Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:50:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506022.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_SRR1506022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:50:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,525,354
Mapped reads	3,994,452 / 72.29%
Unmapped reads	1,530,902 / 27.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	164 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	298,379 / 5.4%
Duplication rate	5.65%
Clipped reads	679,855 / 12.3%

2.2. ACGT Content

Number/percentage of A's	54,657,776 / 29.52%
Number/percentage of C's	38,334,515 / 20.7%
Number/percentage of T's	53,214,811 / 28.74%
Number/percentage of G's	38,347,323 / 20.71%
Number/percentage of N's	603,948 / 0.33%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.5107

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

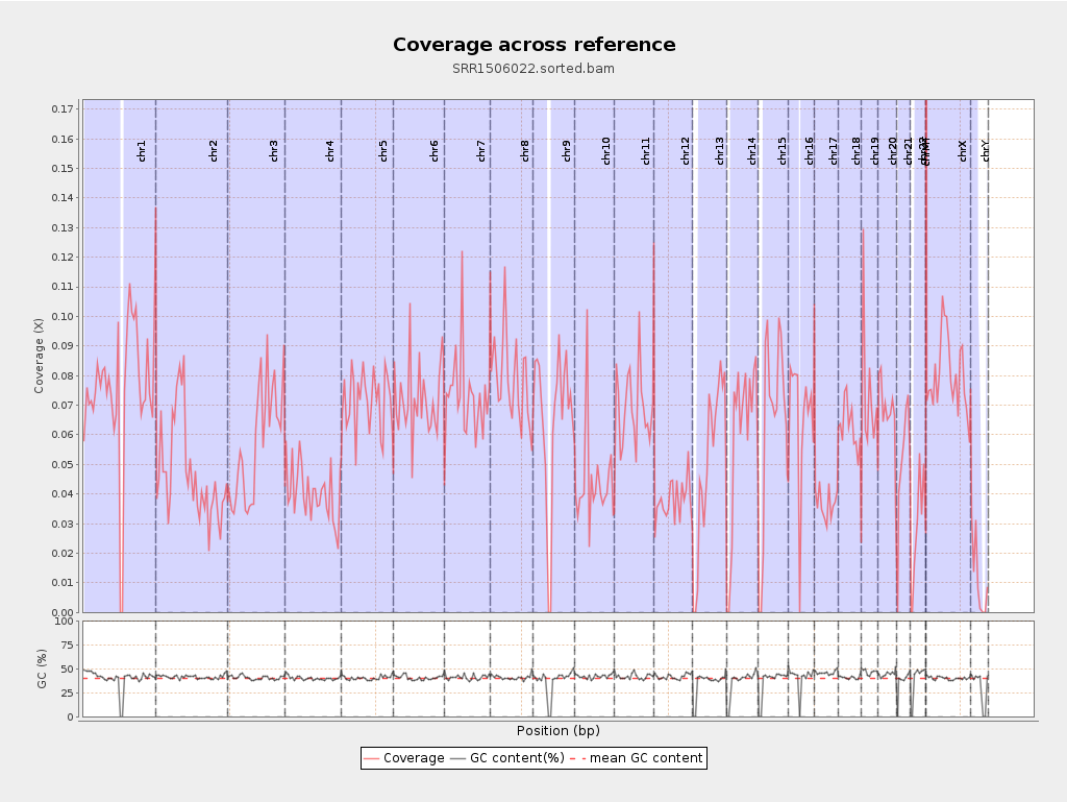
General error rate	0.8%
Mismatches	1,474,456
Insertions	7,727
Mapped reads with at least one insertion	0.19%
Deletions	26,604
Mapped reads with at least one deletion	0.66%
Homopolymer indels	45.38%

2.6. Chromosome stats

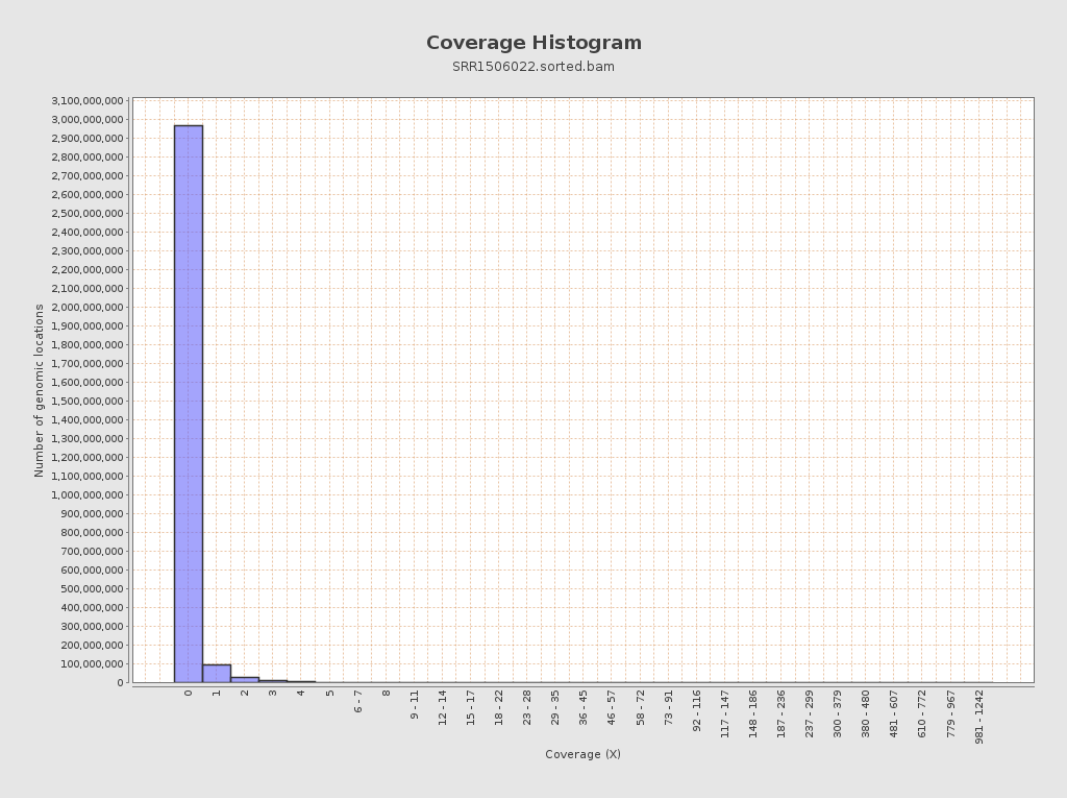
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18919601	0.0759	0.9522
chr2	243199373	11415218	0.0469	0.4028
chr3	198022430	11217781	0.0566	0.325
chr4	191154276	7726235	0.0404	0.2863
chr5	180915260	12863570	0.0711	0.3648
chr6	171115067	12290732	0.0718	0.4379
chr7	159138663	11592266	0.0728	0.7148

chr8	146364022	11424737	0.0781	0.5504
chr9	141213431	9215951	0.0653	0.4213
chr10	135534747	5900442	0.0435	0.5604
chr11	135006516	9282927	0.0688	0.4928
chr12	133851895	5067730	0.0379	0.2772
chr13	115169878	5922689	0.0514	0.3086
chr14	107349540	6481440	0.0604	0.7602
chr15	102531392	6472824	0.0631	0.3399
chr16	90354753	5839808	0.0646	0.3757
chr17	81195210	2975207	0.0366	0.2921
chr18	78077248	4912818	0.0629	0.5768
chr19	59128983	4258691	0.072	0.7588
chr20	63025520	4346760	0.069	0.3652
chr21	48129895	2474818	0.0514	0.3354
chr22	51304566	1488182	0.029	0.2305
chrMT	16571	10794	0.6514	1.2168
chrX	155270560	12437644	0.0801	0.4231
chrY	59373566	656251	0.0111	0.2091

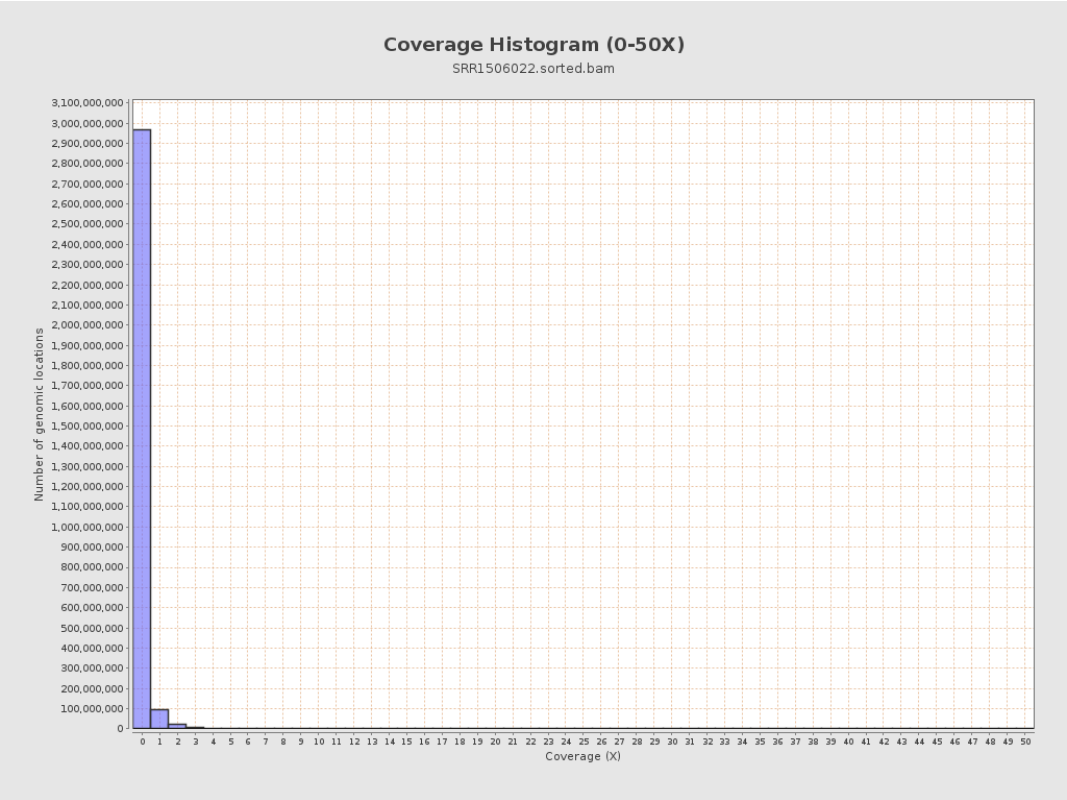
3. Results : Coverage across reference



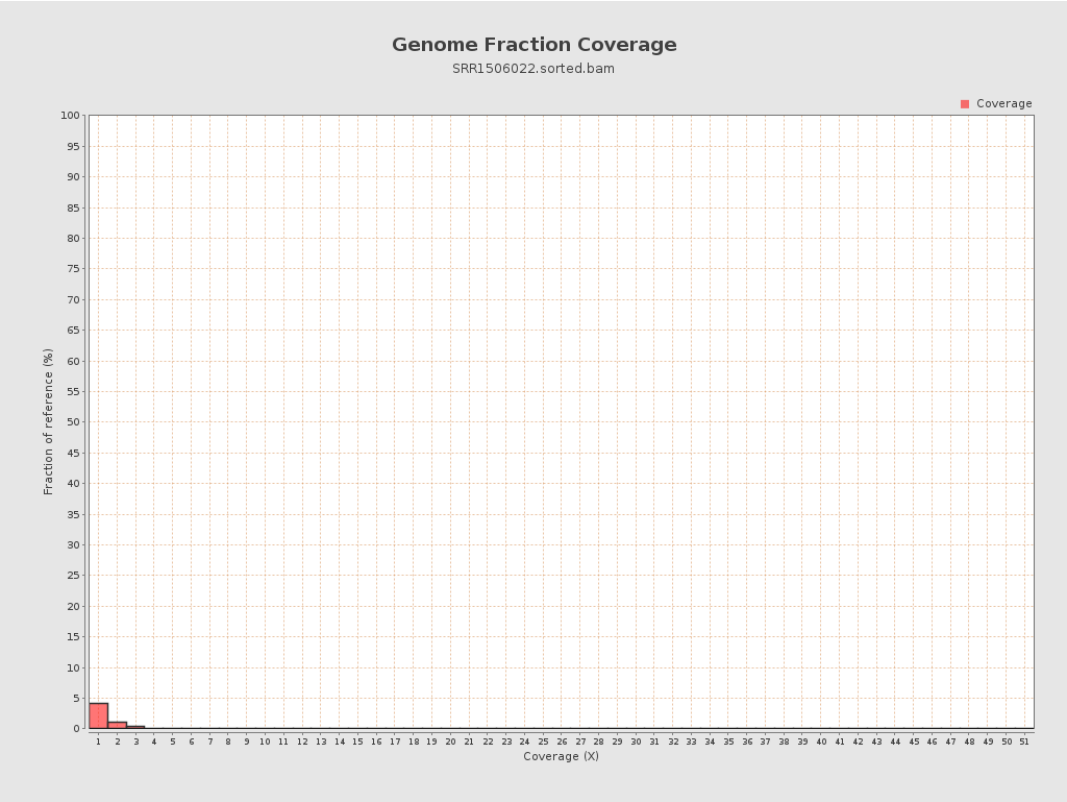
4. Results : Coverage Histogram



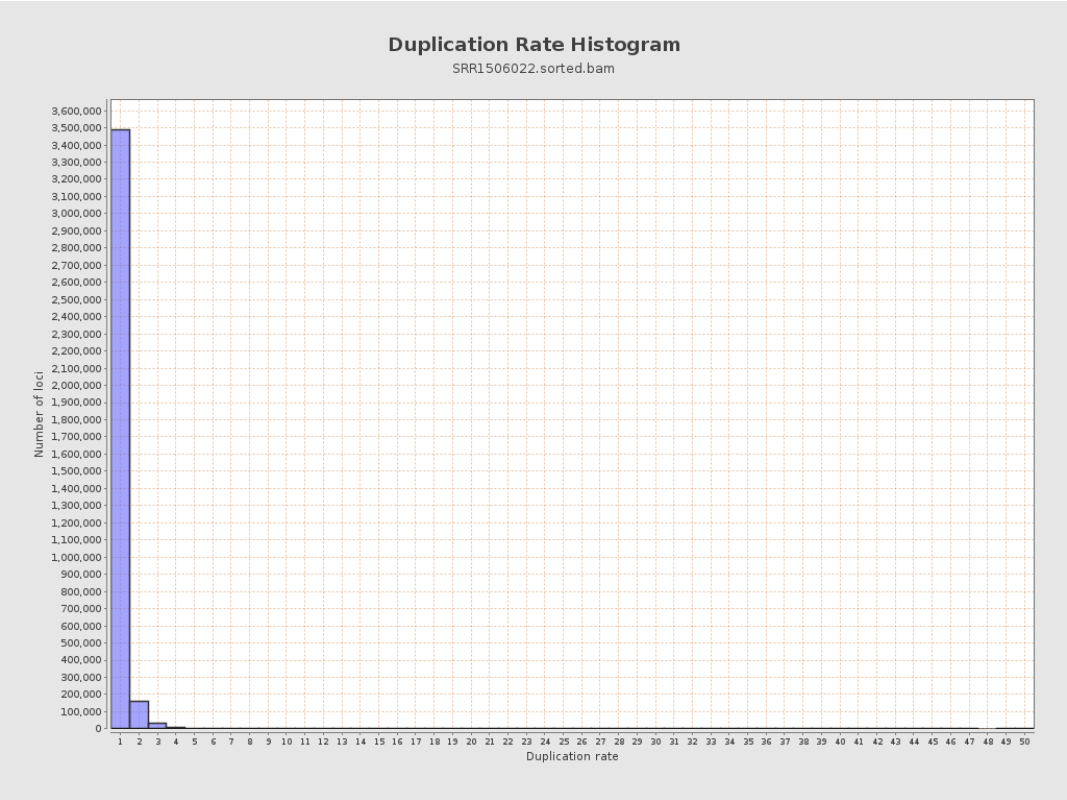
5. Results : Coverage Histogram (0-50X)



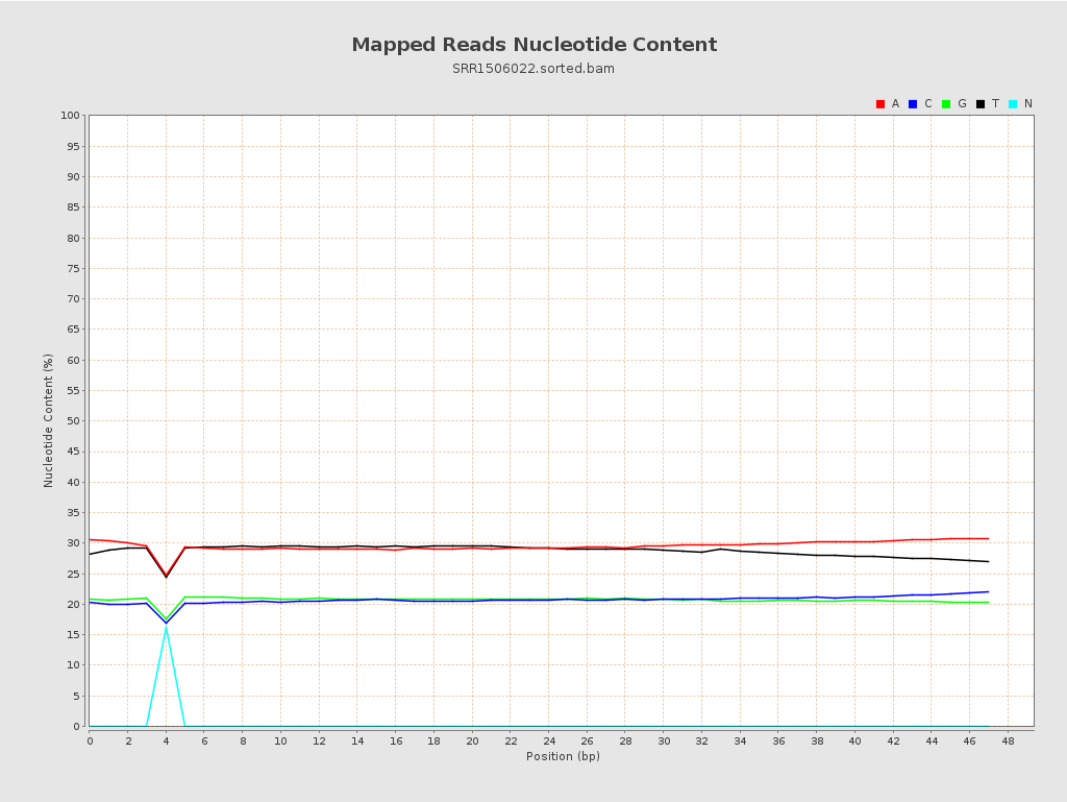
6. Results : Genome Fraction Coverage



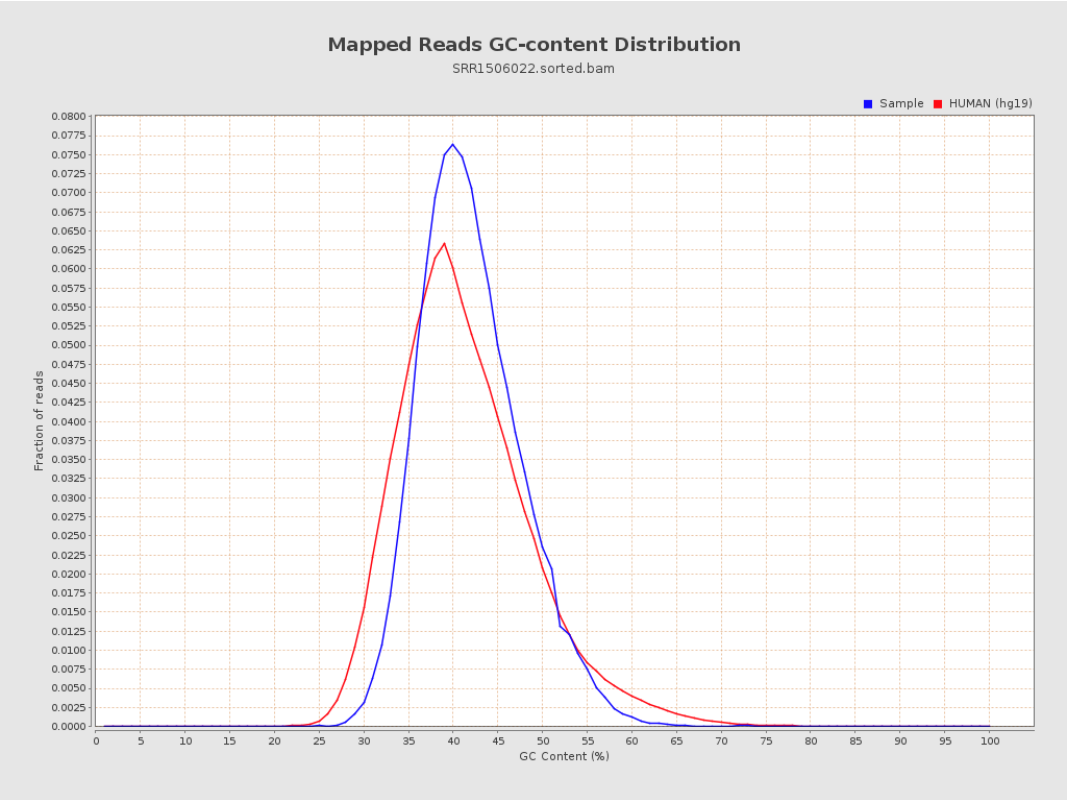
7. Results : Duplication Rate Histogram



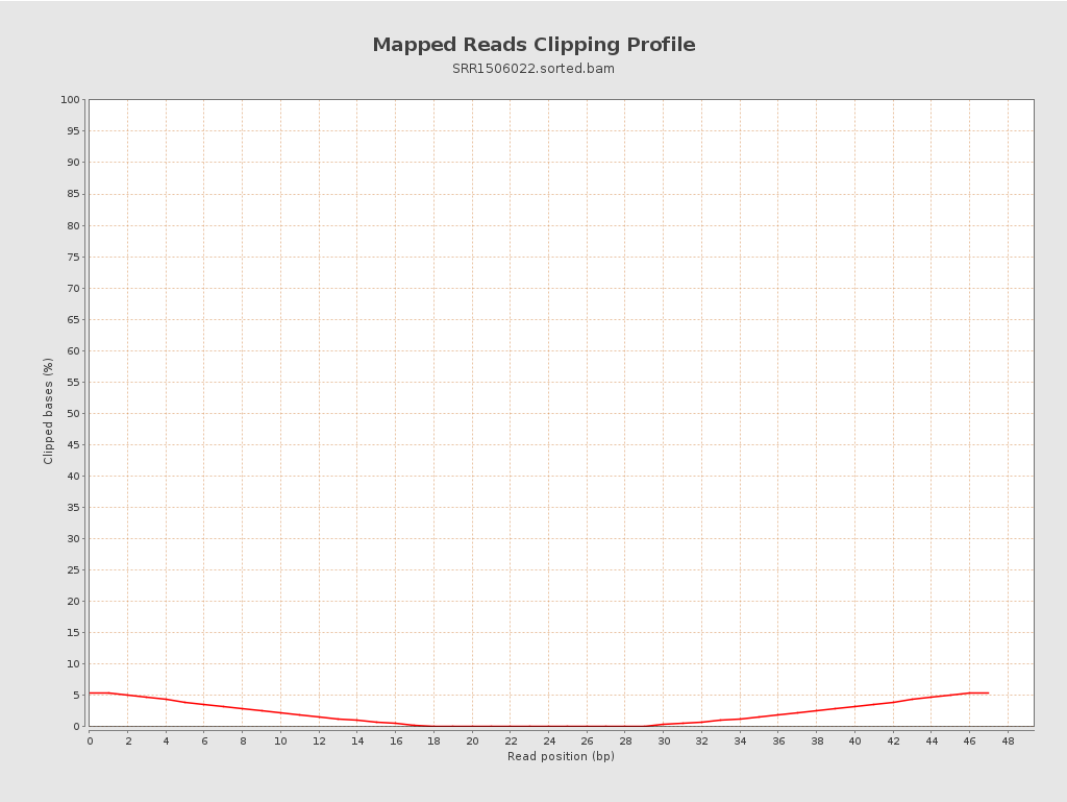
8. Results : Mapped Reads Nucleotide Content



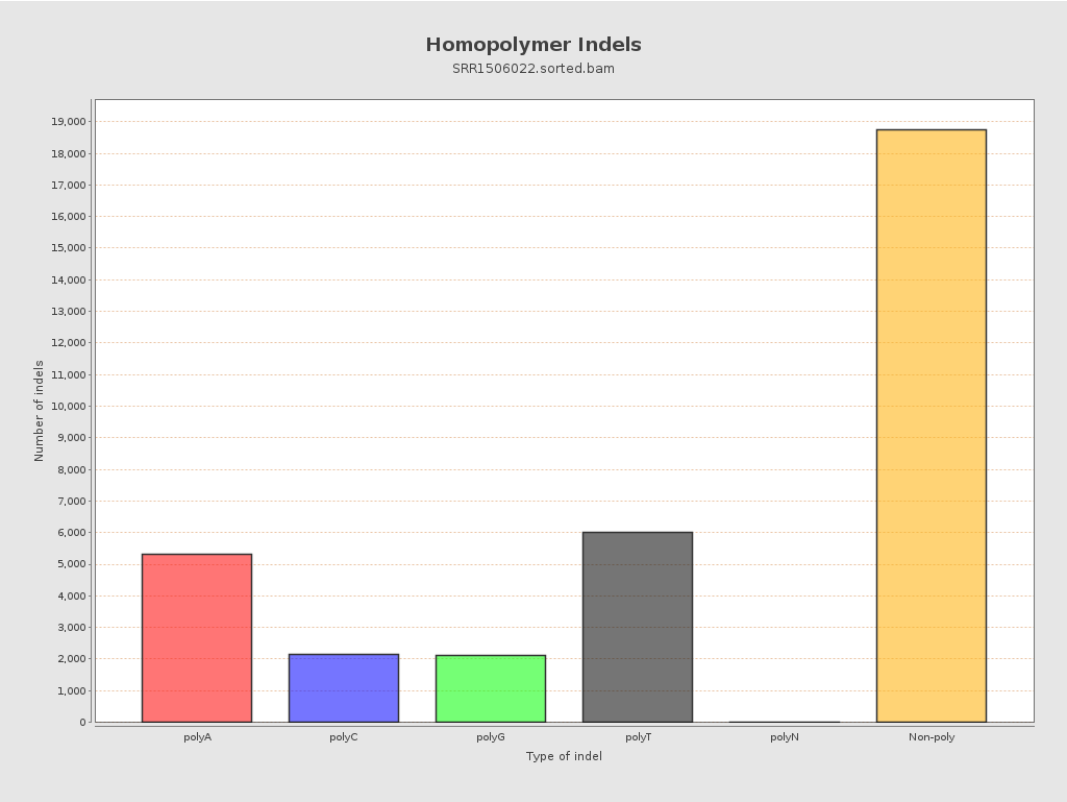
9. Results : Mapped Reads GC-content Distribution



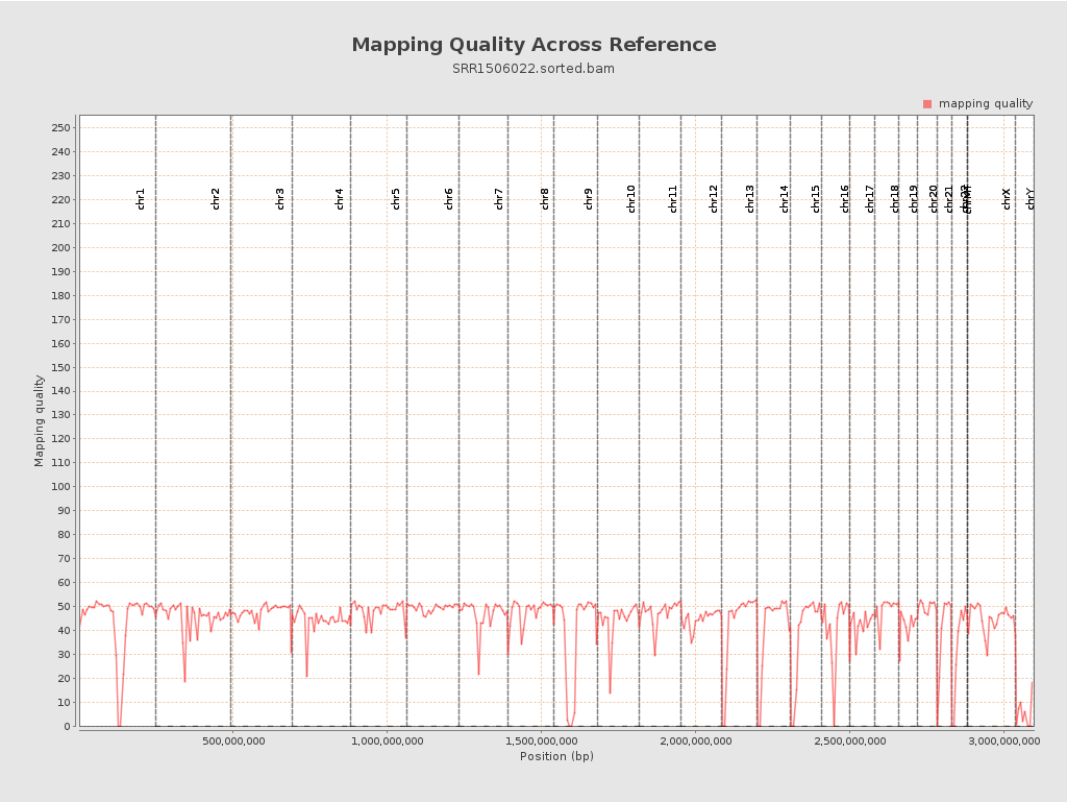
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram