Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:41:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819028.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_SRR1819028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:41:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	502,539
Mapped reads	456,385 / 90.82%
Unmapped reads	46,154 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,979 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	5,664 / 1.13%
Duplication rate	0.98%
Clipped reads	457,024 / 90.94%

2.2. ACGT Content

Number/percentage of A's	6,632,766 / 25.4%
Number/percentage of C's	5,090,526 / 19.5%
Number/percentage of T's	7,722,846 / 29.58%
Number/percentage of G's	6,662,809 / 25.52%
Number/percentage of N's	569 / 0%
GC Percentage	45.02%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1018

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

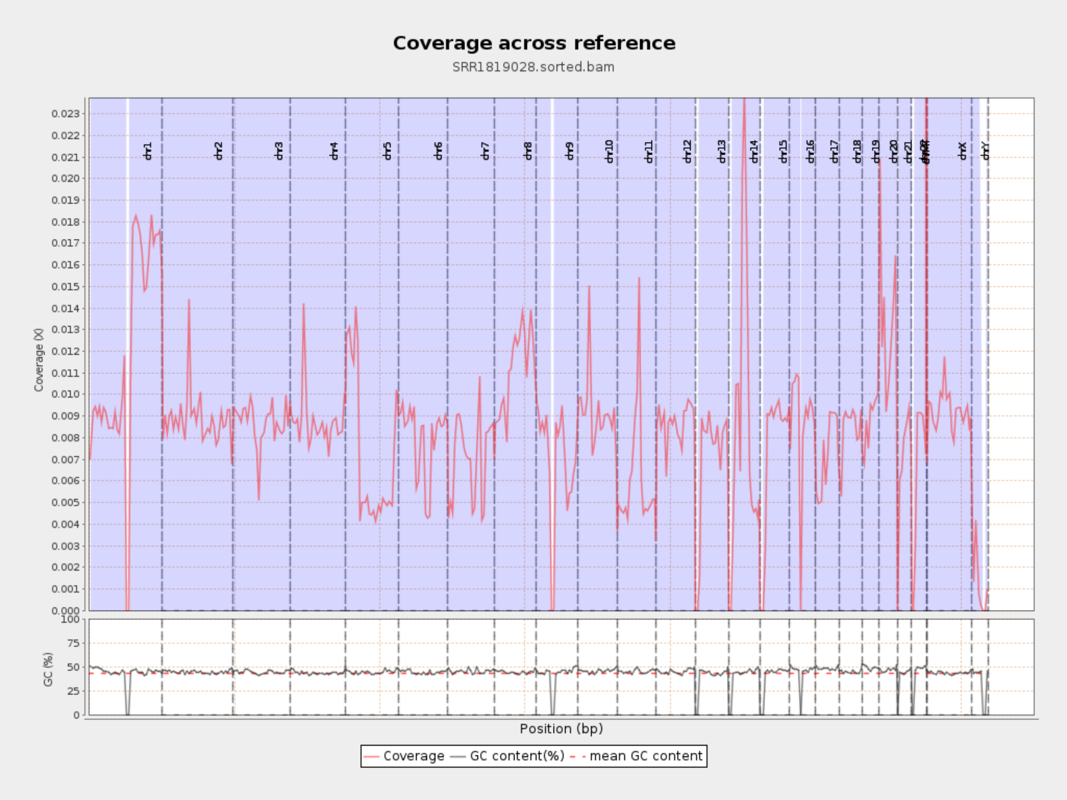
General error rate	0.51%
Mismatches	128,252
Insertions	1,792
Mapped reads with at least one insertion	0.39%
Deletions	4,040
Mapped reads with at least one deletion	0.88%
Homopolymer indels	39.61%

2.6. Chromosome stats

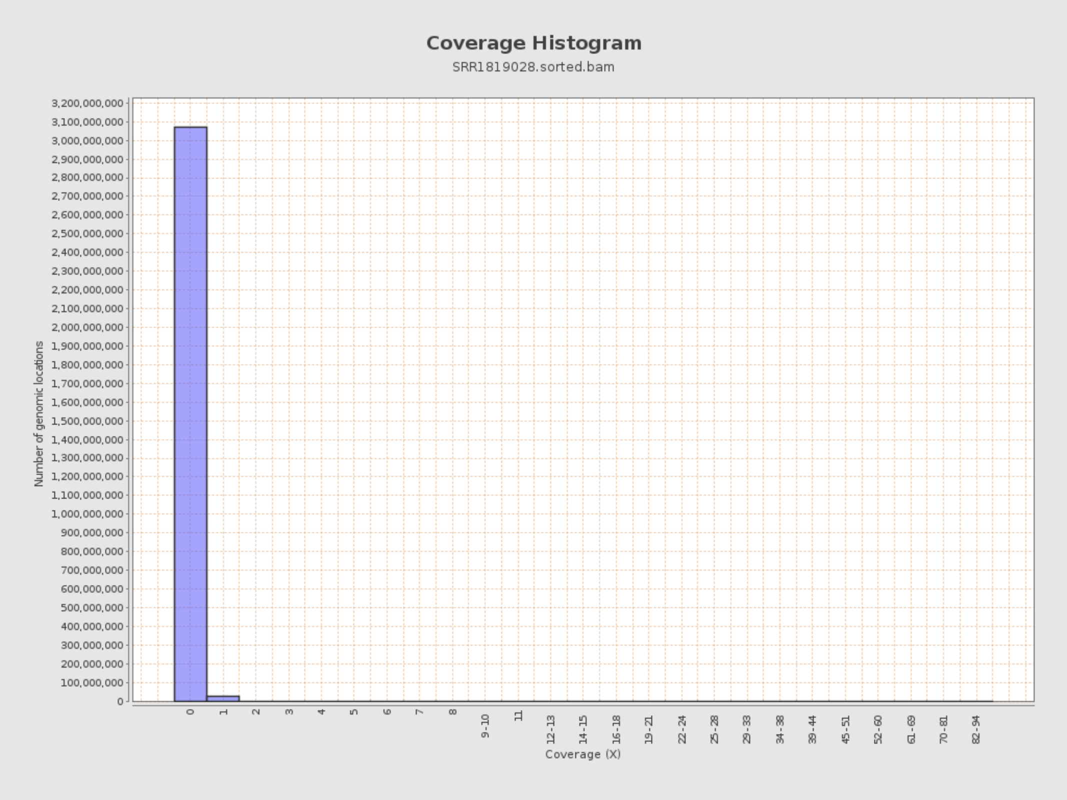
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2945623	0.0118	0.1333
chr2	243199373	2160217	0.0089	0.1095
chr3	198022430	1718574	0.0087	0.0959
chr4	191154276	1664359	0.0087	0.0985
chr5	180915260	1307755	0.0072	0.0879
chr6	171115067	1357454	0.0079	0.093
chr7	159138663	1119299	0.007	0.0913

chr8	146364022	1641517	0.0112	0.1136
chr9	141213431	949815	0.0067	0.0951
chr10	135534747	1244657	0.0092	0.1114
chr11	135006516	825958	0.0061	0.0867
chr12	133851895	1163719	0.0087	0.0962
chr13	115169878	792516	0.0069	0.0852
chr14	107349540	917922	0.0086	0.097
chr15	102531392	751798	0.0073	0.0881
chr16	90354753	790557	0.0087	0.0998
chr17	81195210	591761	0.0073	0.0883
chr18	78077248	652510	0.0084	0.1364
chr19	59128983	524855	0.0089	0.1121
chr20	63025520	834539	0.0132	0.1195
chr21	48129895	336891	0.007	0.0886
chr22	51304566	312191	0.0061	0.0801
chrMT	16571	5971	0.3603	0.6197
chrX	155270560	1430438	0.0092	0.1024
chrY	59373566	75402	0.0013	0.0423

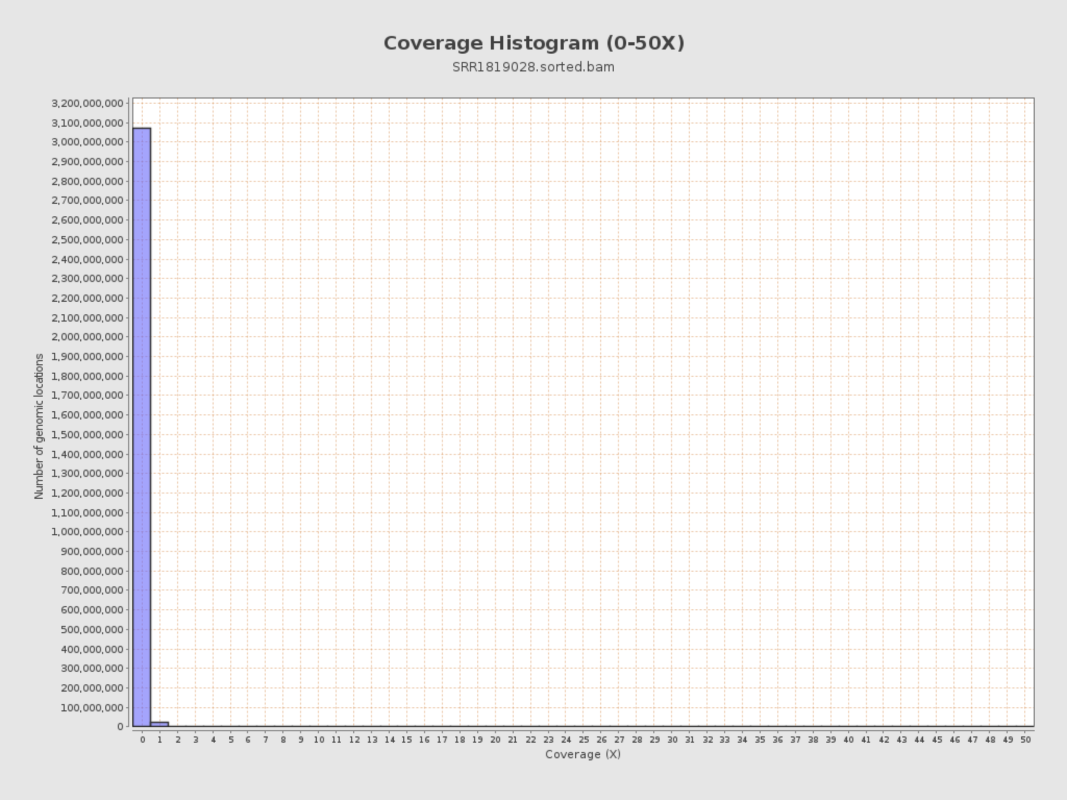
3. Results : Coverage across reference



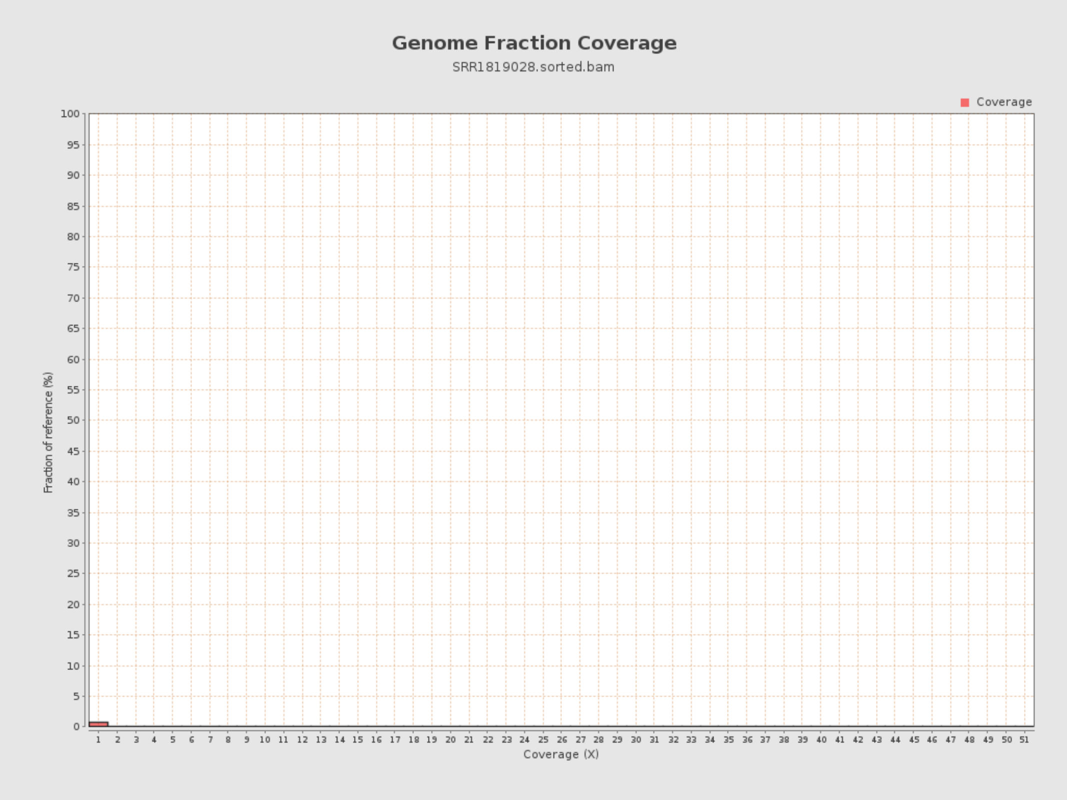
4. Results : Coverage Histogram



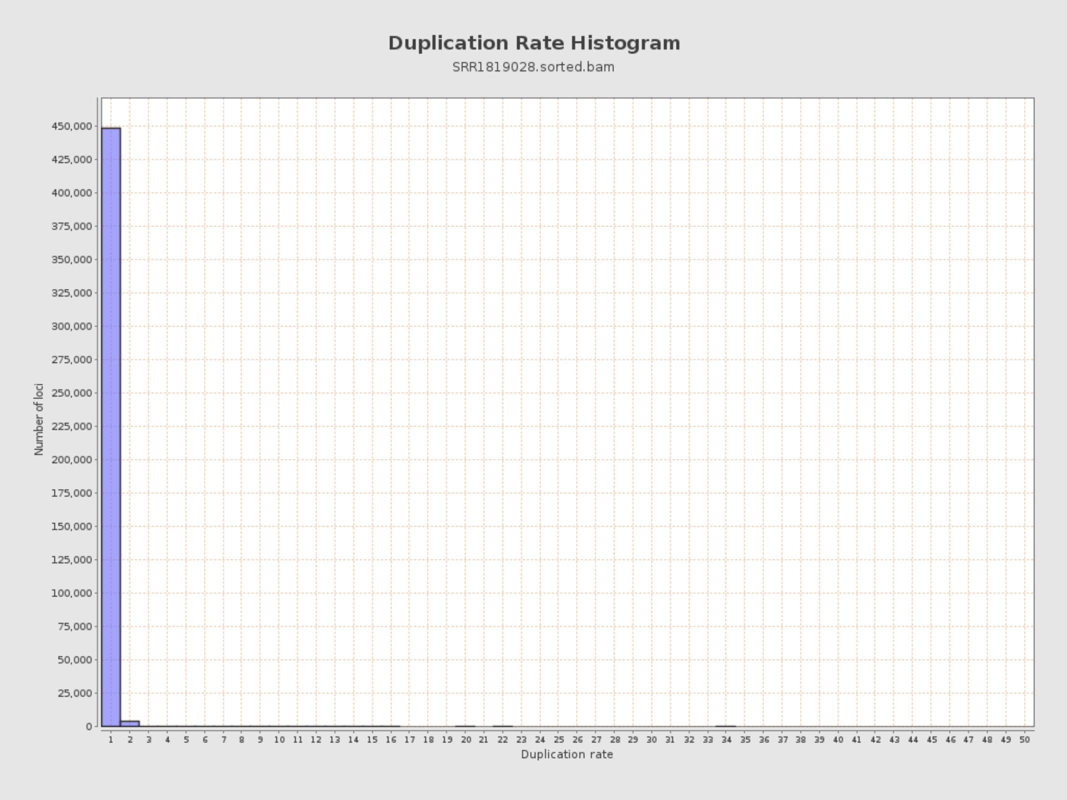
5. Results : Coverage Histogram (0-50X)



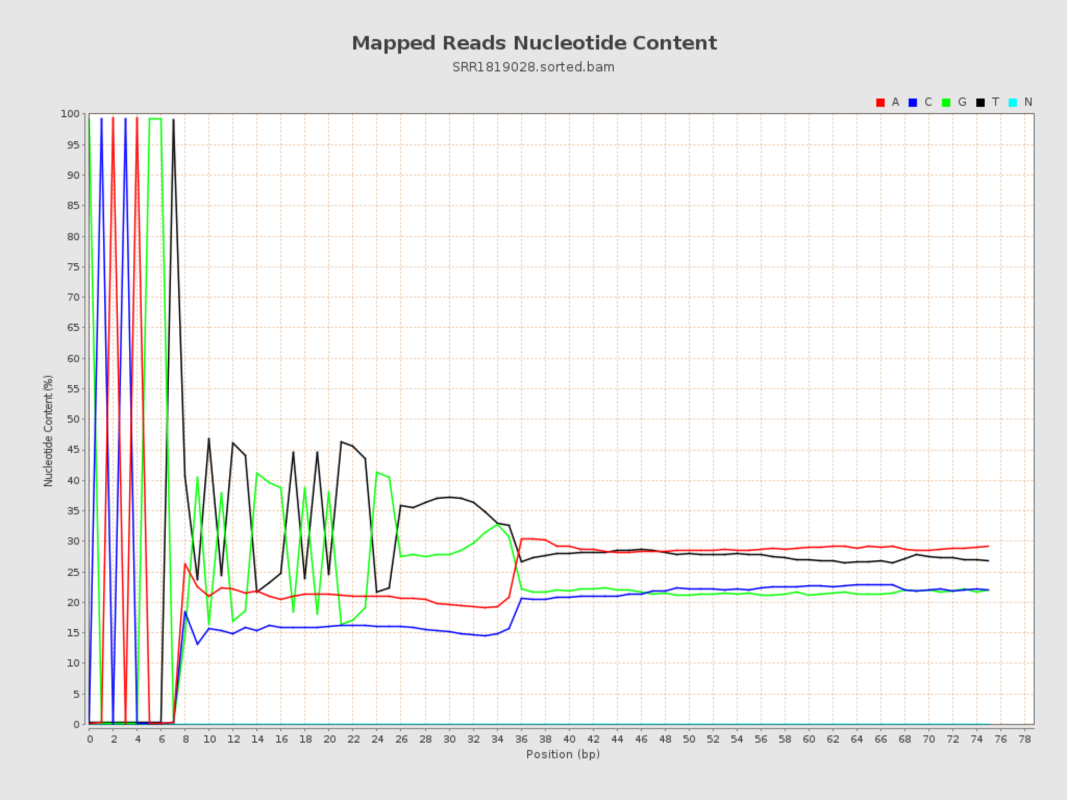
6. Results : Genome Fraction Coverage



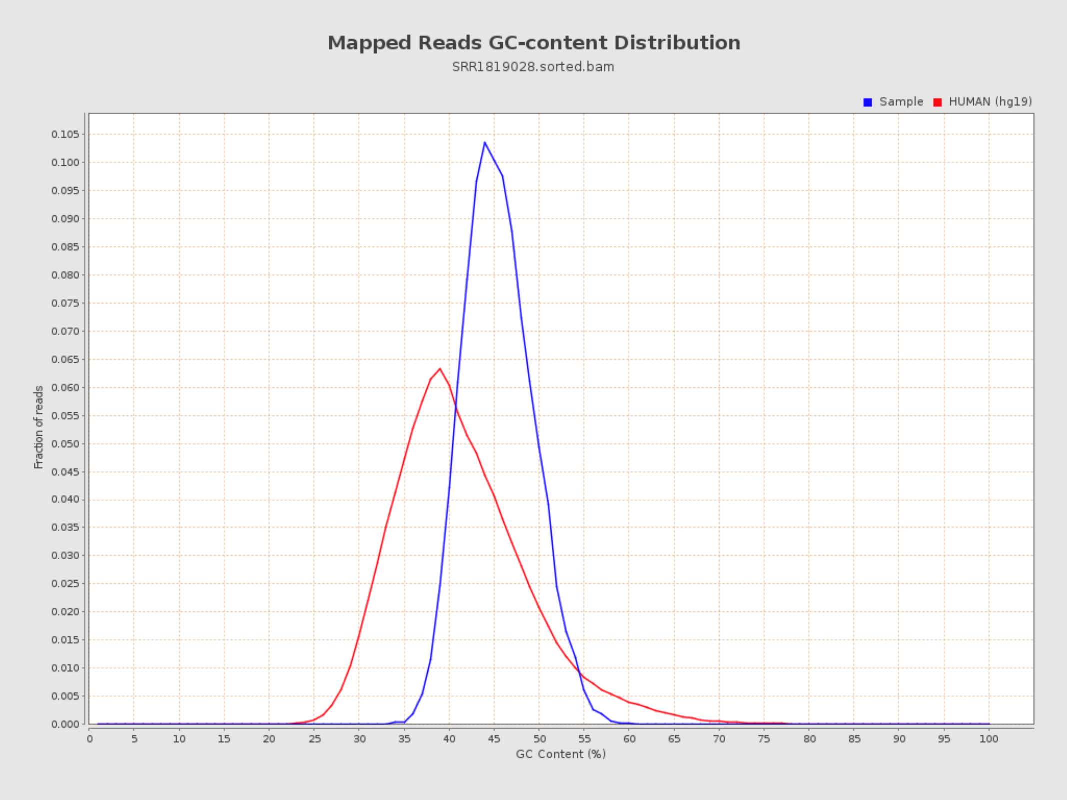
7. Results : Duplication Rate Histogram



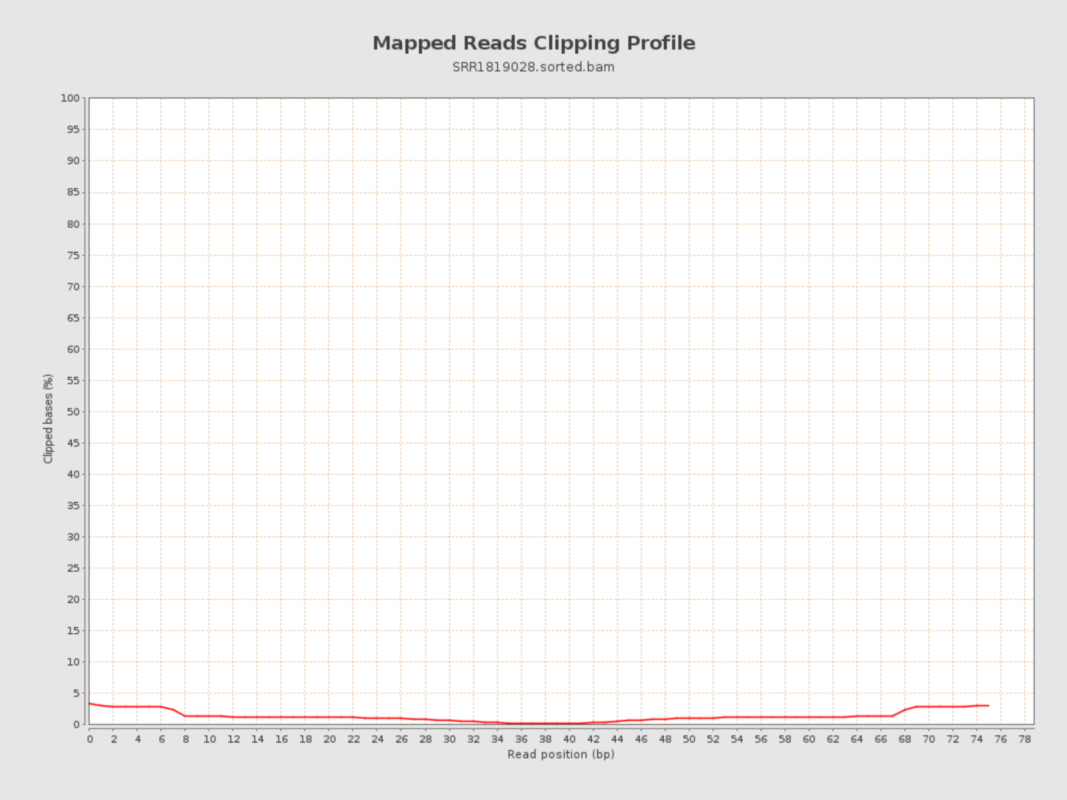
8. Results : Mapped Reads Nucleotide Content



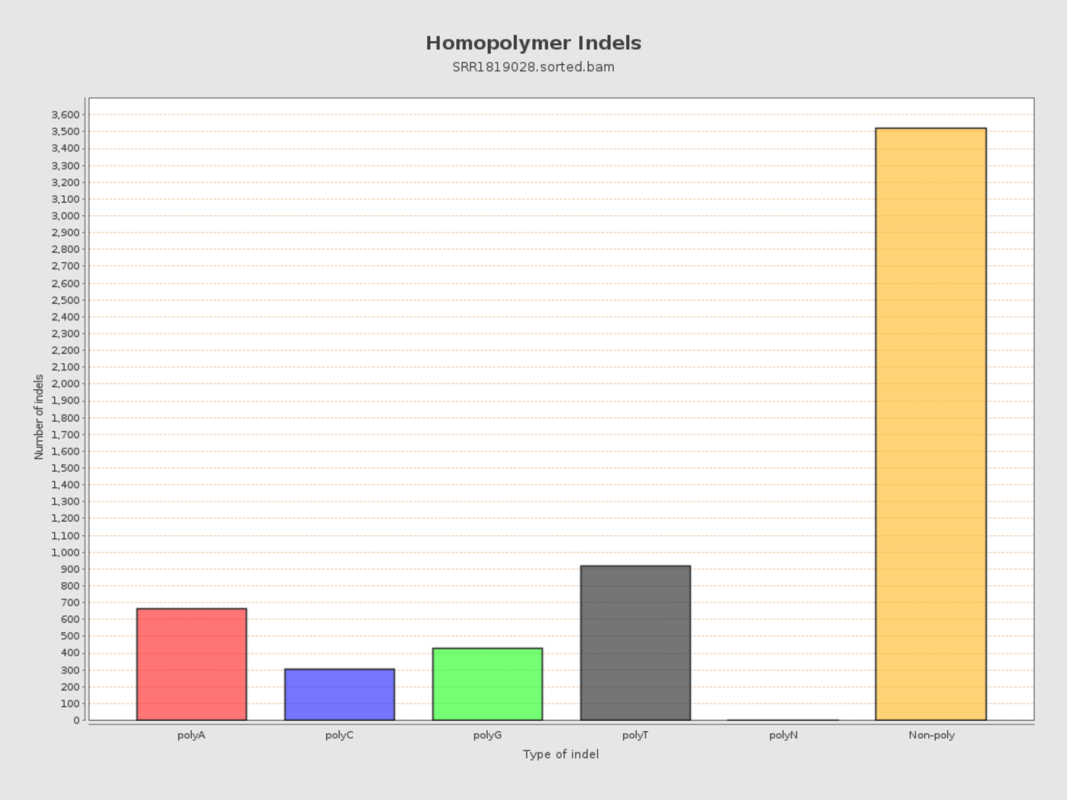
9. Results : Mapped Reads GC-content Distribution



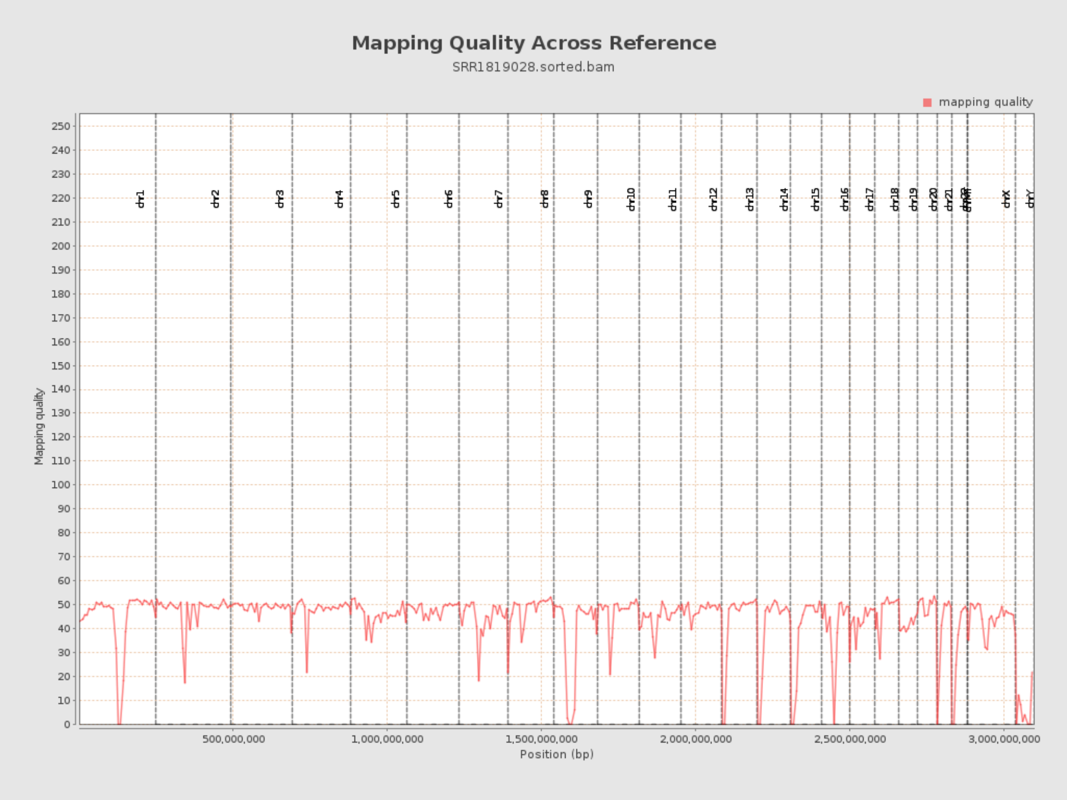
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram