Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:30:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818764.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_SRR1818764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:30:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	294,237
Mapped reads	183,268 / 62.29%
Unmapped reads	110,969 / 37.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,229 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	15,582 / 5.3%
Duplication rate	7.16%
Clipped reads	182,884 / 62.16%

2.2. ACGT Content

Number/percentage of A's	3,555,220 / 28.63%
Number/percentage of C's	2,690,603 / 21.67%
Number/percentage of T's	3,577,102 / 28.81%
Number/percentage of G's	2,592,117 / 20.88%
Number/percentage of N's	752 / 0.01%
GC Percentage	42.55%

2.3. Coverage

Mean	0.004

Standard Deviation	0.0901

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

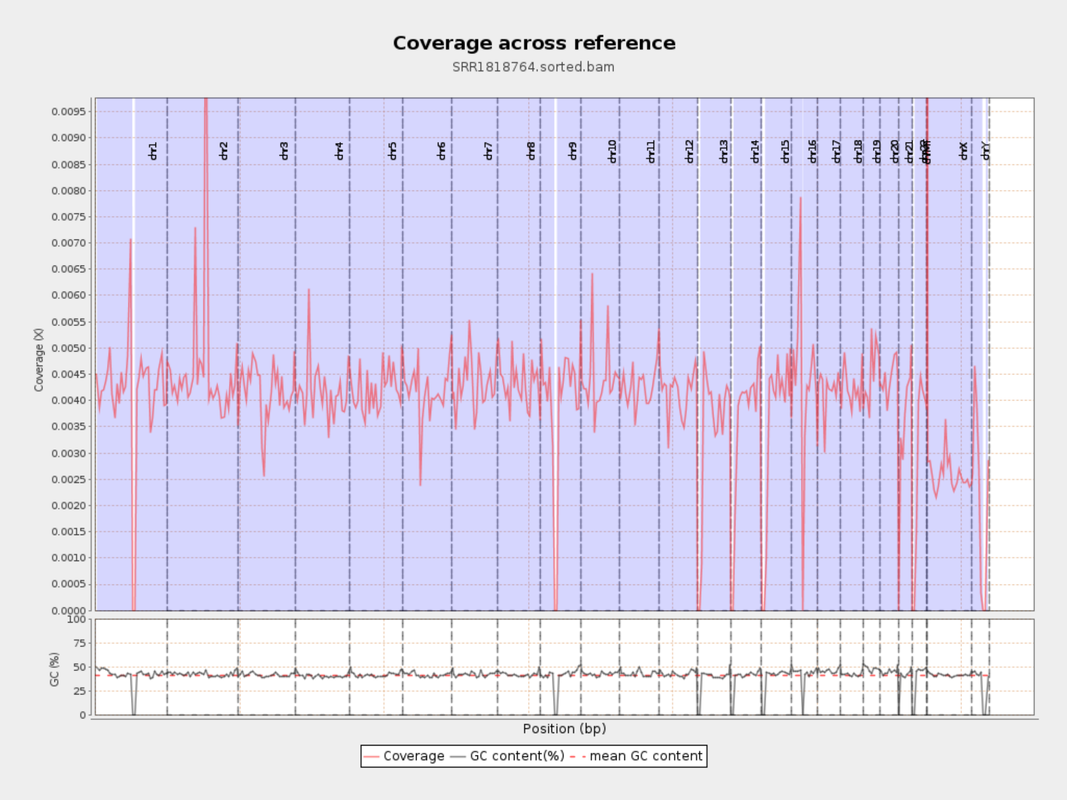
General error rate	0.58%
Mismatches	68,284
Insertions	1,947
Mapped reads with at least one insertion	1.04%
Deletions	3,517
Mapped reads with at least one deletion	1.89%
Homopolymer indels	37.72%

2.6. Chromosome stats

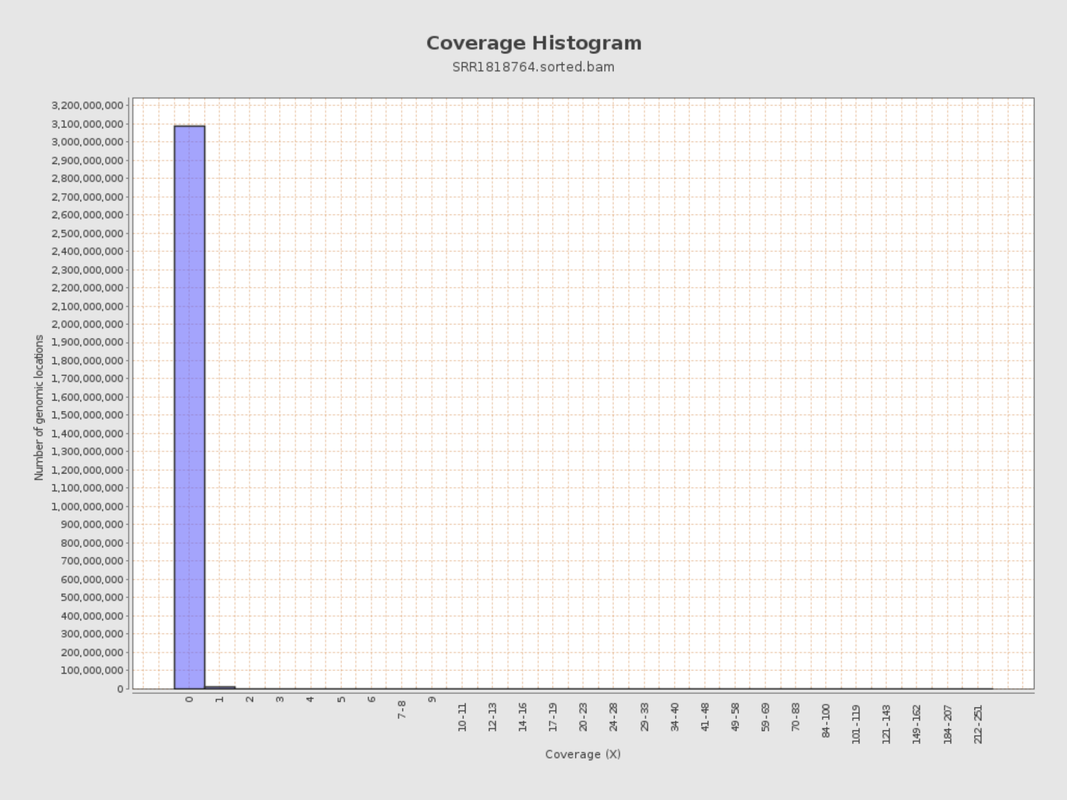
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1026237	0.0041	0.0934
chr2	243199373	1124802	0.0046	0.1646
chr3	198022430	825142	0.0042	0.0708
chr4	191154276	796470	0.0042	0.0782
chr5	180915260	760669	0.0042	0.0745
chr6	171115067	715464	0.0042	0.0752
chr7	159138663	688458	0.0043	0.0769

chr8	146364022	636410	0.0043	0.074
chr9	141213431	546236	0.0039	0.0726
chr10	135534747	598711	0.0044	0.1047
chr11	135006516	572038	0.0042	0.0735
chr12	133851895	556257	0.0042	0.0768
chr13	115169878	386456	0.0034	0.0635
chr14	107349540	376138	0.0035	0.0679
chr15	102531392	359429	0.0035	0.0653
chr16	90354753	389372	0.0043	0.1126
chr17	81195210	340984	0.0042	0.0721
chr18	78077248	329887	0.0042	0.0855
chr19	59128983	265630	0.0045	0.0888
chr20	63025520	279104	0.0044	0.076
chr21	48129895	168821	0.0035	0.0662
chr22	51304566	147414	0.0029	0.0625
chrMT	16571	4495	0.2713	0.5695
chrX	155270560	402092	0.0026	0.0595
chrY	59373566	125469	0.0021	0.1529

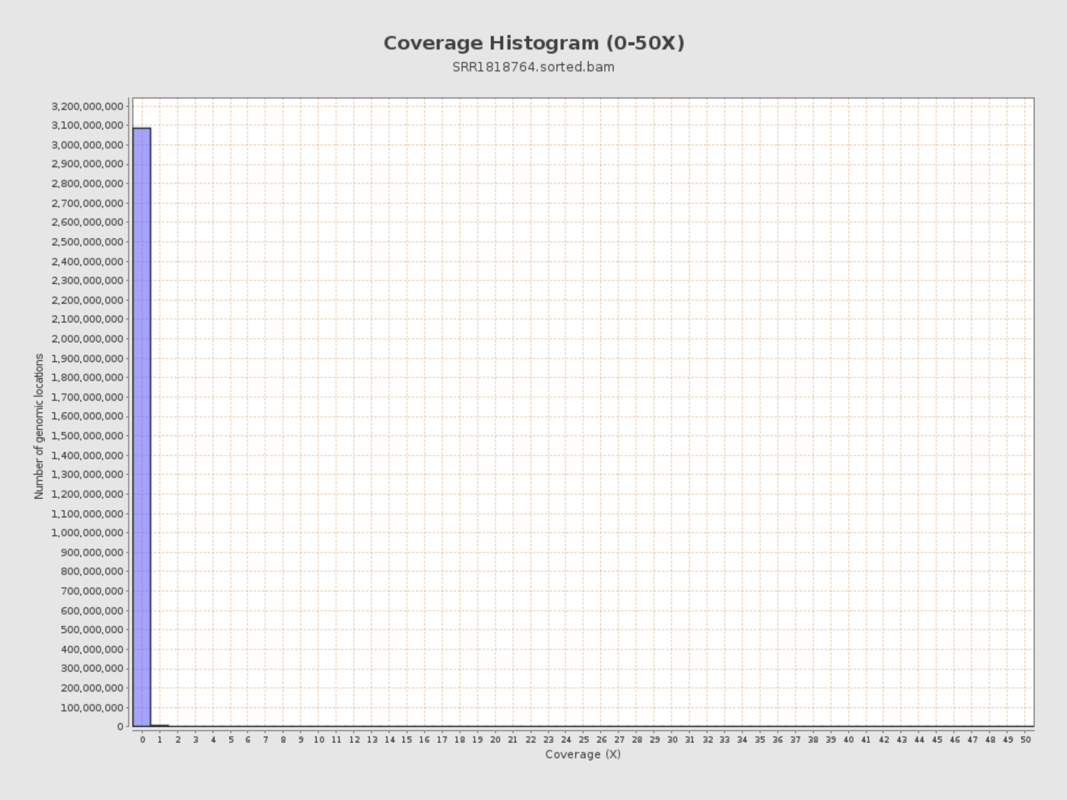
3. Results : Coverage across reference



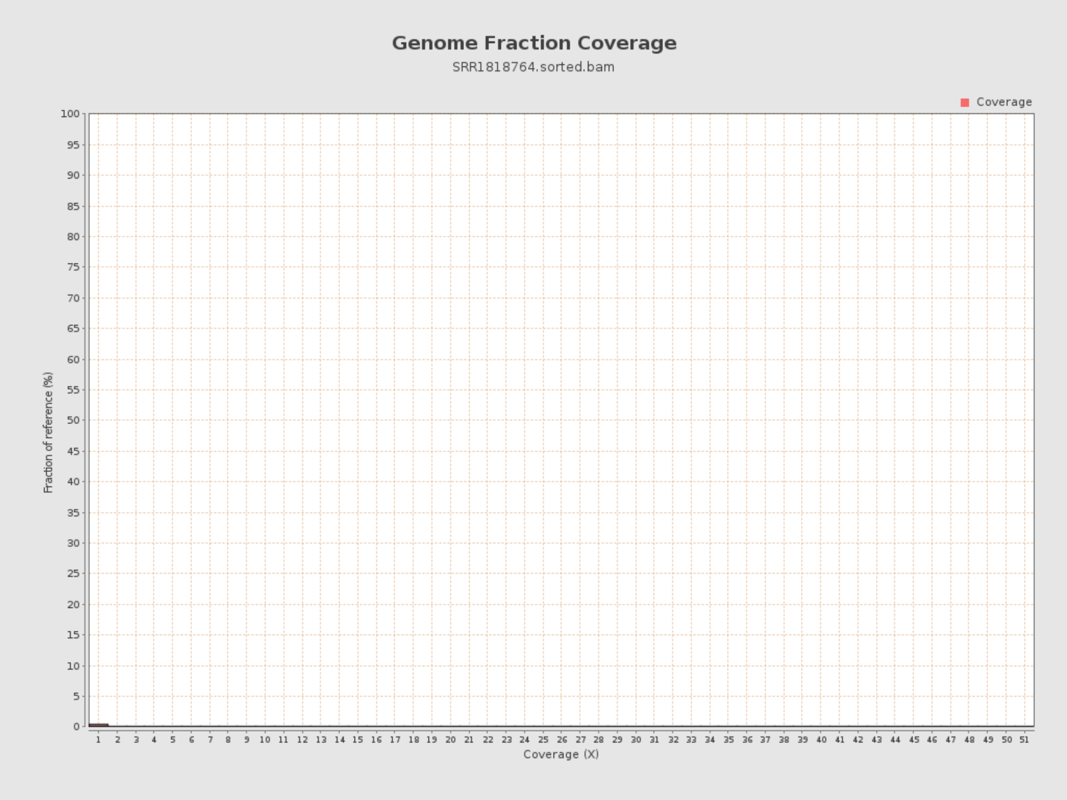
4. Results : Coverage Histogram



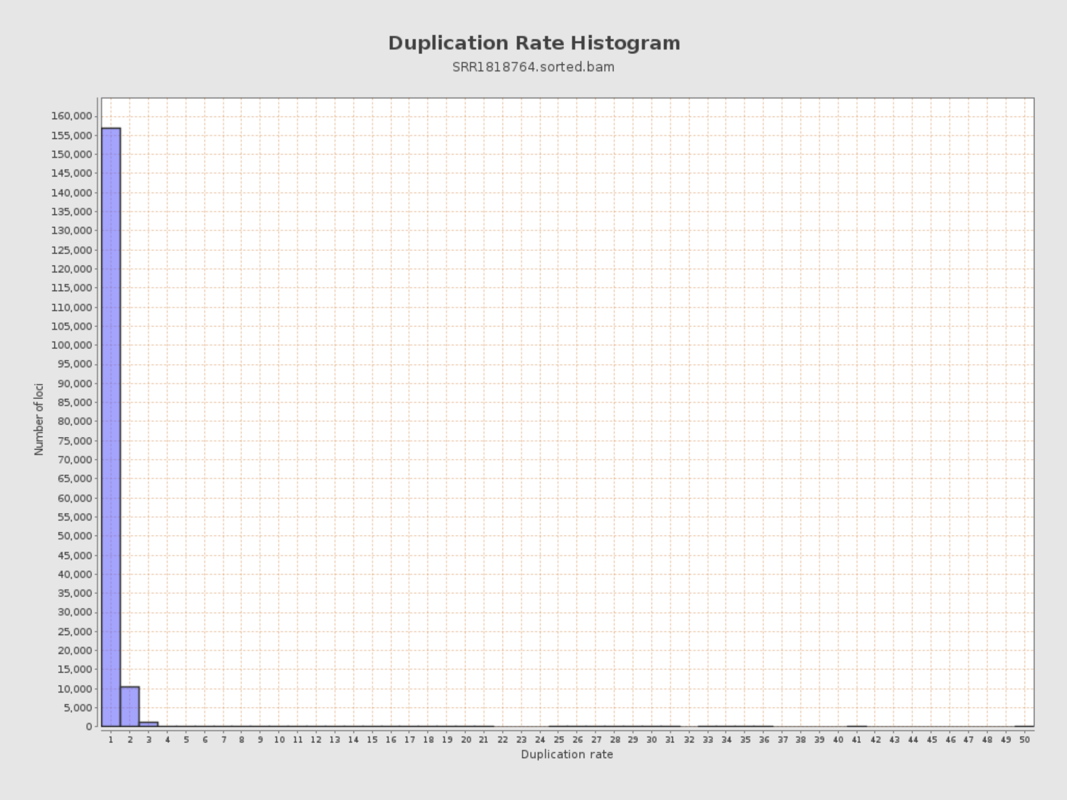
5. Results : Coverage Histogram (0-50X)



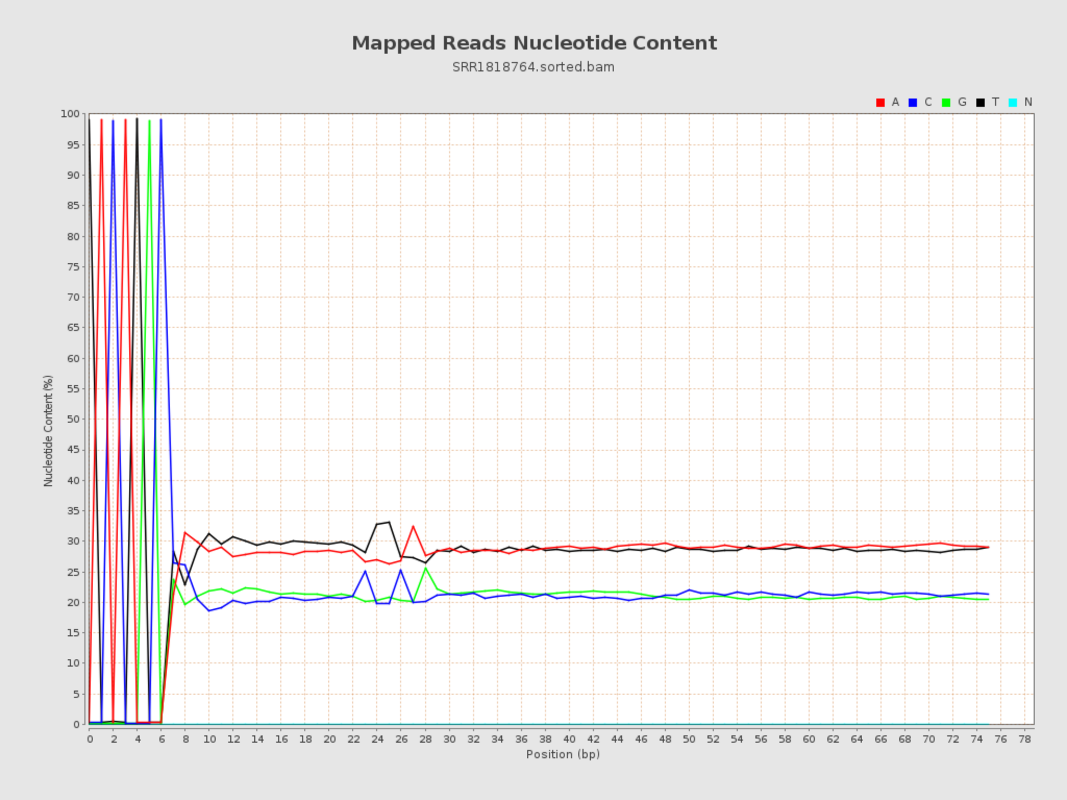
6. Results : Genome Fraction Coverage



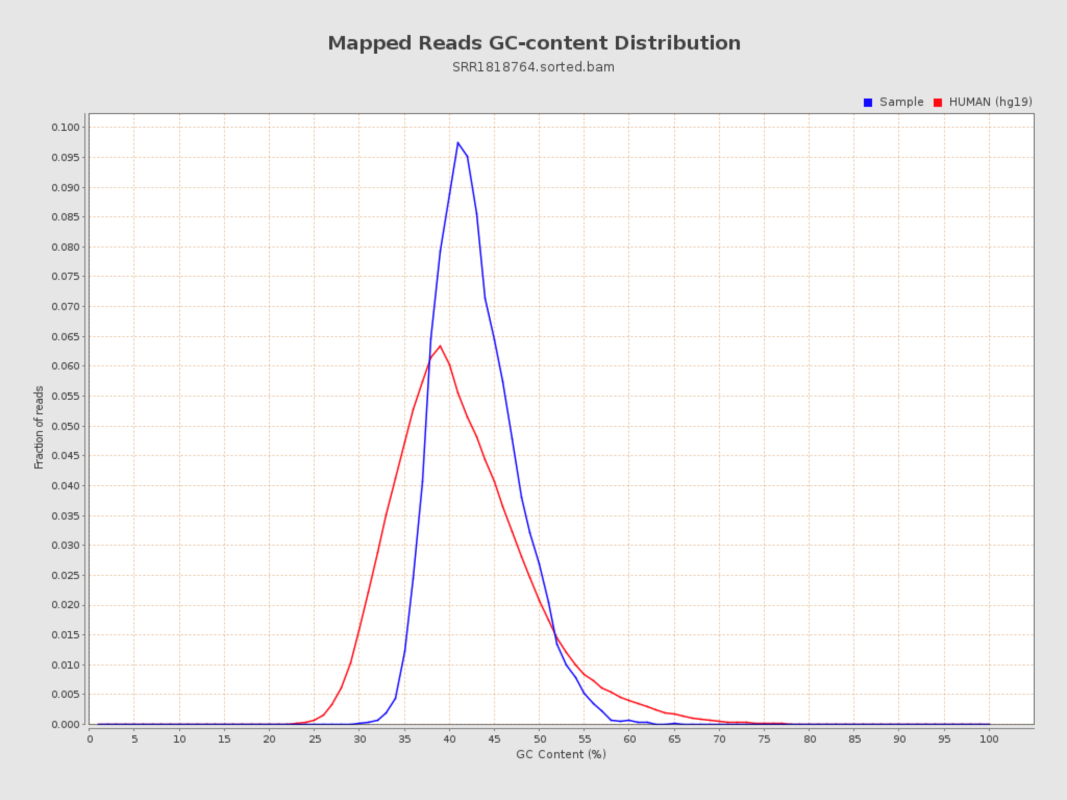
7. Results : Duplication Rate Histogram



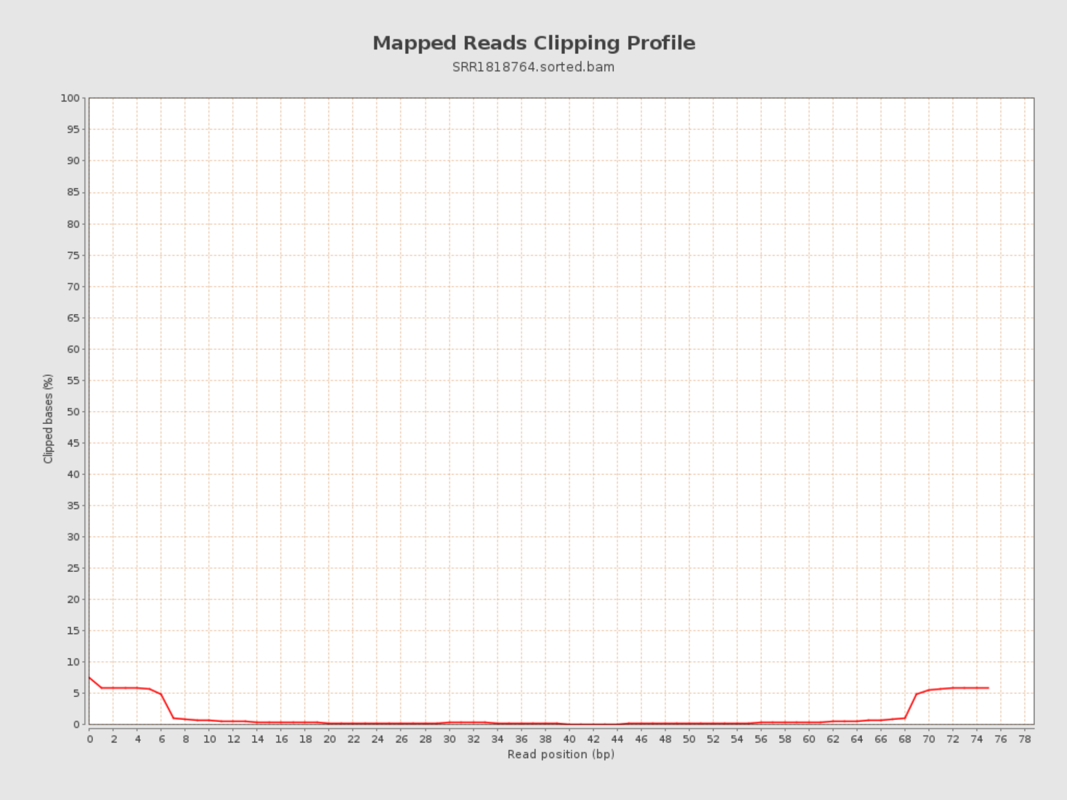
8. Results : Mapped Reads Nucleotide Content



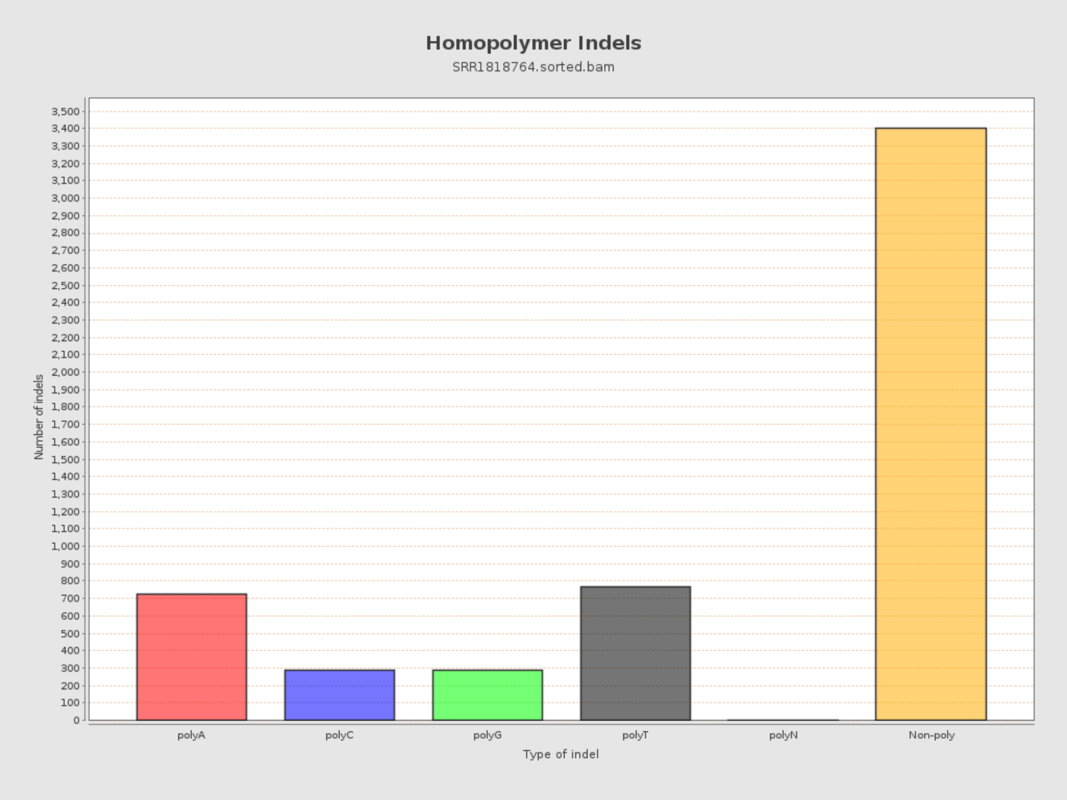
9. Results : Mapped Reads GC-content Distribution



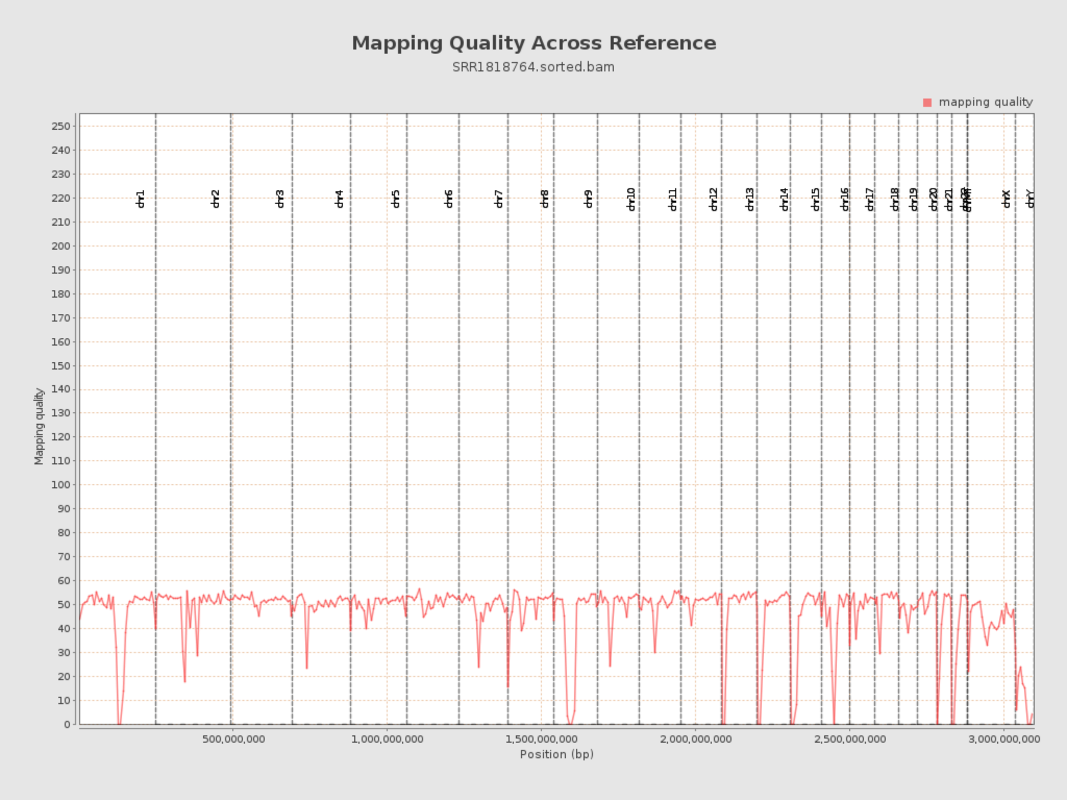
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram