Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:21:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013176.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_SRR6013176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:21:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,097,768
Mapped reads	1,862,104 / 88.77%
Unmapped reads	235,664 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,759 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	56,482 / 2.69%
Duplication rate	2.05%
Clipped reads	947,493 / 45.17%

2.2. ACGT Content

Number/percentage of A's	33,196,528 / 27.44%
Number/percentage of C's	23,227,366 / 19.2%
Number/percentage of T's	36,702,327 / 30.34%
Number/percentage of G's	27,826,674 / 23%
Number/percentage of N's	28,904 / 0.02%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3873

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

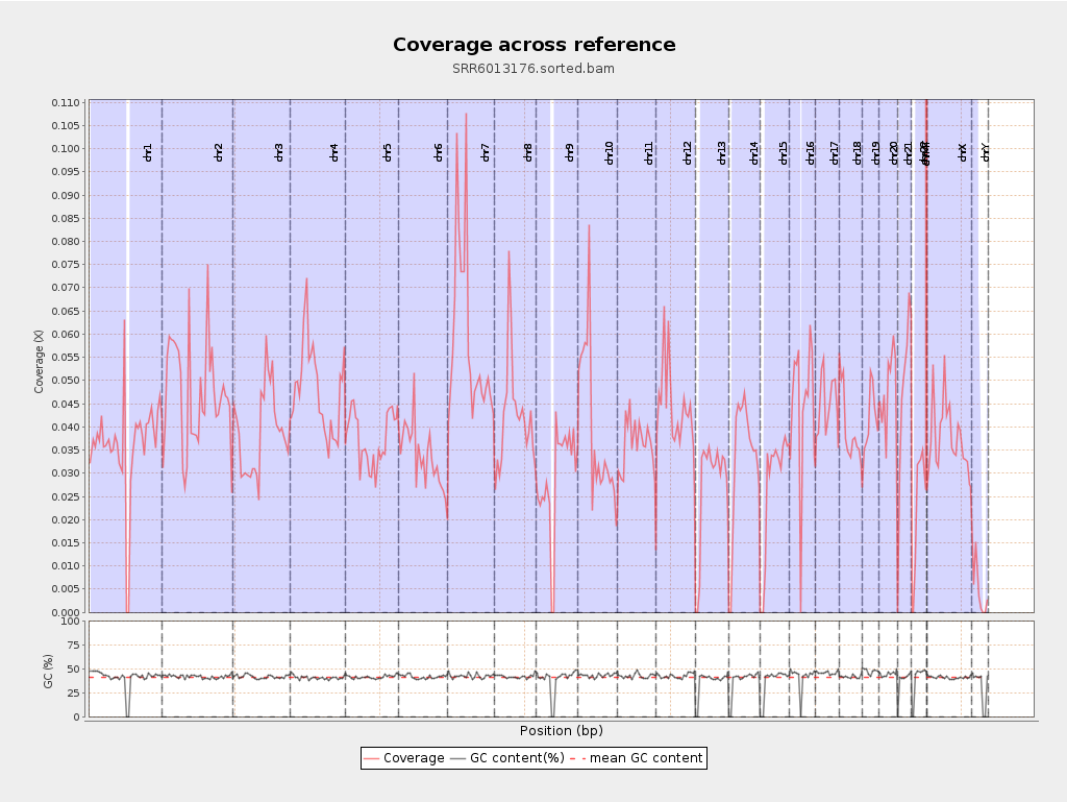
General error rate	0.84%
Mismatches	994,704
Insertions	8,481
Mapped reads with at least one insertion	0.45%
Deletions	34,067
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.19%

2.6. Chromosome stats

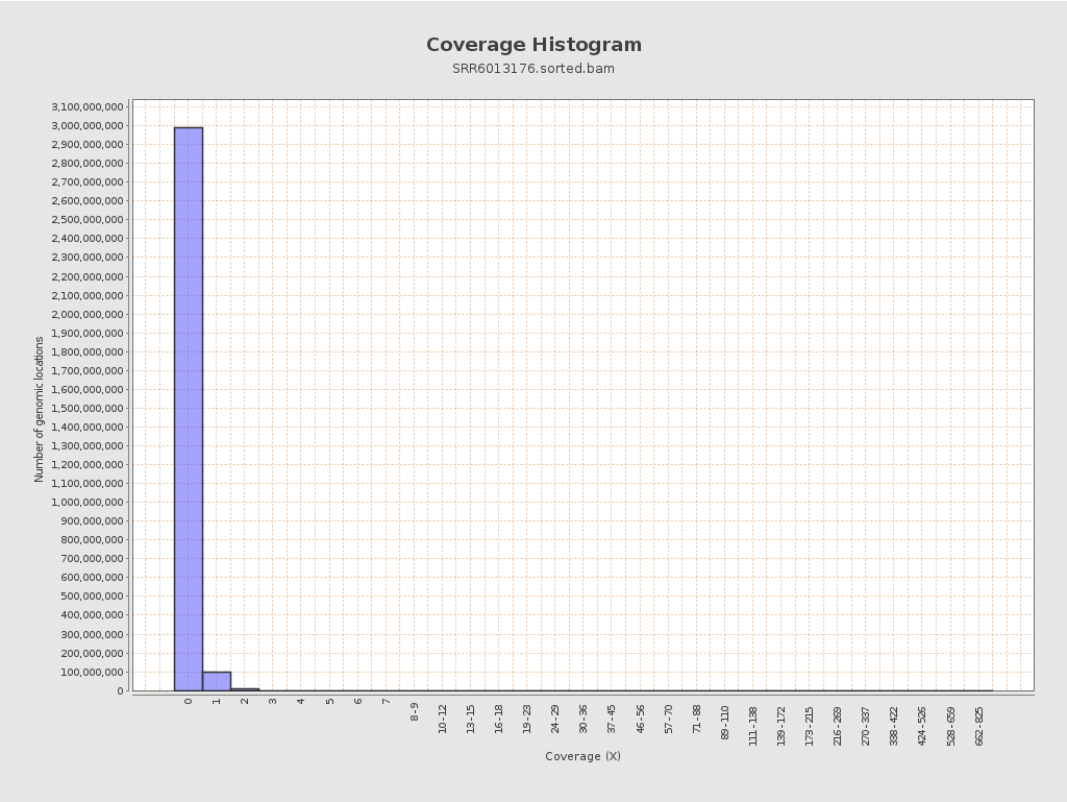
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8965979	0.036	0.708
chr2	243199373	11433933	0.047	0.4248
chr3	198022430	7683842	0.0388	0.2165
chr4	191154276	9164462	0.0479	0.2517
chr5	180915260	6775778	0.0375	0.2104
chr6	171115067	5770541	0.0337	0.2455
chr7	159138663	9391316	0.059	0.7989

chr8	146364022	6183614	0.0422	0.3526
chr9	141213431	4058138	0.0287	0.2949
chr10	135534747	5334689	0.0394	0.4096
chr11	135006516	4857683	0.036	0.2576
chr12	133851895	5925600	0.0443	0.2307
chr13	115169878	3126712	0.0271	0.178
chr14	107349540	3572779	0.0333	0.2338
chr15	102531392	2816237	0.0275	0.1797
chr16	90354753	4043875	0.0448	0.2613
chr17	81195210	3633372	0.0447	0.2727
chr18	78077248	3090054	0.0396	0.524
chr19	59128983	2462934	0.0417	0.5081
chr20	63025520	3003257	0.0477	0.2452
chr21	48129895	2281300	0.0474	0.251
chr22	51304566	1139720	0.0222	0.1596
chrMT	16571	241503	14.5738	9.5428
chrX	155270560	5794053	0.0373	0.2412
chrY	59373566	290119	0.0049	0.1206

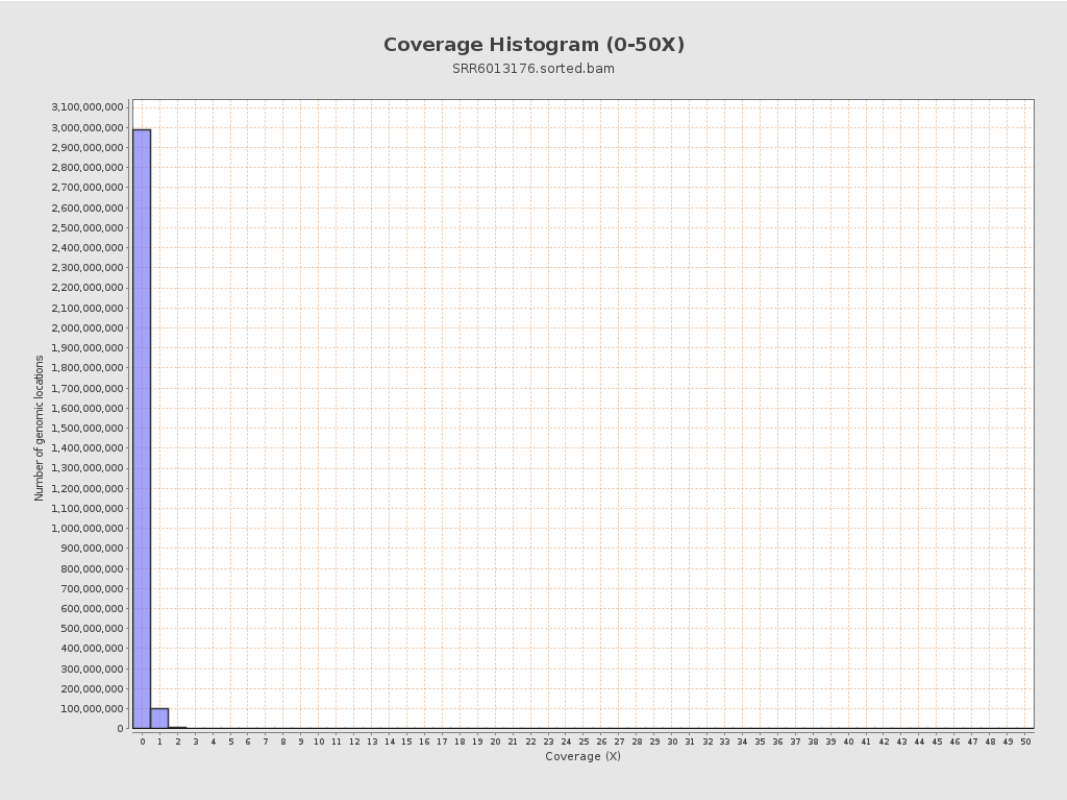
3. Results : Coverage across reference



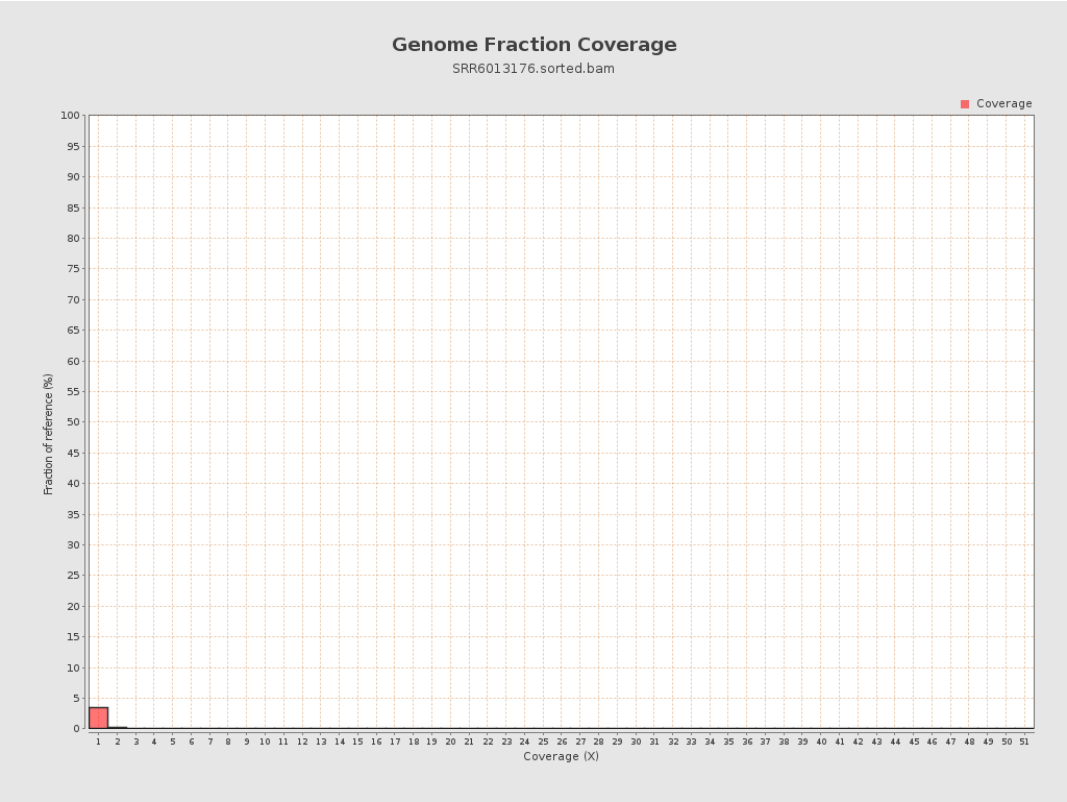
4. Results : Coverage Histogram



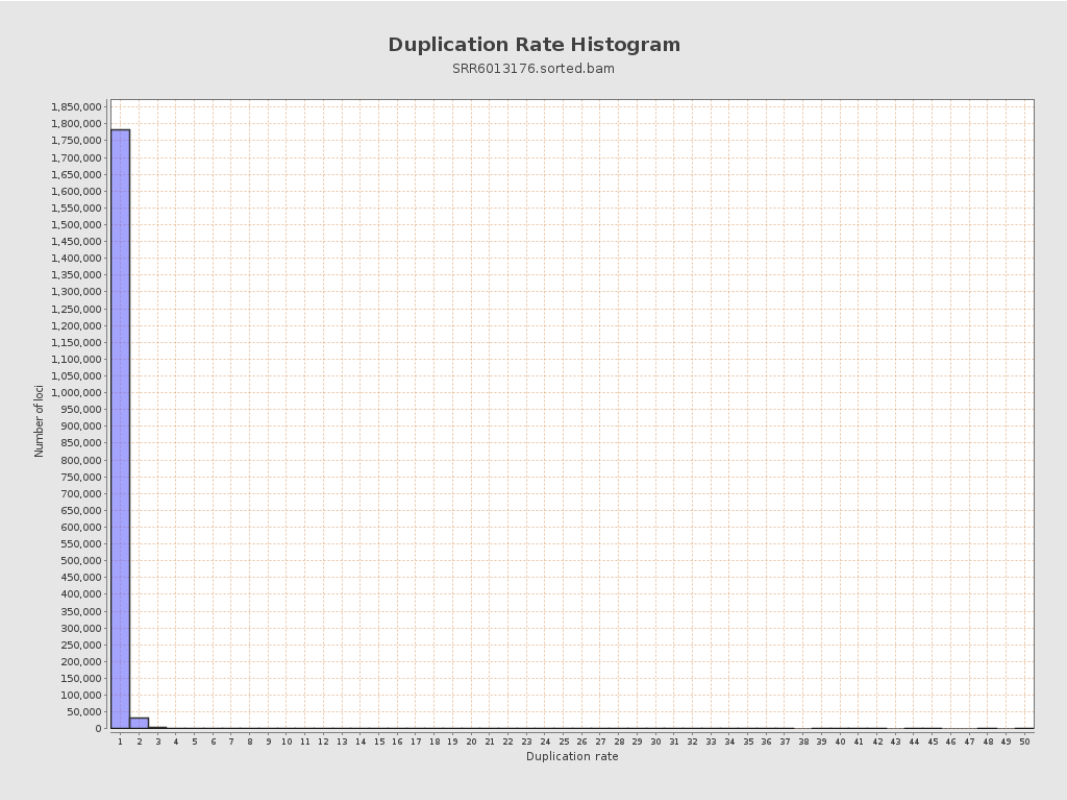
5. Results : Coverage Histogram (0-50X)



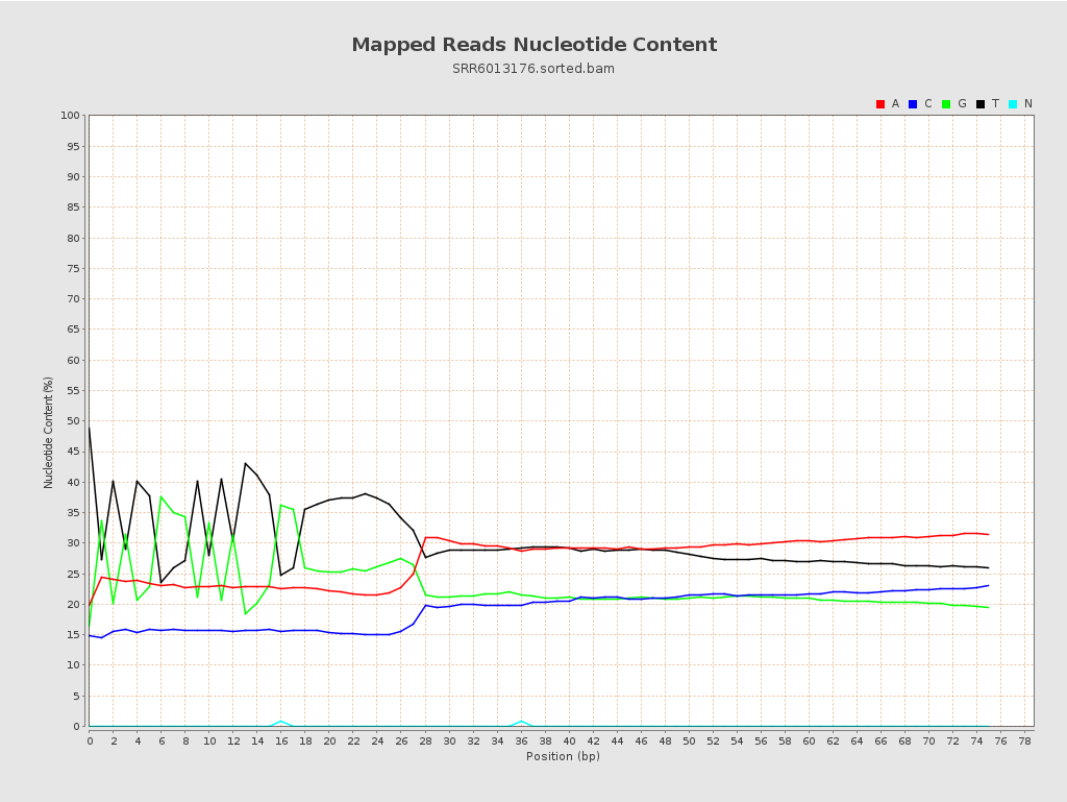
6. Results : Genome Fraction Coverage



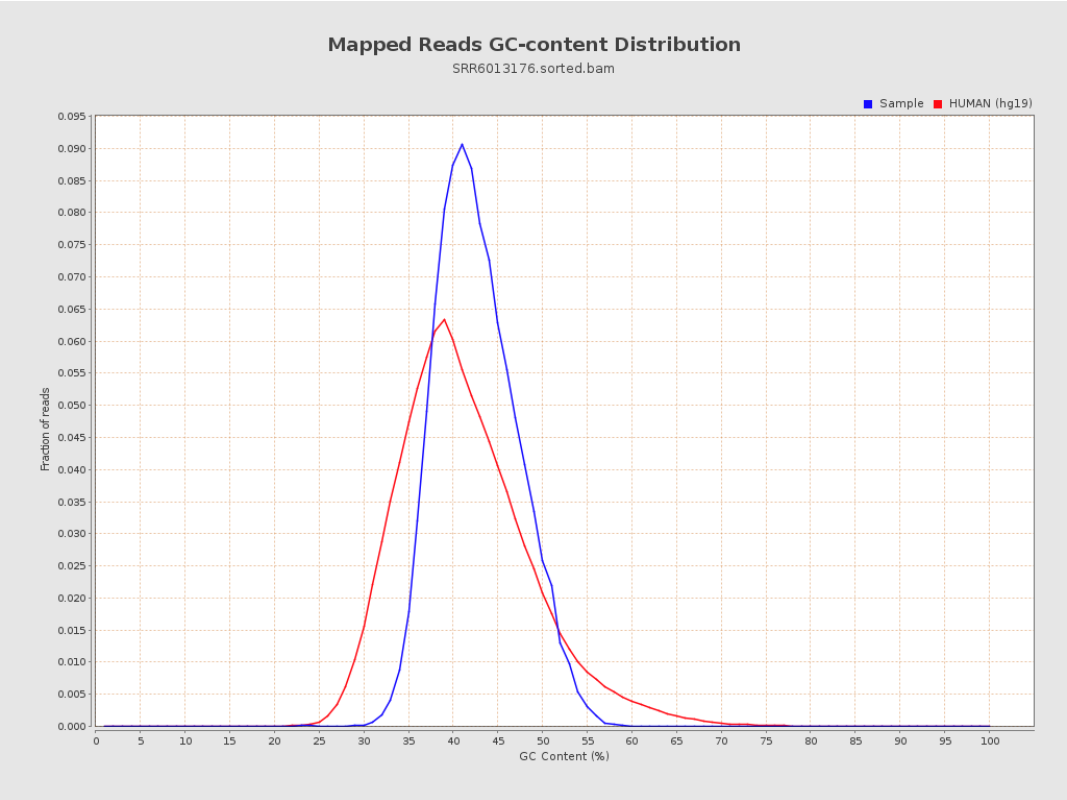
7. Results : Duplication Rate Histogram



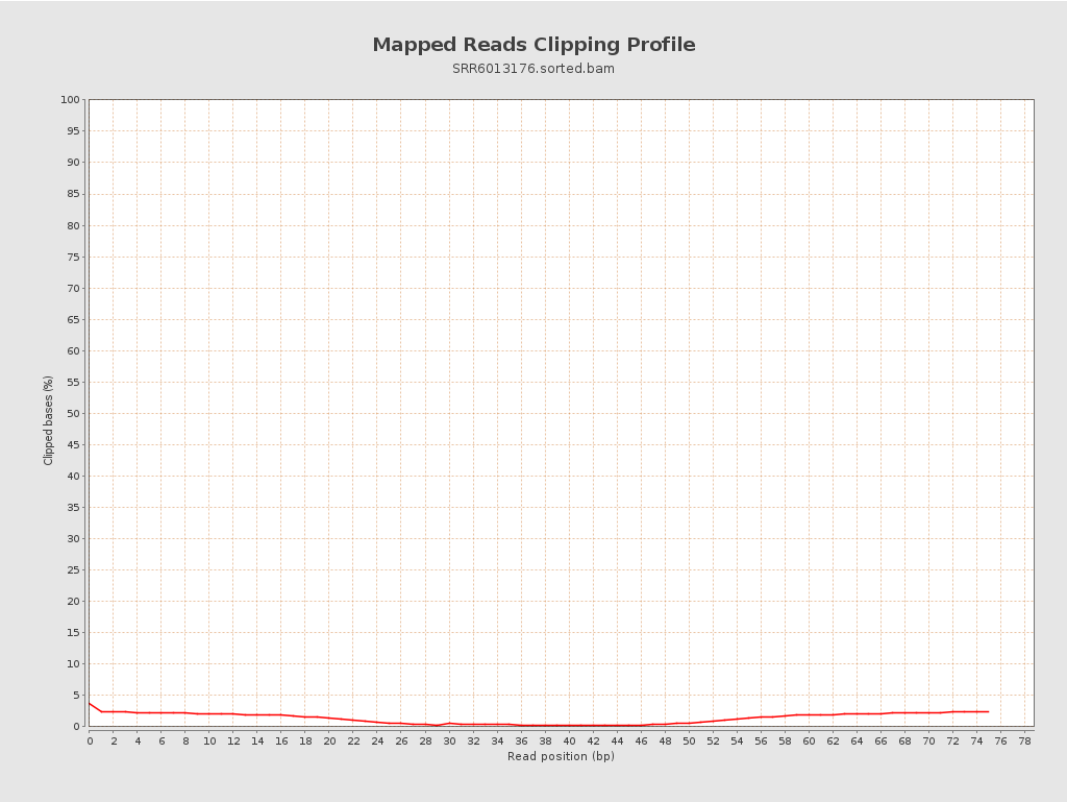
8. Results : Mapped Reads Nucleotide Content



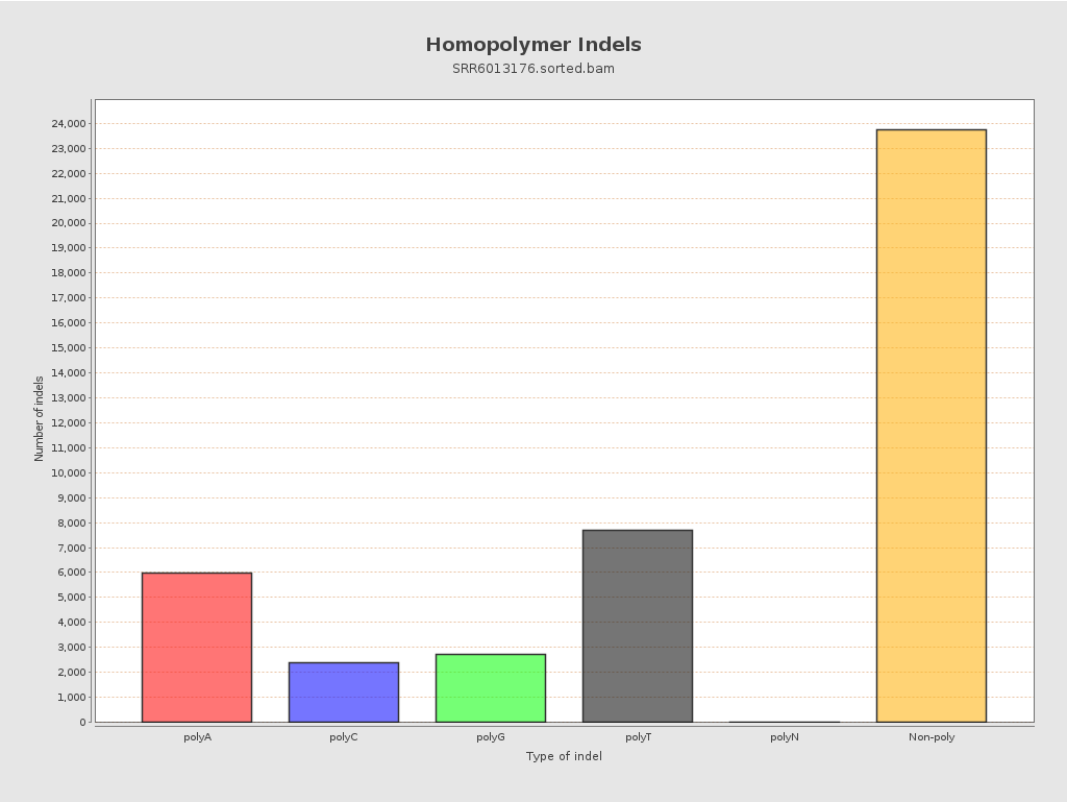
9. Results : Mapped Reads GC-content Distribution



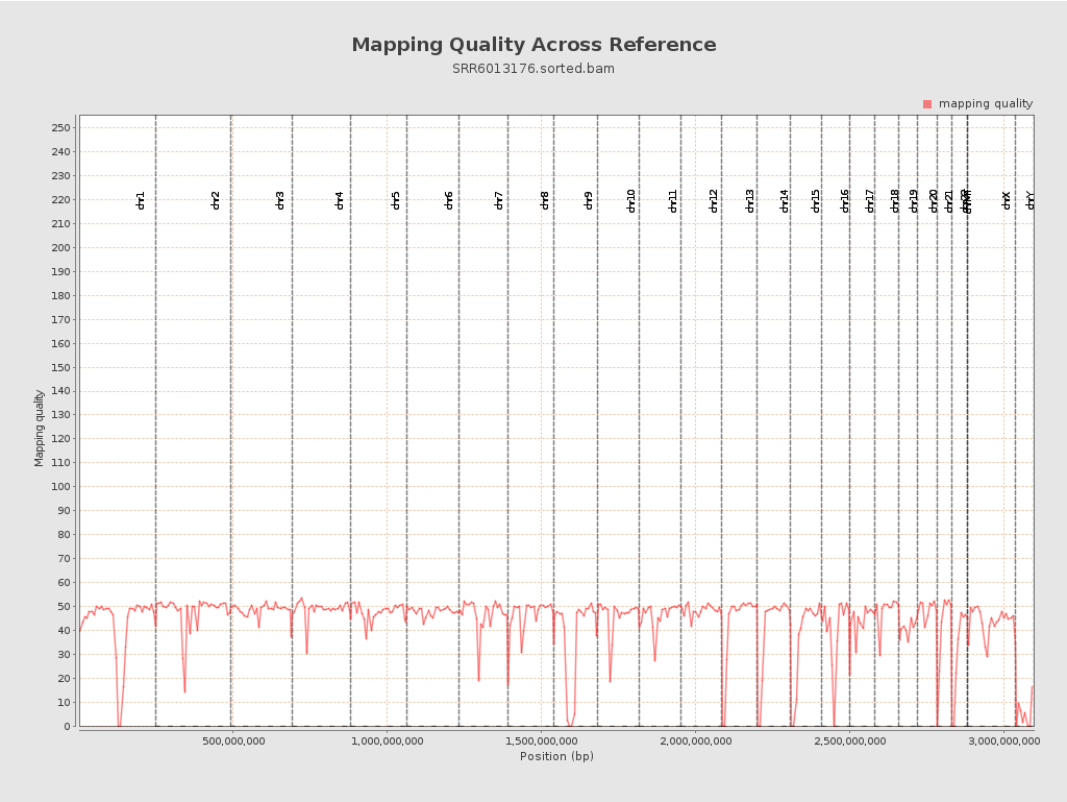
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram