Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818791.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_SRR1818791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:44:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	449,915
Mapped reads	432,247 / 96.07%
Unmapped reads	17,668 / 3.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,622 / 0.81%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	172,140 / 38.26%
Duplication rate	34.36%
Clipped reads	433,610 / 96.38%

2.2. ACGT Content

Number/percentage of A's	8,488,728 / 28.99%
Number/percentage of C's	6,623,784 / 22.62%
Number/percentage of T's	8,179,714 / 27.94%
Number/percentage of G's	5,984,003 / 20.44%
Number/percentage of N's	1,723 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1846

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

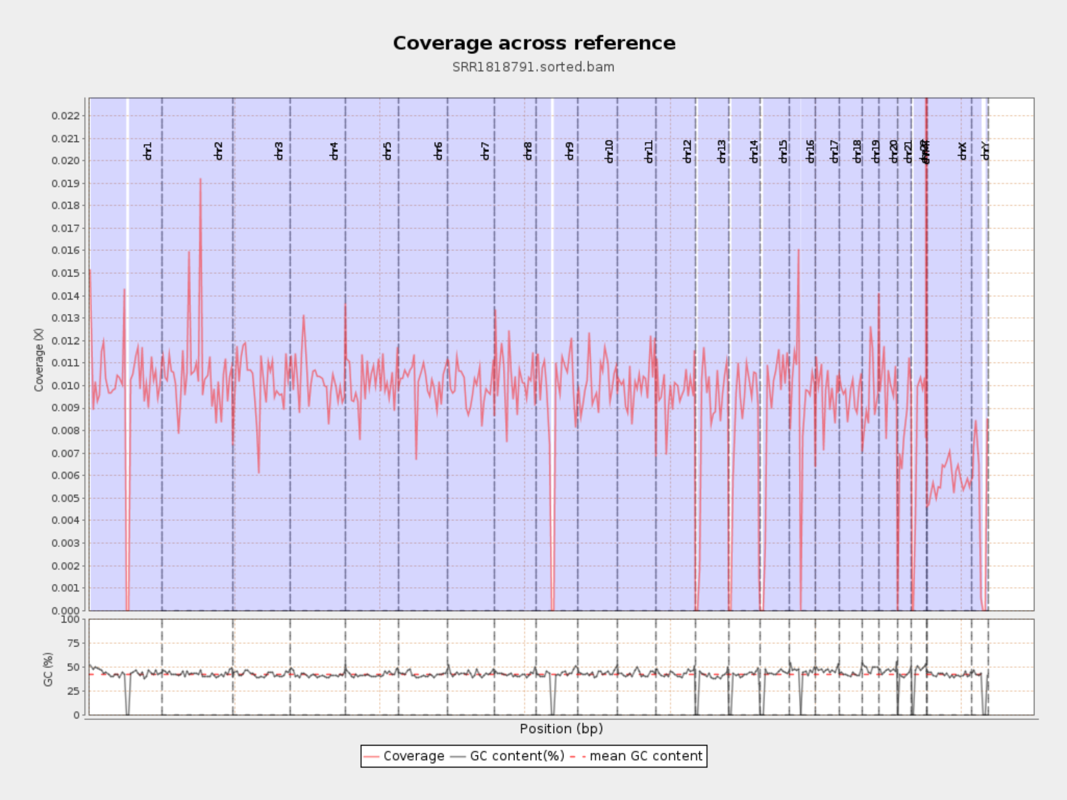
General error rate	0.54%
Mismatches	150,759
Insertions	3,266
Mapped reads with at least one insertion	0.75%
Deletions	7,441
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.26%

2.6. Chromosome stats

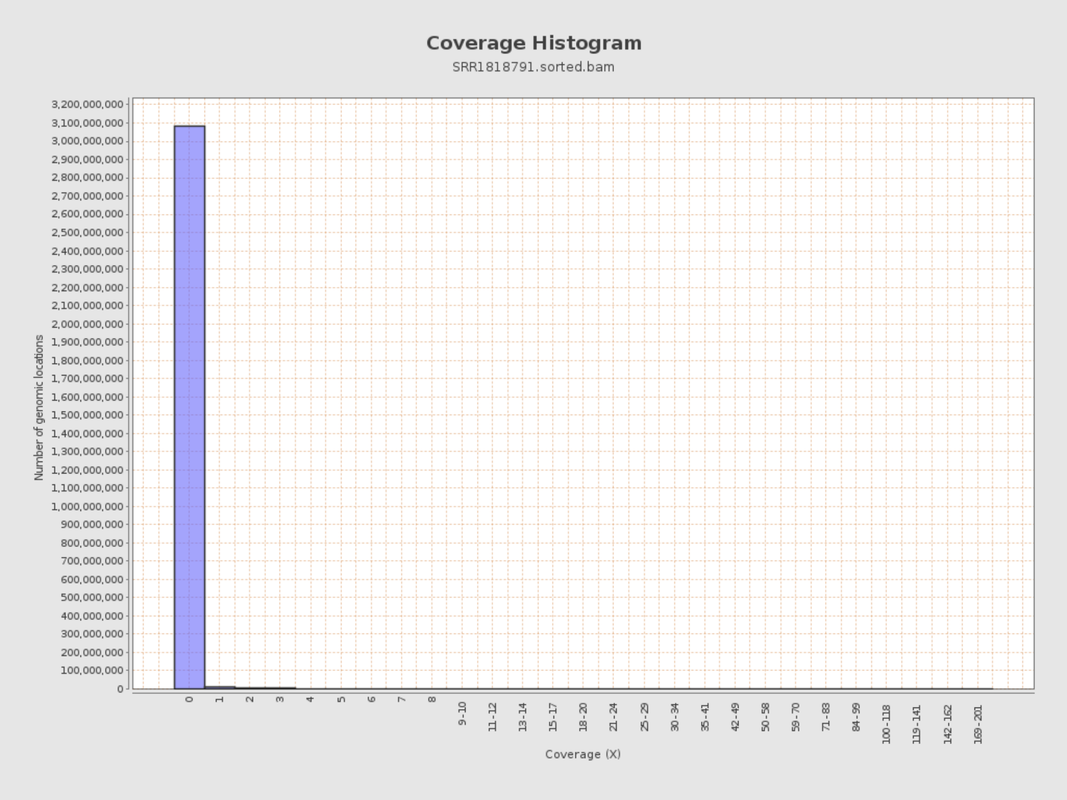
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2467788	0.0099	0.2131
chr2	243199373	2589252	0.0106	0.2371
chr3	198022430	2003678	0.0101	0.1752
chr4	191154276	1949013	0.0102	0.1786
chr5	180915260	1836105	0.0101	0.1743
chr6	171115067	1735737	0.0101	0.1774
chr7	159138663	1577616	0.0099	0.1807

chr8	146364022	1520838	0.0104	0.1781
chr9	141213431	1296238	0.0092	0.1714
chr10	135534747	1368511	0.0101	0.1919
chr11	135006516	1368261	0.0101	0.1775
chr12	133851895	1299055	0.0097	0.1738
chr13	115169878	948759	0.0082	0.1557
chr14	107349540	890576	0.0083	0.1618
chr15	102531392	865900	0.0084	0.1619
chr16	90354753	865327	0.0096	0.1983
chr17	81195210	790639	0.0097	0.1809
chr18	78077248	751238	0.0096	0.1856
chr19	59128983	575145	0.0097	0.207
chr20	63025520	634843	0.0101	0.1817
chr21	48129895	367125	0.0076	0.1512
chr22	51304566	359117	0.007	0.1573
chrMT	16571	59105	3.5668	4.631
chrX	155270560	896397	0.0058	0.1332
chrY	59373566	273065	0.0046	0.2115

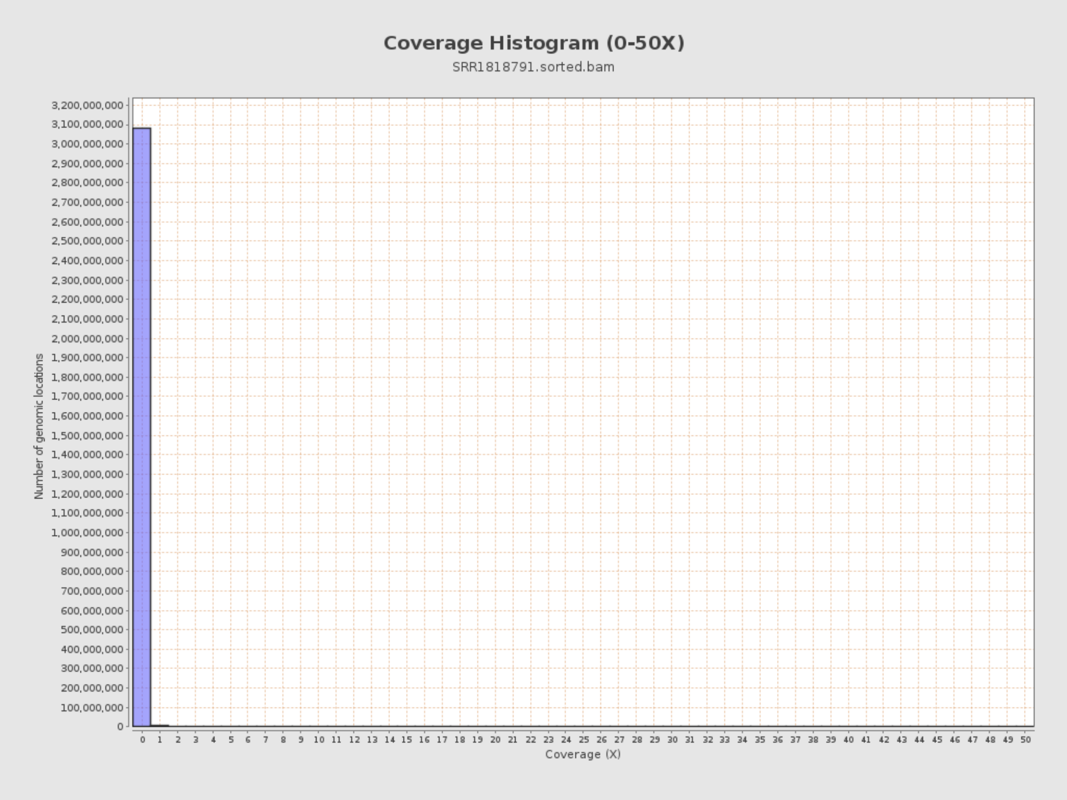
3. Results : Coverage across reference



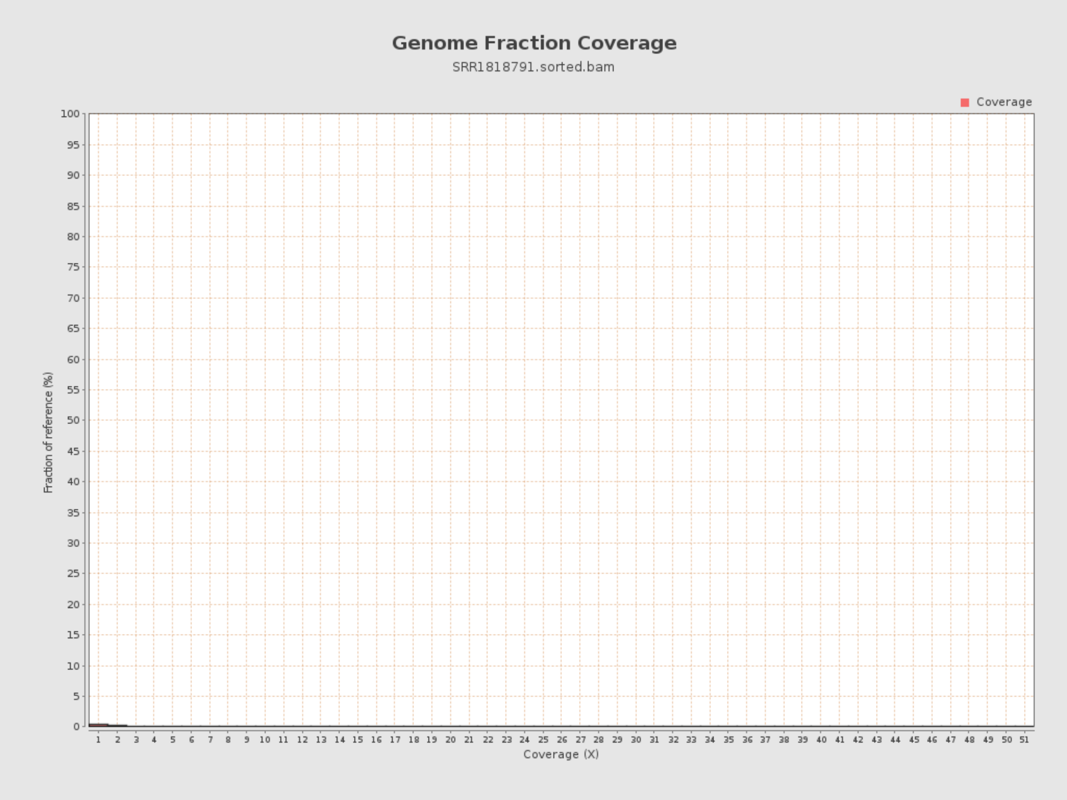
4. Results : Coverage Histogram



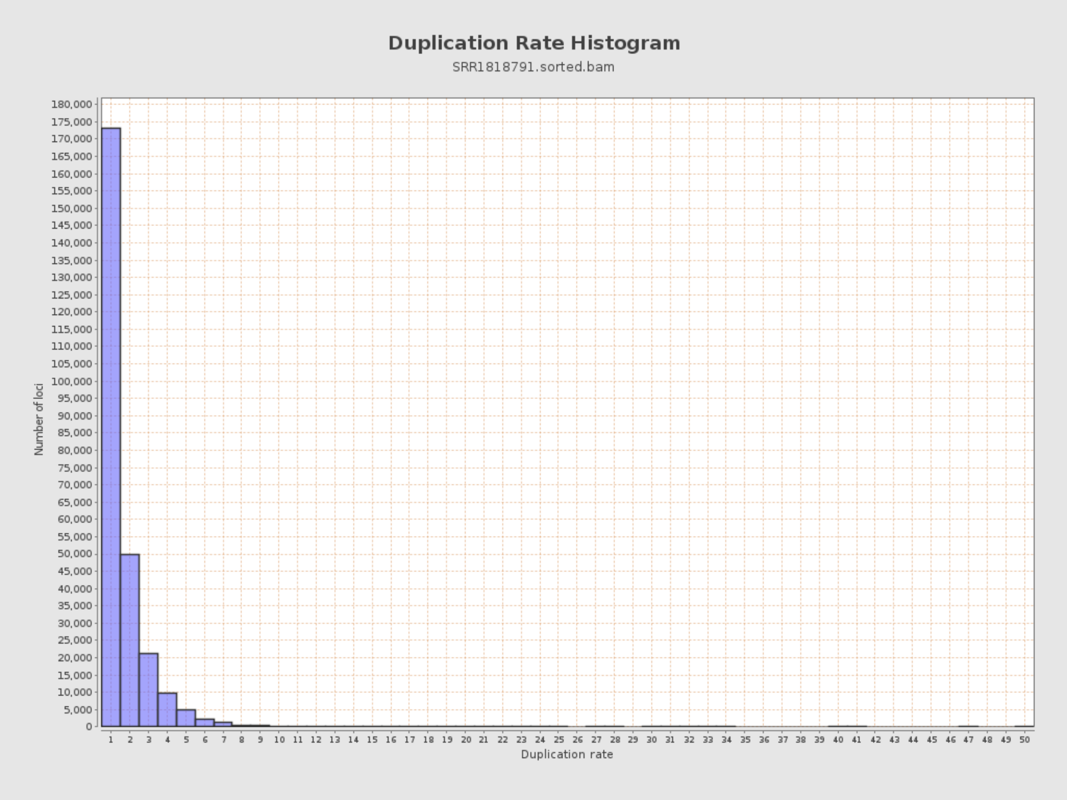
5. Results : Coverage Histogram (0-50X)



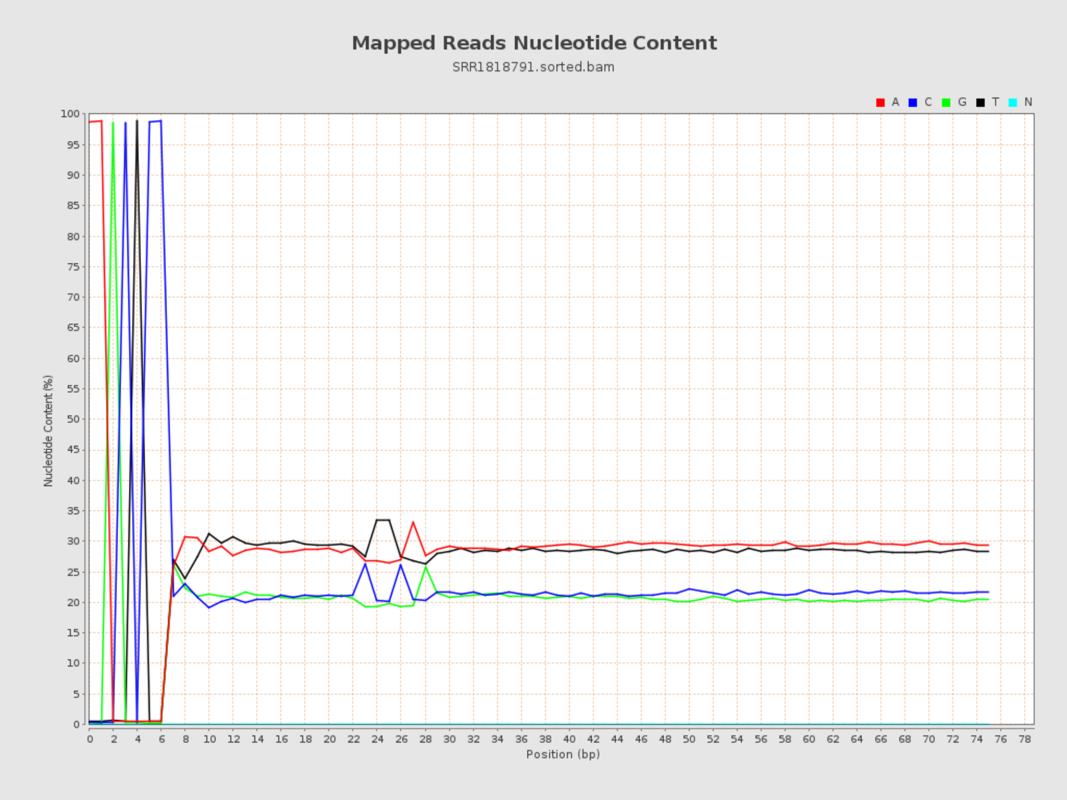
6. Results : Genome Fraction Coverage



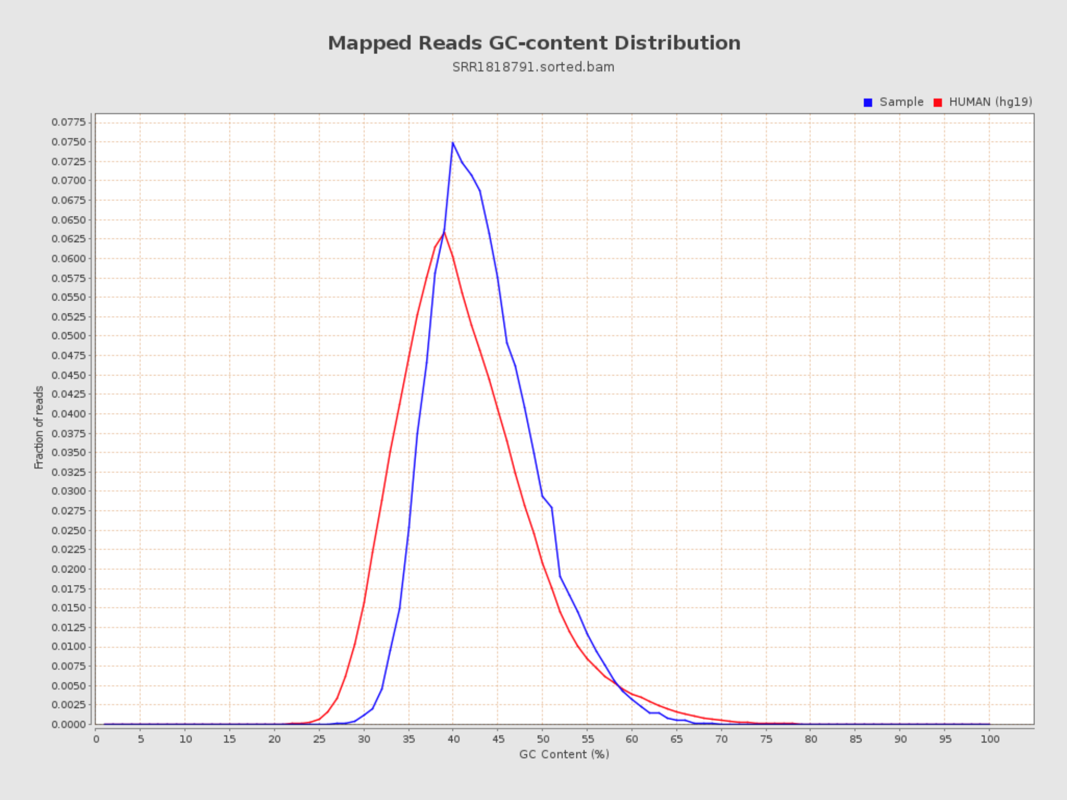
7. Results : Duplication Rate Histogram



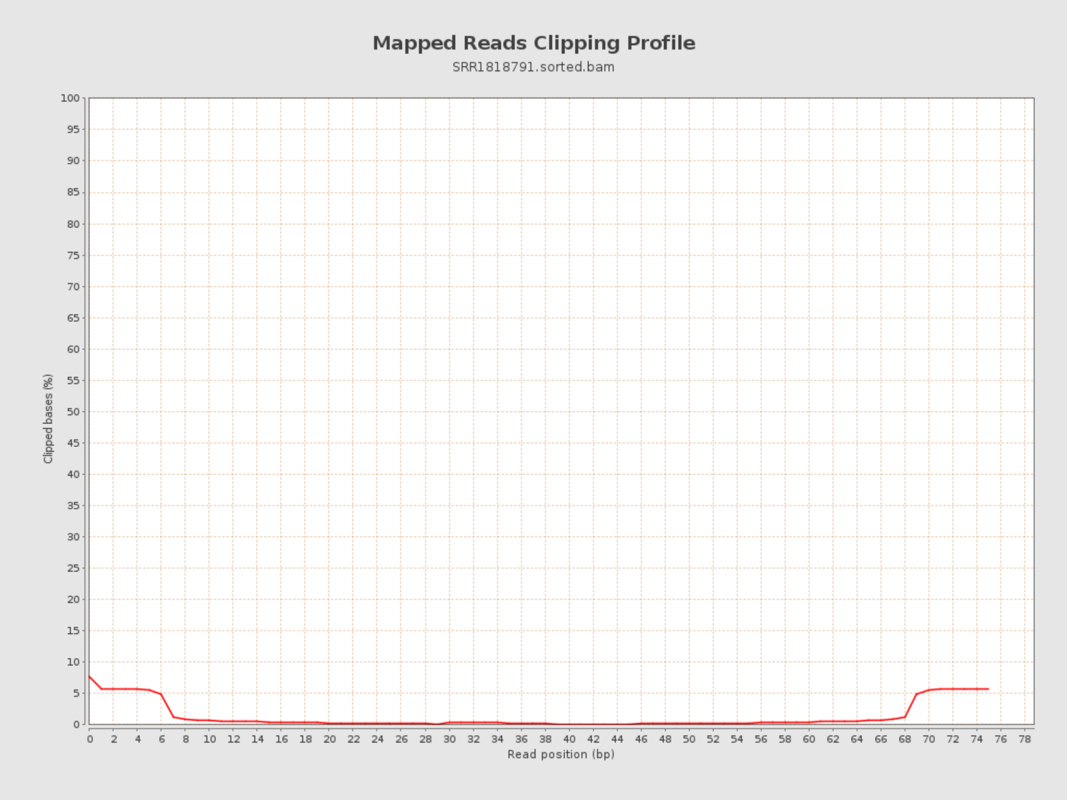
8. Results : Mapped Reads Nucleotide Content



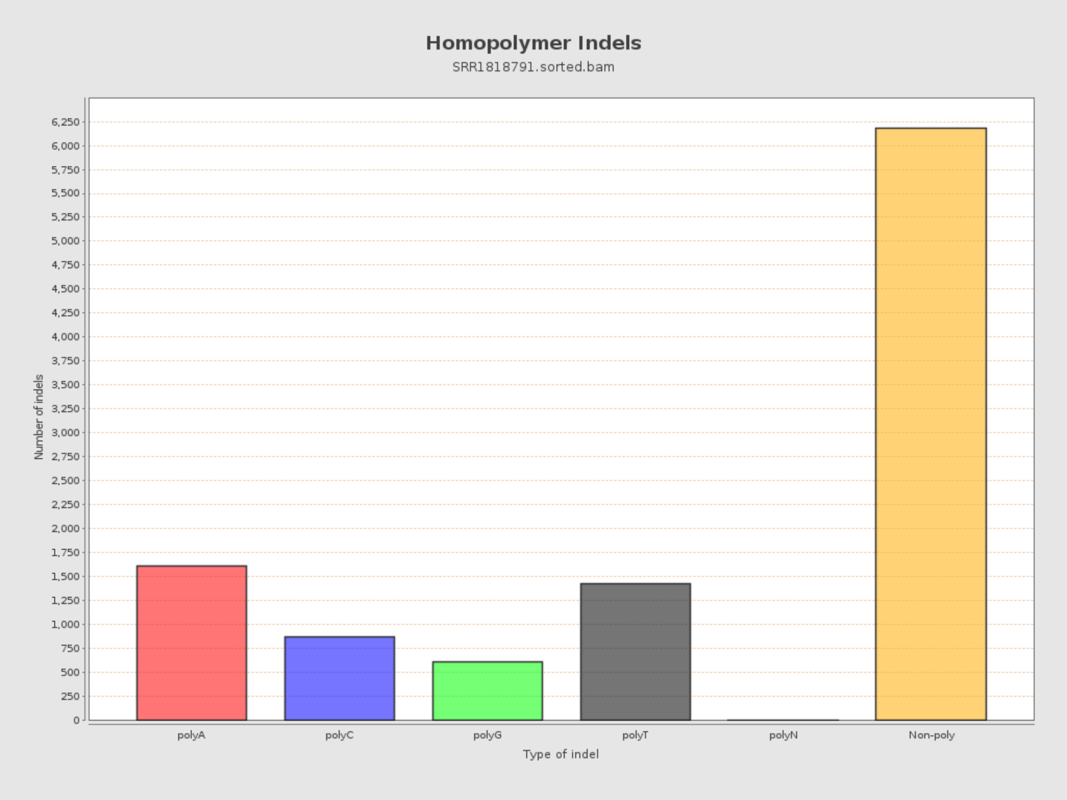
9. Results : Mapped Reads GC-content Distribution



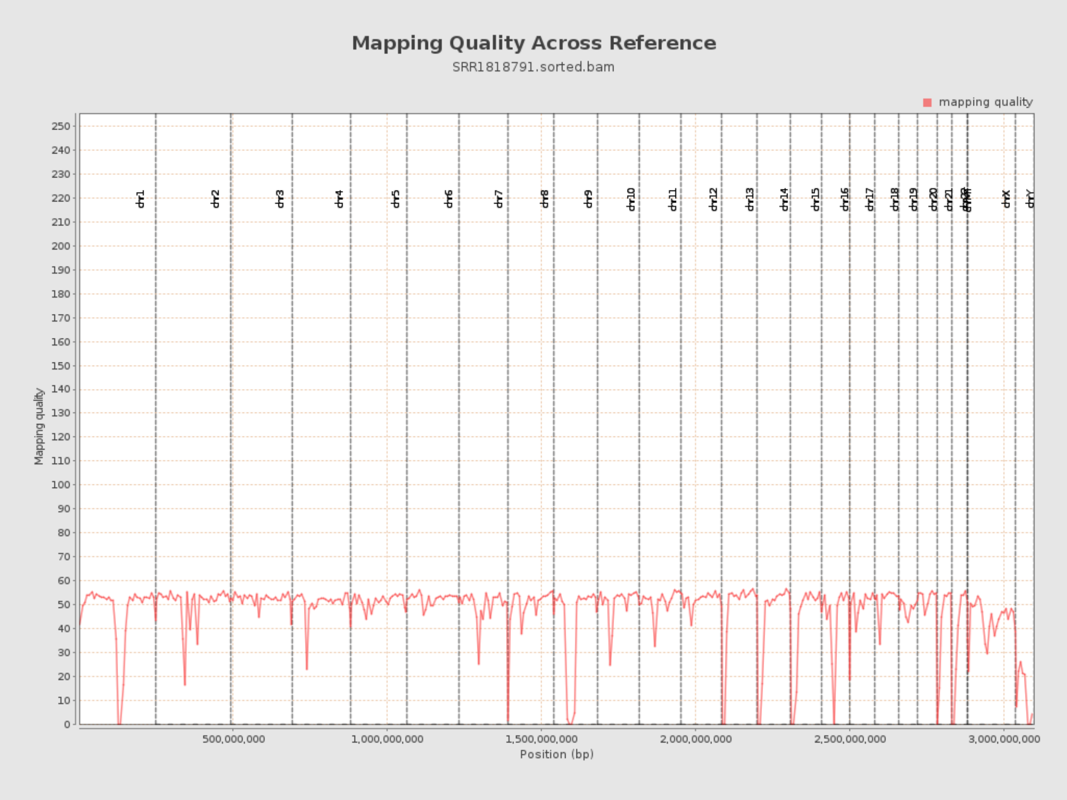
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram