Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:56:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818793.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_SRR1818793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:56:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	529,928
Mapped reads	516,137 / 97.4%
Unmapped reads	13,791 / 2.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,426 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	103,972 / 19.62%
Duplication rate	18.51%
Clipped reads	510,091 / 96.26%

2.2. ACGT Content

Number/percentage of A's	9,905,894 / 28.23%
Number/percentage of C's	7,170,294 / 20.44%
Number/percentage of T's	9,920,584 / 28.27%
Number/percentage of G's	8,088,378 / 23.05%
Number/percentage of N's	1,722 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1654

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

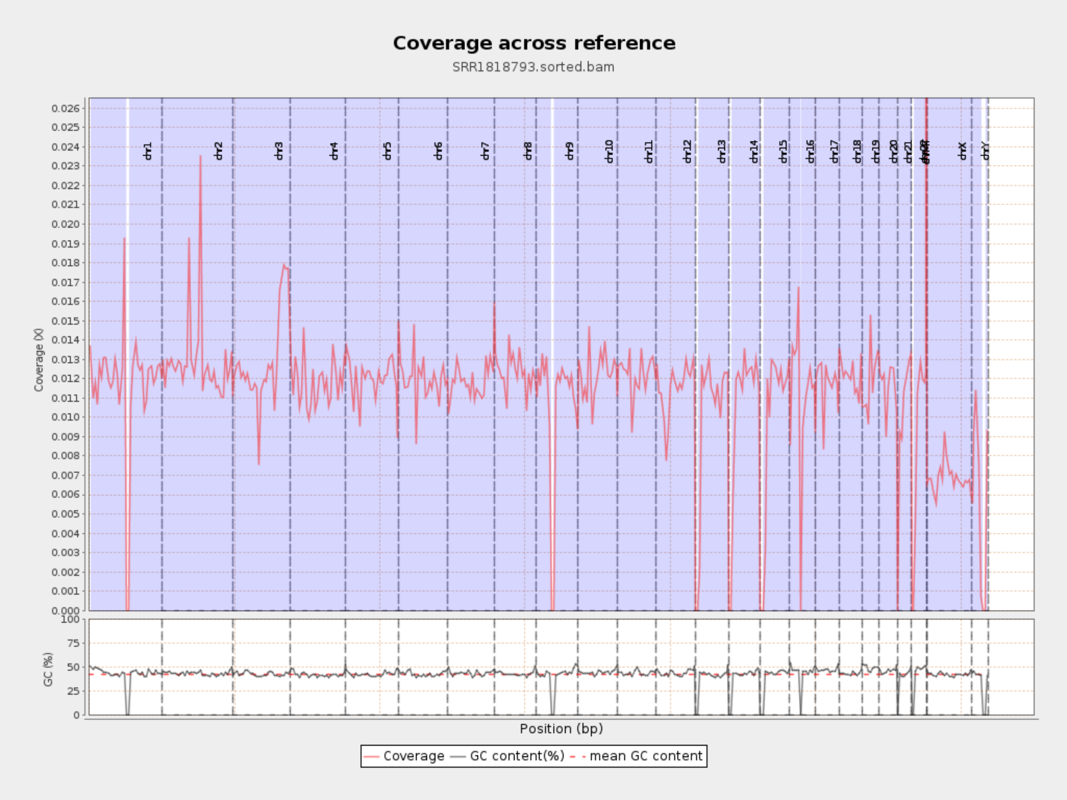
General error rate	0.54%
Mismatches	179,365
Insertions	4,896
Mapped reads with at least one insertion	0.94%
Deletions	8,847
Mapped reads with at least one deletion	1.7%
Homopolymer indels	39.07%

2.6. Chromosome stats

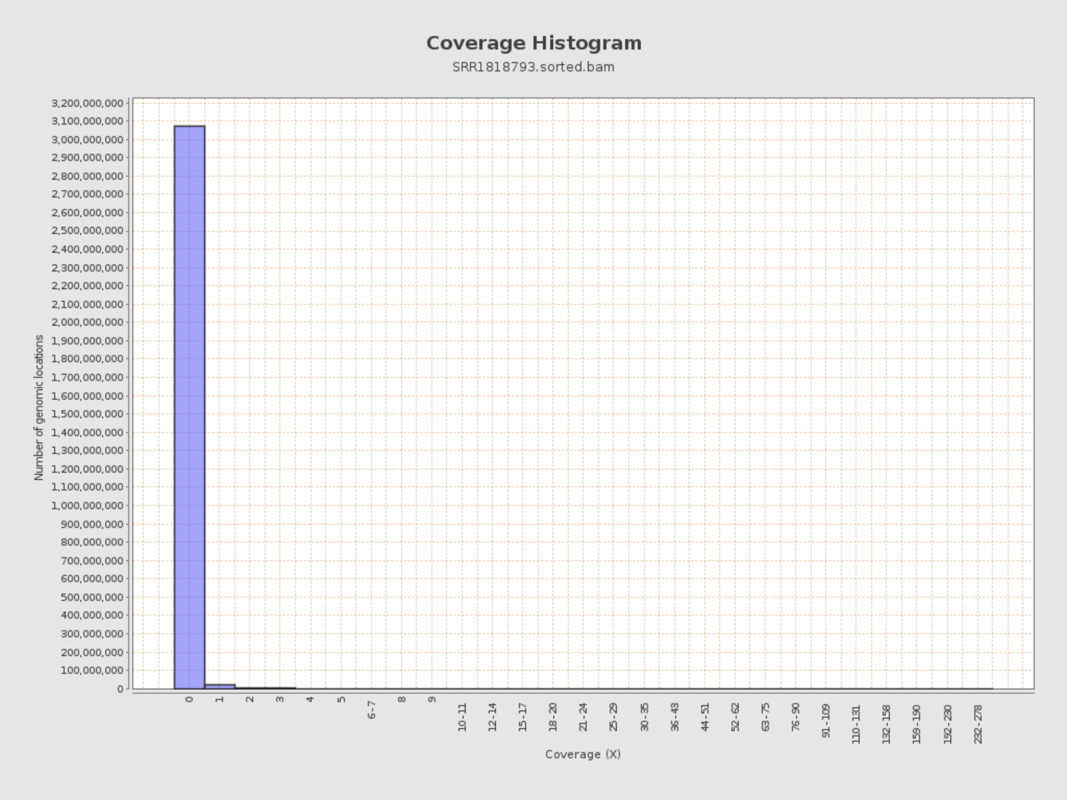
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2896746	0.0116	0.2195
chr2	243199373	3154943	0.013	0.2401
chr3	198022430	2555365	0.0129	0.1474
chr4	191154276	2243280	0.0117	0.1481
chr5	180915260	2170844	0.012	0.1432
chr6	171115067	2059985	0.012	0.15
chr7	159138663	1881720	0.0118	0.1546

chr8	146364022	1809117	0.0124	0.1517
chr9	141213431	1490230	0.0106	0.1412
chr10	135534747	1661335	0.0123	0.1692
chr11	135006516	1654269	0.0123	0.1505
chr12	133851895	1540244	0.0115	0.1412
chr13	115169878	1135416	0.0099	0.1298
chr14	107349540	1106119	0.0103	0.1397
chr15	102531392	988432	0.0096	0.1269
chr16	90354753	1015214	0.0112	0.1705
chr17	81195210	951454	0.0117	0.1452
chr18	78077248	948392	0.0121	0.171
chr19	59128983	704130	0.0119	0.1928
chr20	63025520	730181	0.0116	0.1465
chr21	48129895	488840	0.0102	0.1373
chr22	51304566	430365	0.0084	0.1249
chrMT	16571	89143	5.3795	5.2451
chrX	155270560	1070867	0.0069	0.1111
chrY	59373566	324706	0.0055	0.2102

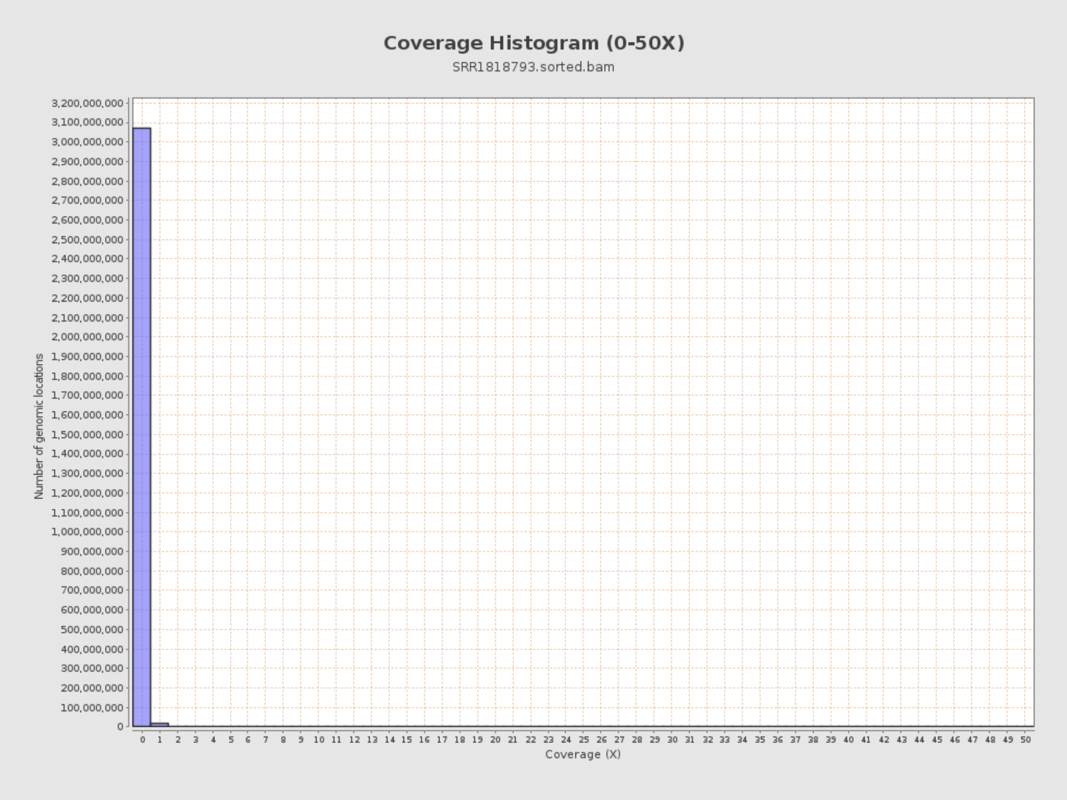
3. Results : Coverage across reference



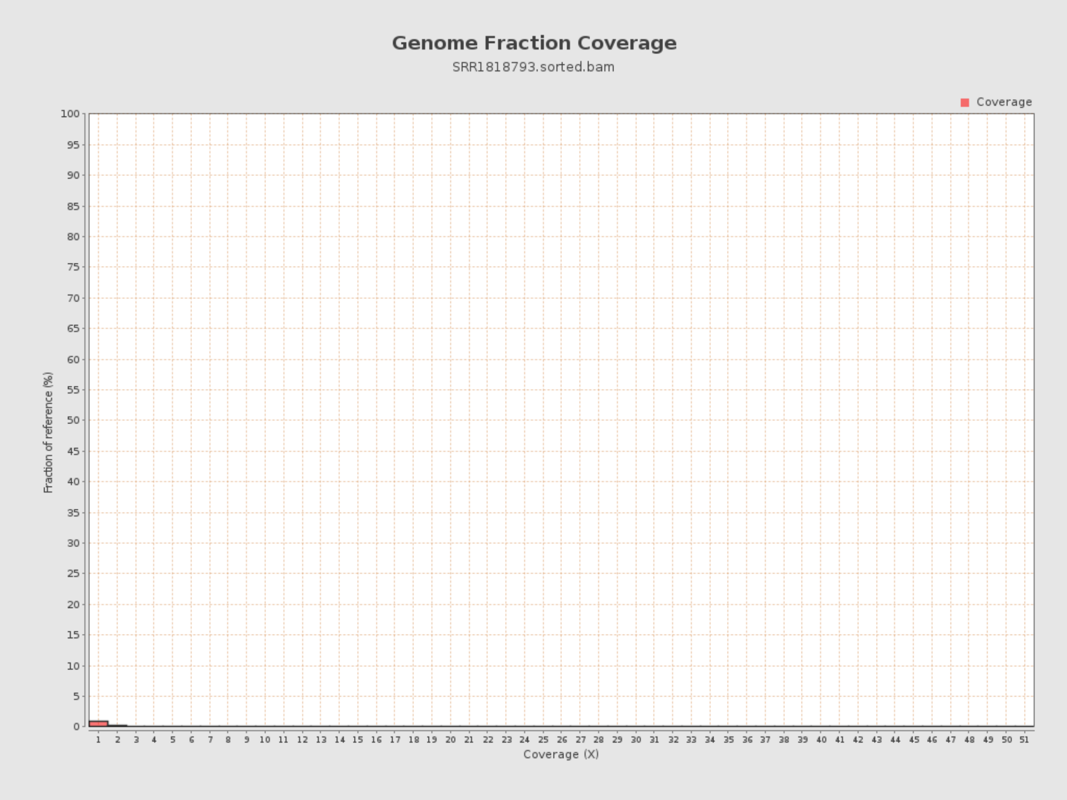
4. Results : Coverage Histogram



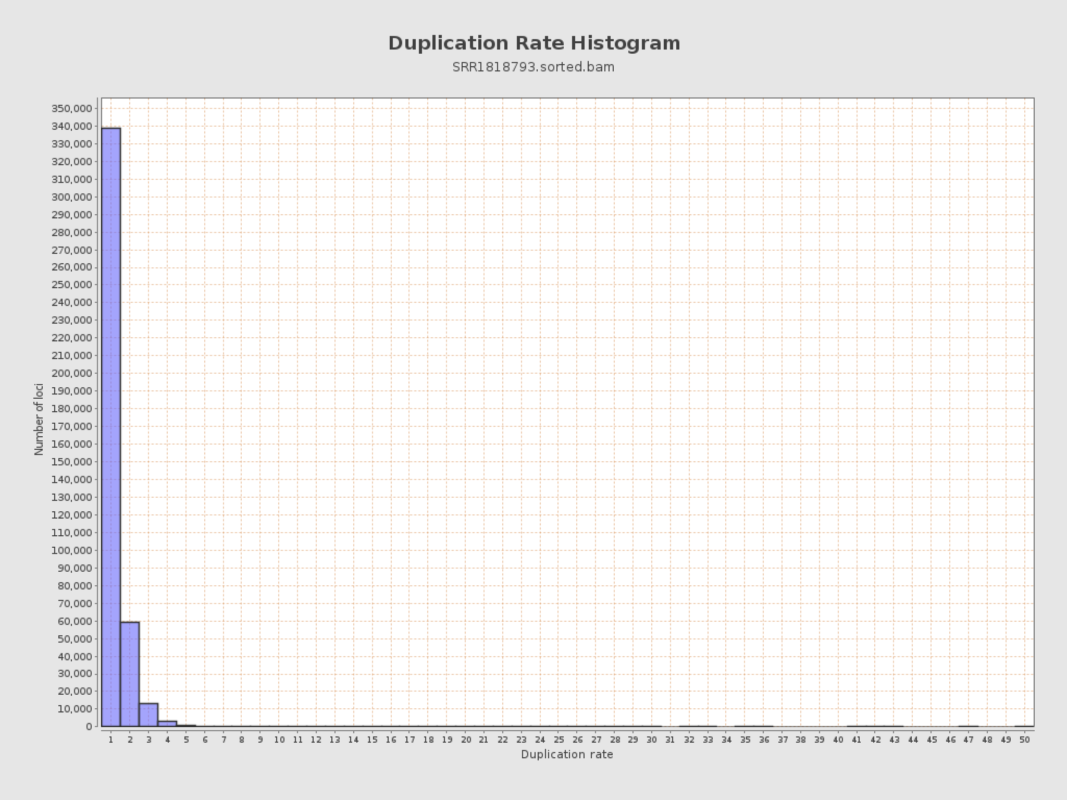
5. Results : Coverage Histogram (0-50X)



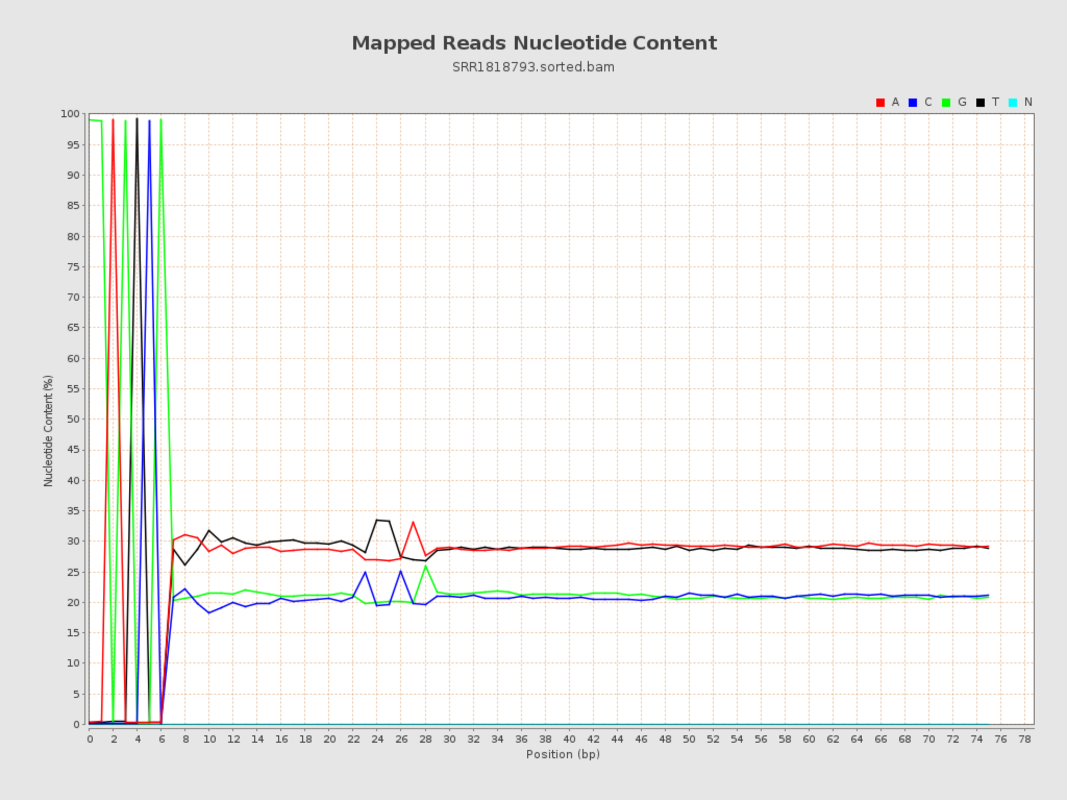
6. Results : Genome Fraction Coverage



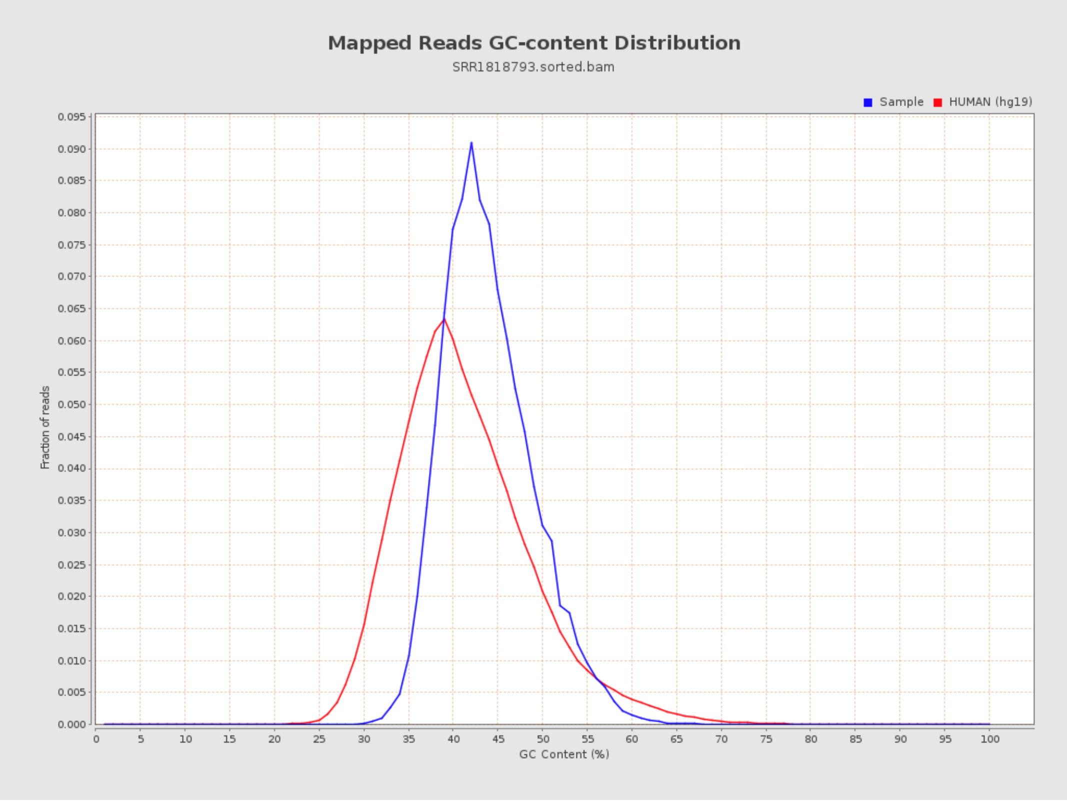
7. Results : Duplication Rate Histogram



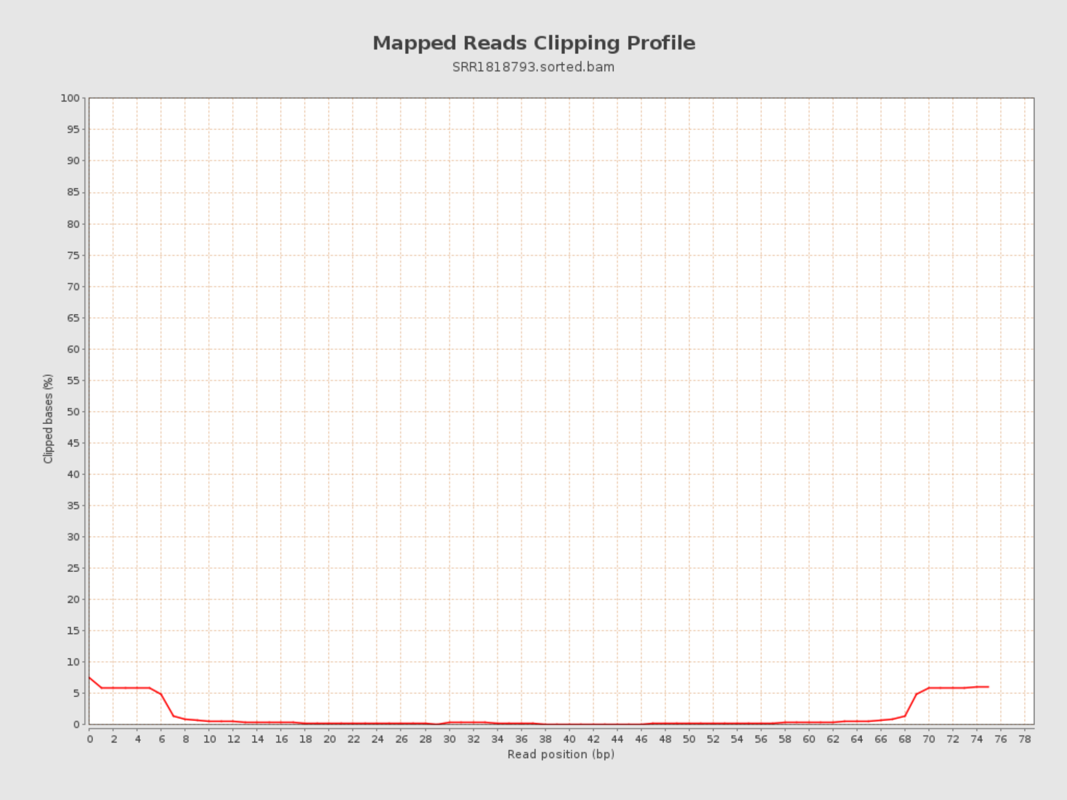
8. Results : Mapped Reads Nucleotide Content



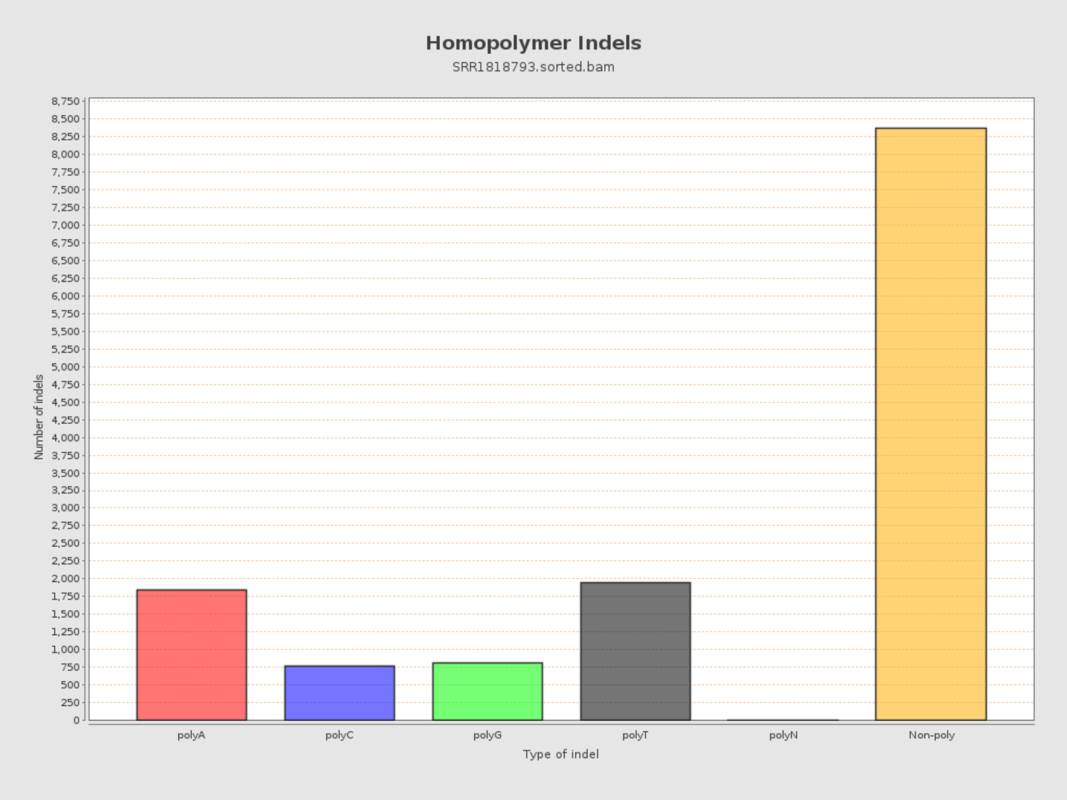
9. Results : Mapped Reads GC-content Distribution



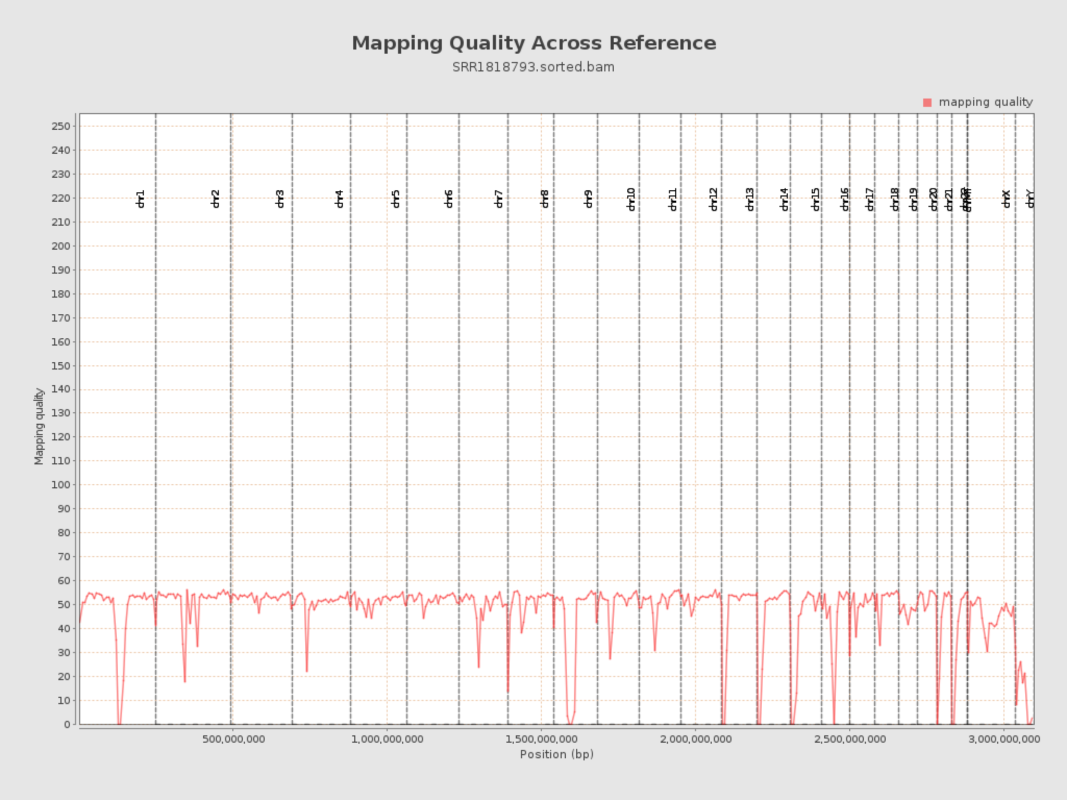
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram