Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:35:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506018.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_SRR1506018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:35:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,445,379
Mapped reads	1,049,401 / 72.6%
Unmapped reads	395,978 / 27.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	29,087 / 2.01%
Duplication rate	2.19%
Clipped reads	165,359 / 11.44%

2.2. ACGT Content

Number/percentage of A's	14,315,872 / 29.36%
Number/percentage of C's	10,068,161 / 20.65%
Number/percentage of T's	14,066,845 / 28.85%
Number/percentage of G's	10,154,313 / 20.82%
Number/percentage of N's	160,426 / 0.33%
GC Percentage	41.47%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1846

2.4. Mapping Quality

Mean Mapping Quality	44.24

2.5. Mismatches and indels

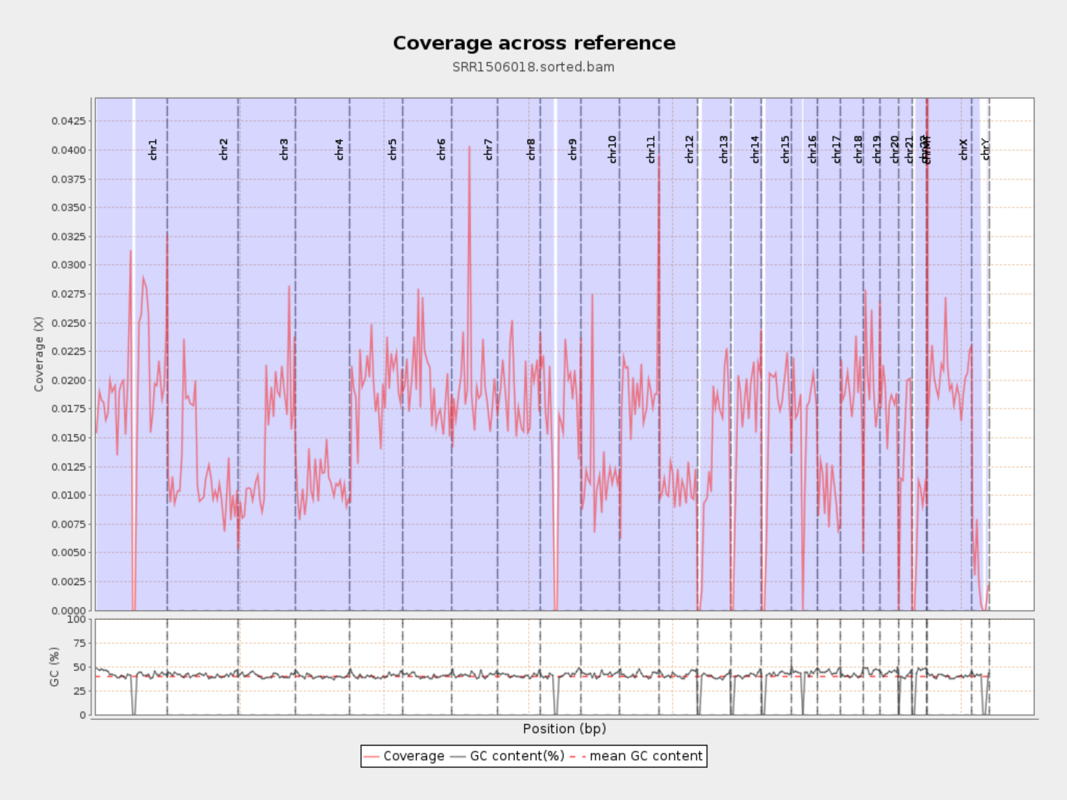
General error rate	0.81%
Mismatches	390,787
Insertions	2,080
Mapped reads with at least one insertion	0.2%
Deletions	7,016
Mapped reads with at least one deletion	0.67%
Homopolymer indels	45.94%

2.6. Chromosome stats

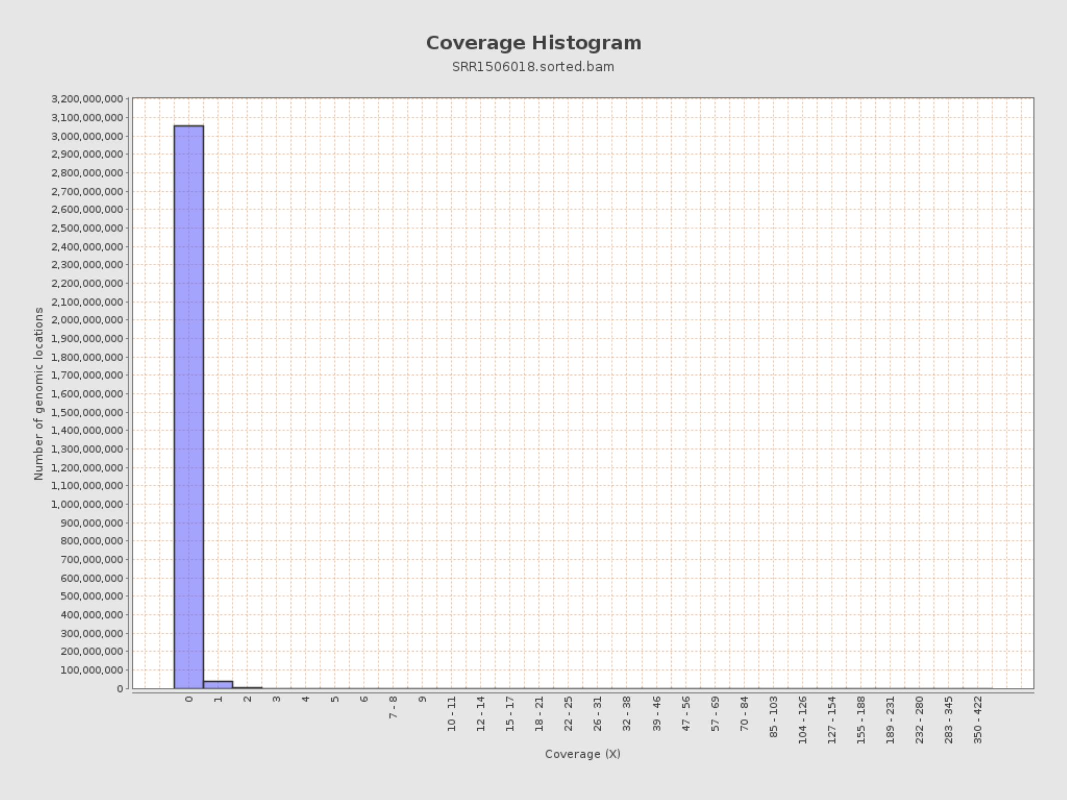
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4737263	0.019	0.3182
chr2	243199373	2932051	0.0121	0.144
chr3	198022430	2912199	0.0147	0.1323
chr4	191154276	2097283	0.011	0.1168
chr5	180915260	3570004	0.0197	0.1535
chr6	171115067	3375355	0.0197	0.1707
chr7	159138663	3154210	0.0198	0.3175

chr8	146364022	2762251	0.0189	0.2076
chr9	141213431	2309868	0.0164	0.1541
chr10	135534747	1592428	0.0117	0.1687
chr11	135006516	2525700	0.0187	0.1761
chr12	133851895	1433834	0.0107	0.1167
chr13	115169878	1541123	0.0134	0.1253
chr14	107349540	1710093	0.0159	0.1527
chr15	102531392	1616798	0.0158	0.1364
chr16	90354753	1457670	0.0161	0.1435
chr17	81195210	814986	0.01	0.1171
chr18	78077248	1519369	0.0195	0.2147
chr19	59128983	1201486	0.0203	0.2636
chr20	63025520	1132535	0.018	0.1476
chr21	48129895	688804	0.0143	0.1381
chr22	51304566	381851	0.0074	0.0932
chrMT	16571	17098	1.0318	1.1335
chrX	155270560	3131273	0.0202	0.1665
chrY	59373566	159837	0.0027	0.0694

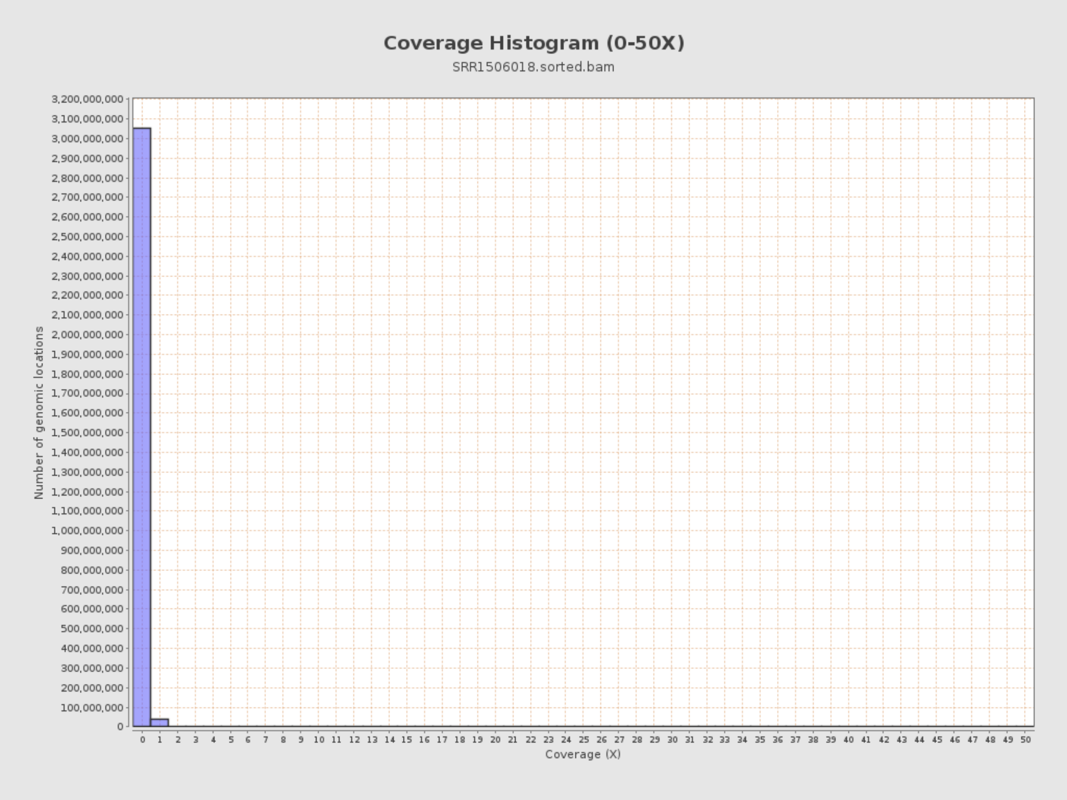
3. Results : Coverage across reference



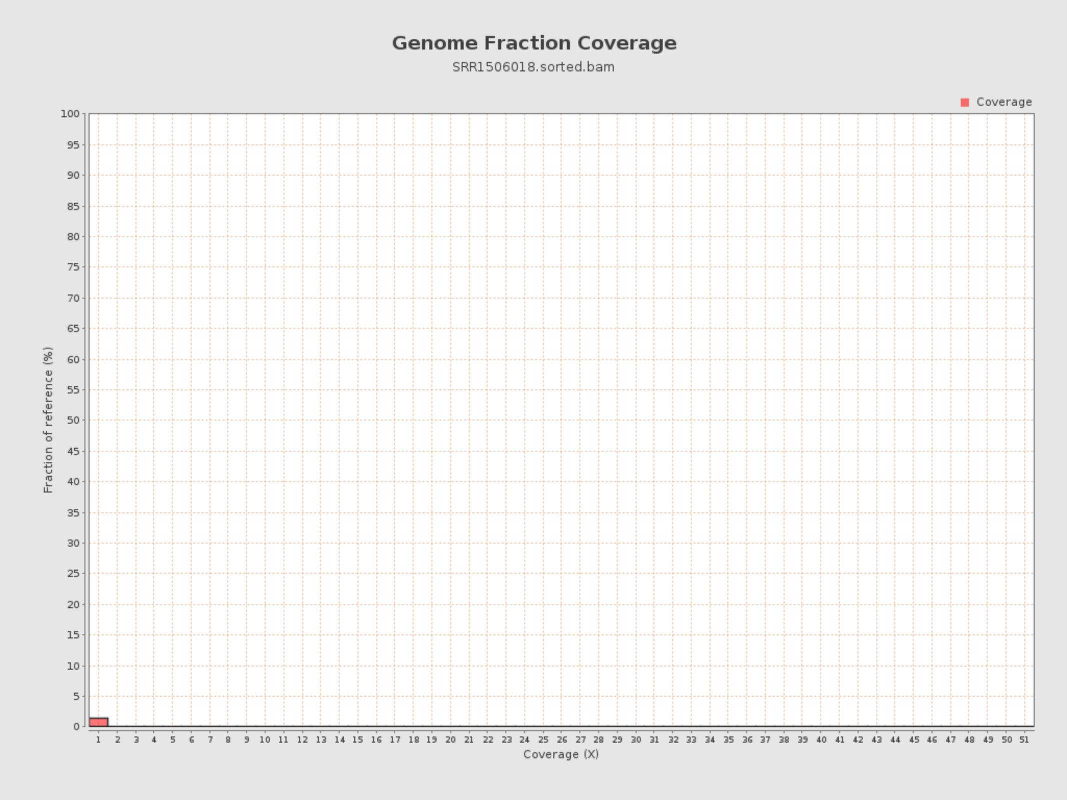
4. Results : Coverage Histogram



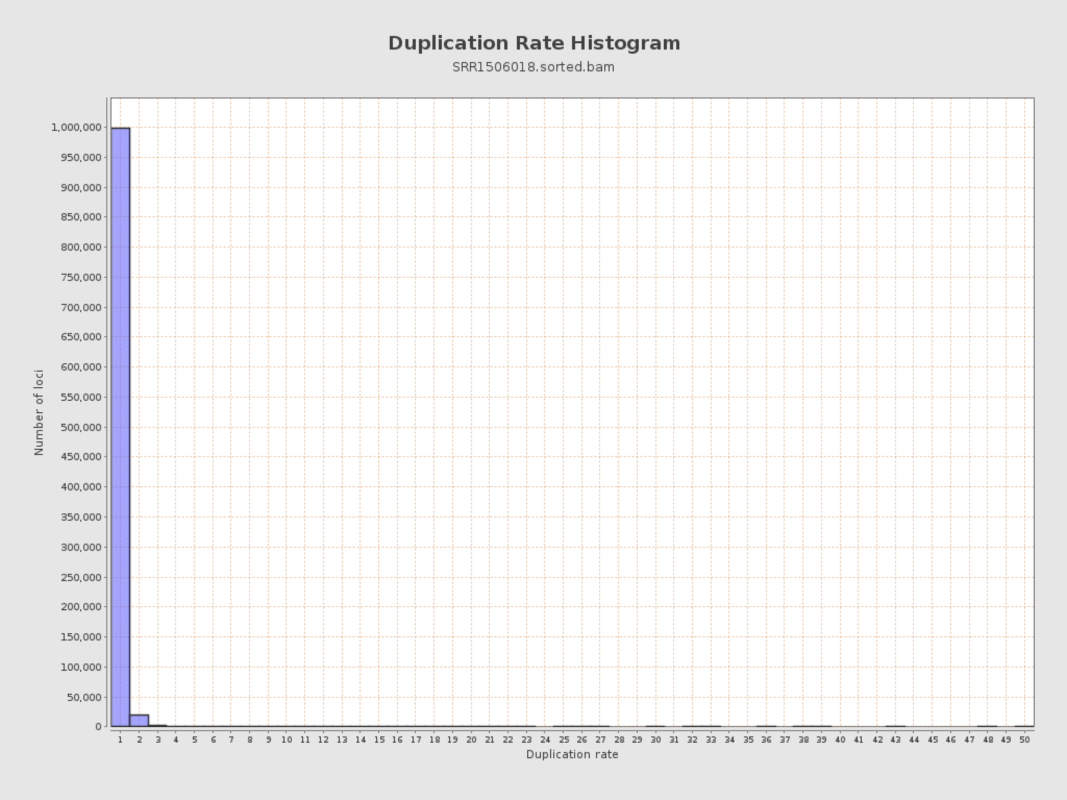
5. Results : Coverage Histogram (0-50X)



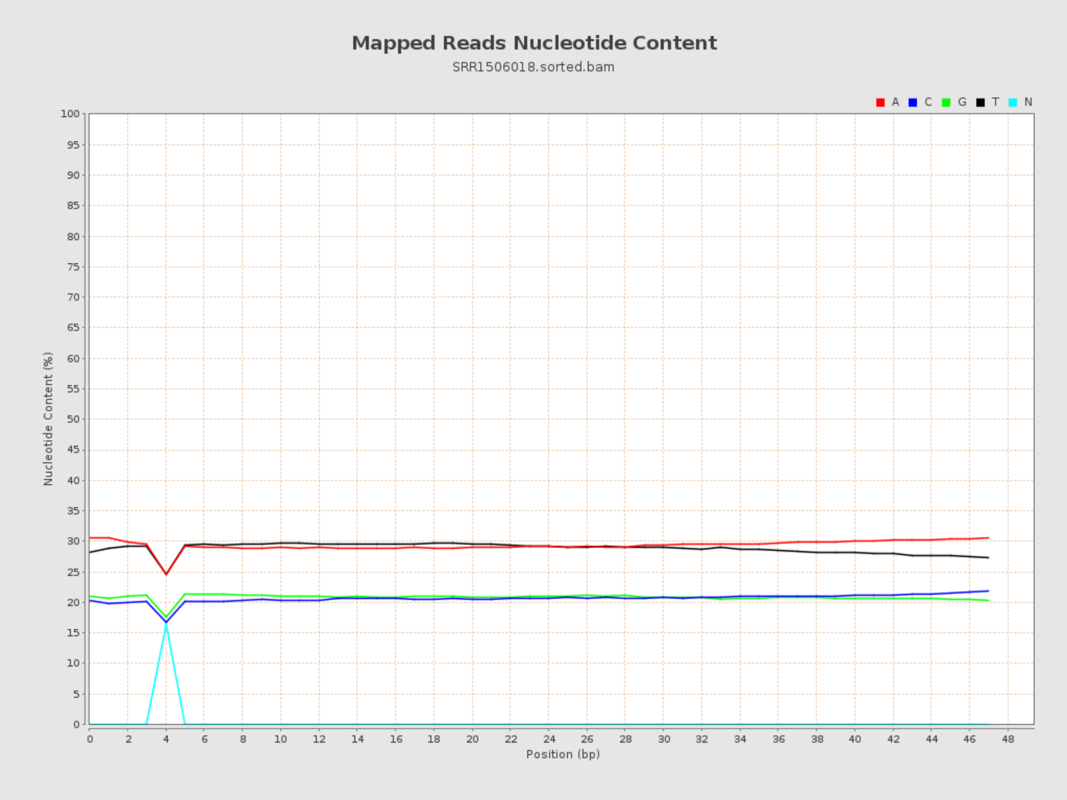
6. Results : Genome Fraction Coverage



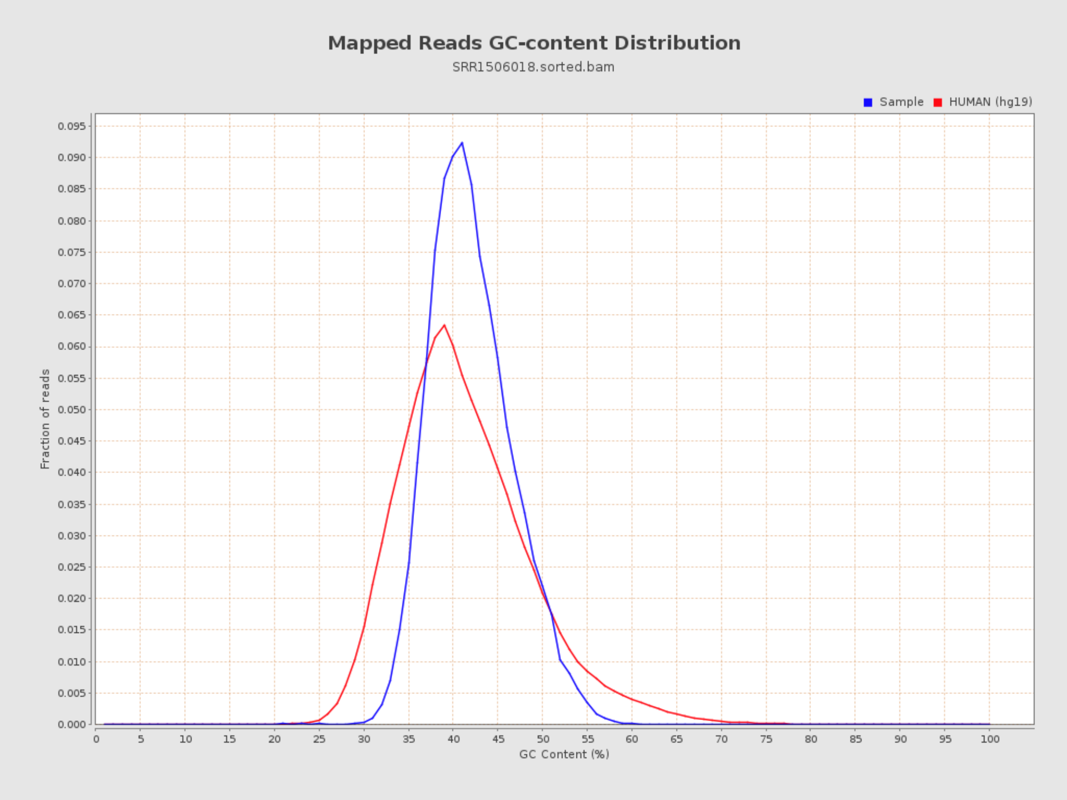
7. Results : Duplication Rate Histogram



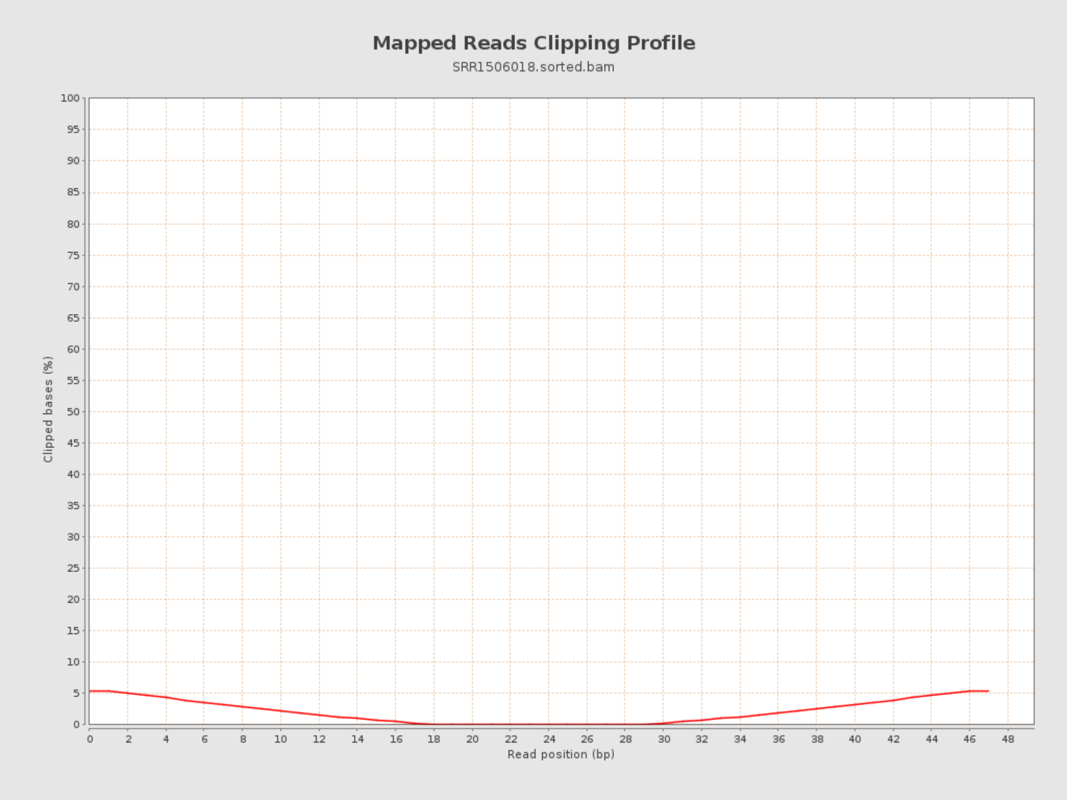
8. Results : Mapped Reads Nucleotide Content



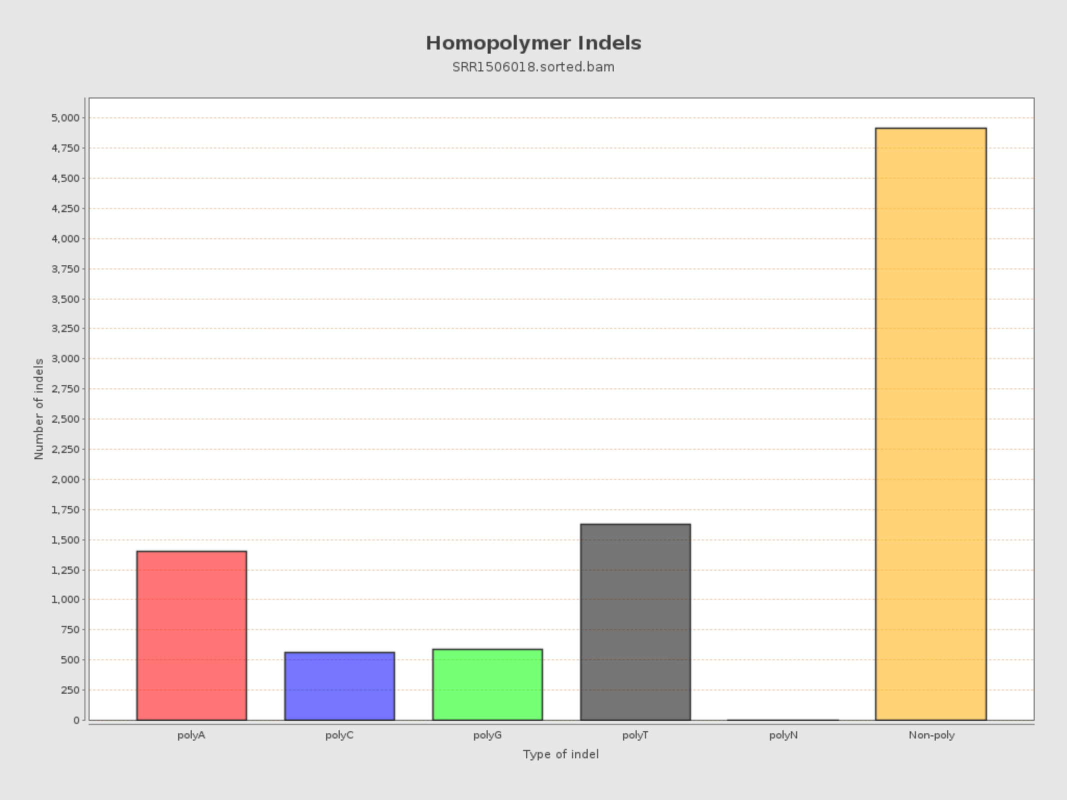
9. Results : Mapped Reads GC-content Distribution



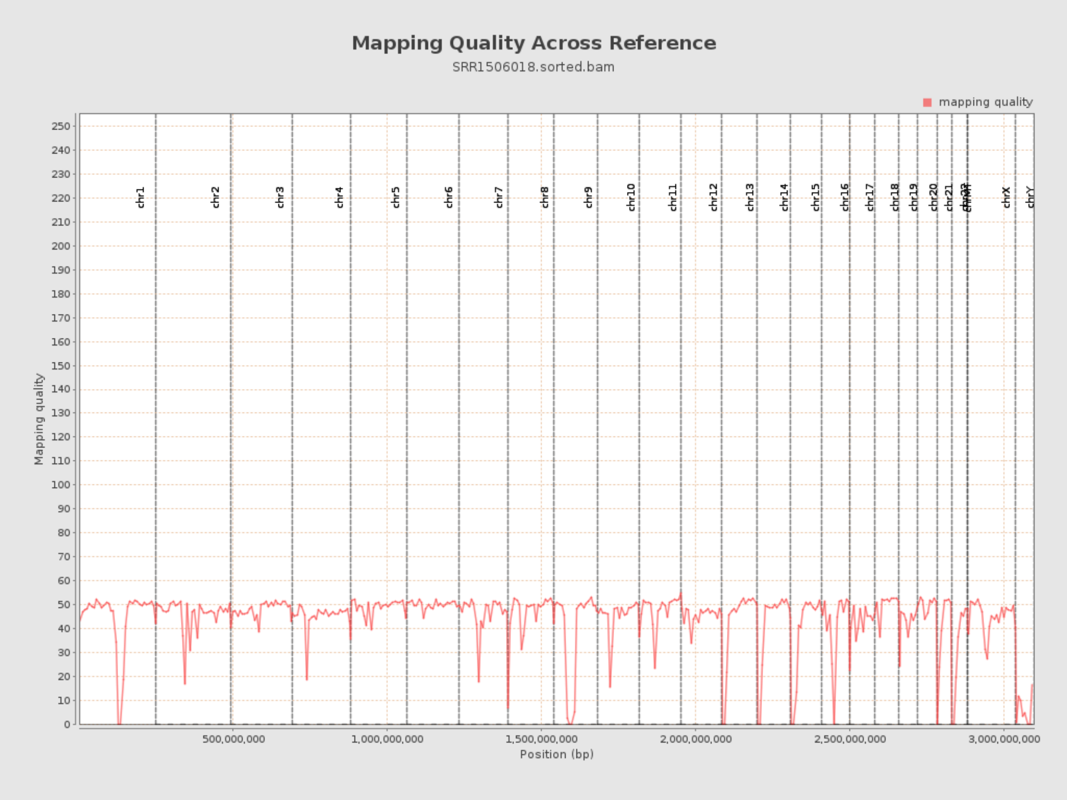
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram