Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818814.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_SRR1818814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:42:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	459,288
Mapped reads	442,360 / 96.31%
Unmapped reads	16,928 / 3.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,875 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	73,589 / 16.02%
Duplication rate	14.95%
Clipped reads	441,038 / 96.03%

2.2. ACGT Content

Number/percentage of A's	8,519,951 / 28.42%
Number/percentage of C's	6,596,607 / 22%
Number/percentage of T's	8,432,129 / 28.13%
Number/percentage of G's	6,430,237 / 21.45%
Number/percentage of N's	1,785 / 0.01%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1543

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

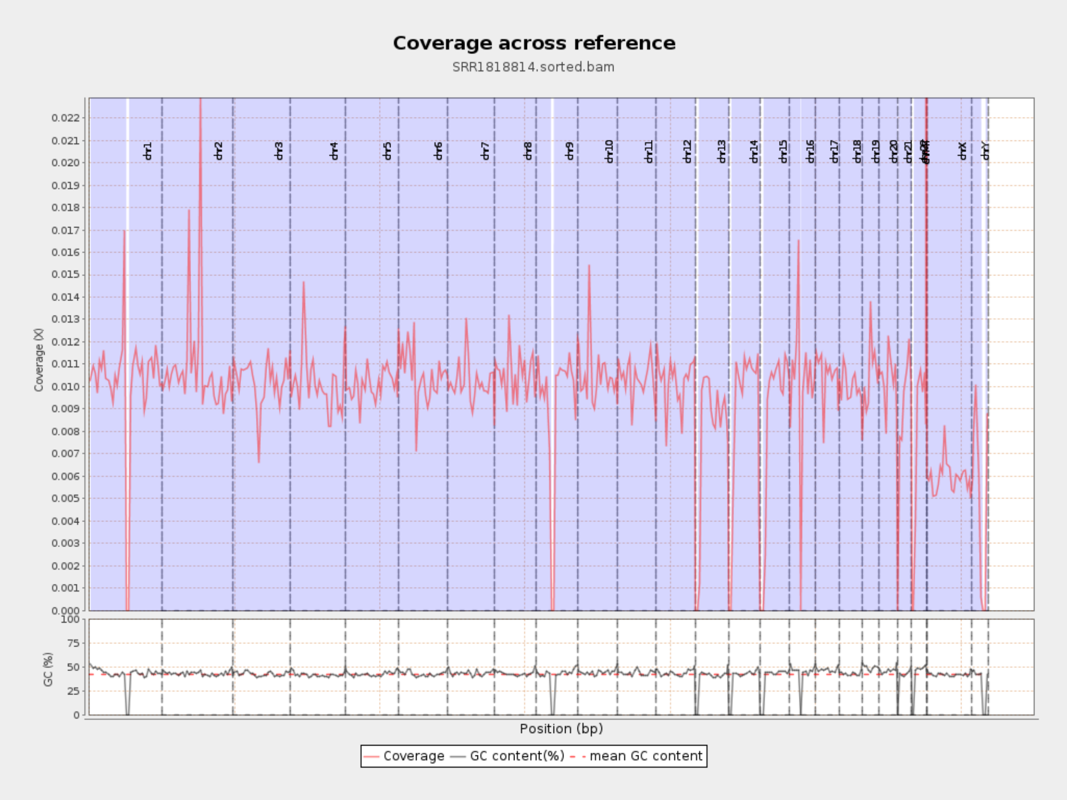
General error rate	0.55%
Mismatches	158,165
Insertions	3,830
Mapped reads with at least one insertion	0.85%
Deletions	7,863
Mapped reads with at least one deletion	1.76%
Homopolymer indels	40.14%

2.6. Chromosome stats

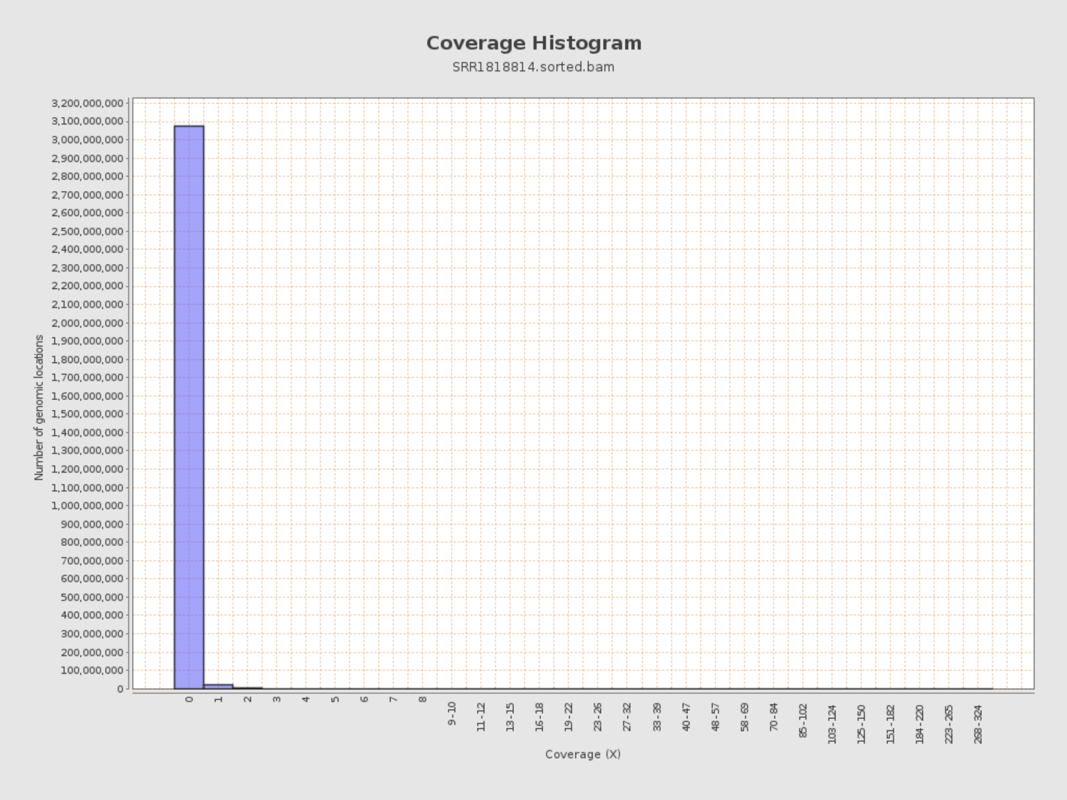
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2524131	0.0101	0.1971
chr2	243199373	2653975	0.0109	0.2497
chr3	198022430	2023645	0.0102	0.124
chr4	191154276	1929838	0.0101	0.1359
chr5	180915260	1831223	0.0101	0.1255
chr6	171115067	1802868	0.0105	0.1337
chr7	159138663	1628902	0.0102	0.1386

chr8	146364022	1548488	0.0106	0.1337
chr9	141213431	1282515	0.0091	0.1268
chr10	135534747	1428359	0.0105	0.1662
chr11	135006516	1398613	0.0104	0.1323
chr12	133851895	1370852	0.0102	0.1283
chr13	115169878	888444	0.0077	0.1075
chr14	107349540	958400	0.0089	0.1267
chr15	102531392	859249	0.0084	0.112
chr16	90354753	910703	0.0101	0.1763
chr17	81195210	852802	0.0105	0.1298
chr18	78077248	788306	0.0101	0.1585
chr19	59128983	623325	0.0105	0.1766
chr20	63025520	654607	0.0104	0.1344
chr21	48129895	422912	0.0088	0.1182
chr22	51304566	364732	0.0071	0.1066
chrMT	16571	27057	1.6328	1.8689
chrX	155270560	929603	0.006	0.1035
chrY	59373566	290158	0.0049	0.2467

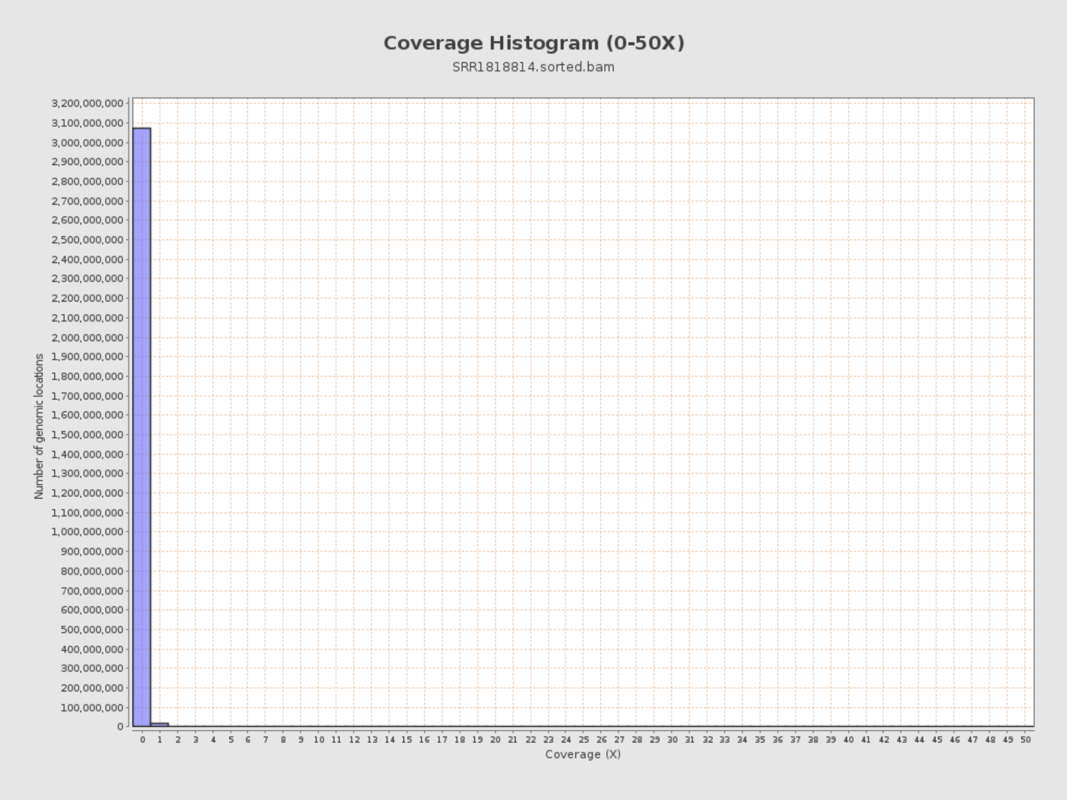
3. Results : Coverage across reference



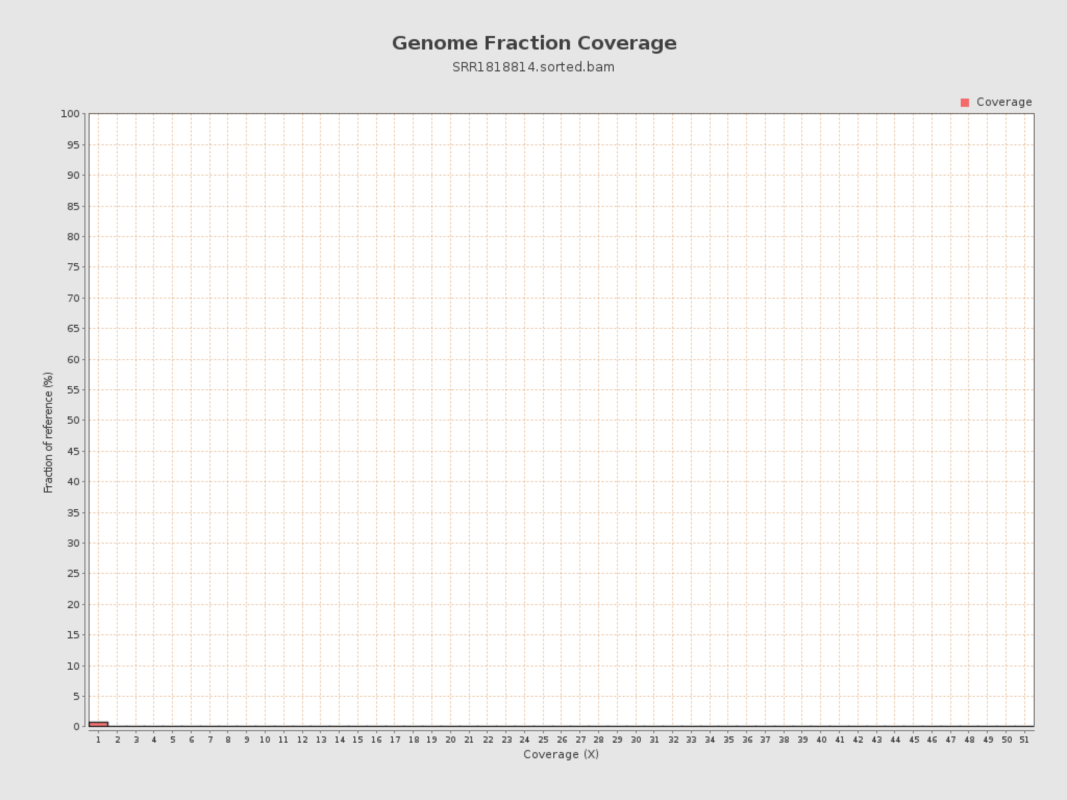
4. Results : Coverage Histogram



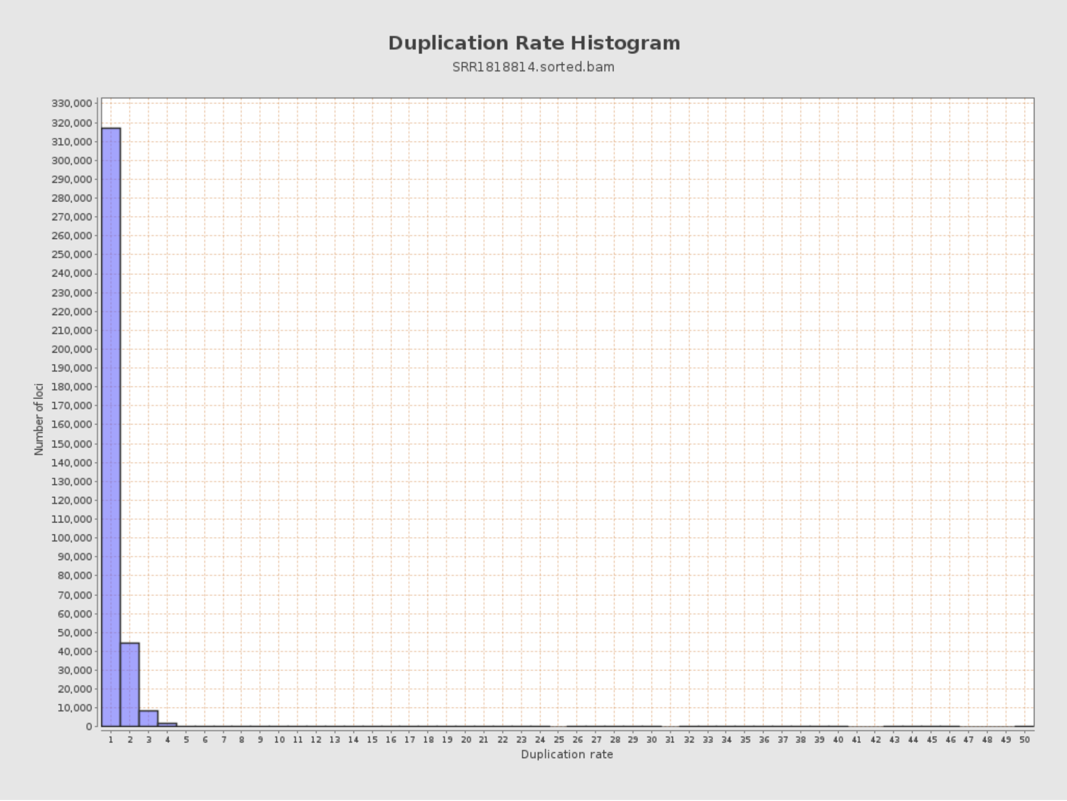
5. Results : Coverage Histogram (0-50X)



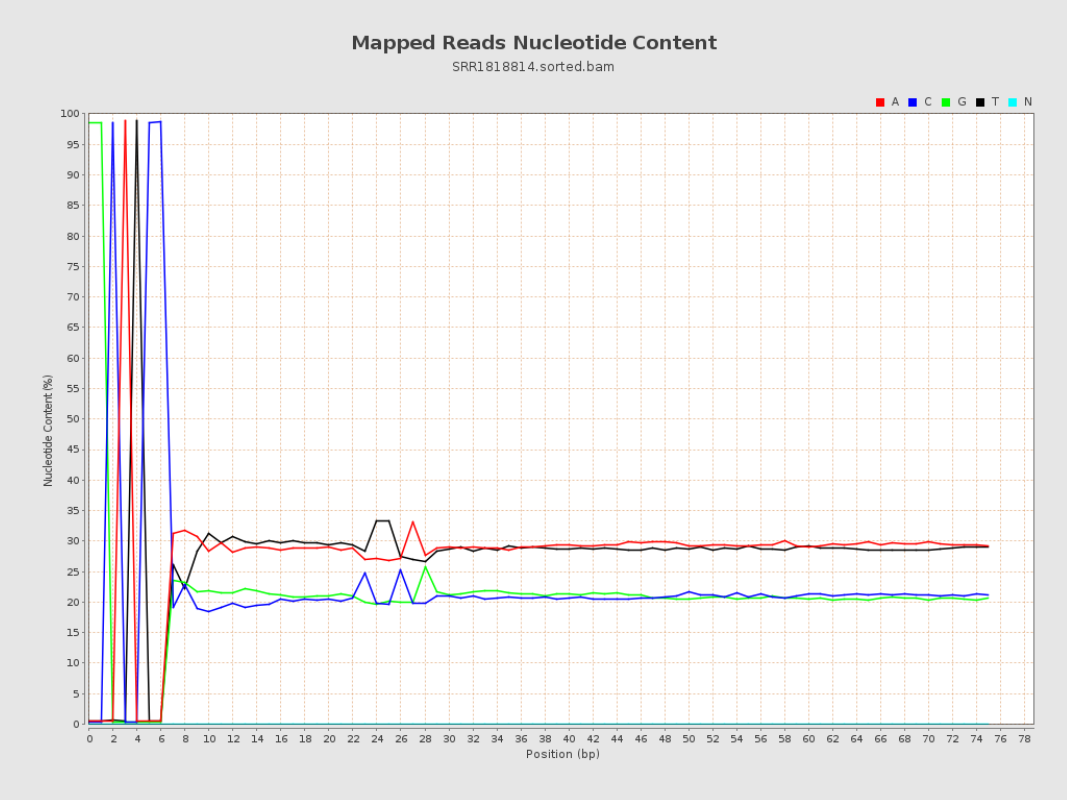
6. Results : Genome Fraction Coverage



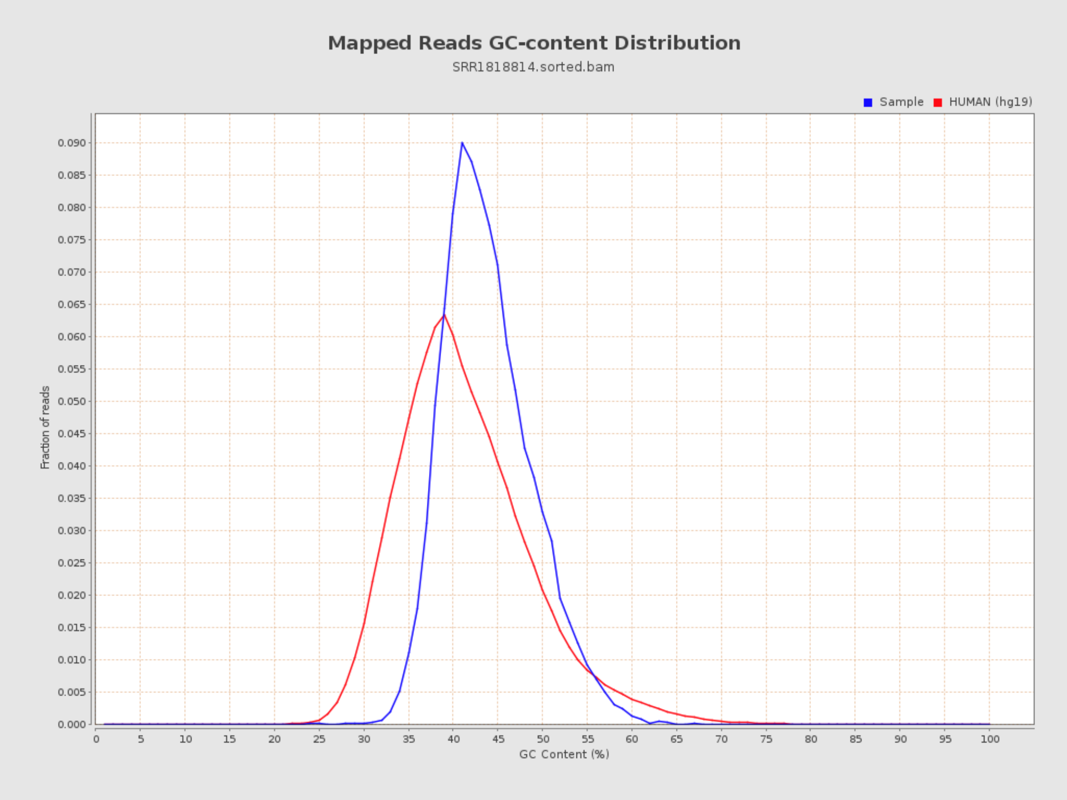
7. Results : Duplication Rate Histogram



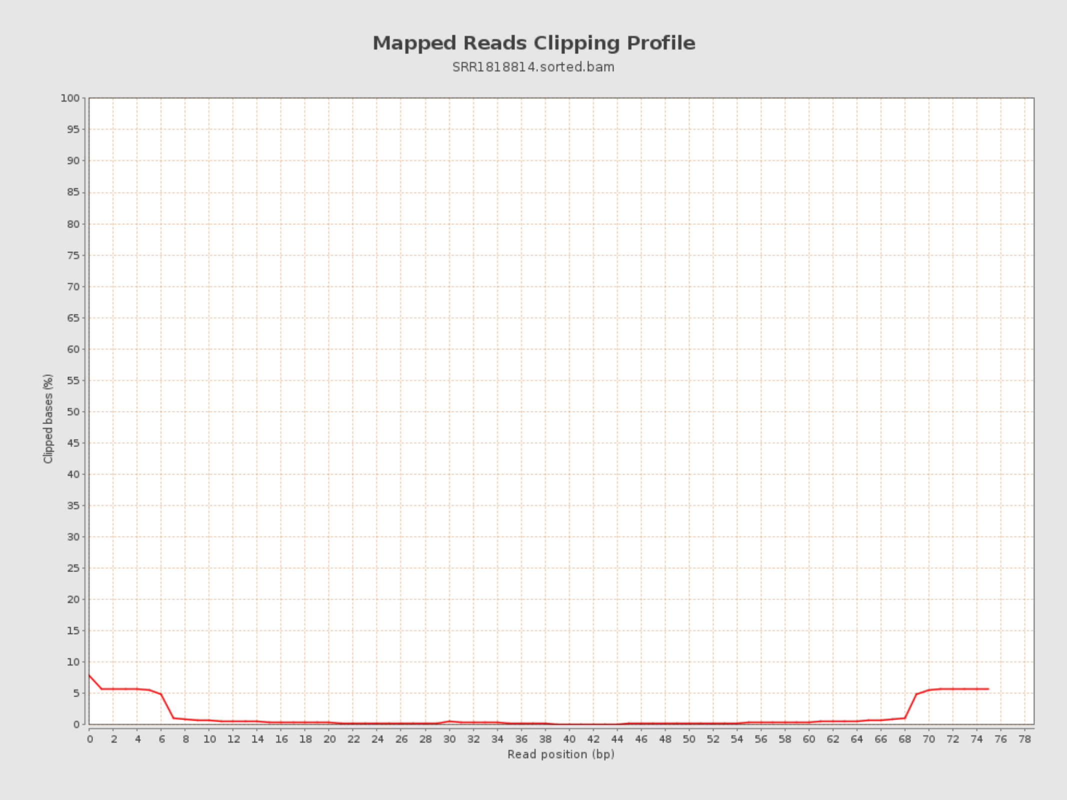
8. Results : Mapped Reads Nucleotide Content



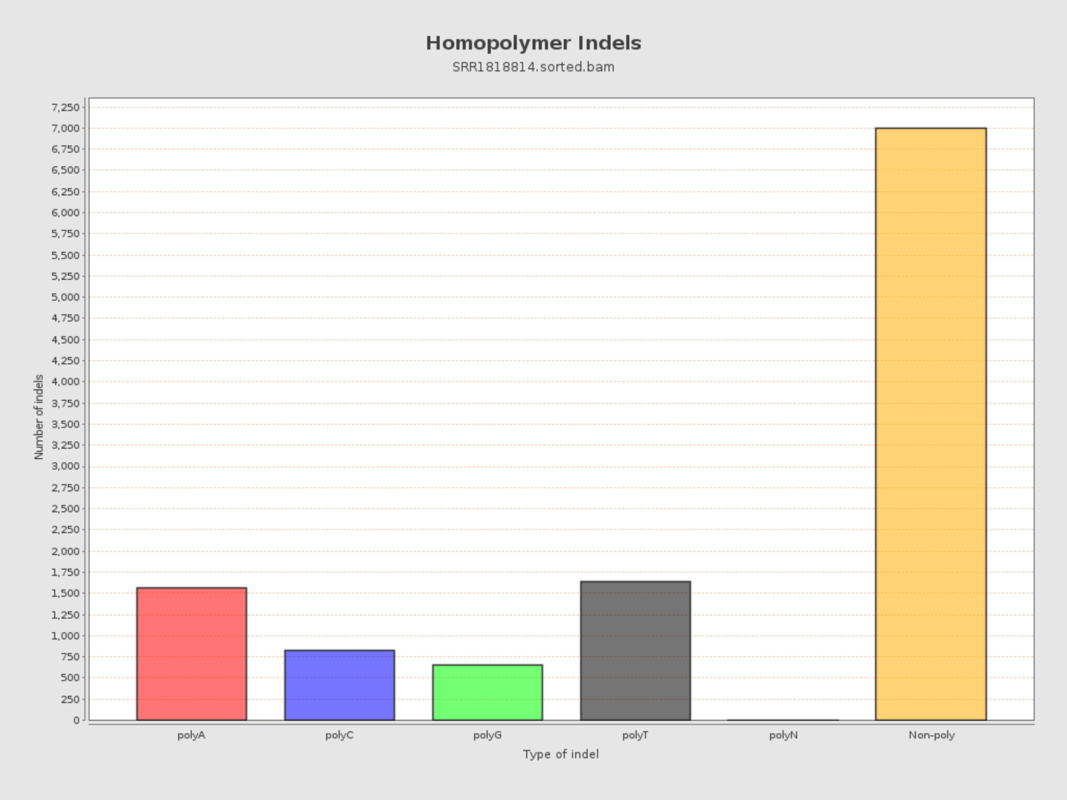
9. Results : Mapped Reads GC-content Distribution



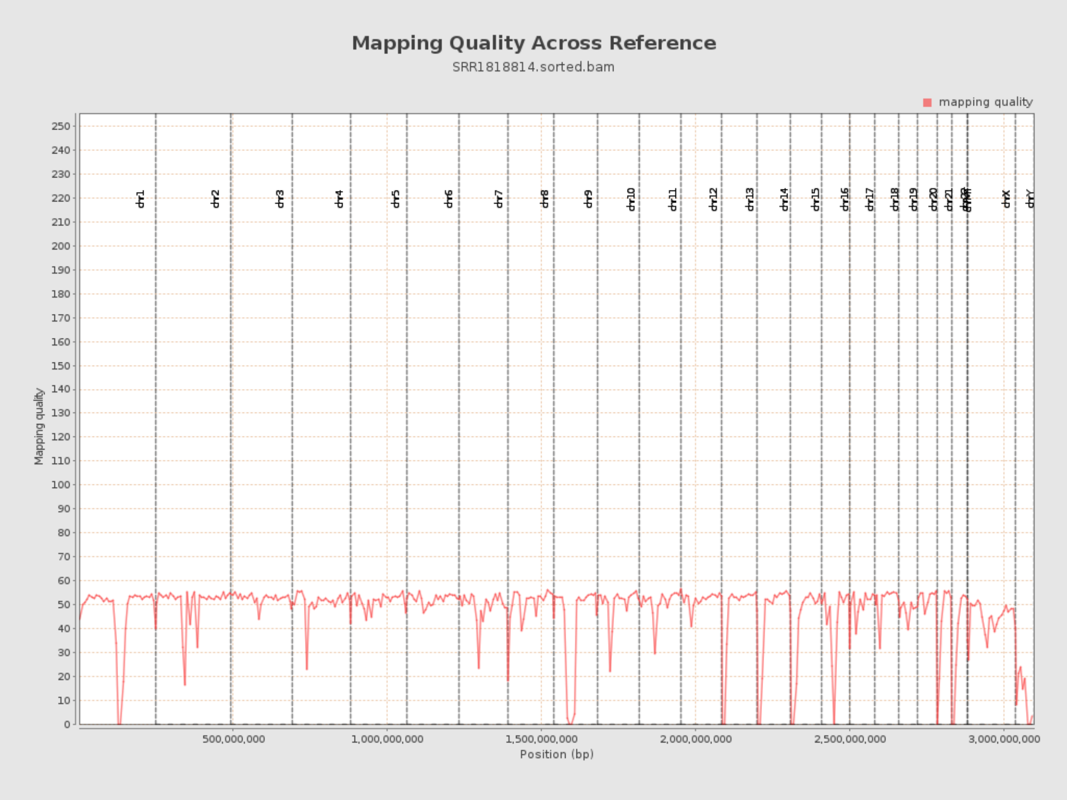
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram