Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:04:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818932.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_SRR1818932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:04:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	668,107
Mapped reads	658,892 / 98.62%
Unmapped reads	9,215 / 1.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,774 / 1.16%
Read min/max/mean length	30 / 101 / 101.45
Duplicated reads (estimated)	155,975 / 23.35%
Duplication rate	20.83%
Clipped reads	666,055 / 99.69%

2.2. ACGT Content

Number/percentage of A's	17,089,903 / 27.99%
Number/percentage of C's	13,189,920 / 21.6%
Number/percentage of T's	17,159,526 / 28.1%
Number/percentage of G's	13,624,790 / 22.31%
Number/percentage of N's	2,581 / 0%
GC Percentage	43.91%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2466

2.4. Mapping Quality

Mean Mapping Quality	49.3

2.5. Mismatches and indels

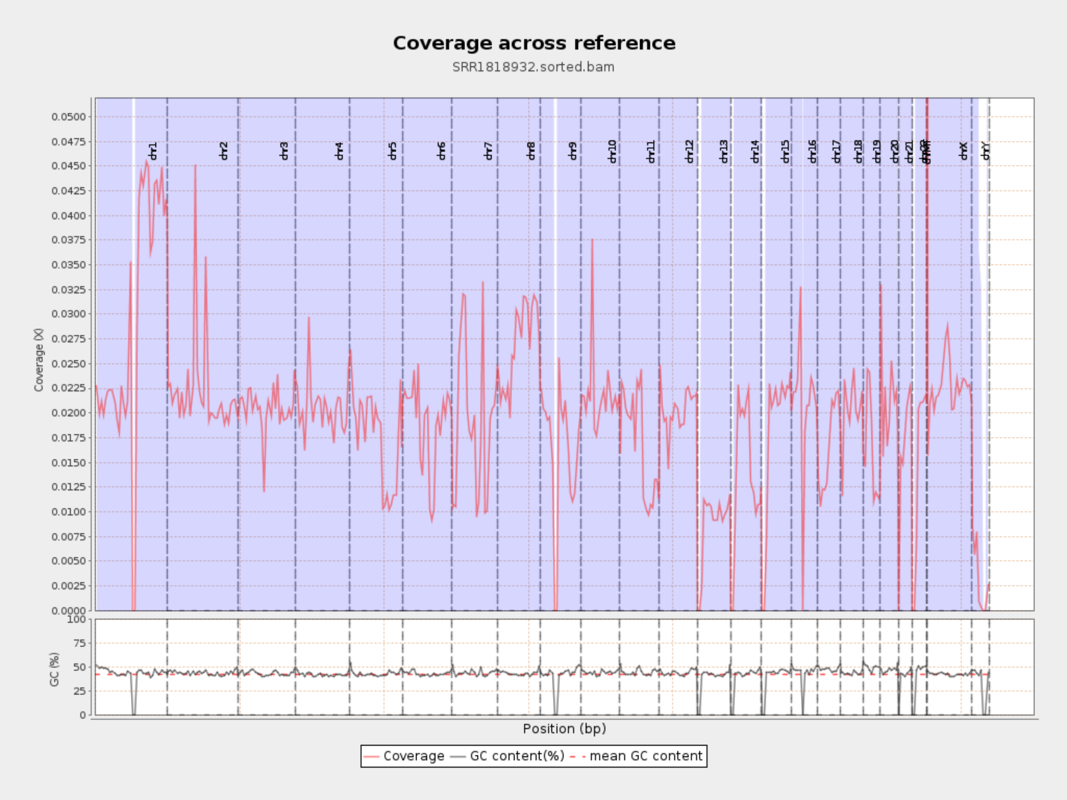
General error rate	0.65%
Mismatches	381,741
Insertions	6,647
Mapped reads with at least one insertion	0.98%
Deletions	18,139
Mapped reads with at least one deletion	2.69%
Homopolymer indels	42.76%

2.6. Chromosome stats

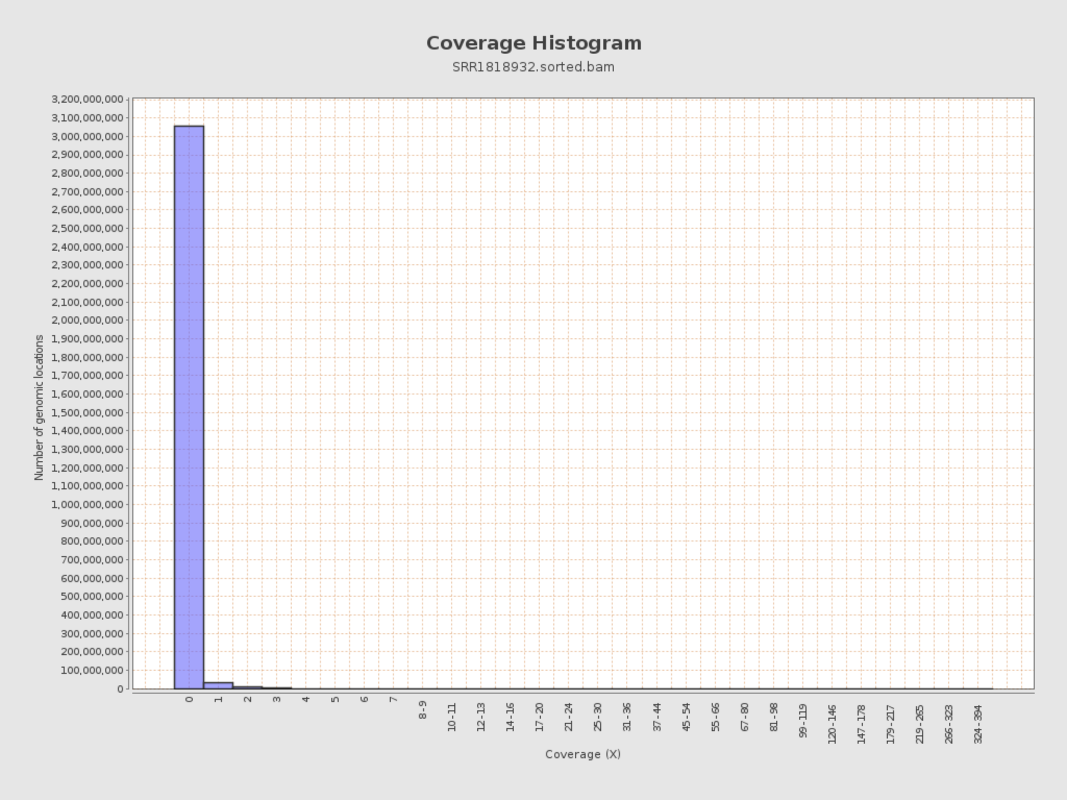
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7229779	0.029	0.389
chr2	243199373	5399944	0.0222	0.3194
chr3	198022430	4030781	0.0204	0.1954
chr4	191154276	3947803	0.0207	0.2051
chr5	180915260	3153970	0.0174	0.1831
chr6	171115067	3236525	0.0189	0.1978
chr7	159138663	3062271	0.0192	0.2246

chr8	146364022	3952563	0.027	0.2397
chr9	141213431	2265246	0.016	0.2619
chr10	135534747	2982985	0.022	0.2831
chr11	135006516	2319260	0.0172	0.1941
chr12	133851895	2717408	0.0203	0.1986
chr13	115169878	982673	0.0085	0.1253
chr14	107349540	1494130	0.0139	0.1695
chr15	102531392	1814431	0.0177	0.1832
chr16	90354753	1862455	0.0206	0.2691
chr17	81195210	1340242	0.0165	0.1847
chr18	78077248	1561632	0.02	0.3365
chr19	59128983	974329	0.0165	0.3144
chr20	63025520	1347472	0.0214	0.2088
chr21	48129895	816021	0.017	0.185
chr22	51304566	744298	0.0145	0.1723
chrMT	16571	146903	8.8651	6.7835
chrX	155270560	3536122	0.0228	0.2256
chrY	59373566	180011	0.003	0.1708

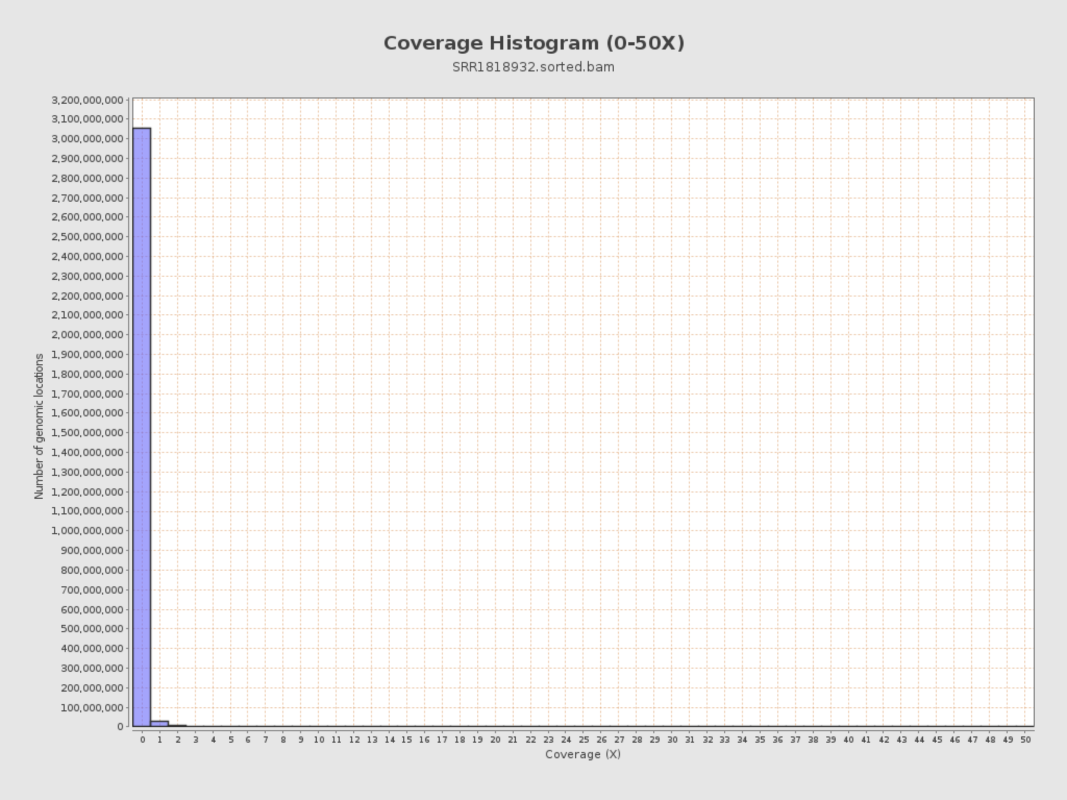
3. Results : Coverage across reference



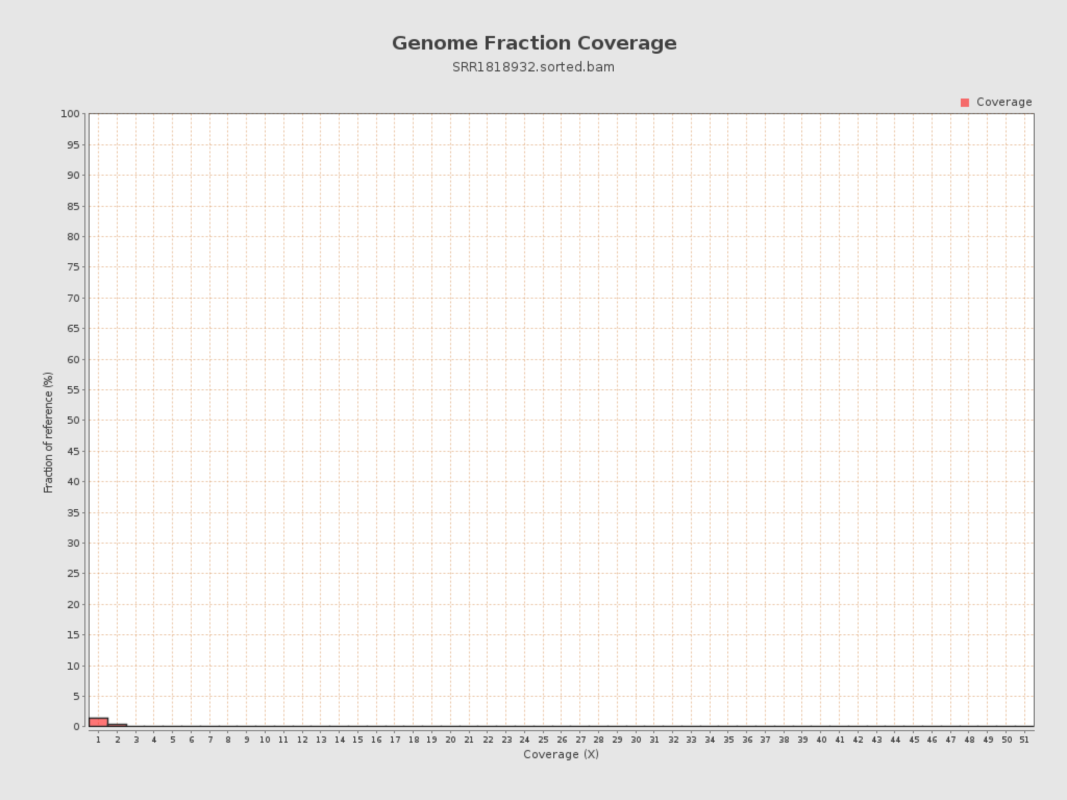
4. Results : Coverage Histogram



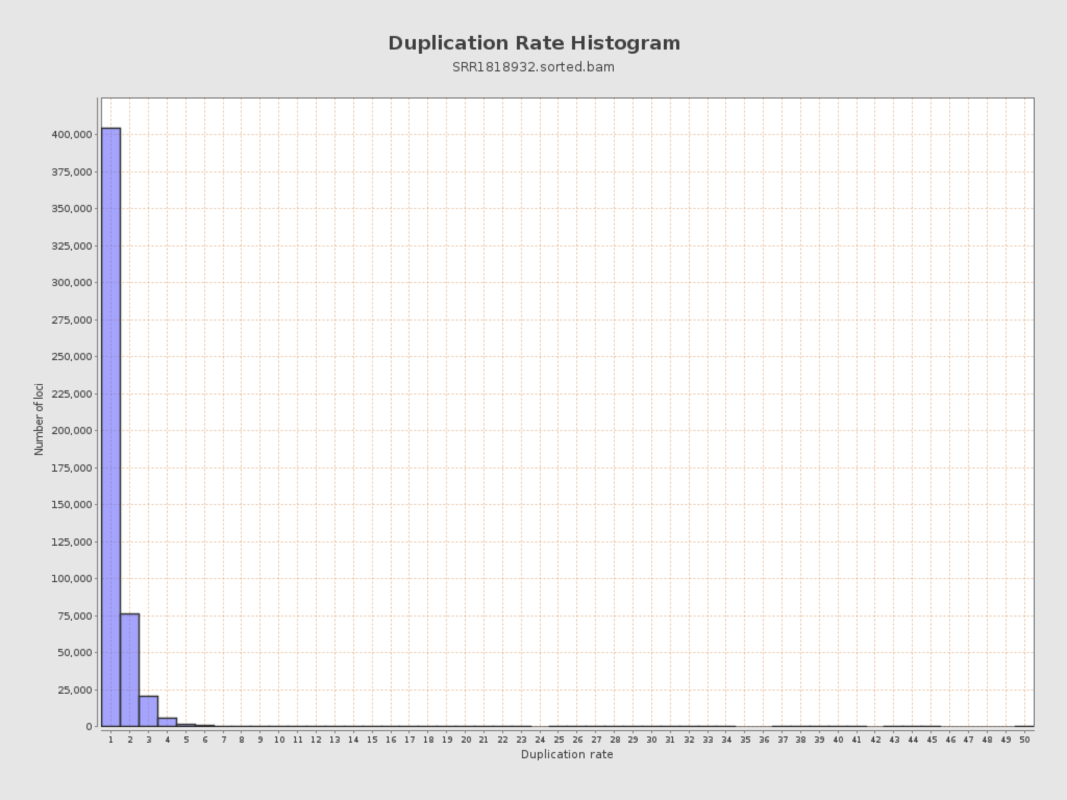
5. Results : Coverage Histogram (0-50X)



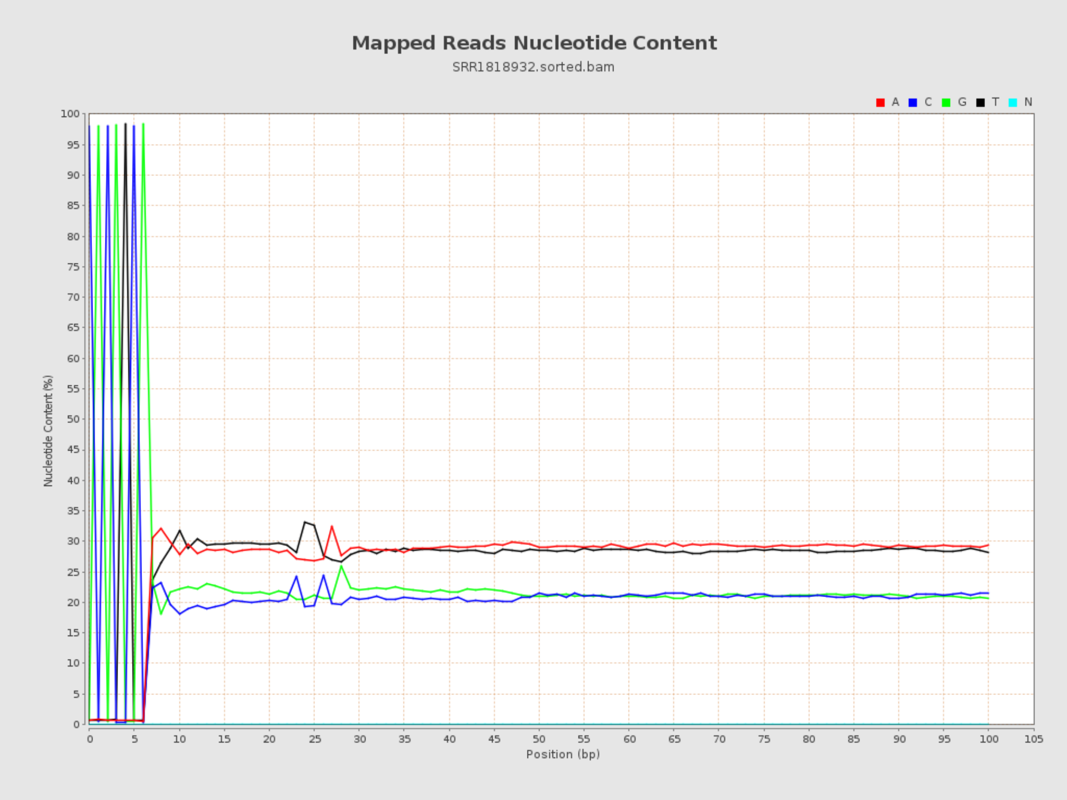
6. Results : Genome Fraction Coverage



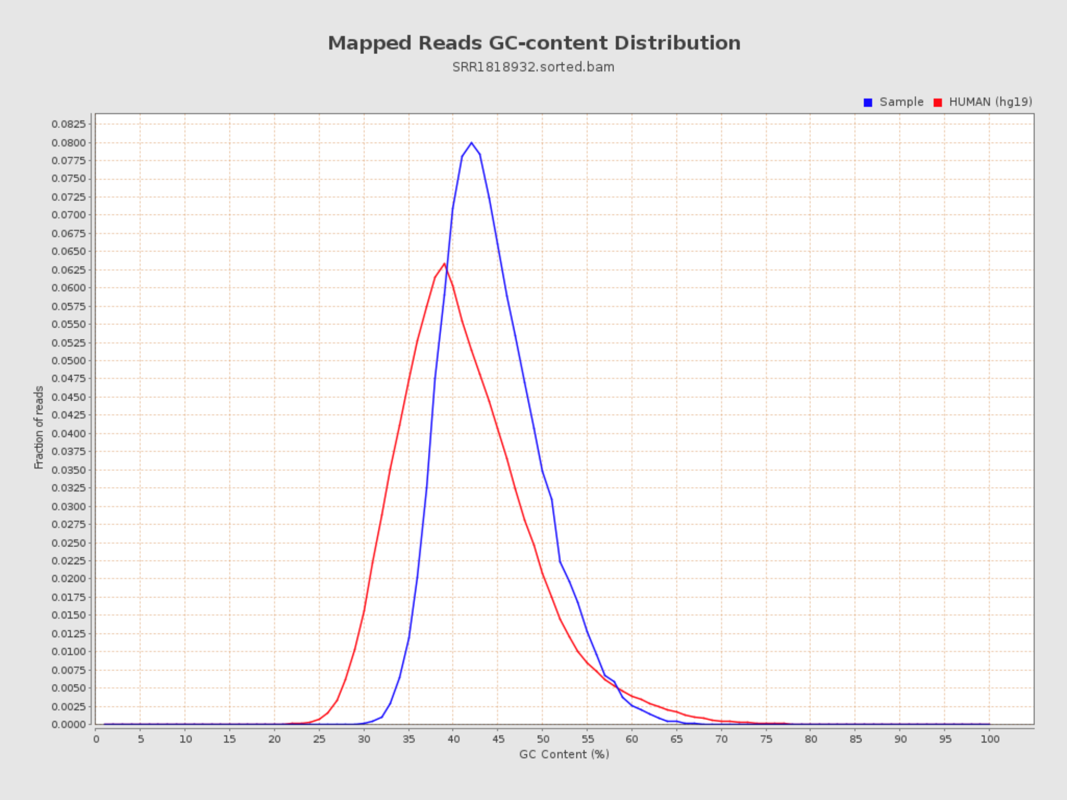
7. Results : Duplication Rate Histogram



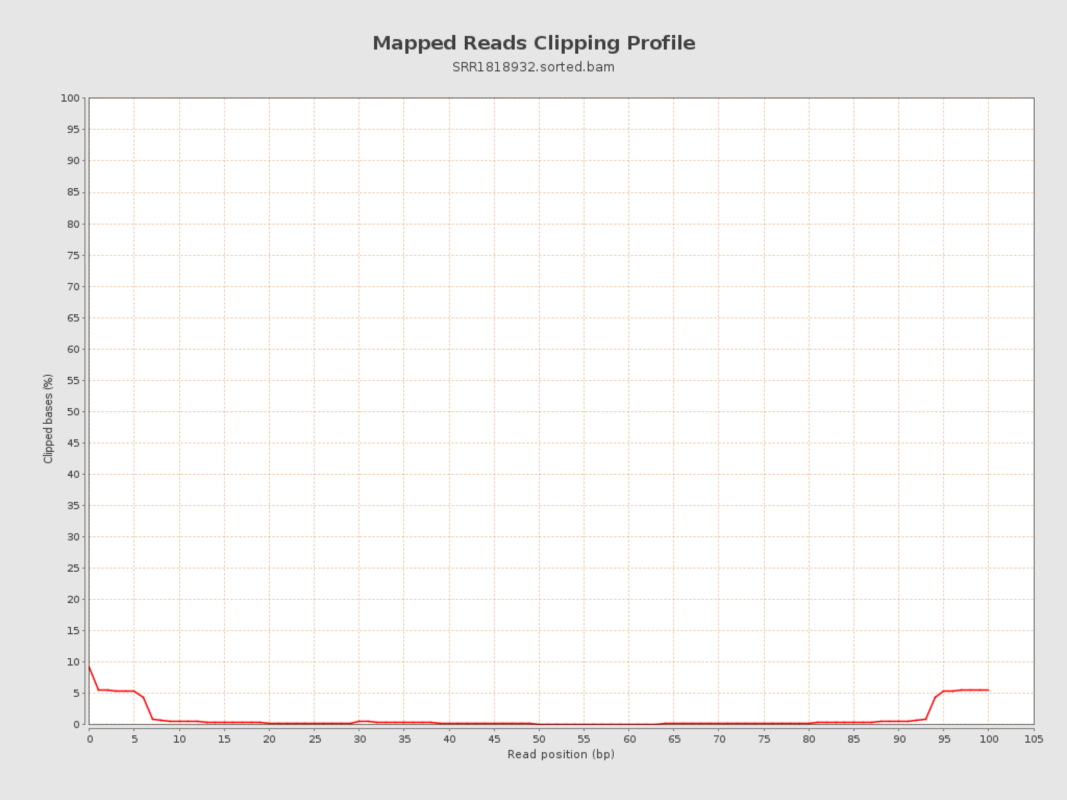
8. Results : Mapped Reads Nucleotide Content



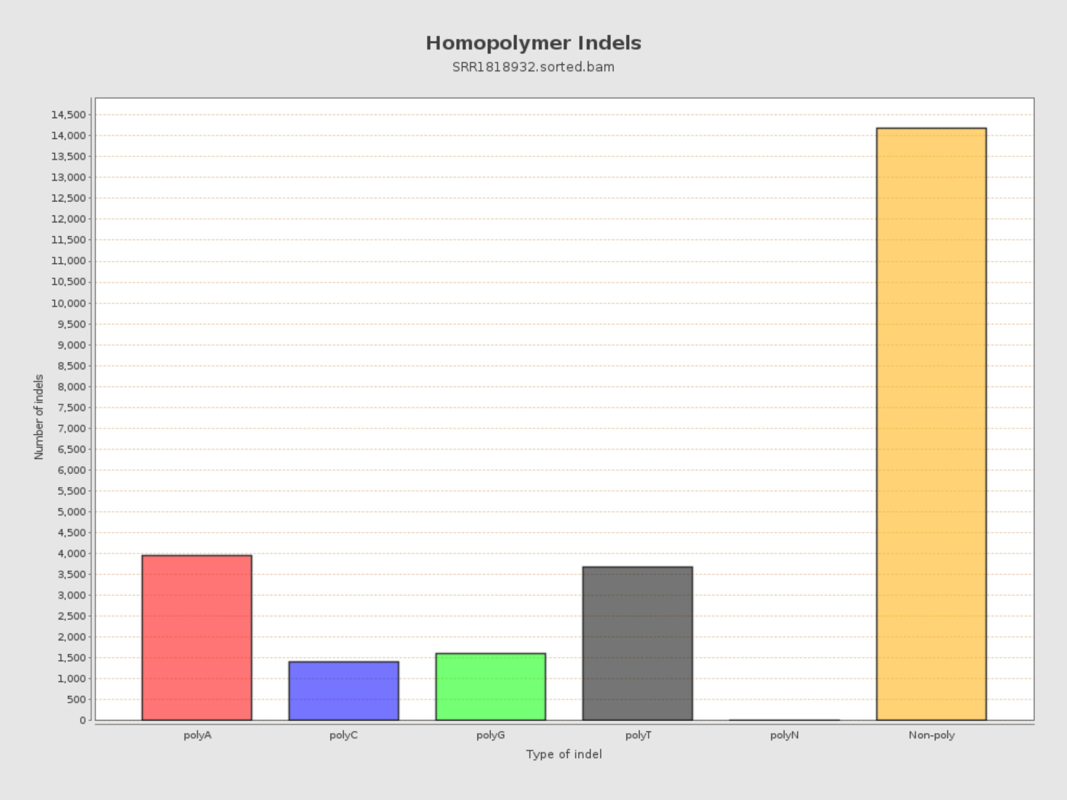
9. Results : Mapped Reads GC-content Distribution



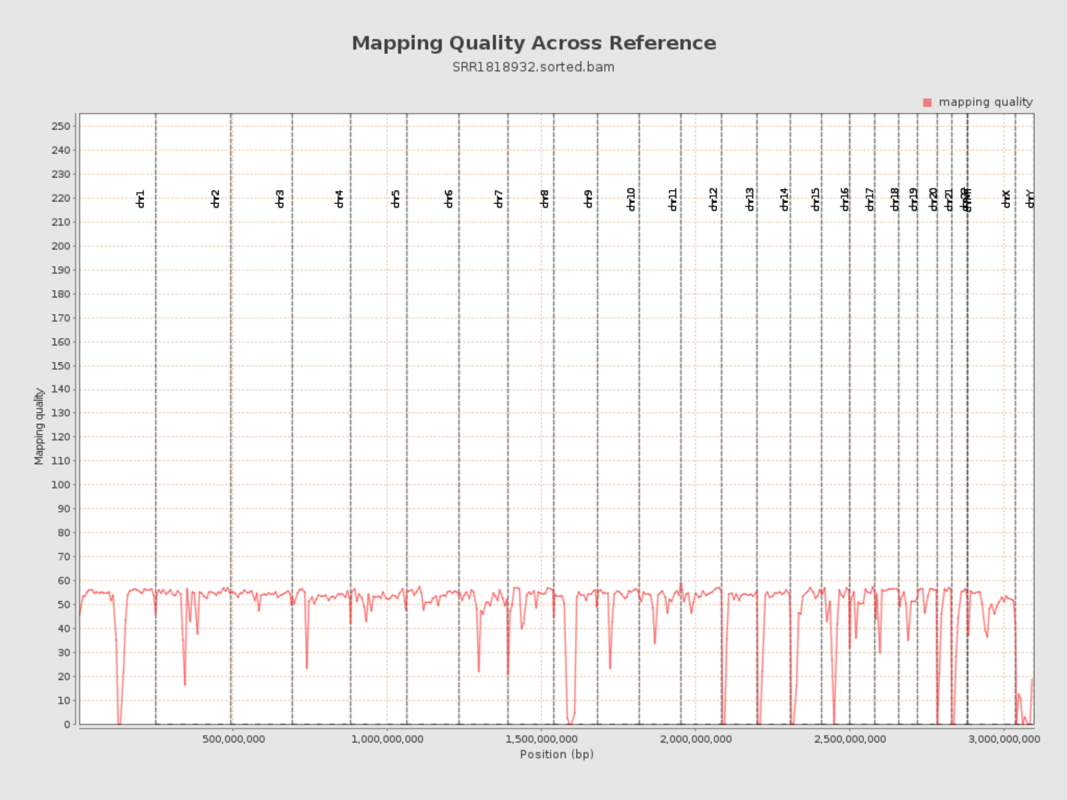
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram