Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:11:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013316.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_SRR6013316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013316.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,580,146
Mapped reads	1,400,906 / 88.66%
Unmapped reads	179,240 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,474 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	48,294 / 3.06%
Duplication rate	2.67%
Clipped reads	637,749 / 40.36%

2.2. ACGT Content

Number/percentage of A's	25,468,059 / 27.55%
Number/percentage of C's	16,853,394 / 18.23%
Number/percentage of T's	29,382,619 / 31.79%
Number/percentage of G's	20,732,561 / 22.43%
Number/percentage of N's	1,367 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.2878

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Mismatches and indels

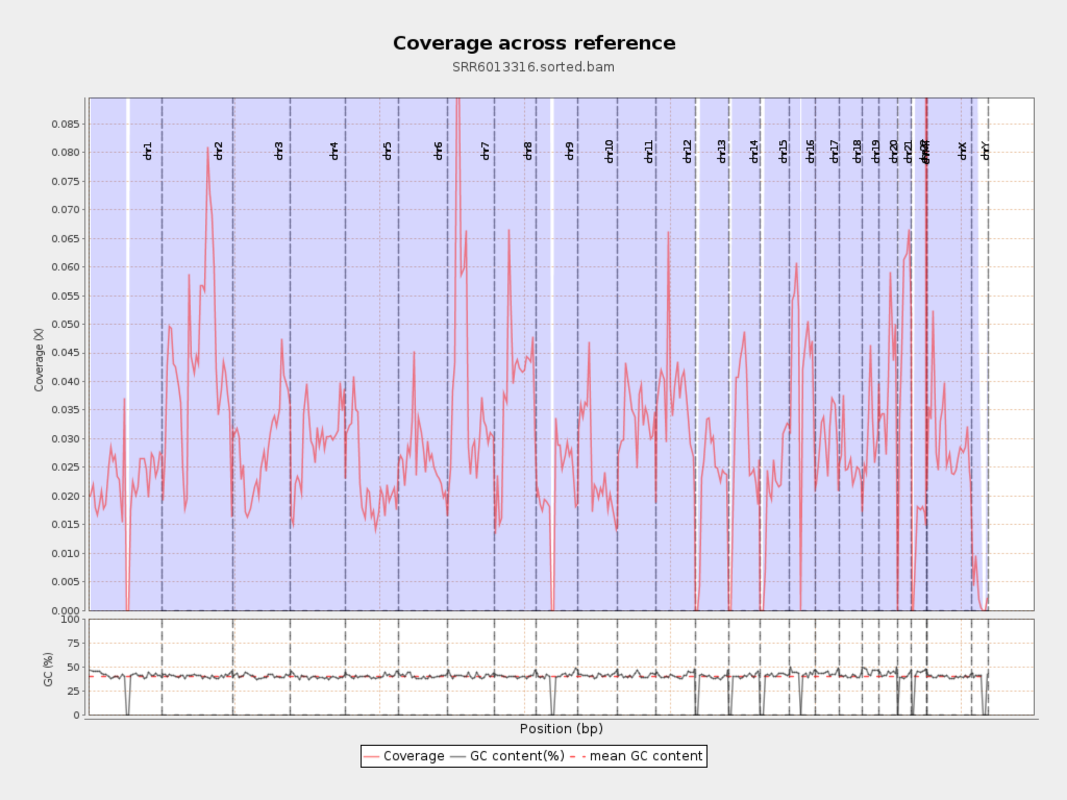
General error rate	0.71%
Mismatches	645,021
Insertions	6,003
Mapped reads with at least one insertion	0.43%
Deletions	23,289
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.55%

2.6. Chromosome stats

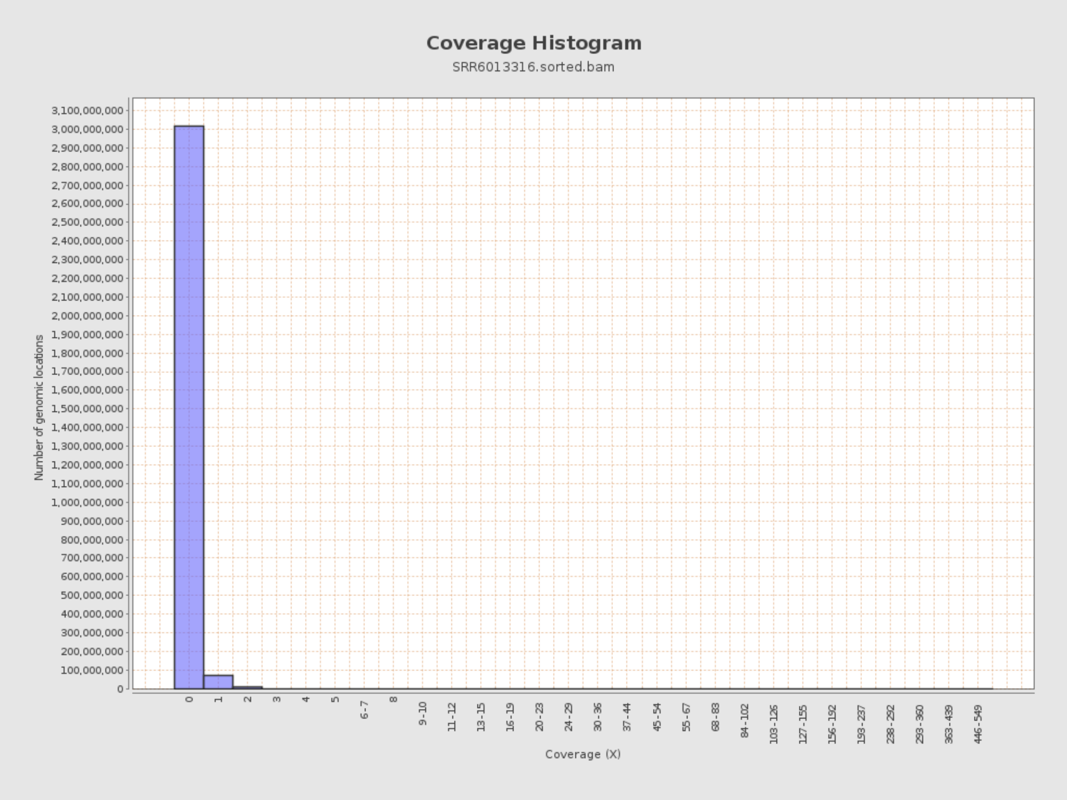
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5414522	0.0217	0.4708
chr2	243199373	10639905	0.0437	0.3147
chr3	198022430	5680240	0.0287	0.1872
chr4	191154276	5593631	0.0293	0.1944
chr5	180915260	4153886	0.023	0.1689
chr6	171115067	4582957	0.0268	0.2405
chr7	159138663	6548514	0.0411	0.5491

chr8	146364022	5579673	0.0381	0.2983
chr9	141213431	3001304	0.0213	0.243
chr10	135534747	3438438	0.0254	0.2691
chr11	135006516	4517366	0.0335	0.2631
chr12	133851895	5112400	0.0382	0.2177
chr13	115169878	2540747	0.0221	0.161
chr14	107349540	3068388	0.0286	0.1968
chr15	102531392	2105351	0.0205	0.161
chr16	90354753	3900323	0.0432	0.2447
chr17	81195210	2410596	0.0297	0.2322
chr18	78077248	2023842	0.0259	0.3921
chr19	59128983	1829055	0.0309	0.3392
chr20	63025520	2510702	0.0398	0.2226
chr21	48129895	2339100	0.0486	0.2533
chr22	51304566	647901	0.0126	0.1243
chrMT	16571	22924	1.3834	1.4196
chrX	155270560	4624722	0.0298	0.2107
chrY	59373566	192524	0.0032	0.0781

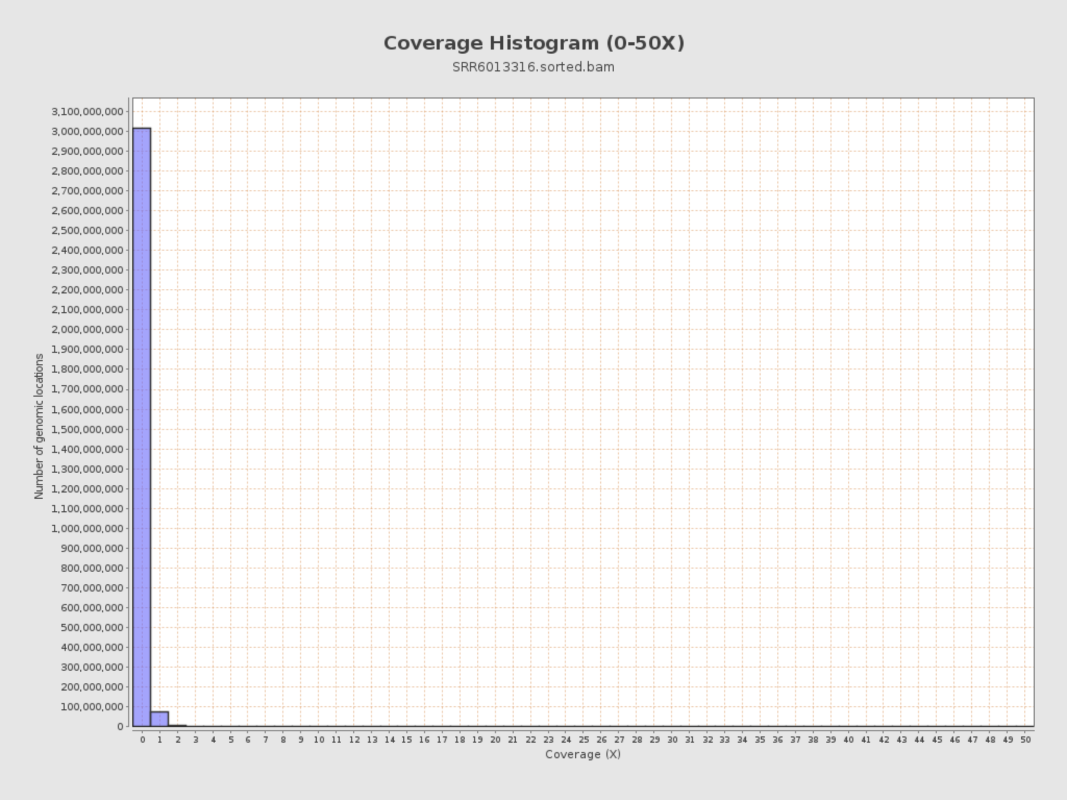
3. Results : Coverage across reference



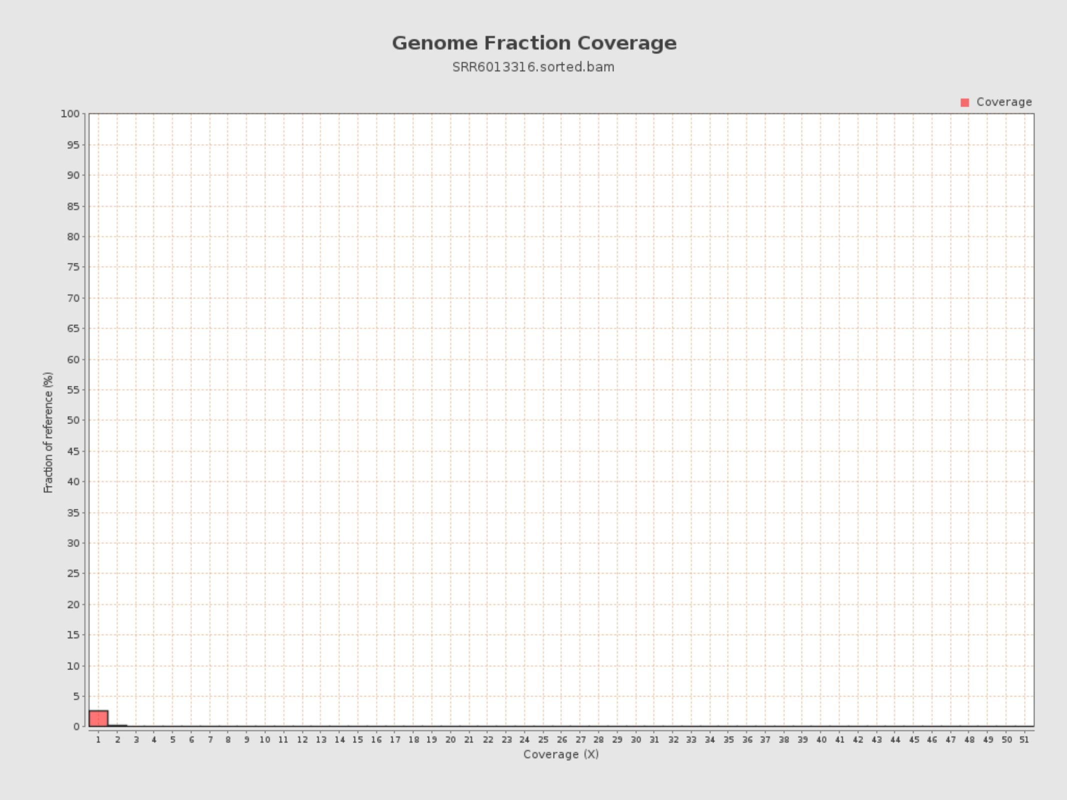
4. Results : Coverage Histogram



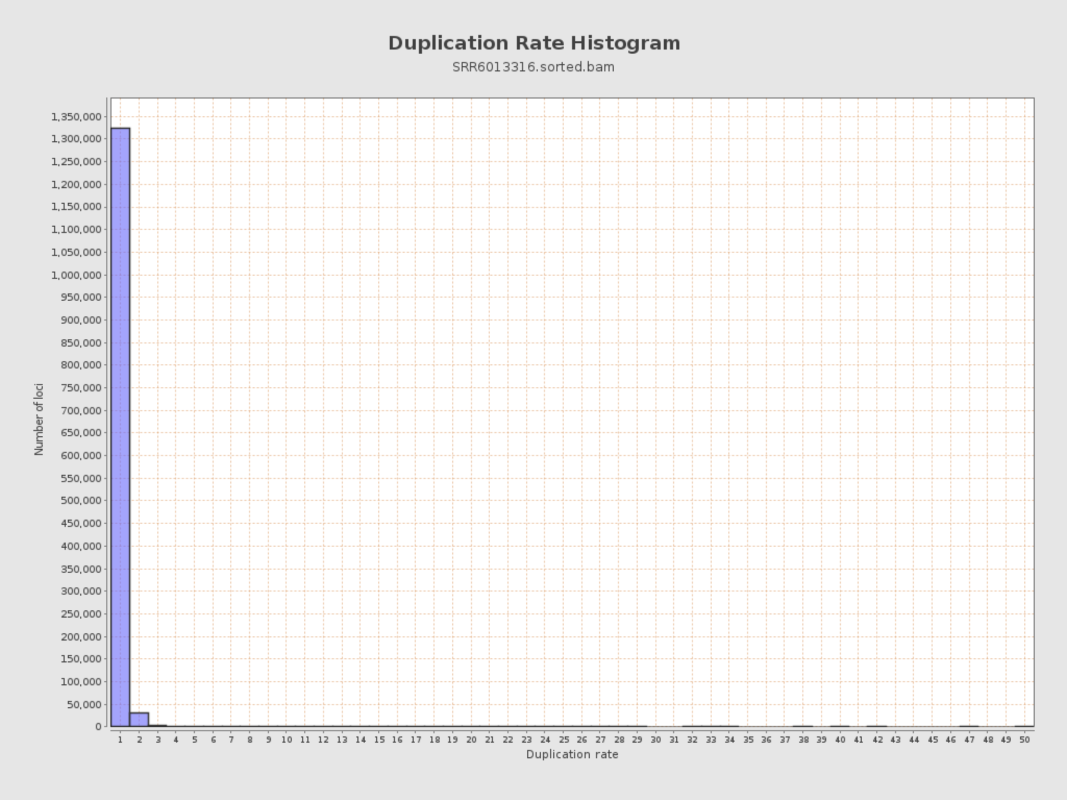
5. Results : Coverage Histogram (0-50X)



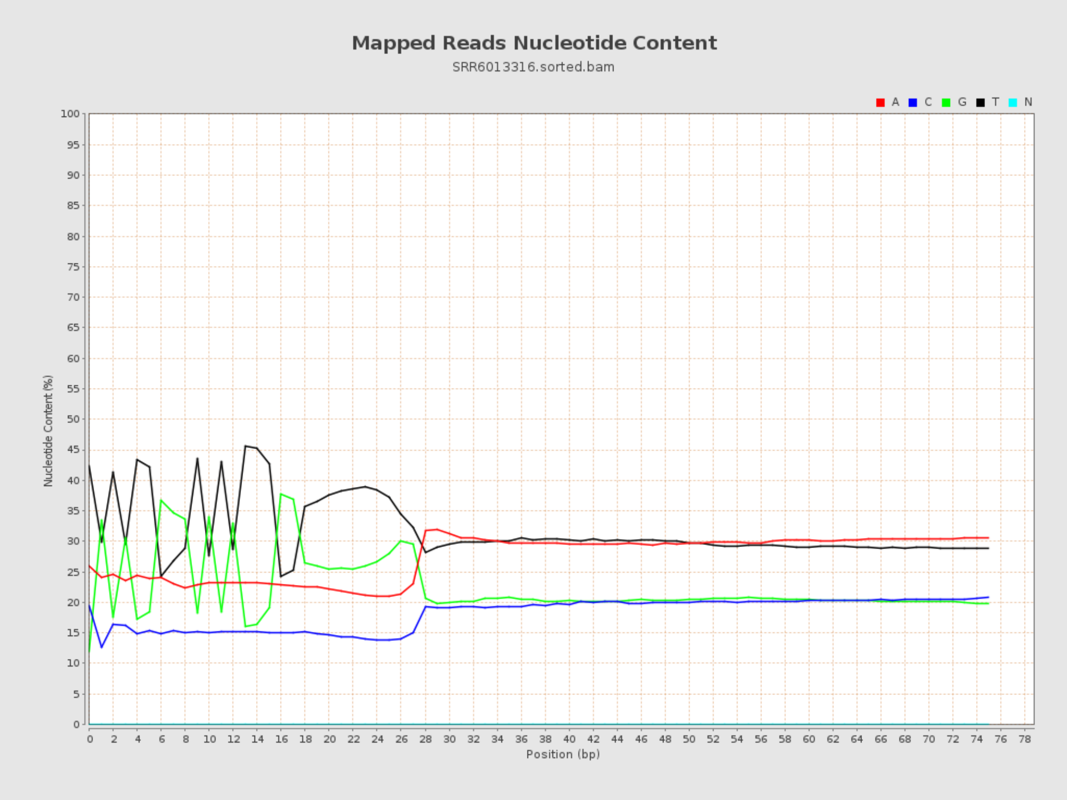
6. Results : Genome Fraction Coverage



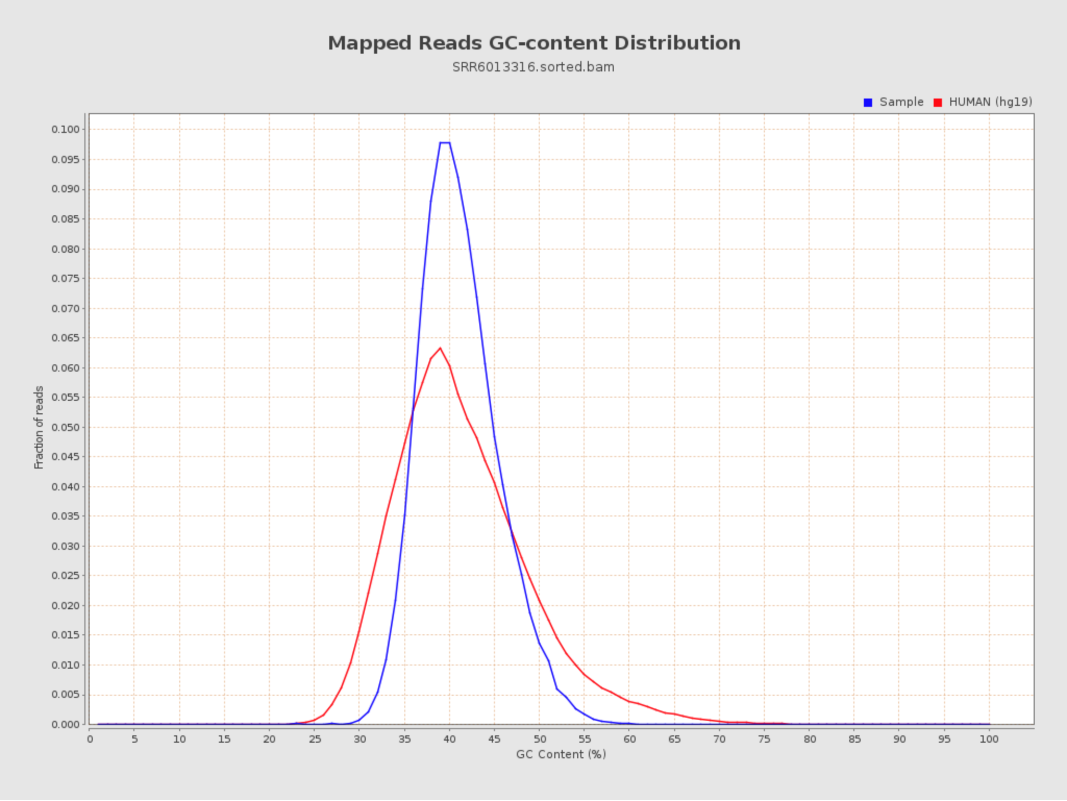
7. Results : Duplication Rate Histogram



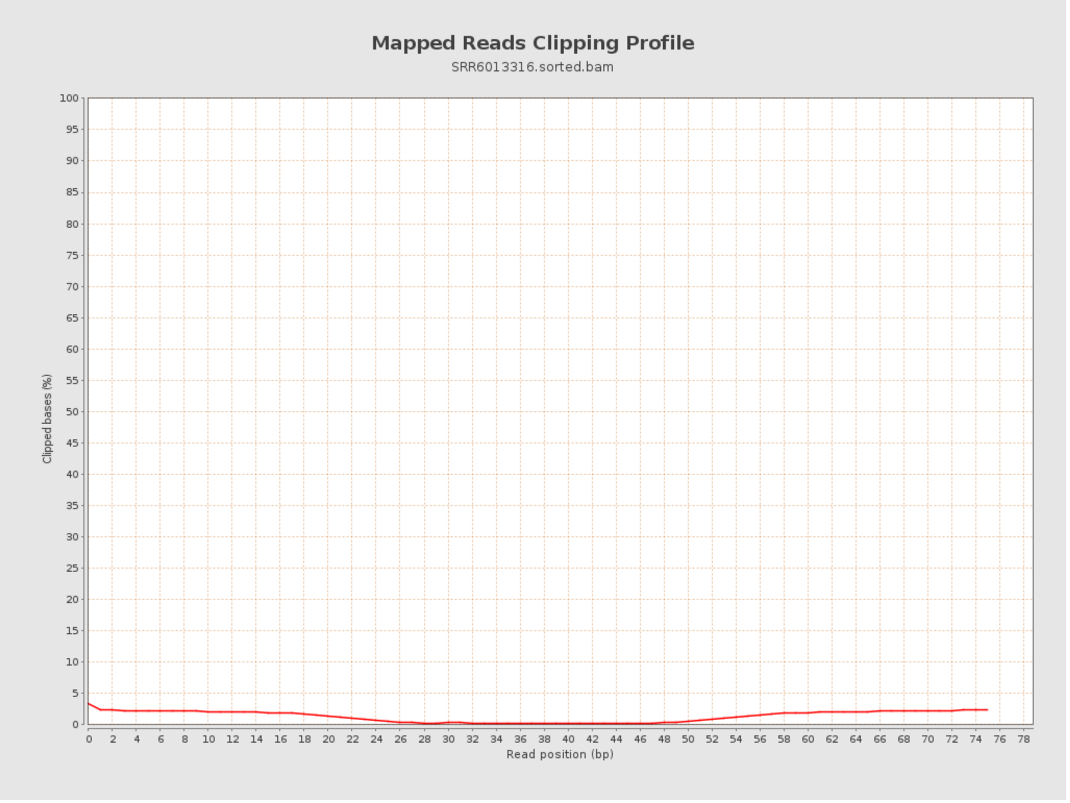
8. Results : Mapped Reads Nucleotide Content



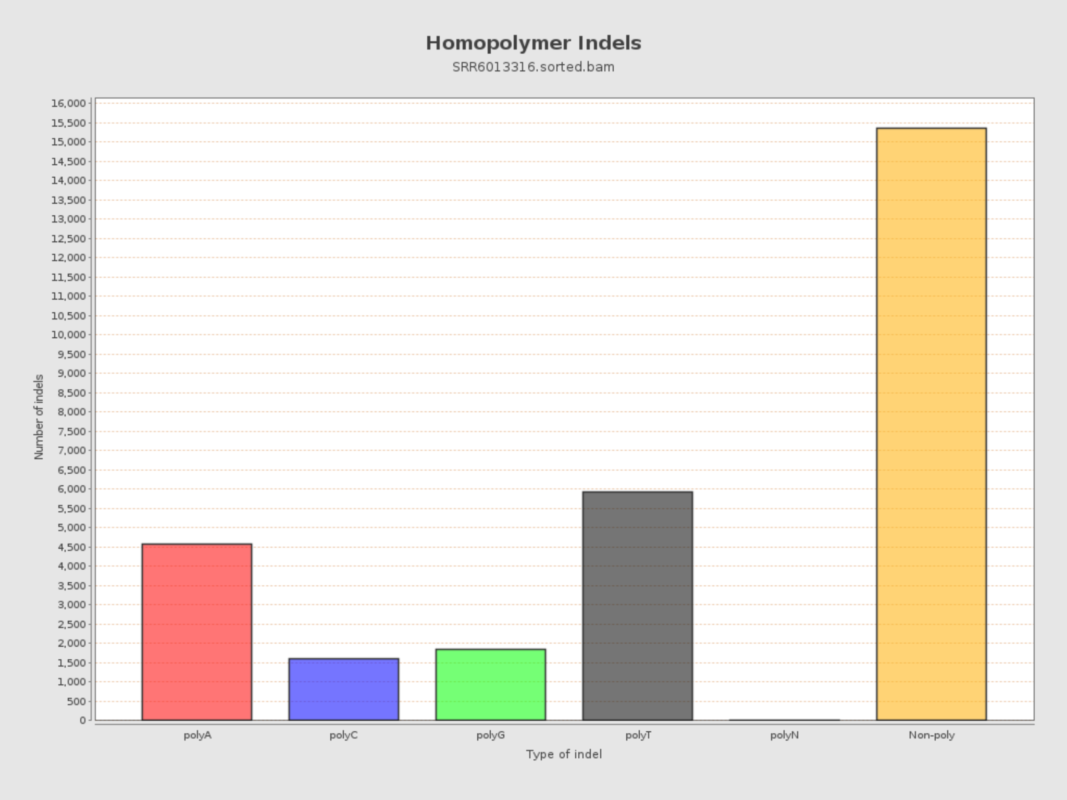
9. Results : Mapped Reads GC-content Distribution



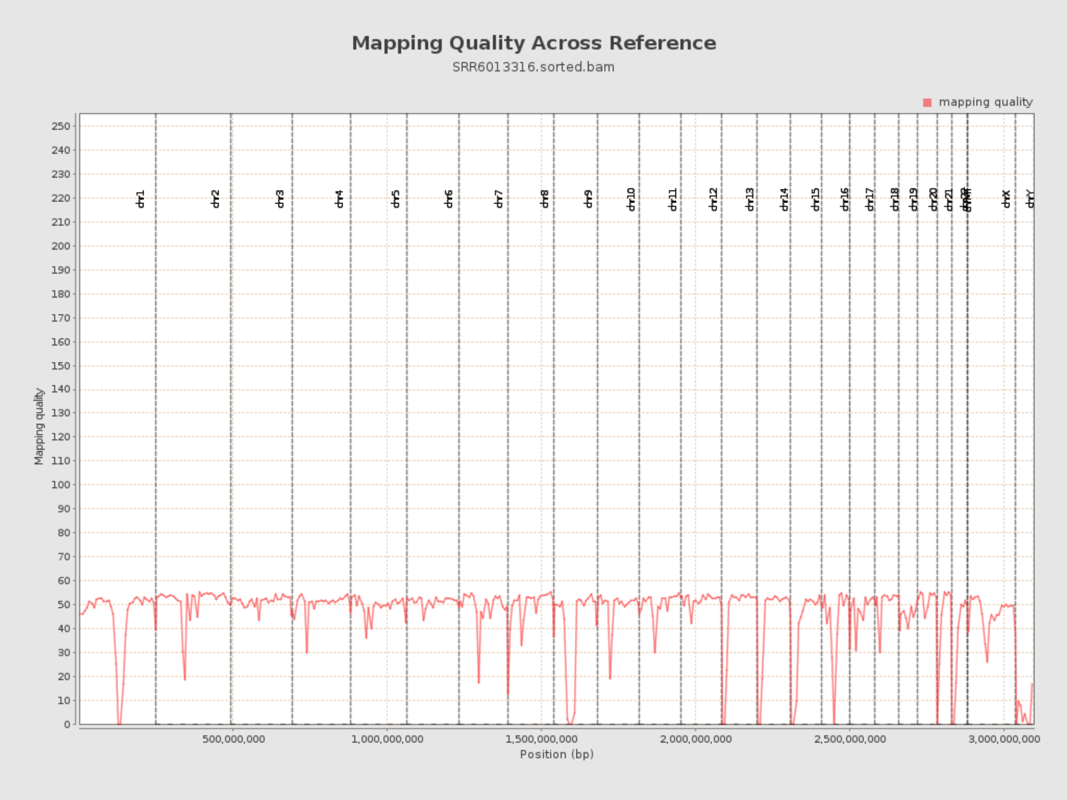
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram