Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:39:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013182.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_SRR6013182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:39:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,413,033
Mapped reads	1,279,047 / 90.52%
Unmapped reads	133,986 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,099 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	33,745 / 2.39%
Duplication rate	1.88%
Clipped reads	548,820 / 38.84%

2.2. ACGT Content

Number/percentage of A's	24,312,816 / 28.39%
Number/percentage of C's	15,850,682 / 18.51%
Number/percentage of T's	26,799,611 / 31.3%
Number/percentage of G's	18,643,734 / 21.77%
Number/percentage of N's	20,941 / 0.02%
GC Percentage	40.28%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2785

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

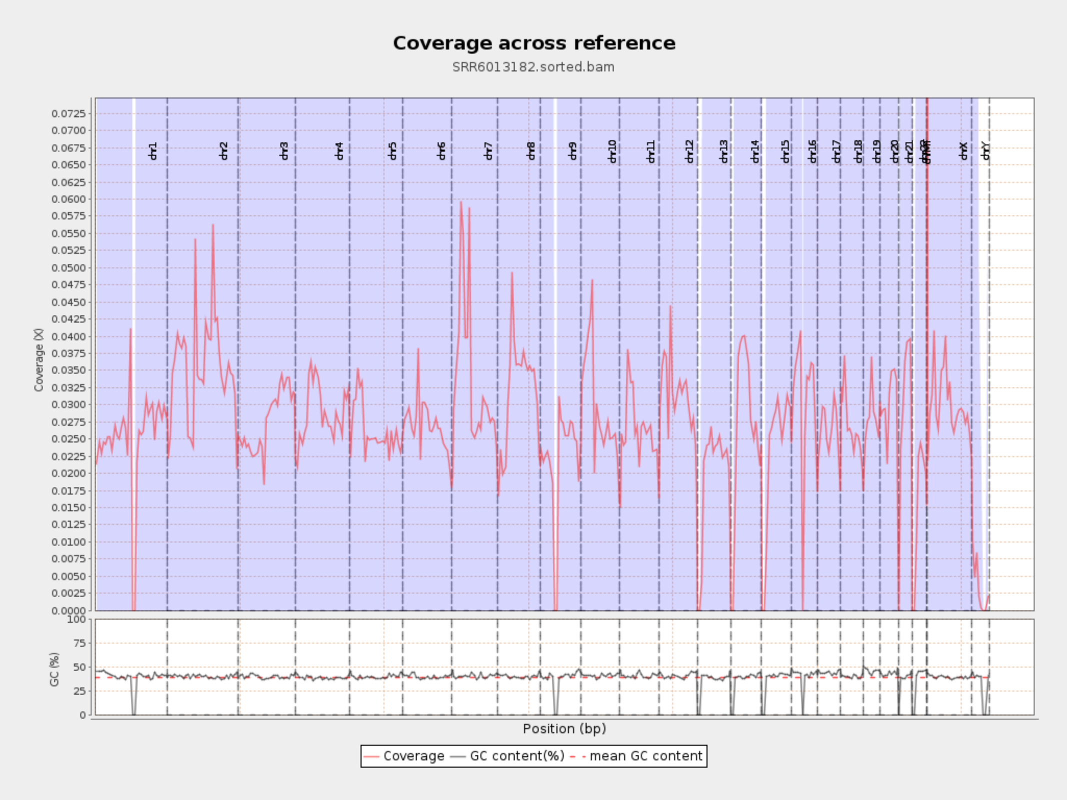
General error rate	0.84%
Mismatches	703,935
Insertions	6,413
Mapped reads with at least one insertion	0.5%
Deletions	25,100
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.05%

2.6. Chromosome stats

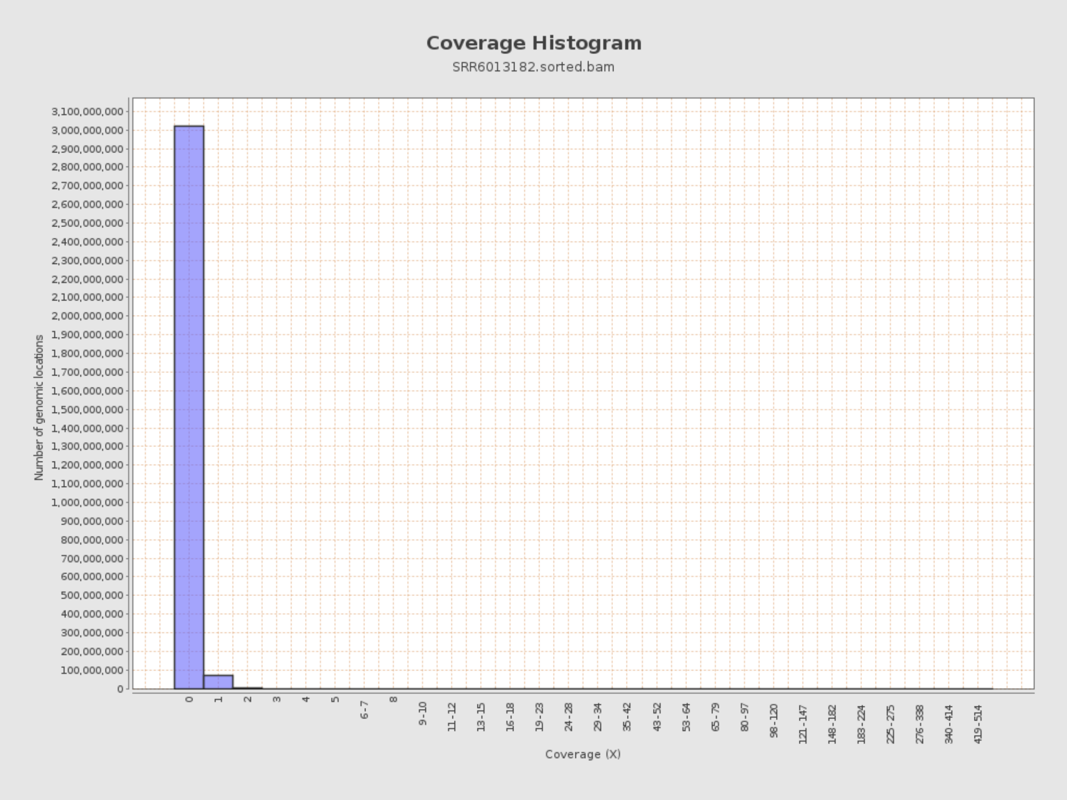
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6268524	0.0251	0.4586
chr2	243199373	8690070	0.0357	0.314
chr3	198022430	5460706	0.0276	0.1793
chr4	191154276	5499207	0.0288	0.1863
chr5	180915260	4757053	0.0263	0.1761
chr6	171115067	4605901	0.0269	0.2098
chr7	159138663	5399091	0.0339	0.4906

chr8	146364022	4714513	0.0322	0.3469
chr9	141213431	3077340	0.0218	0.23
chr10	135534747	4048427	0.0299	0.2785
chr11	135006516	3584767	0.0266	0.2211
chr12	133851895	4240408	0.0317	0.1929
chr13	115169878	2255948	0.0196	0.1515
chr14	107349540	2894925	0.027	0.1896
chr15	102531392	2346119	0.0229	0.1627
chr16	90354753	2710884	0.03	0.206
chr17	81195210	2129484	0.0262	0.189
chr18	78077248	2108416	0.027	0.4217
chr19	59128983	1660929	0.0281	0.3376
chr20	63025520	1882790	0.0299	0.1895
chr21	48129895	1449468	0.0301	0.1955
chr22	51304566	802579	0.0156	0.135
chrMT	16571	206396	12.4553	8.2937
chrX	155270560	4685679	0.0302	0.2027
chrY	59373566	191659	0.0032	0.0779

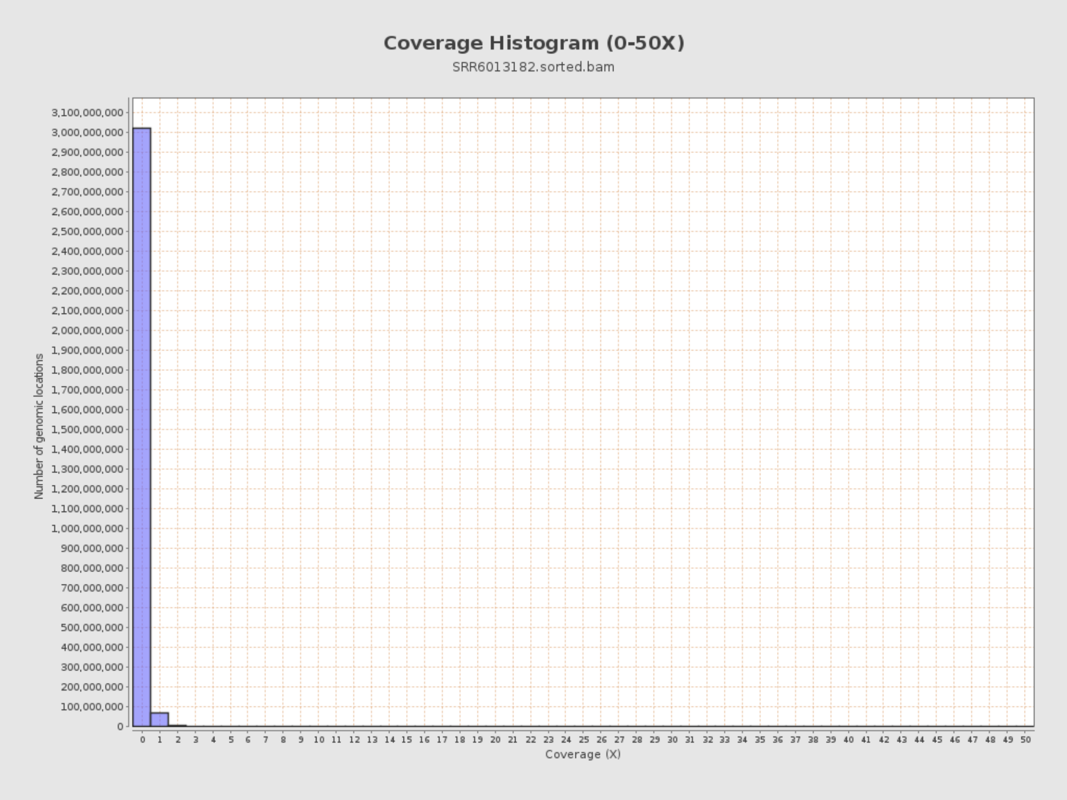
3. Results : Coverage across reference



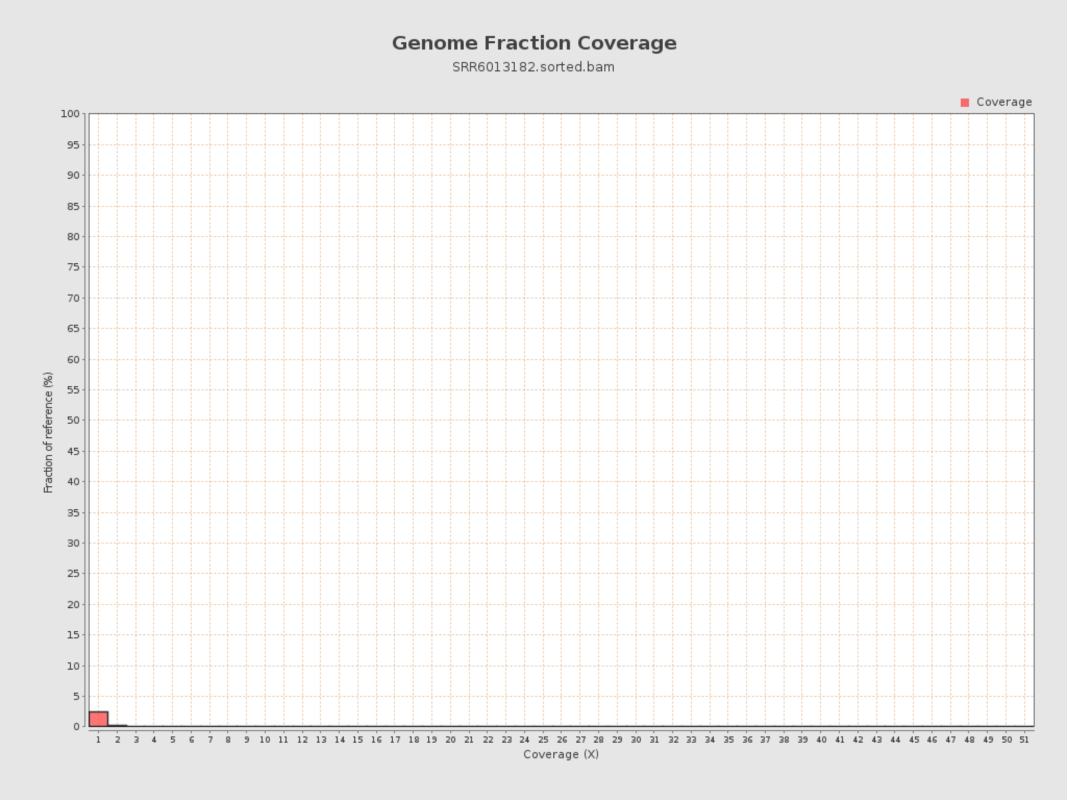
4. Results : Coverage Histogram



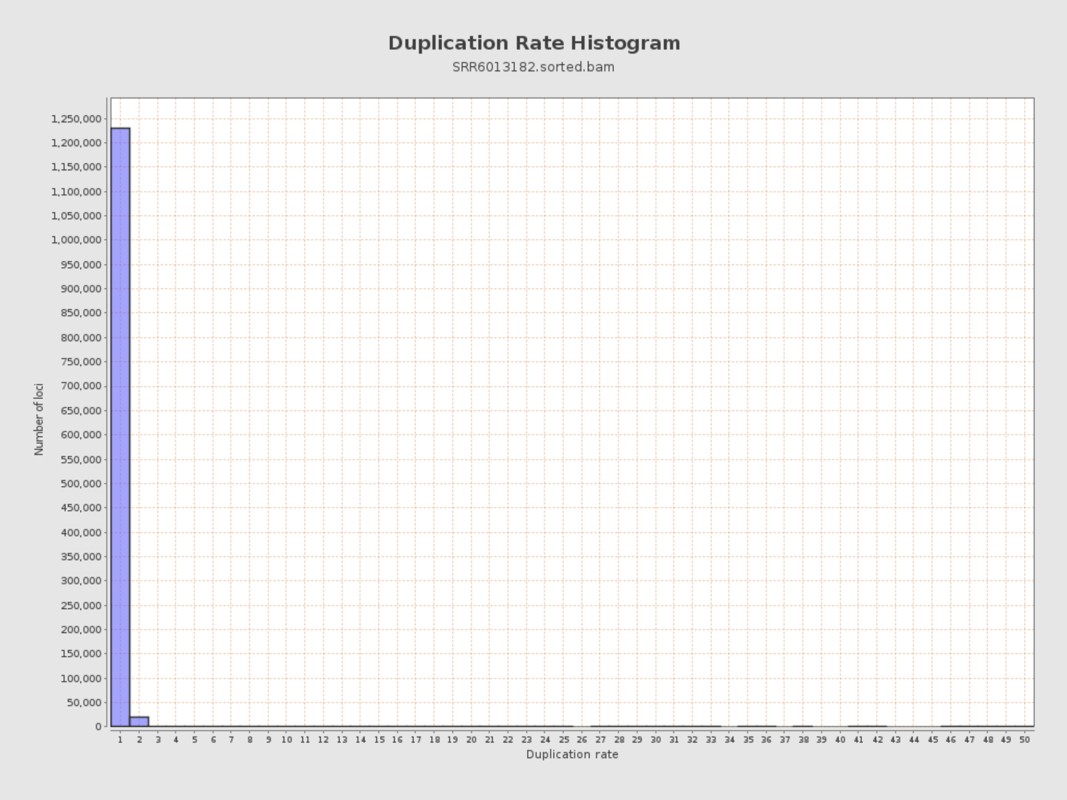
5. Results : Coverage Histogram (0-50X)



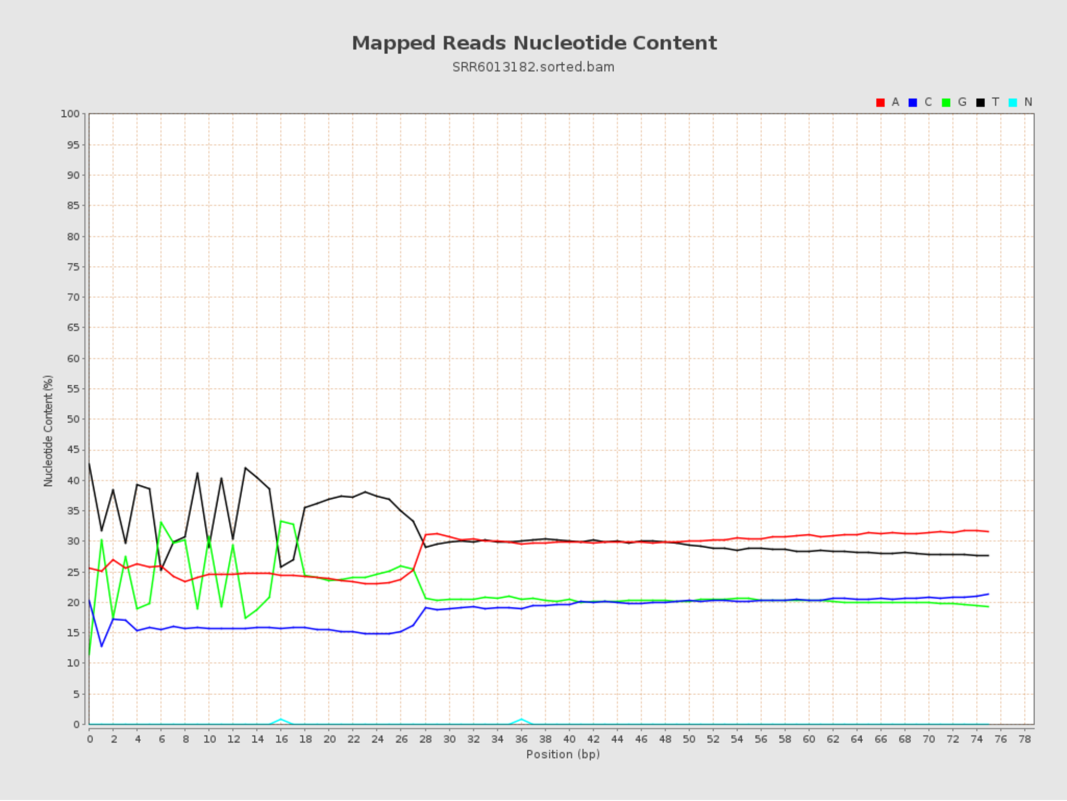
6. Results : Genome Fraction Coverage



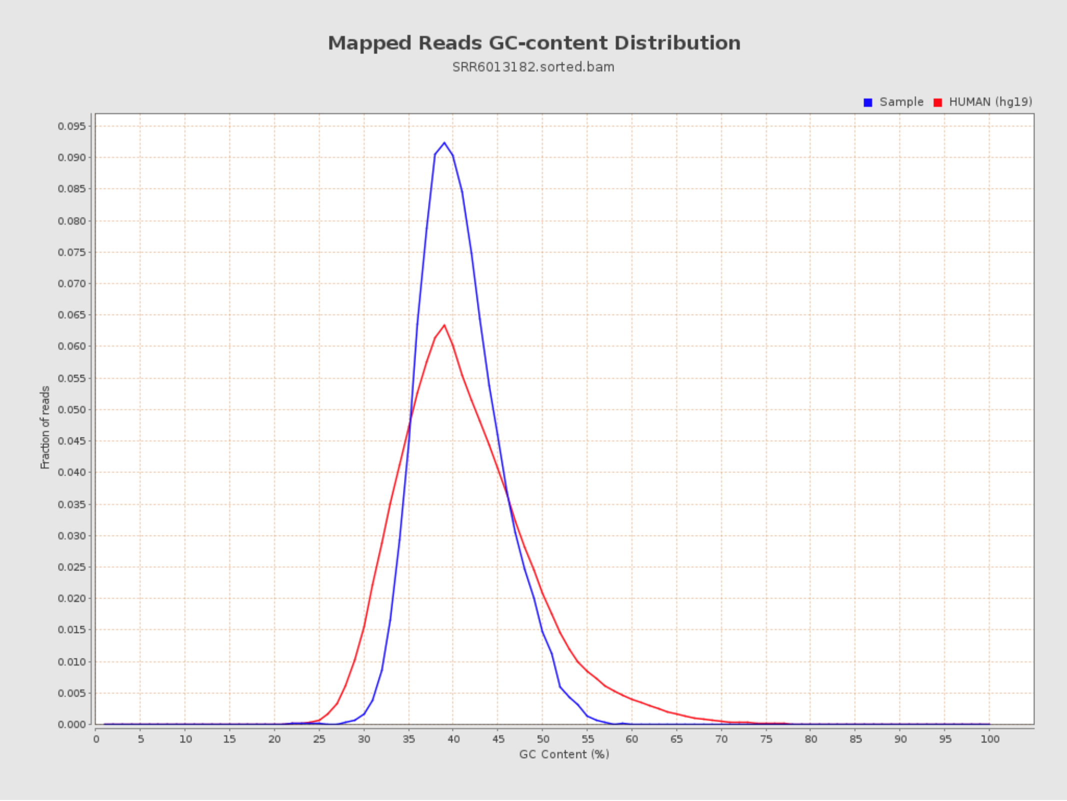
7. Results : Duplication Rate Histogram



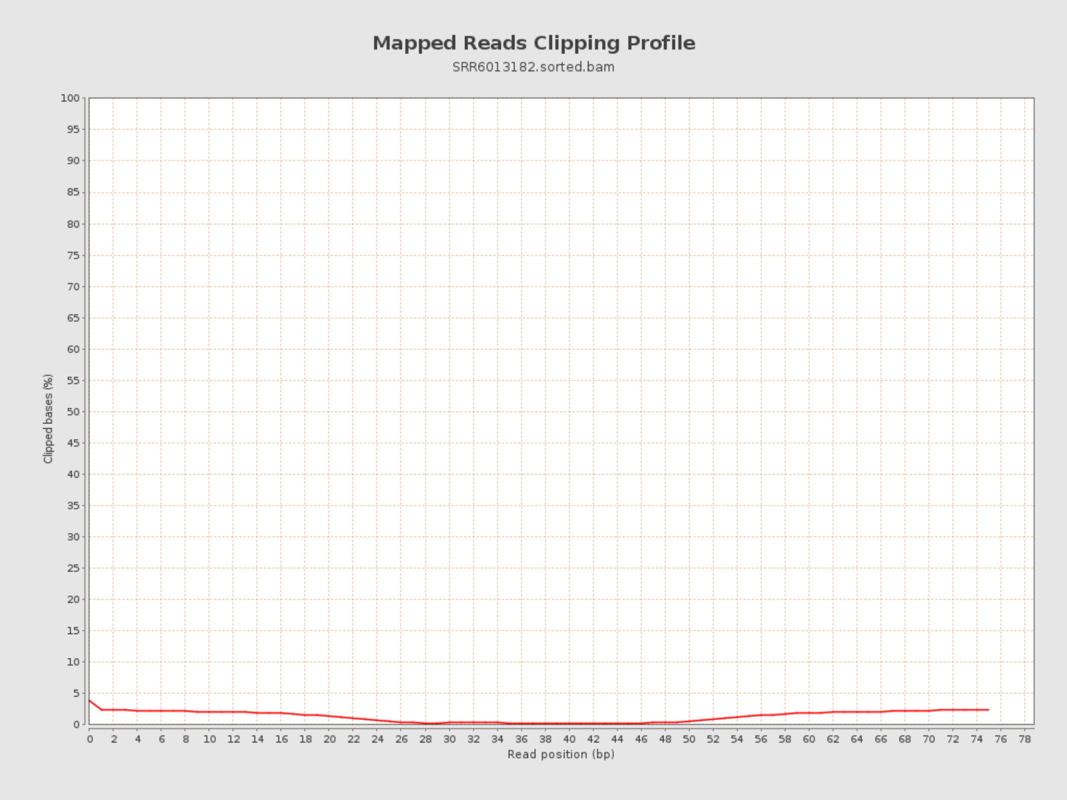
8. Results : Mapped Reads Nucleotide Content



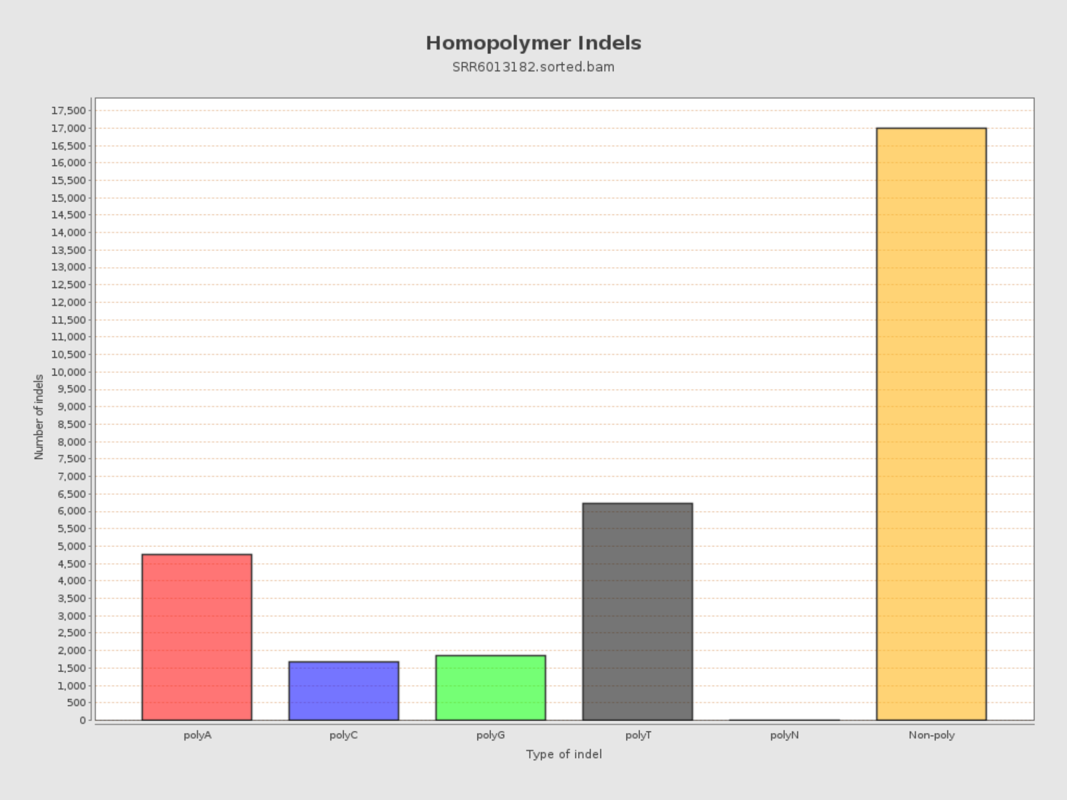
9. Results : Mapped Reads GC-content Distribution



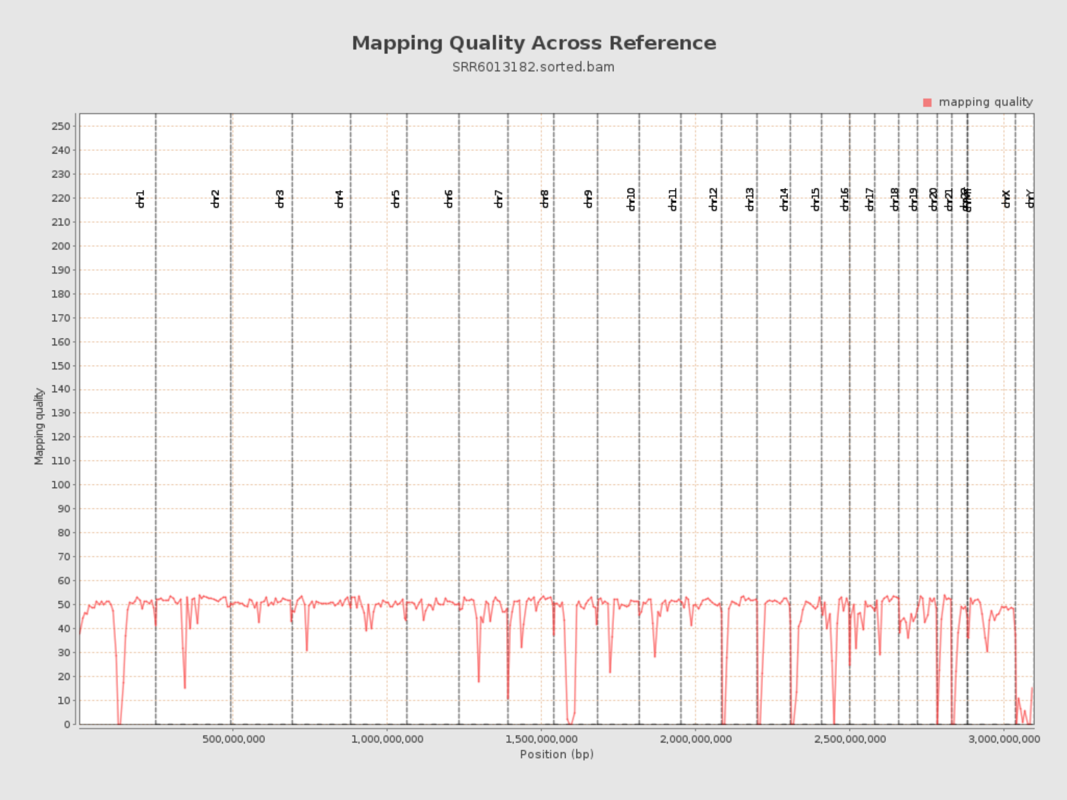
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram