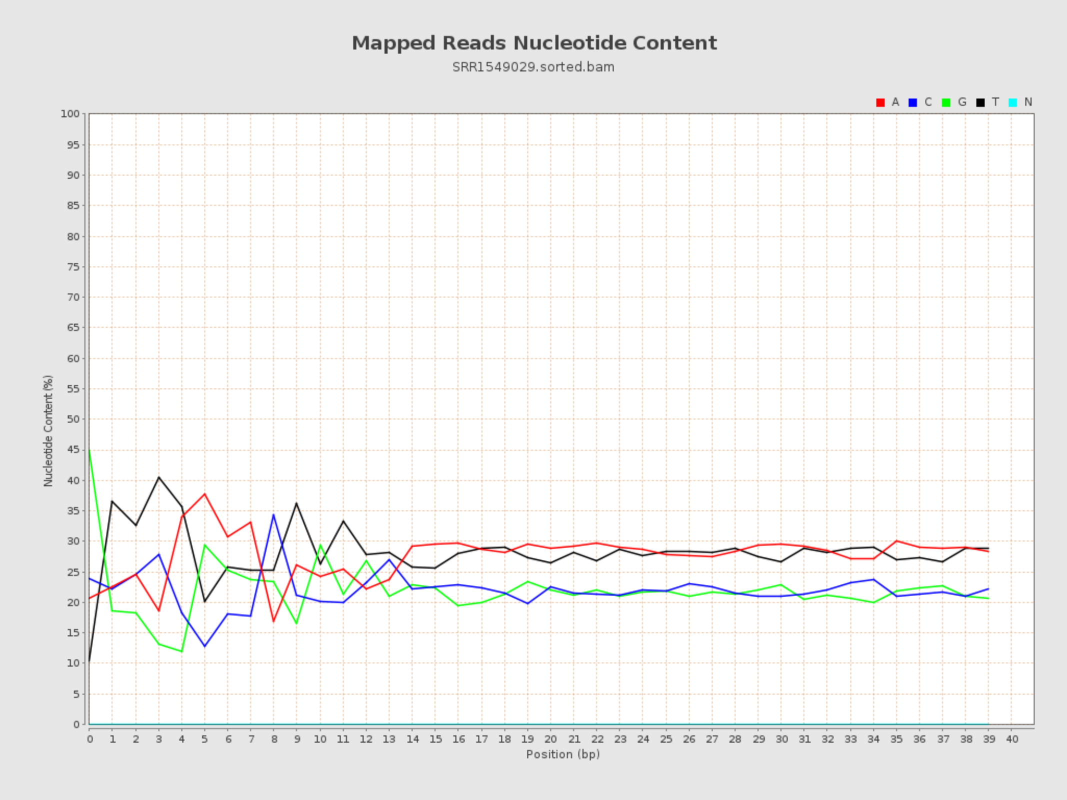
6. Results : Genome Fraction Coverage



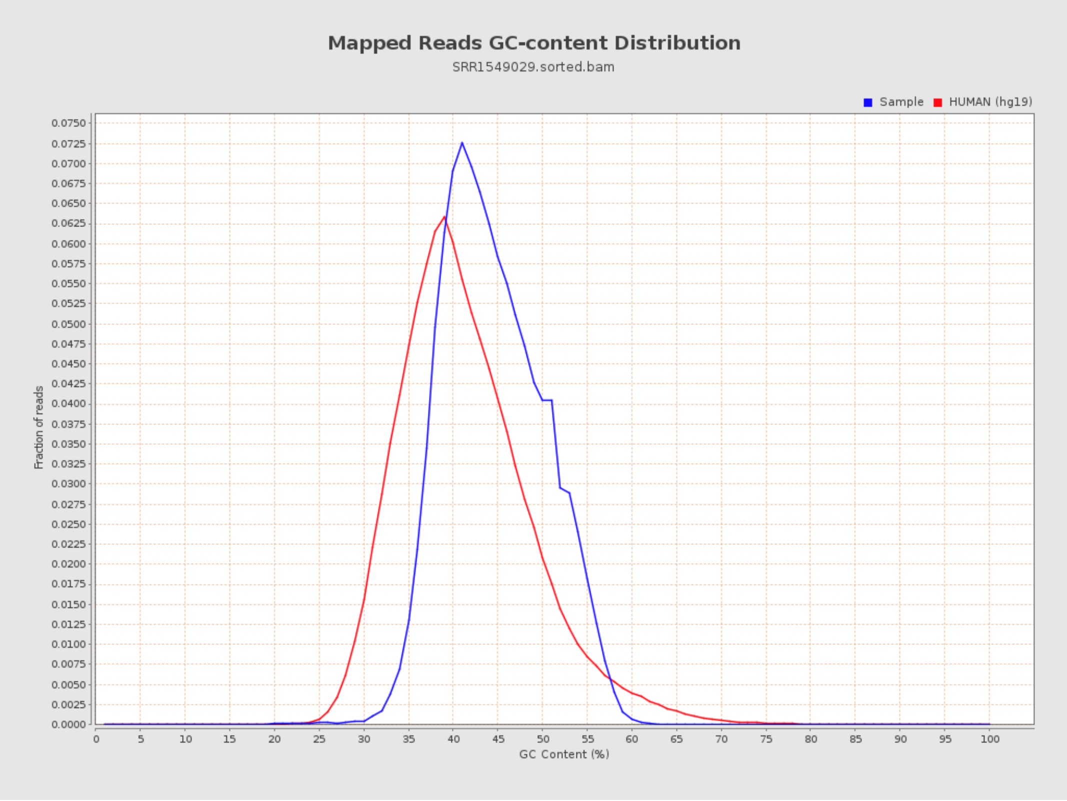
7. Results : Duplication Rate Histogram



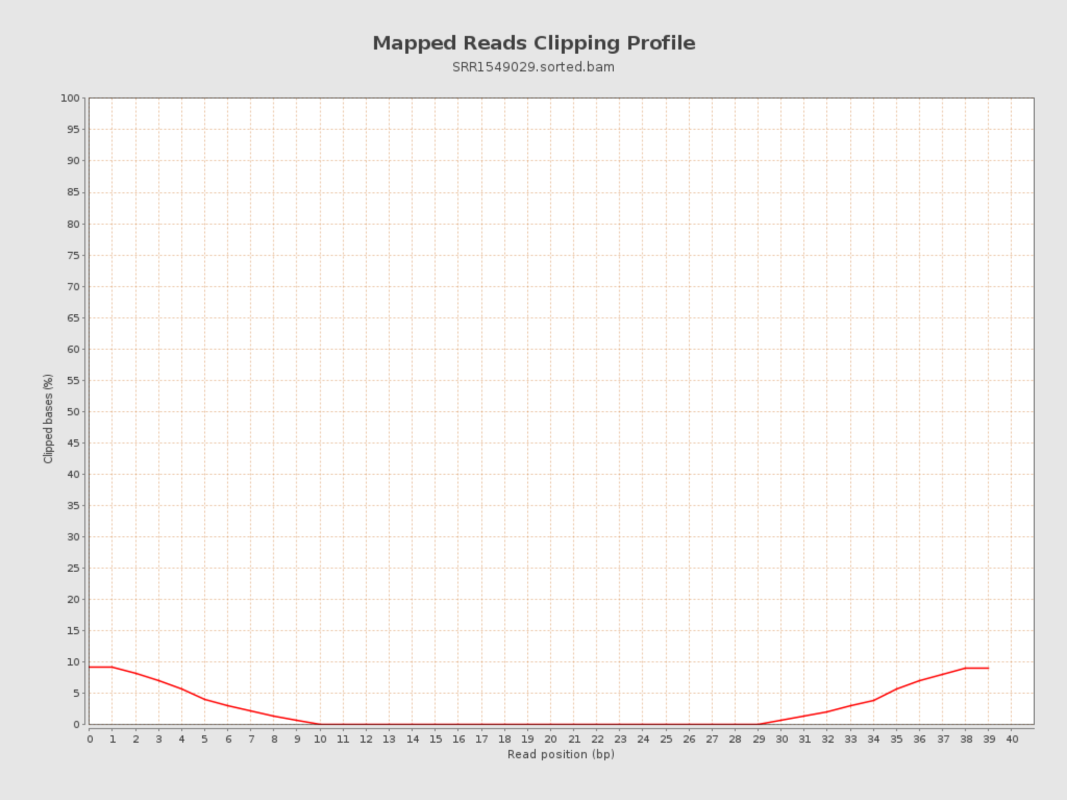
8. Results : Mapped Reads Nucleotide Content



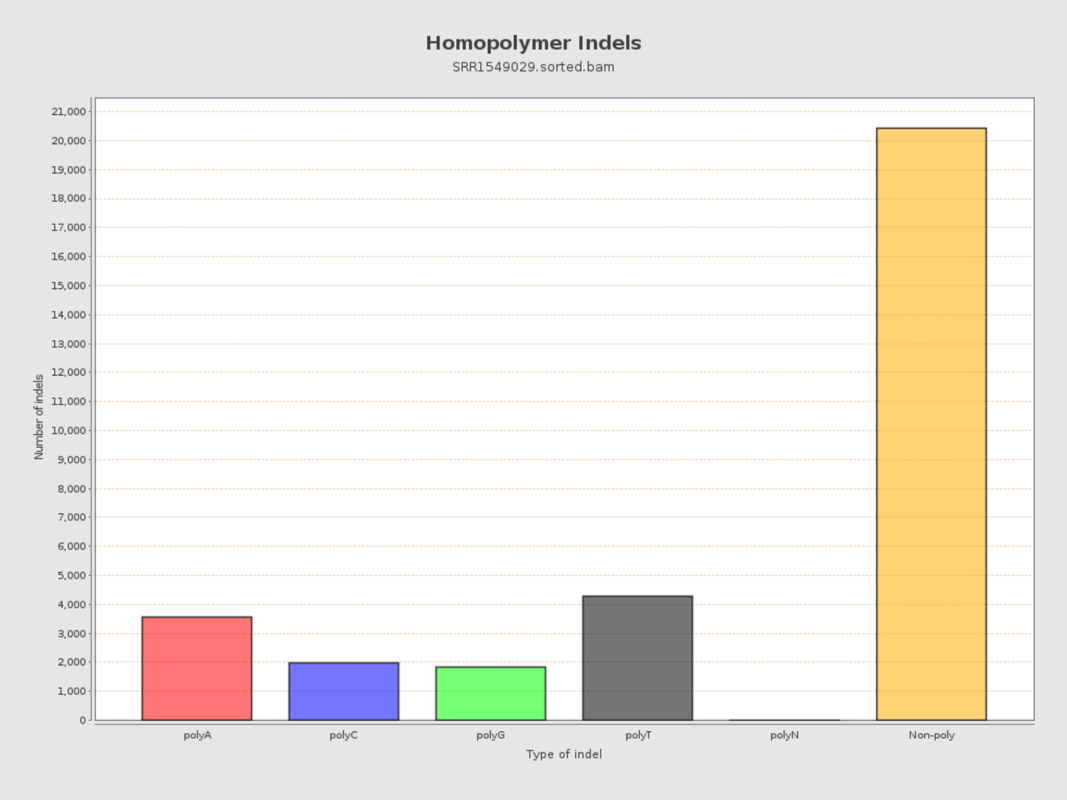
9. Results : Mapped Reads GC-content Distribution



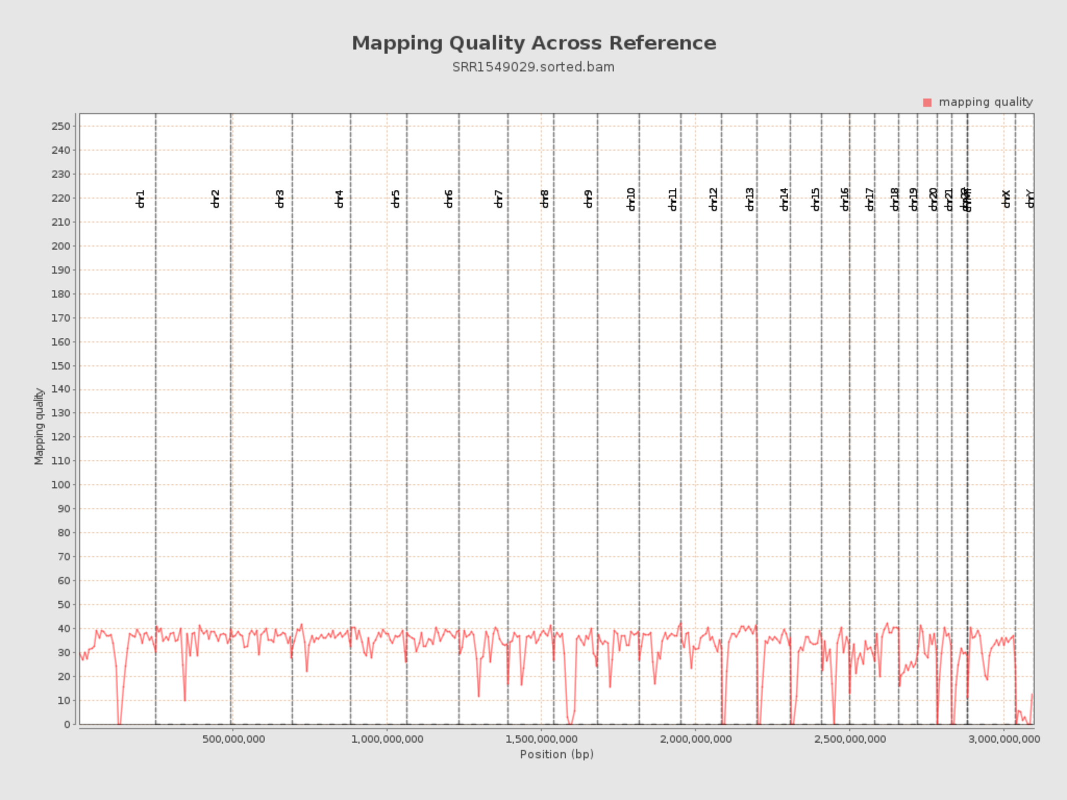
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram