Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:23:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819058.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_SRR1819058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:23:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,232,192
Mapped reads	1,111,921 / 90.24%
Unmapped reads	120,271 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,677 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,857 / 2.02%
Duplication rate	1.73%
Clipped reads	1,115,705 / 90.55%

2.2. ACGT Content

Number/percentage of A's	16,103,486 / 25.44%
Number/percentage of C's	12,776,502 / 20.18%
Number/percentage of T's	19,339,391 / 30.55%
Number/percentage of G's	15,087,204 / 23.83%
Number/percentage of N's	1,305 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.179

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

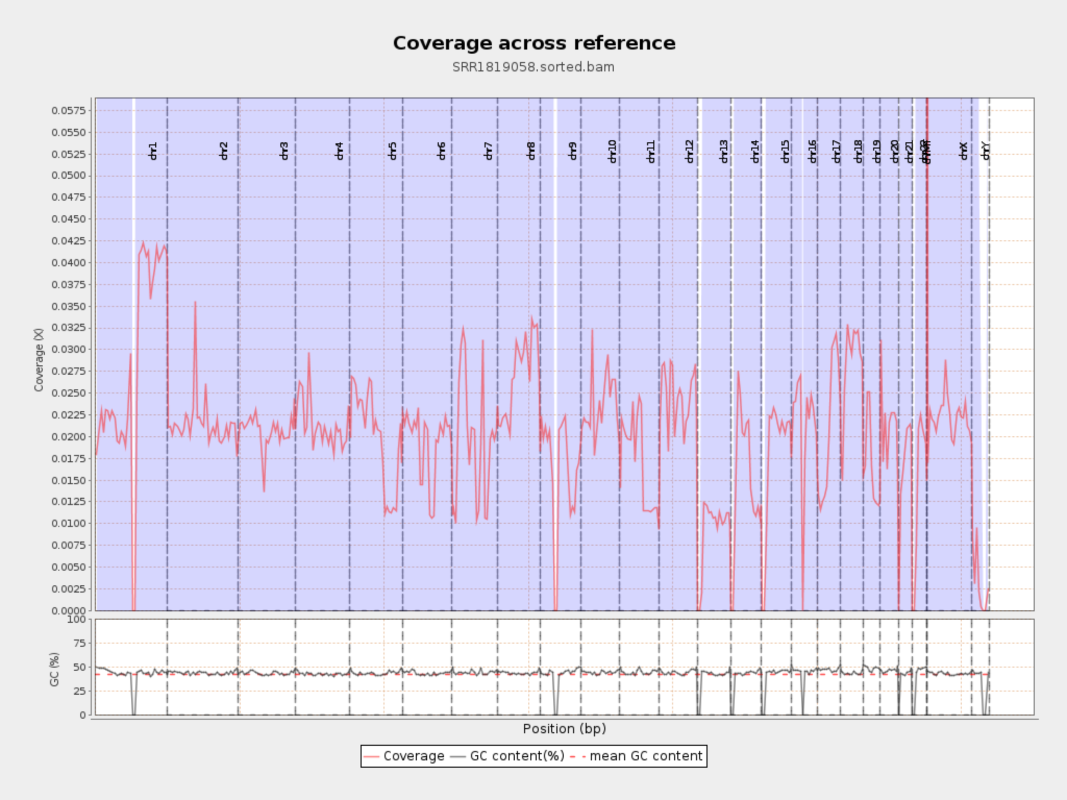
General error rate	0.49%
Mismatches	307,735
Insertions	3,135
Mapped reads with at least one insertion	0.28%
Deletions	9,451
Mapped reads with at least one deletion	0.84%
Homopolymer indels	42.12%

2.6. Chromosome stats

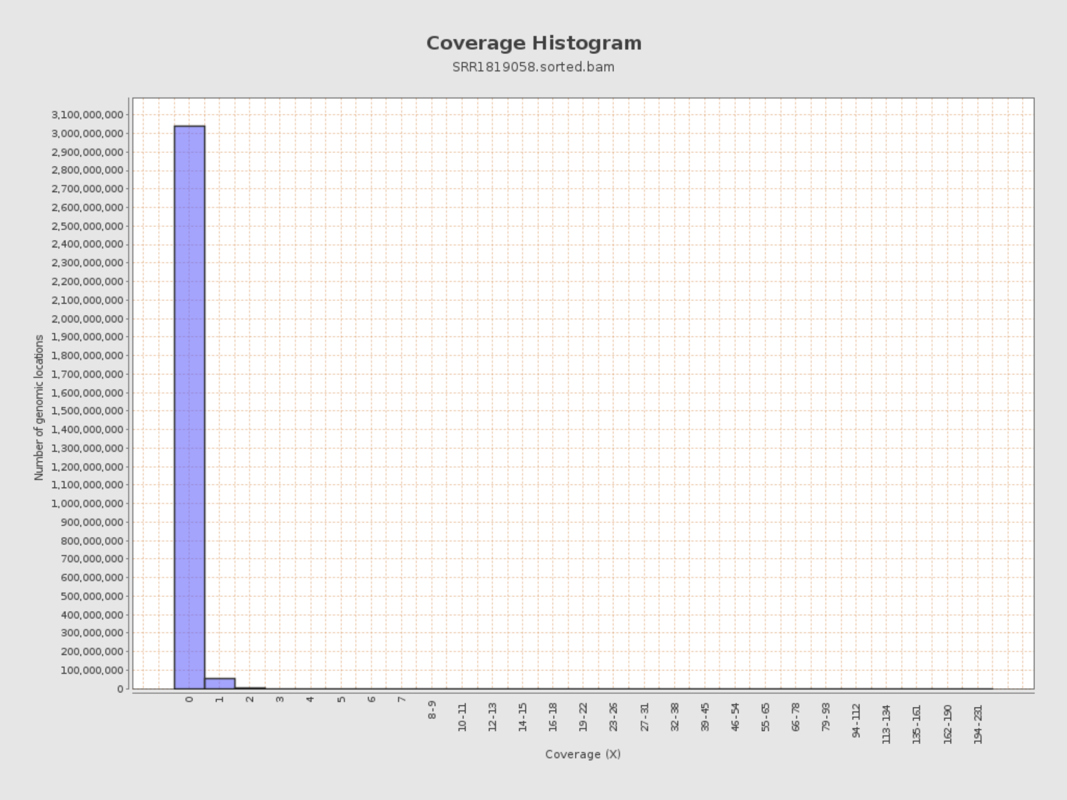
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7008482	0.0281	0.2556
chr2	243199373	5245998	0.0216	0.2043
chr3	198022430	4073548	0.0206	0.1525
chr4	191154276	4095325	0.0214	0.1628
chr5	180915260	3606692	0.0199	0.1514
chr6	171115067	3293575	0.0192	0.1549
chr7	159138663	3104420	0.0195	0.165

chr8	146364022	3969277	0.0271	0.193
chr9	141213431	2261874	0.016	0.172
chr10	135534747	3209131	0.0237	0.1952
chr11	135006516	2335658	0.0173	0.1704
chr12	133851895	3296751	0.0246	0.1686
chr13	115169878	1055394	0.0092	0.1008
chr14	107349540	1606193	0.015	0.1371
chr15	102531392	1813926	0.0177	0.1421
chr16	90354753	1900154	0.021	0.1608
chr17	81195210	1693646	0.0209	0.1567
chr18	78077248	2207185	0.0283	0.3119
chr19	59128983	1005604	0.017	0.1984
chr20	63025520	1348118	0.0214	0.1579
chr21	48129895	799529	0.0166	0.1464
chr22	51304566	737587	0.0144	0.1269
chrMT	16571	13869	0.8369	0.9769
chrX	155270560	3462171	0.0223	0.1718
chrY	59373566	179841	0.003	0.0754

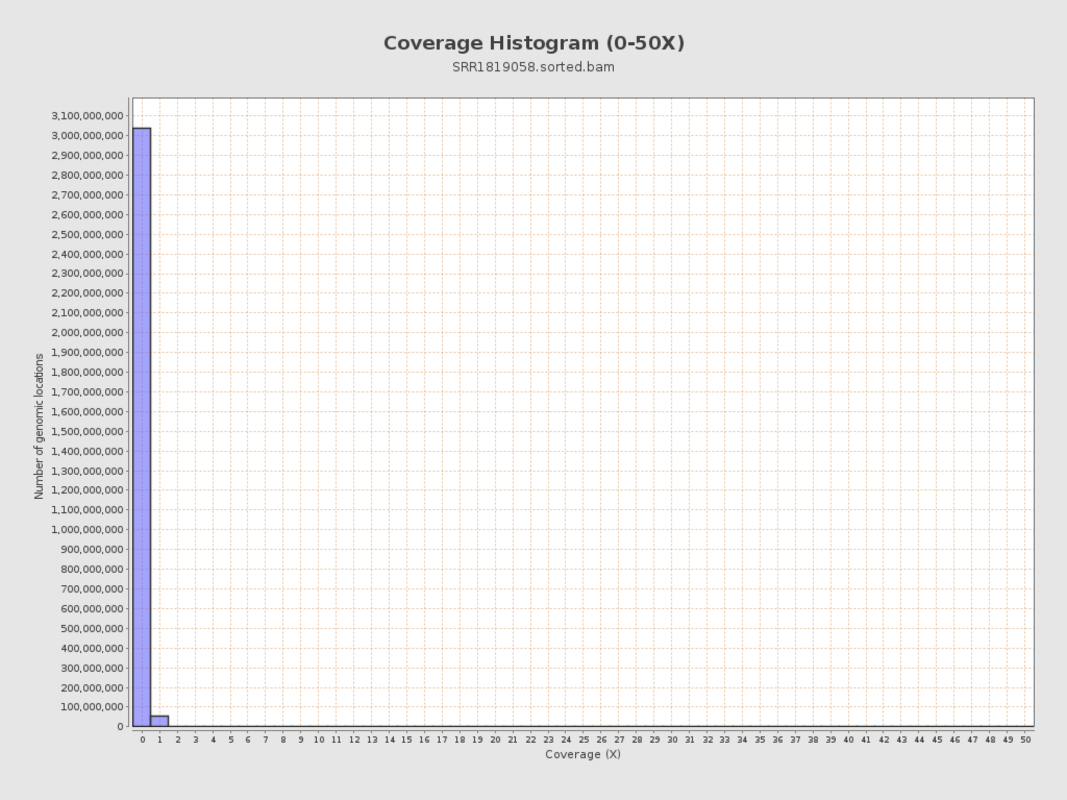
3. Results : Coverage across reference



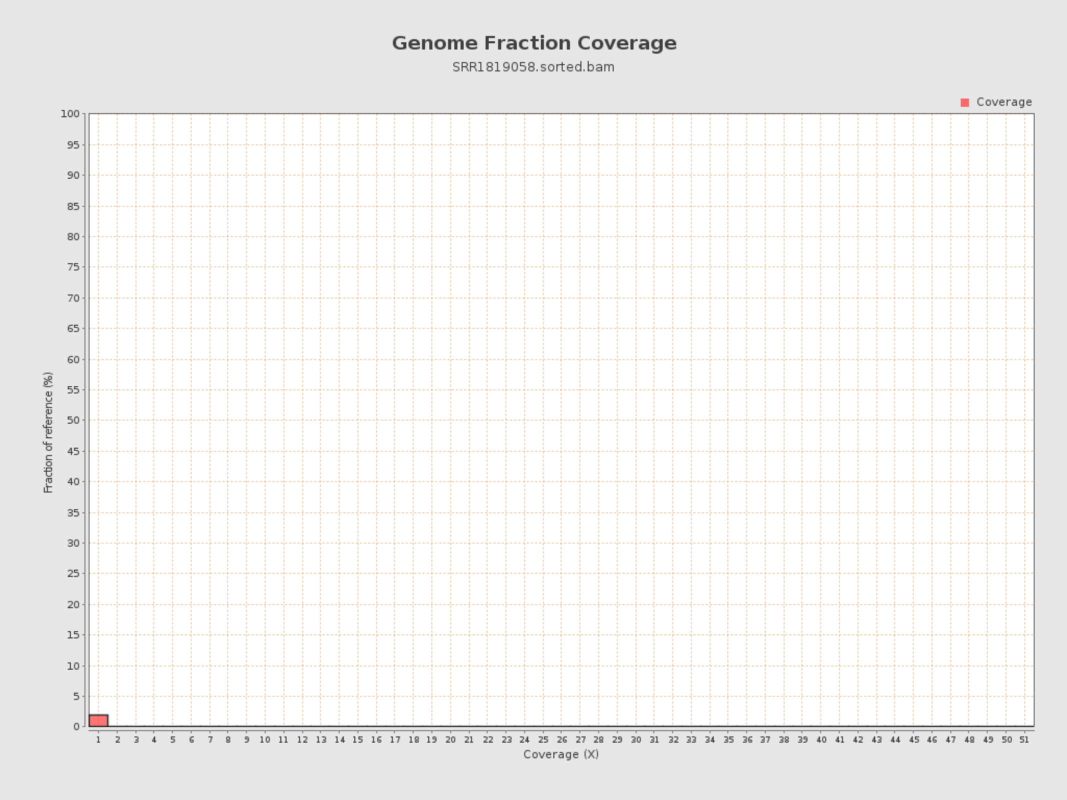
4. Results : Coverage Histogram



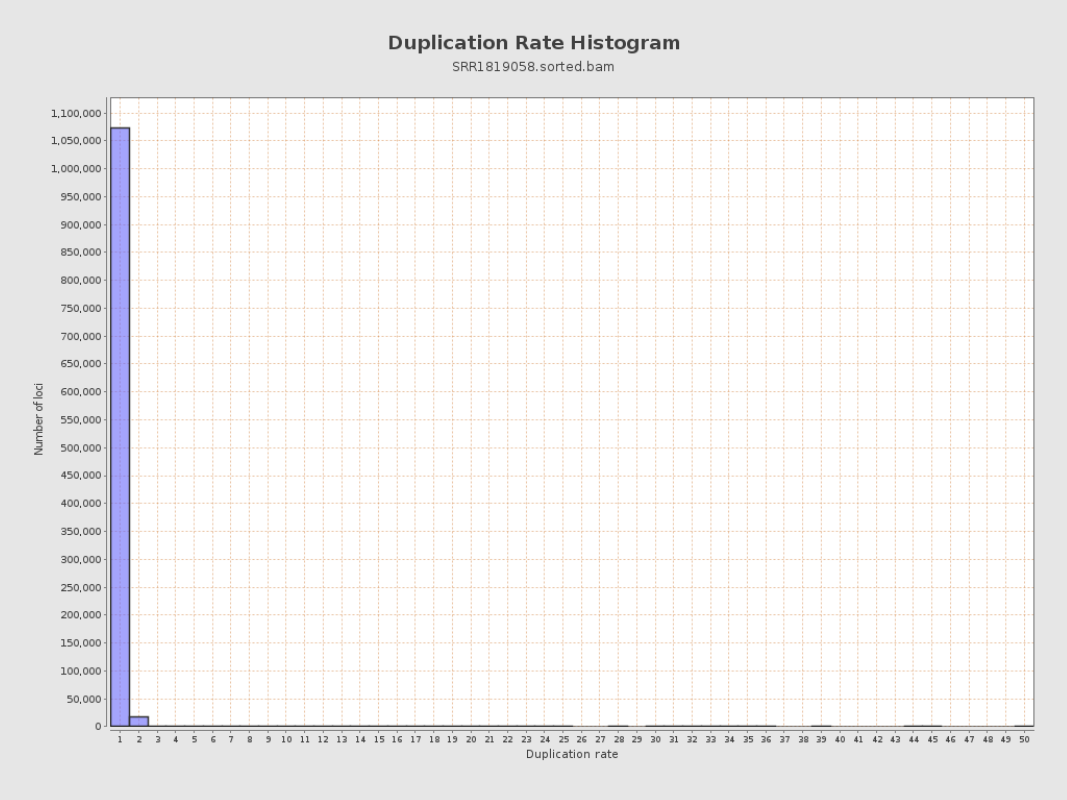
5. Results : Coverage Histogram (0-50X)



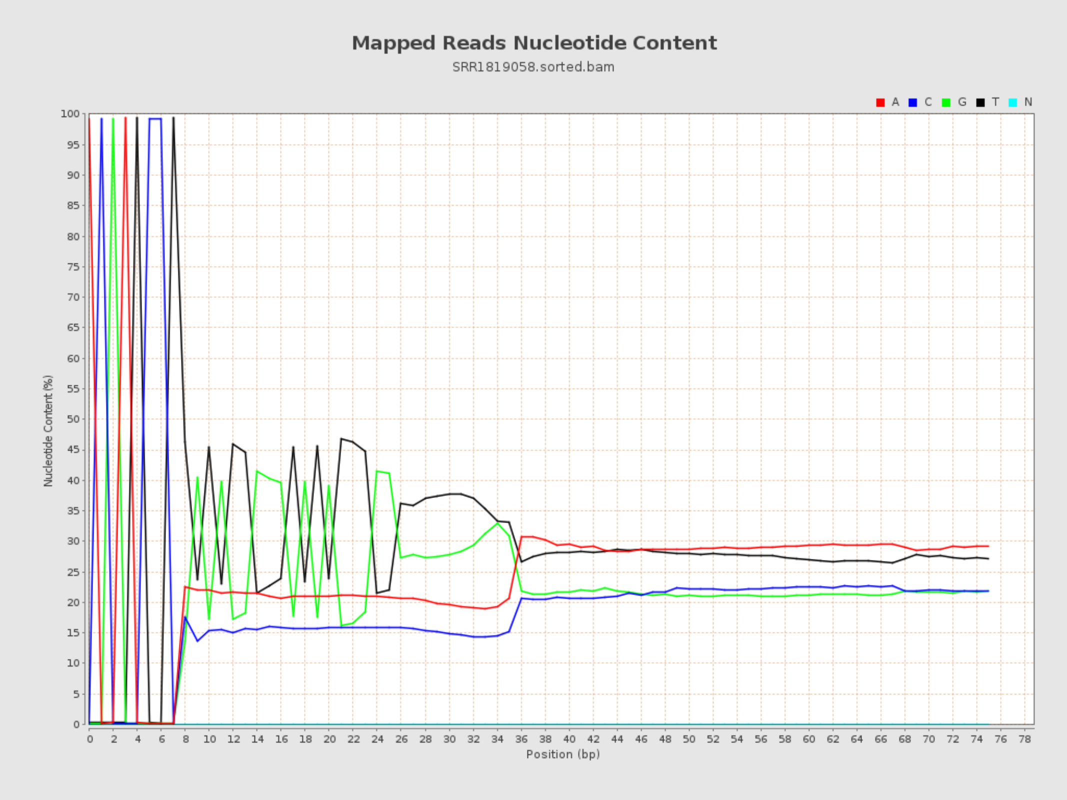
6. Results : Genome Fraction Coverage



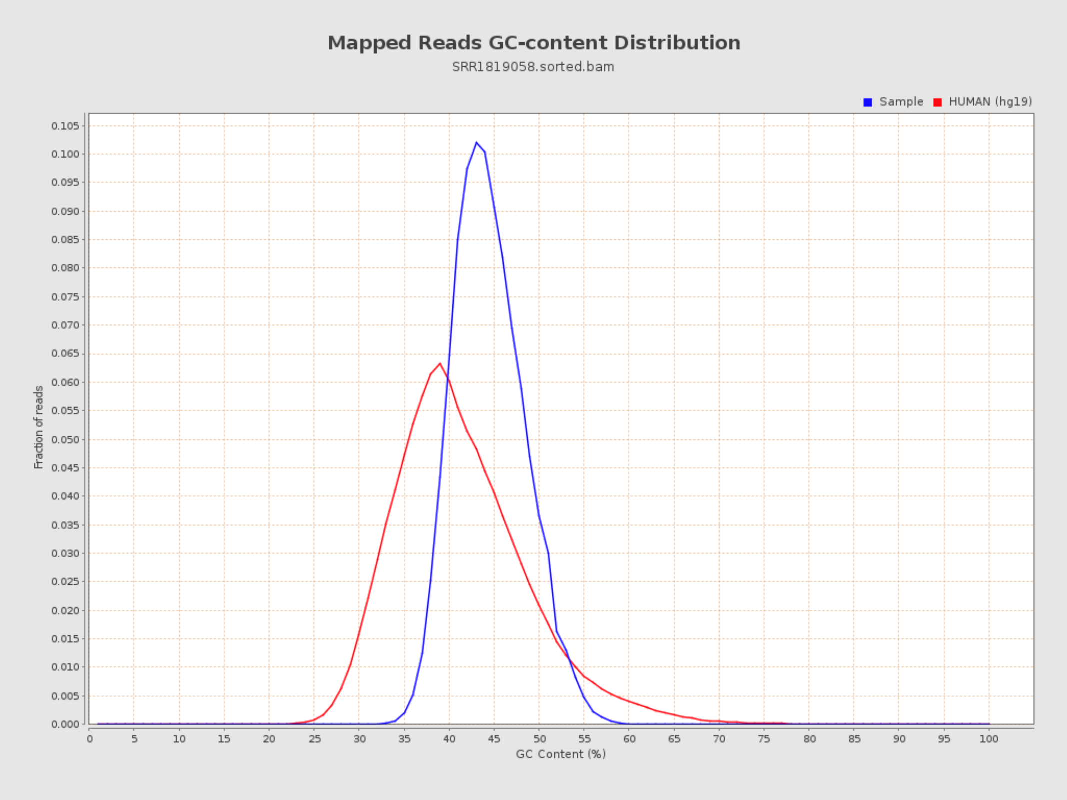
7. Results : Duplication Rate Histogram



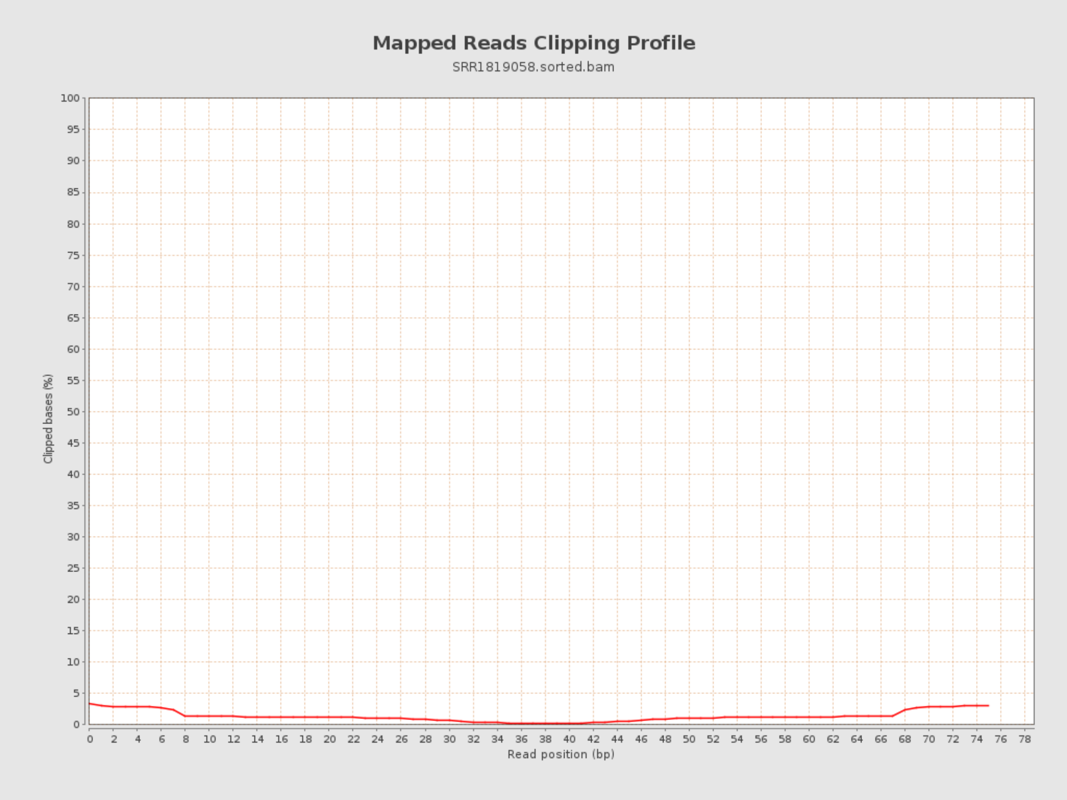
8. Results : Mapped Reads Nucleotide Content



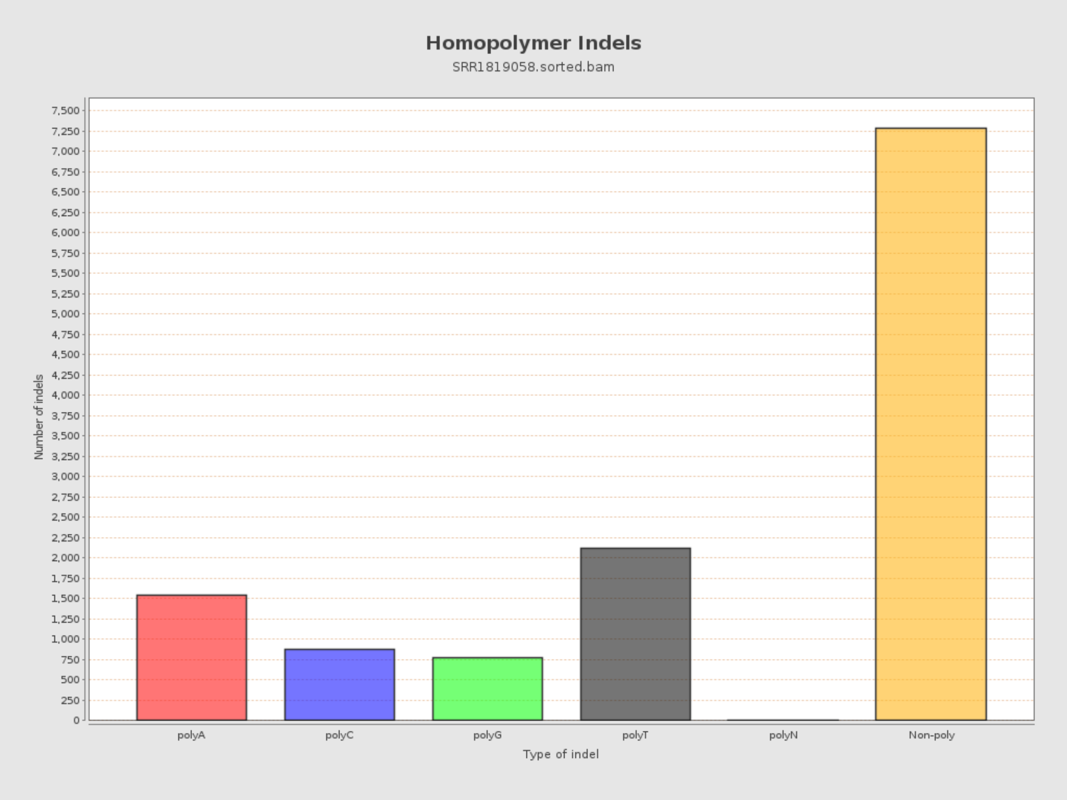
9. Results : Mapped Reads GC-content Distribution



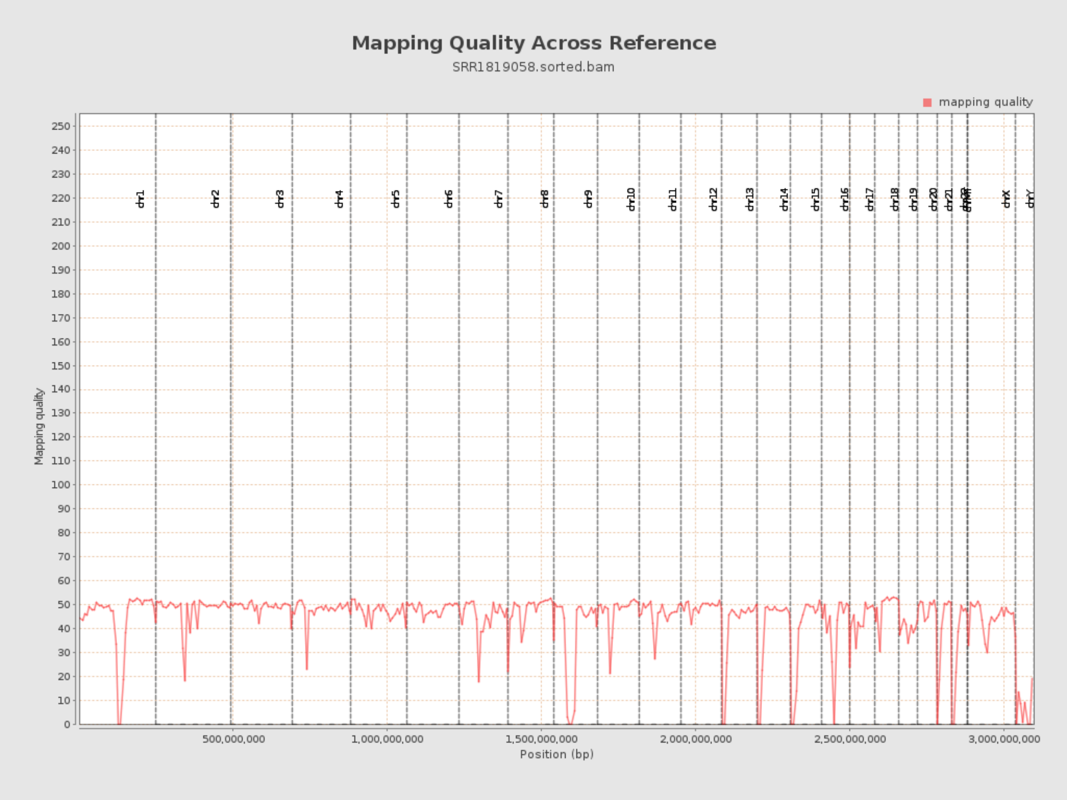
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram