Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:31:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506017.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_SRR1506017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:31:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,160,001
Mapped reads	4,443,933 / 72.14%
Unmapped reads	1,716,068 / 27.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	254 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	219,523 / 3.56%
Duplication rate	3.6%
Clipped reads	681,550 / 11.06%

2.2. ACGT Content

Number/percentage of A's	60,830,411 / 29.43%
Number/percentage of C's	42,425,314 / 20.53%
Number/percentage of T's	59,877,291 / 28.97%
Number/percentage of G's	42,910,766 / 20.76%
Number/percentage of N's	645,217 / 0.31%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0668

Standard Deviation	0.6102

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

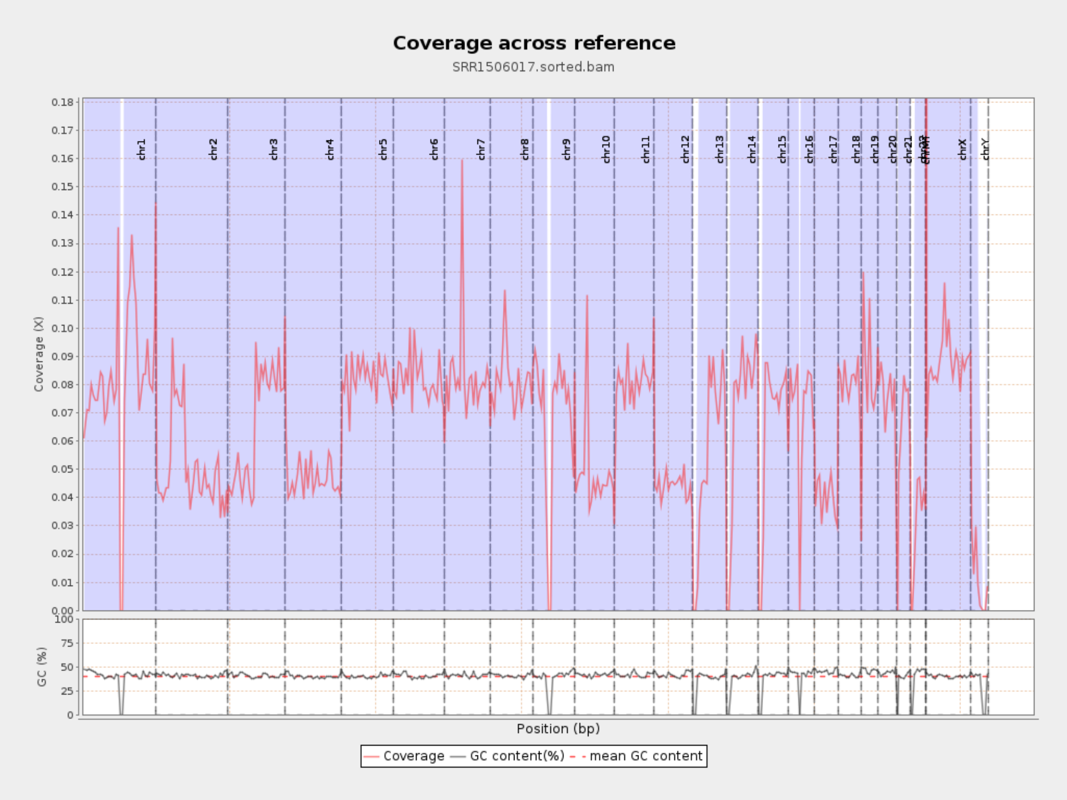
General error rate	0.79%
Mismatches	1,614,718
Insertions	8,986
Mapped reads with at least one insertion	0.2%
Deletions	30,340
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.26%

2.6. Chromosome stats

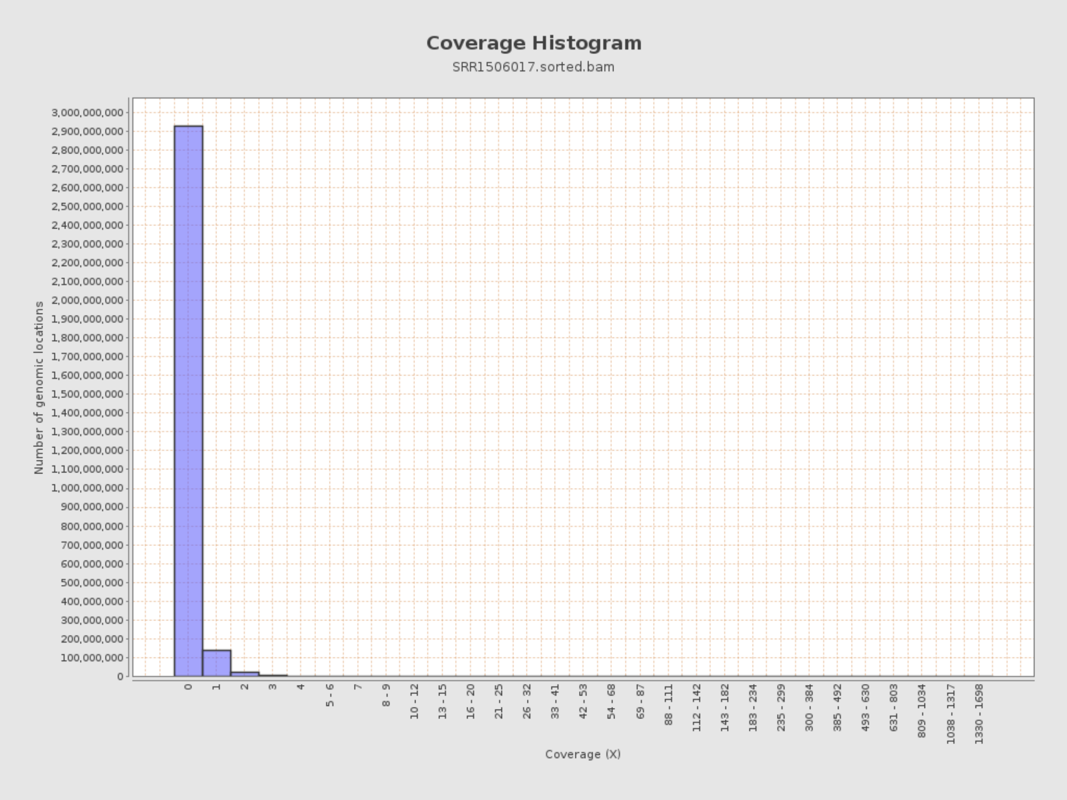
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20298809	0.0814	1.1955
chr2	243199373	12402097	0.051	0.4322
chr3	198022430	12857364	0.0649	0.3064
chr4	191154276	8944846	0.0468	0.2728
chr5	180915260	14942085	0.0826	0.3494
chr6	171115067	14032211	0.082	0.4353
chr7	159138663	13254810	0.0833	1.1731

chr8	146364022	11887930	0.0812	0.6997
chr9	141213431	9611739	0.0681	0.4285
chr10	135534747	6538380	0.0482	0.5506
chr11	135006516	10819283	0.0801	0.4955
chr12	133851895	5908751	0.0441	0.2803
chr13	115169878	6545483	0.0568	0.2813
chr14	107349540	7539888	0.0702	0.9323
chr15	102531392	6576040	0.0641	0.3002
chr16	90354753	6239566	0.0691	0.3535
chr17	81195210	3265304	0.0402	0.2696
chr18	78077248	6336905	0.0812	0.7414
chr19	59128983	5027042	0.085	0.8712
chr20	63025520	4826805	0.0766	0.3455
chr21	48129895	2989370	0.0621	0.3361
chr22	51304566	1513125	0.0295	0.2026
chrMT	16571	42805	2.5831	2.2882
chrX	155270560	13700156	0.0882	0.4208
chrY	59373566	630199	0.0106	0.1738

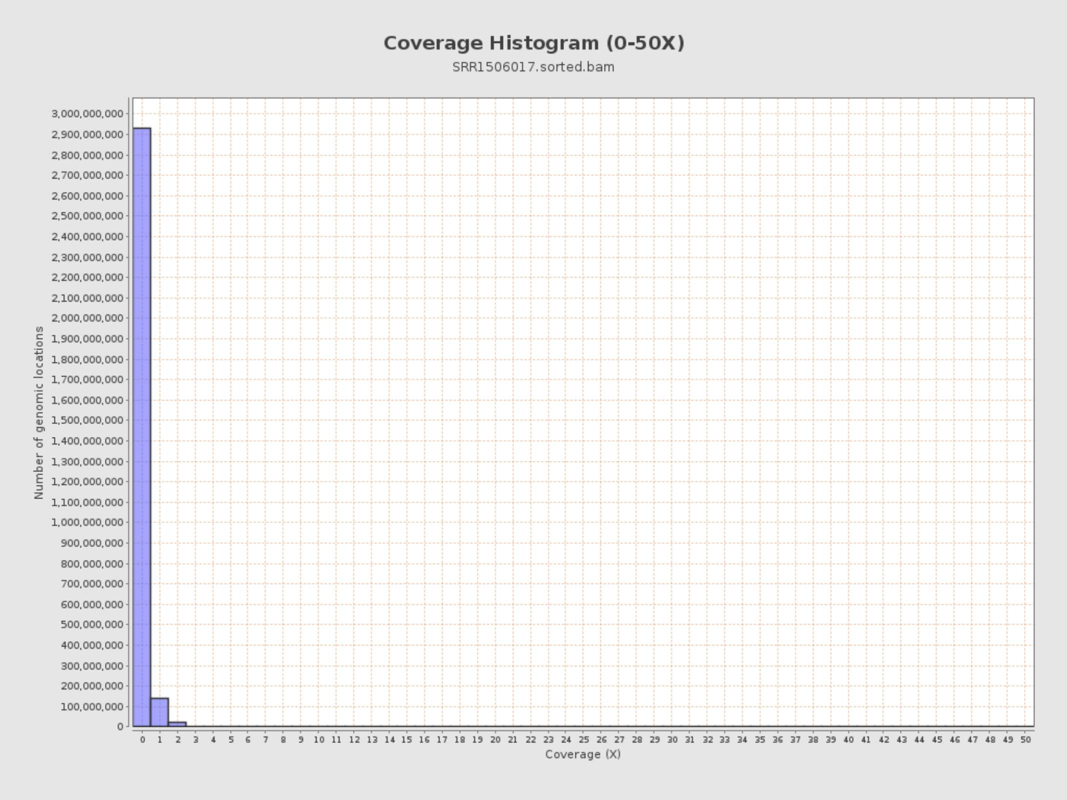
3. Results : Coverage across reference



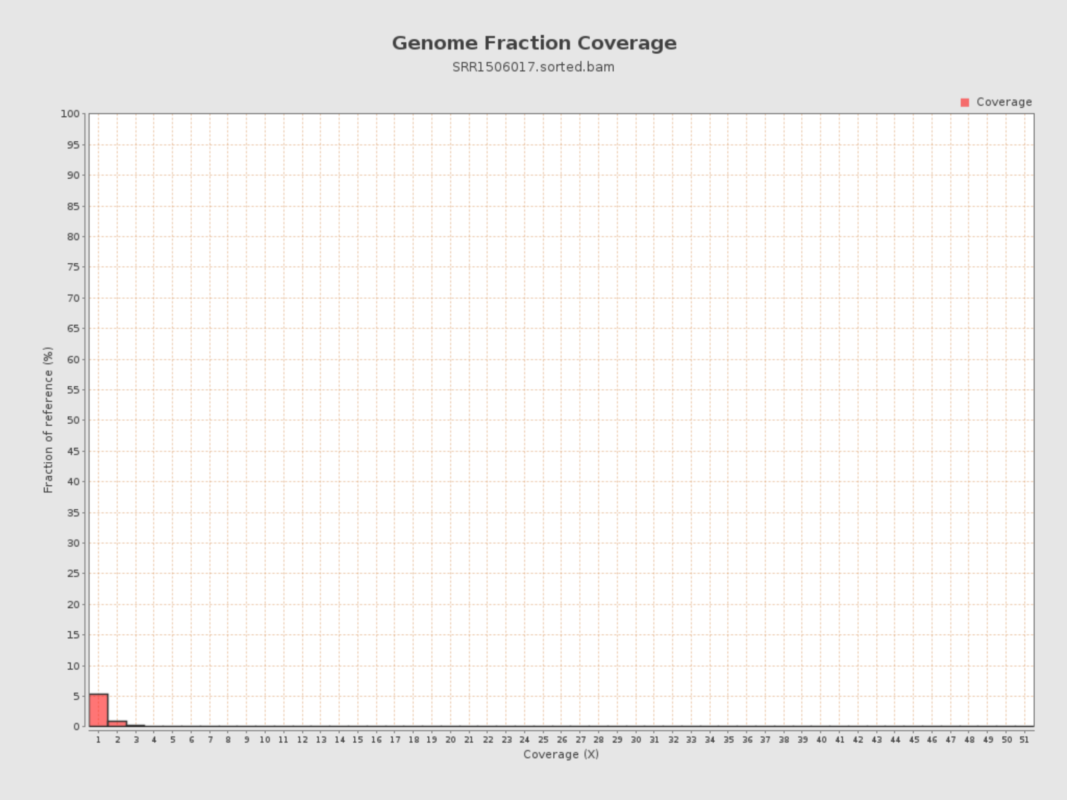
4. Results : Coverage Histogram



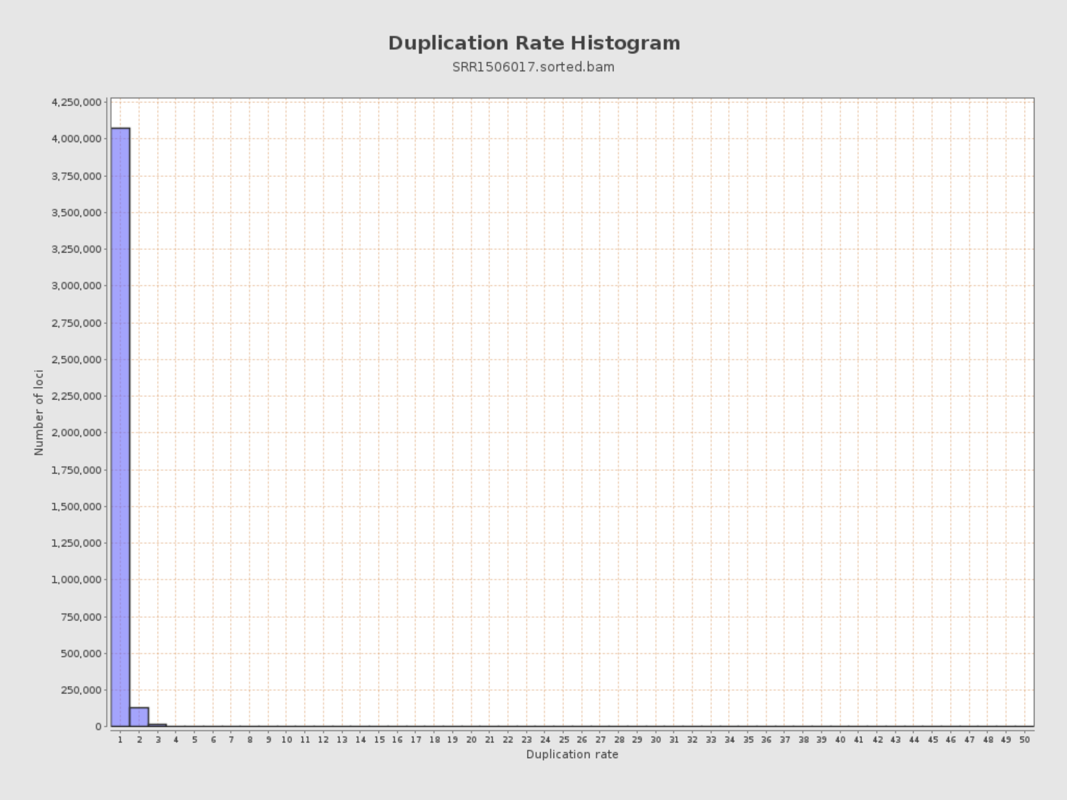
5. Results : Coverage Histogram (0-50X)



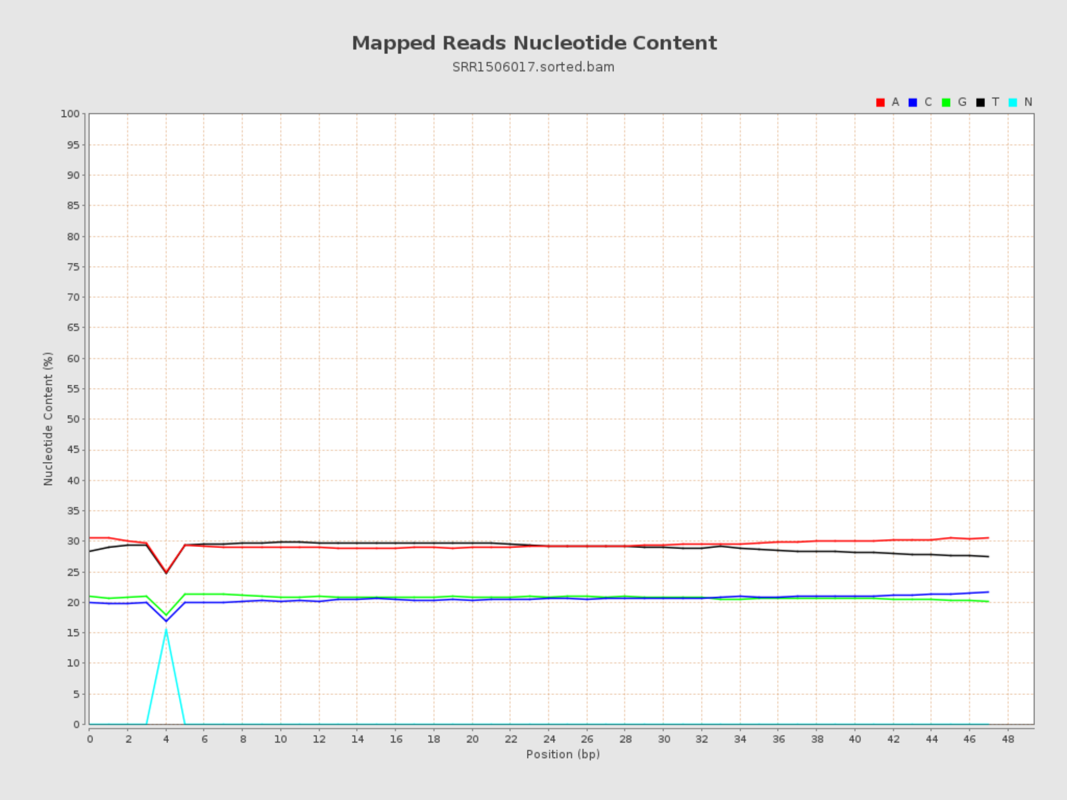
6. Results : Genome Fraction Coverage



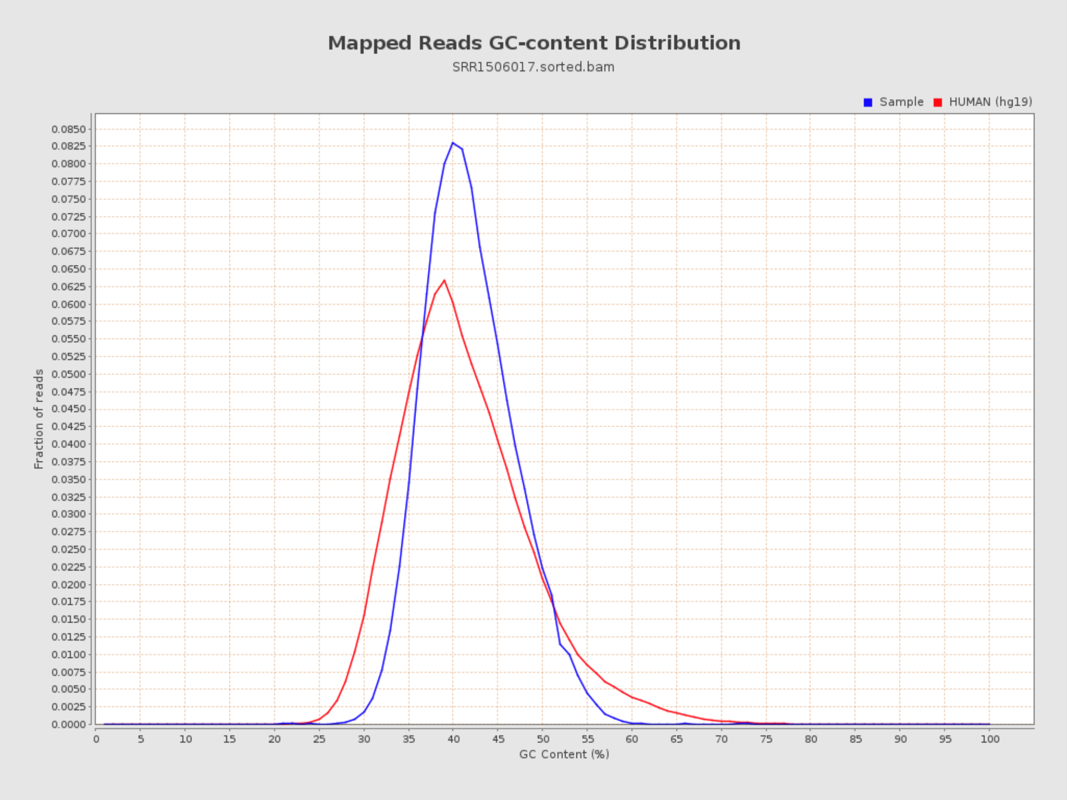
7. Results : Duplication Rate Histogram



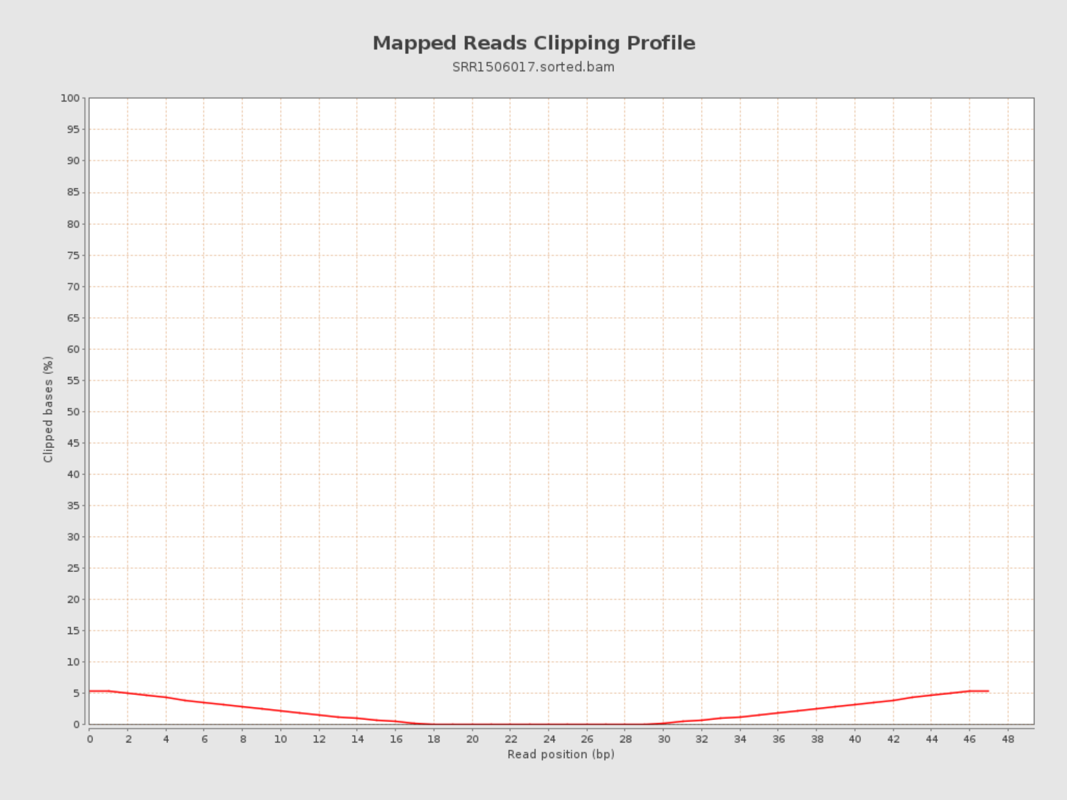
8. Results : Mapped Reads Nucleotide Content



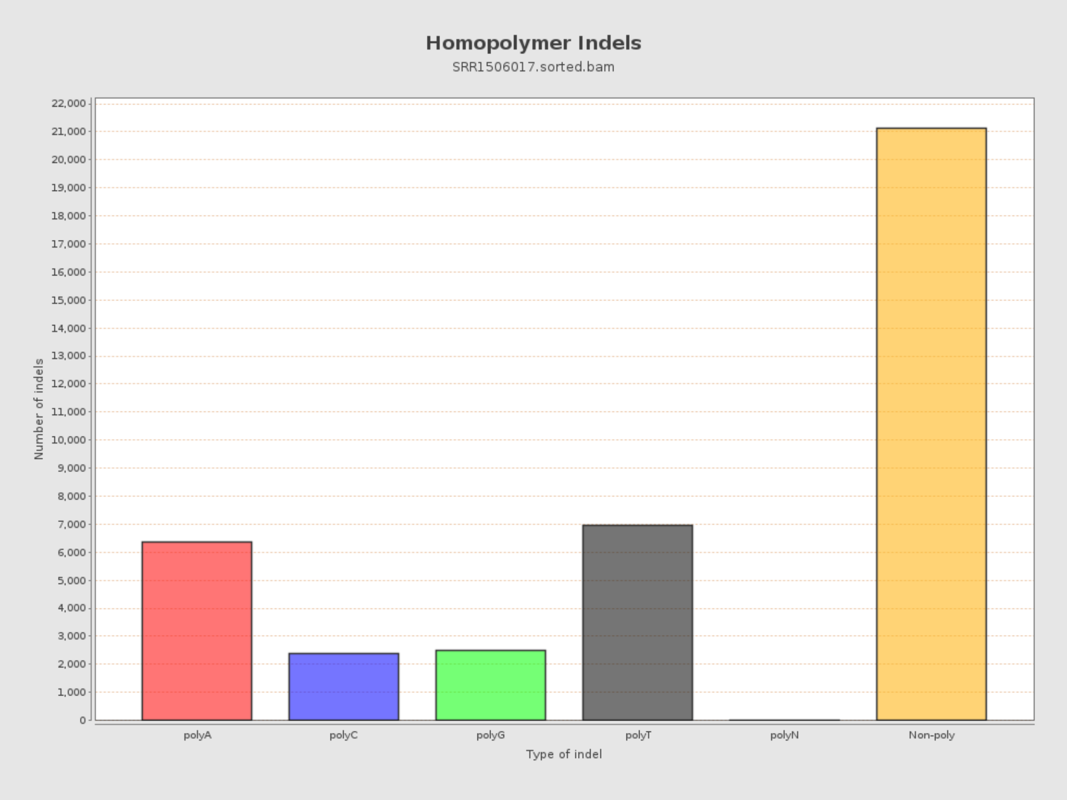
9. Results : Mapped Reads GC-content Distribution



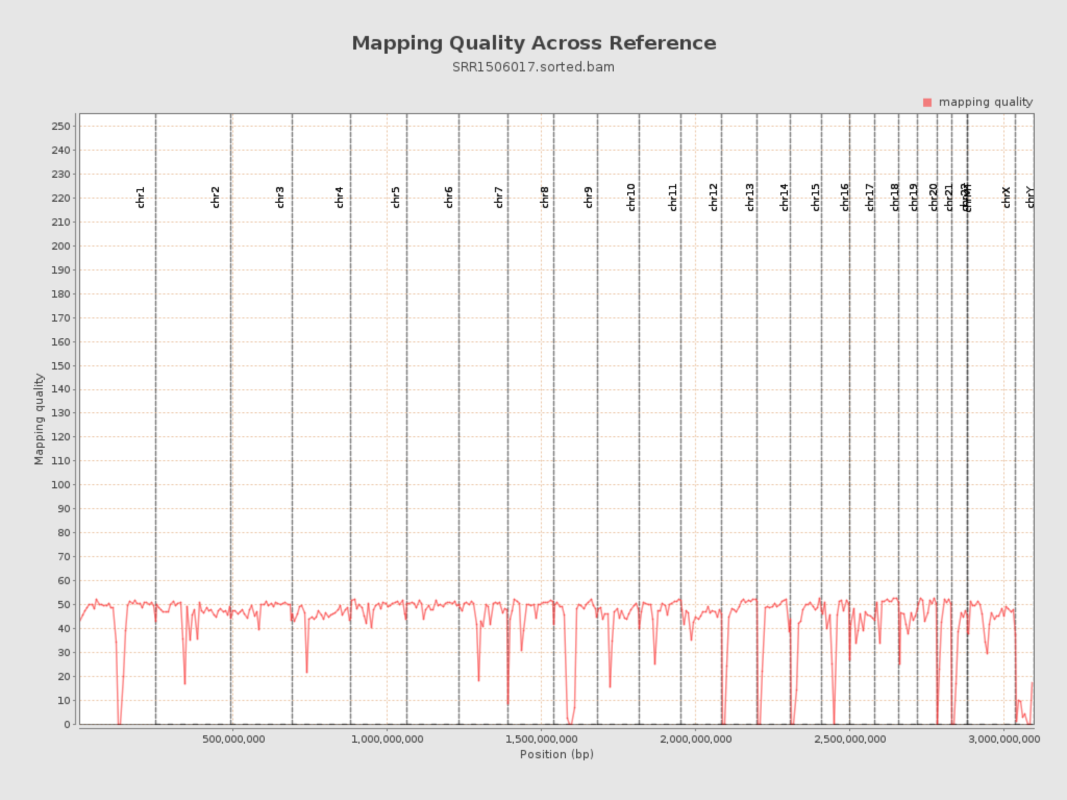
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram