Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:09:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013357.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_SRR6013357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013357.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:09:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,438,245
Mapped reads	1,247,972 / 86.77%
Unmapped reads	190,273 / 13.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,384 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	134,369 / 9.34%
Duplication rate	9.01%
Clipped reads	685,282 / 47.65%

2.2. ACGT Content

Number/percentage of A's	21,346,926 / 26.68%
Number/percentage of C's	14,385,369 / 17.98%
Number/percentage of T's	25,825,614 / 32.28%
Number/percentage of G's	18,445,825 / 23.06%
Number/percentage of N's	1,117 / 0%
GC Percentage	41.04%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.2795

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

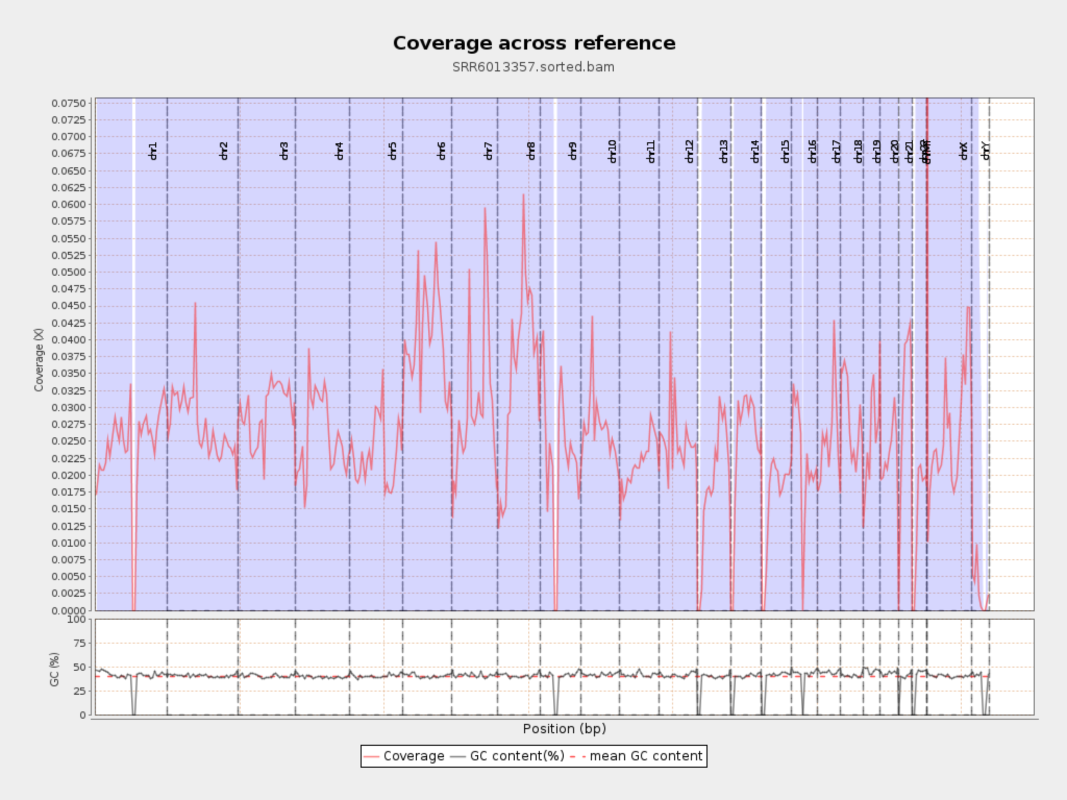
General error rate	0.82%
Mismatches	644,343
Insertions	5,784
Mapped reads with at least one insertion	0.46%
Deletions	25,183
Mapped reads with at least one deletion	1.99%
Homopolymer indels	48.79%

2.6. Chromosome stats

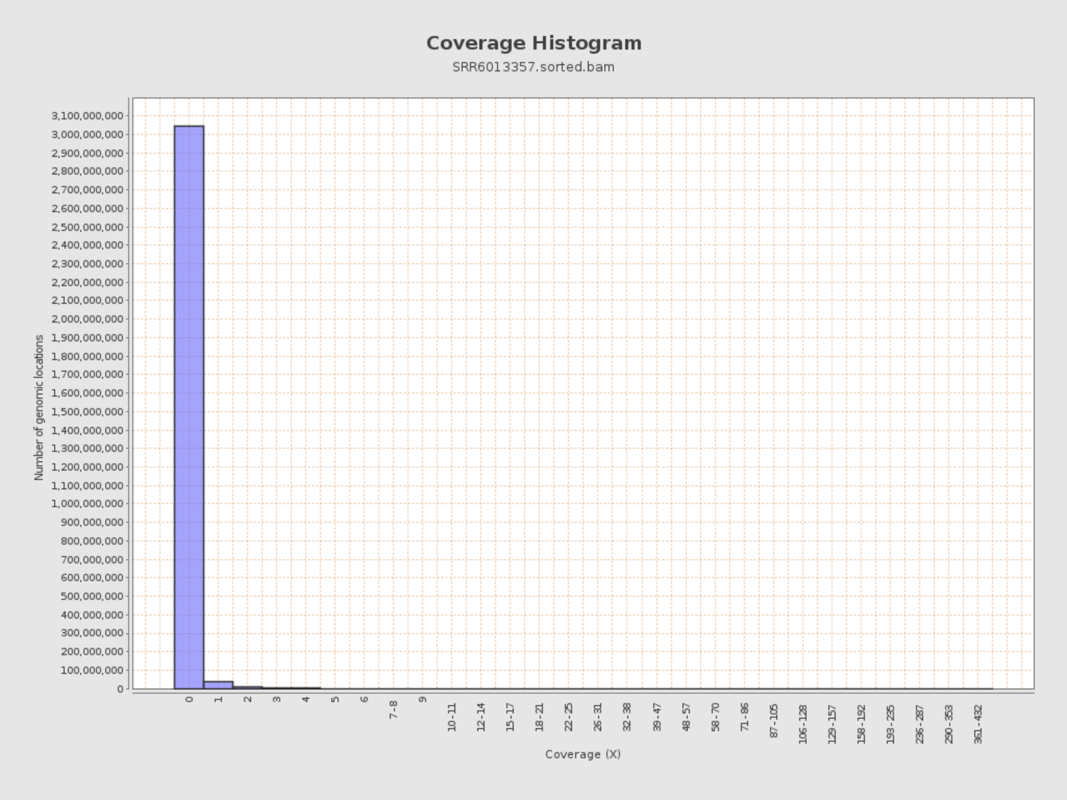
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6001823	0.0241	0.3313
chr2	243199373	6672349	0.0274	0.3372
chr3	198022430	5841363	0.0295	0.2417
chr4	191154276	4946939	0.0259	0.2374
chr5	180915260	4195567	0.0232	0.2119
chr6	171115067	6861035	0.0401	0.3091
chr7	159138663	4788596	0.0301	0.4642

chr8	146364022	5190111	0.0355	0.3383
chr9	141213431	3307065	0.0234	0.2574
chr10	135534747	3666430	0.0271	0.2787
chr11	135006516	2967895	0.022	0.2337
chr12	133851895	3391052	0.0253	0.2259
chr13	115169878	2137422	0.0186	0.1898
chr14	107349540	2597357	0.0242	0.2239
chr15	102531392	1653032	0.0161	0.1814
chr16	90354753	1962190	0.0217	0.2106
chr17	81195210	2084282	0.0257	0.231
chr18	78077248	2213208	0.0283	0.3914
chr19	59128983	1518432	0.0257	0.2823
chr20	63025520	1466757	0.0233	0.215
chr21	48129895	1492937	0.031	0.2547
chr22	51304566	736361	0.0144	0.1654
chrMT	16571	31011	1.8714	2.0826
chrX	155270560	4151184	0.0267	0.2359
chrY	59373566	175777	0.003	0.0962

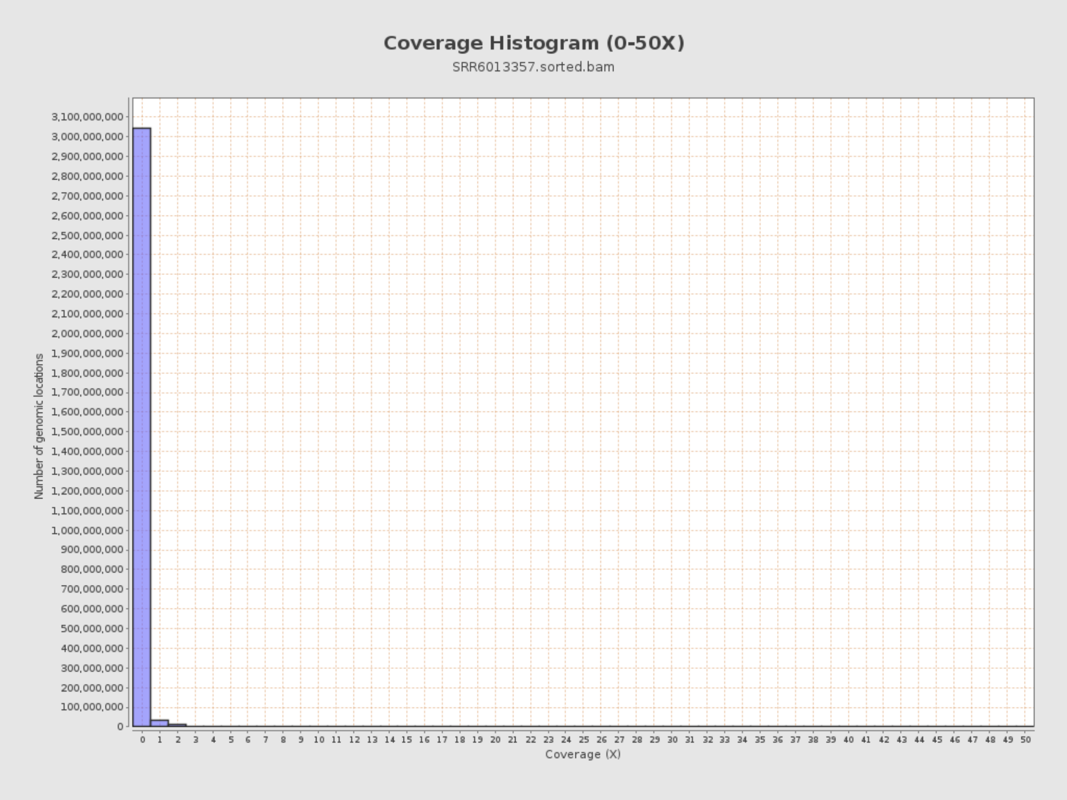
3. Results : Coverage across reference



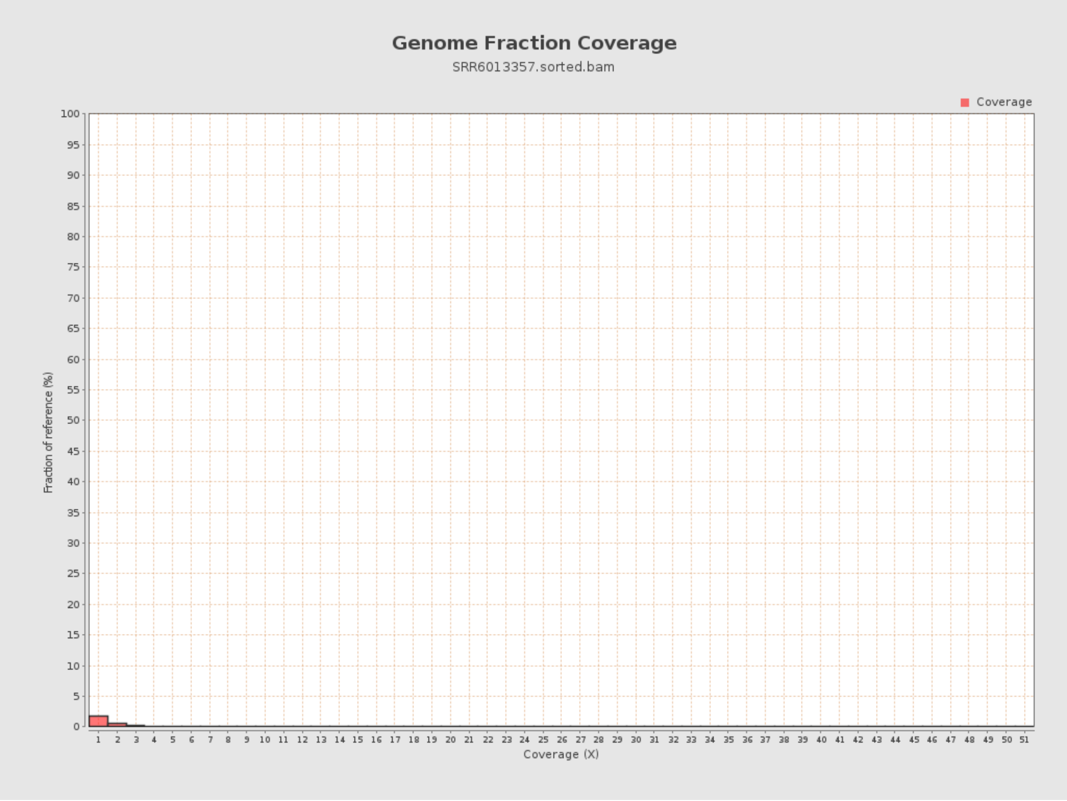
4. Results : Coverage Histogram



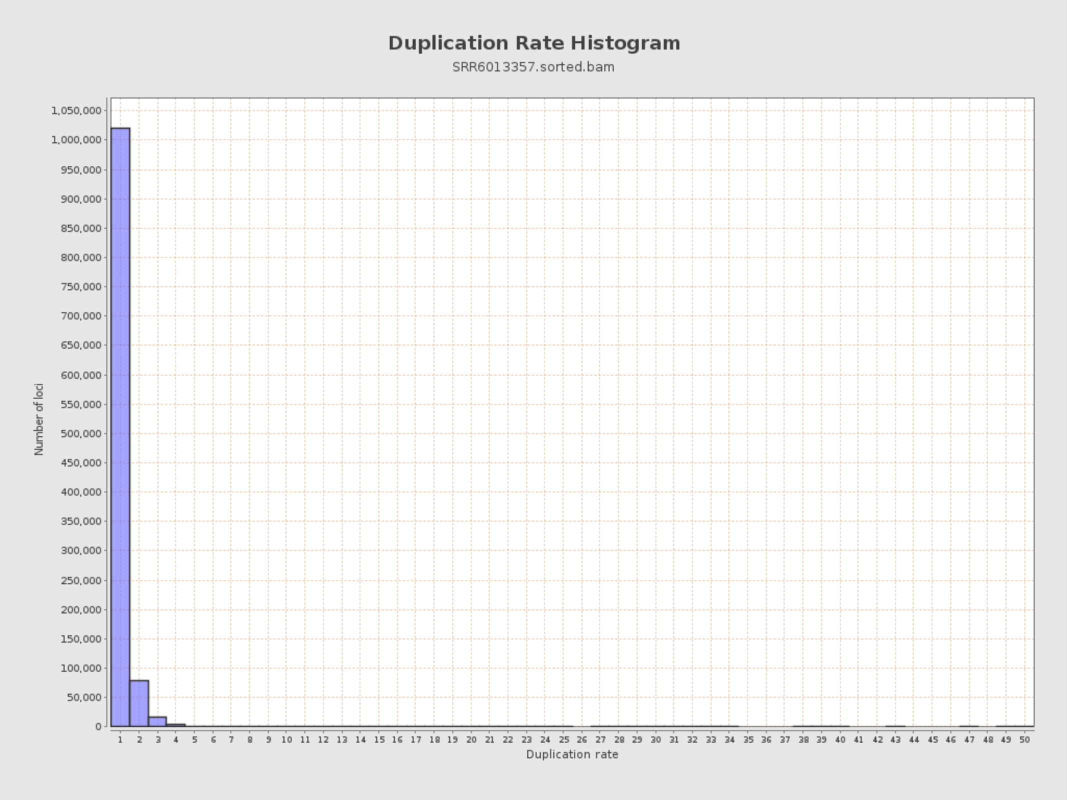
5. Results : Coverage Histogram (0-50X)



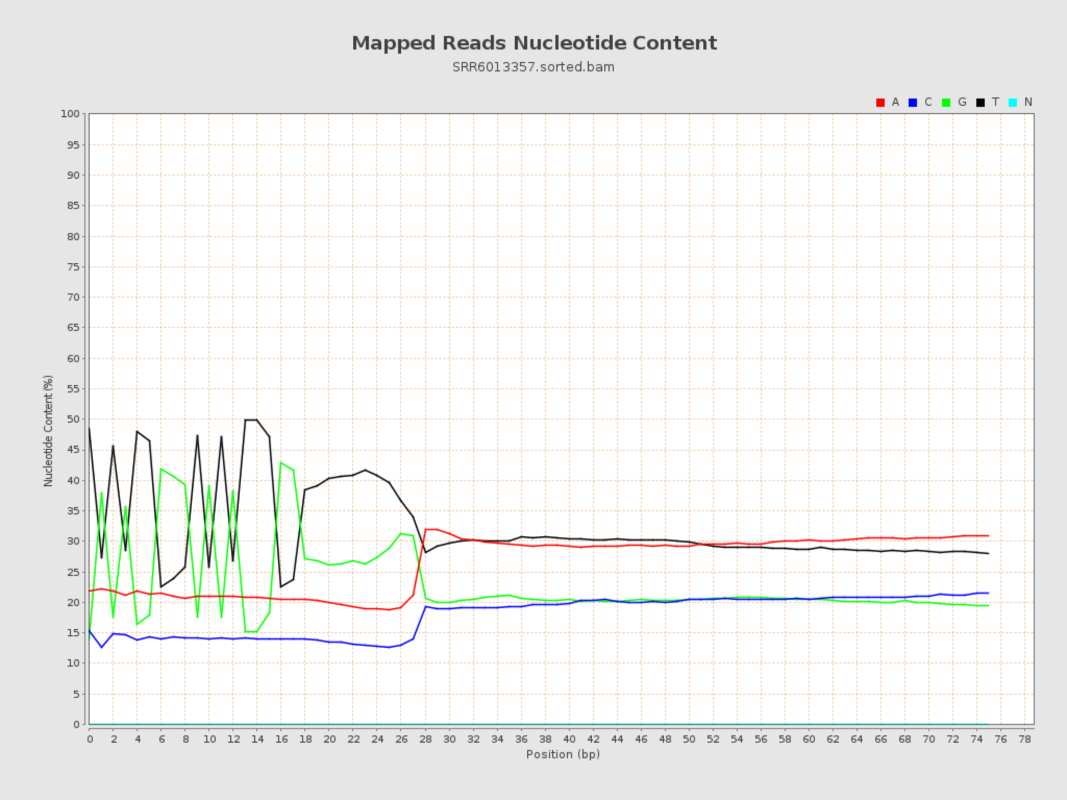
6. Results : Genome Fraction Coverage



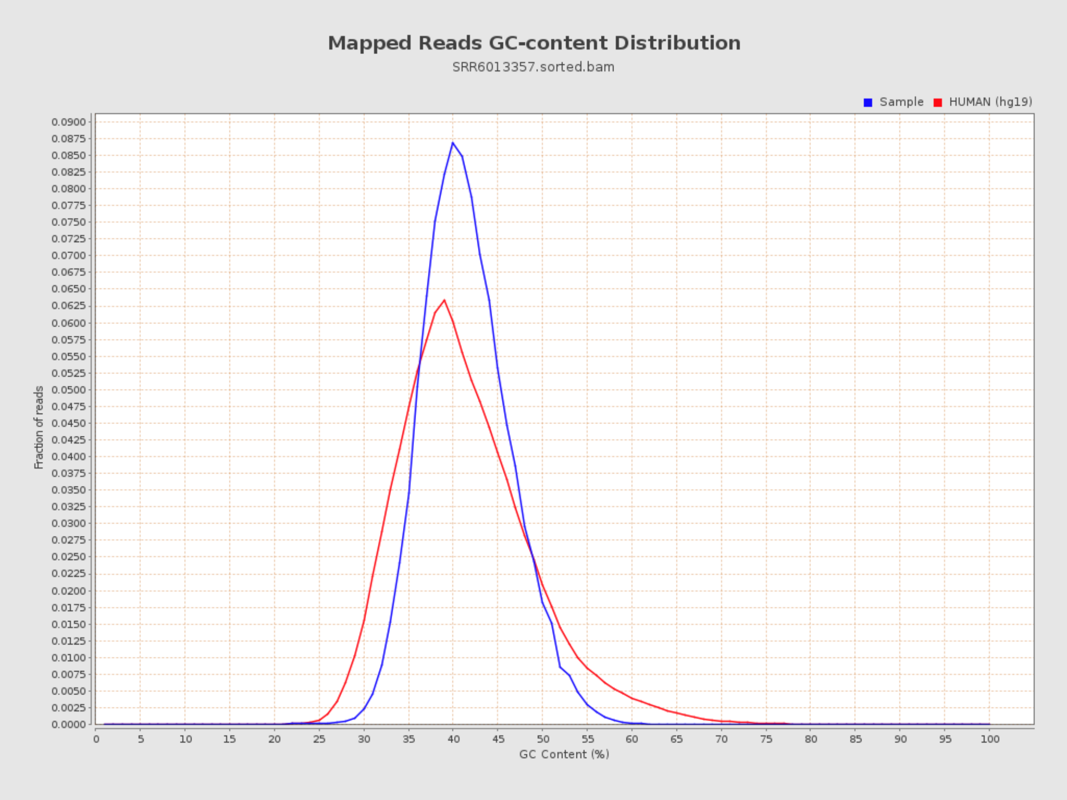
7. Results : Duplication Rate Histogram



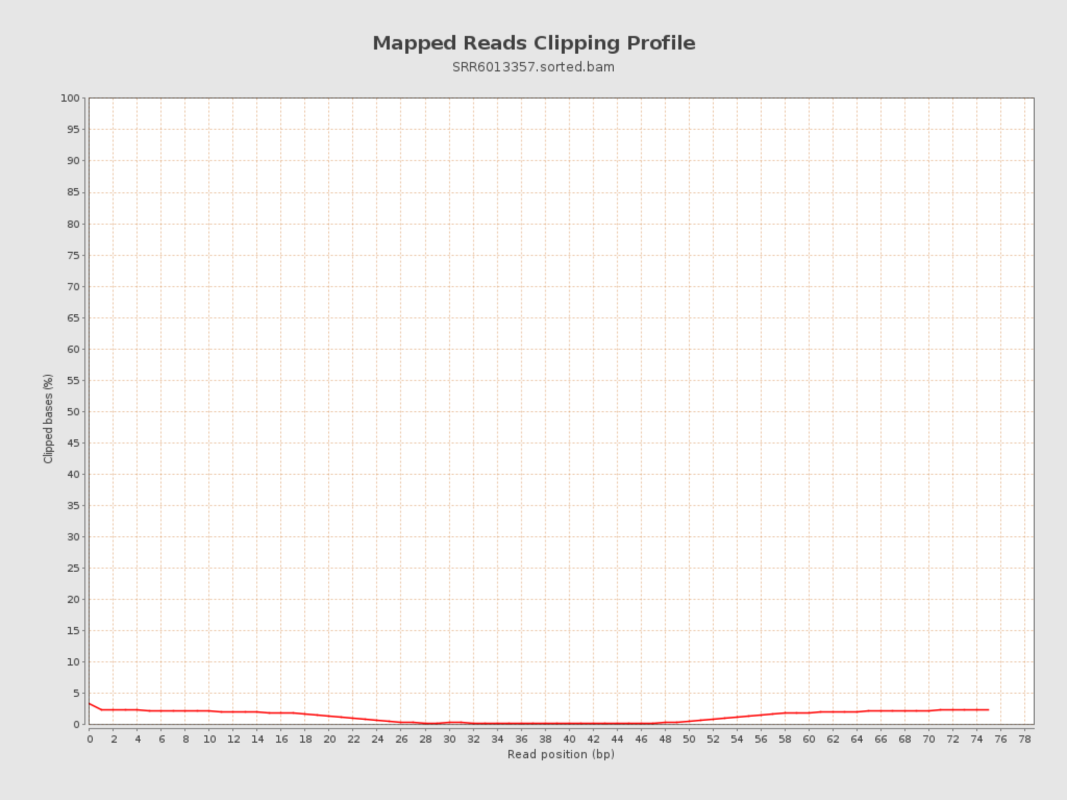
8. Results : Mapped Reads Nucleotide Content



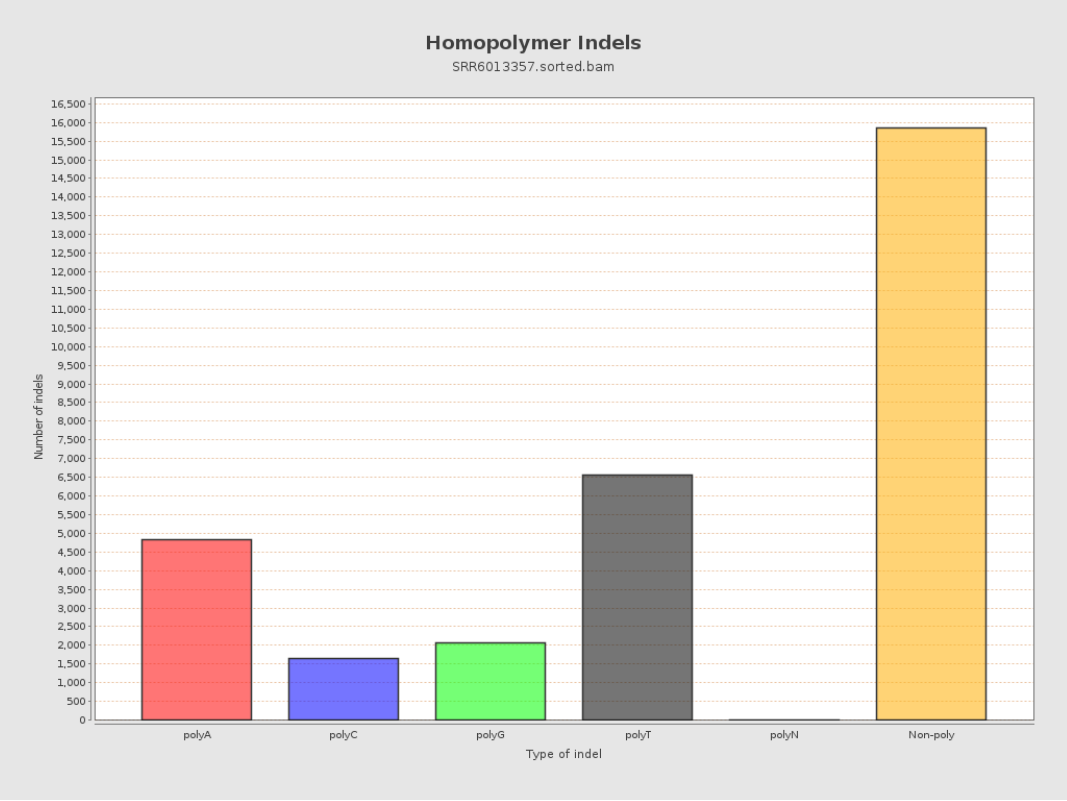
9. Results : Mapped Reads GC-content Distribution



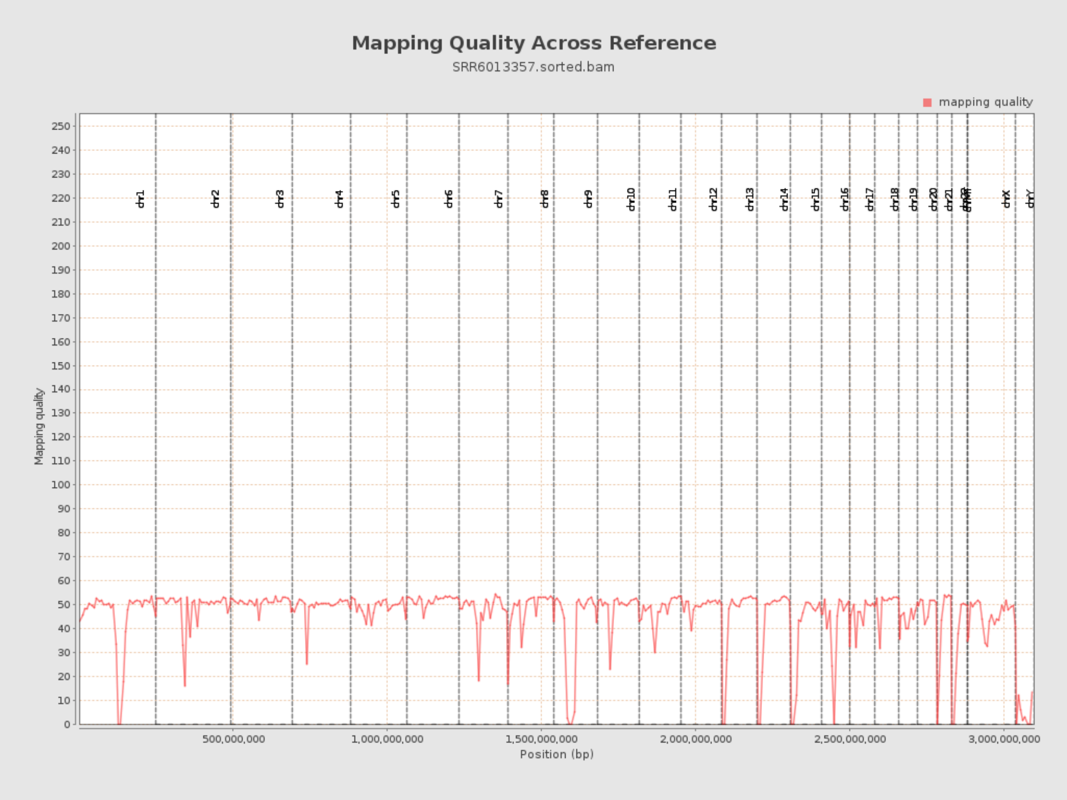
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram