Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:41:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013368.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_SRR6013368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013368.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:41:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013368.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,598,597
Mapped reads	2,309,879 / 88.89%
Unmapped reads	288,718 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,231 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	116,259 / 4.47%
Duplication rate	3.33%
Clipped reads	1,065,530 / 41%

2.2. ACGT Content

Number/percentage of A's	42,398,463 / 27.62%
Number/percentage of C's	28,399,478 / 18.5%
Number/percentage of T's	48,276,729 / 31.45%
Number/percentage of G's	34,408,046 / 22.41%
Number/percentage of N's	31,110 / 0.02%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0496

Standard Deviation	0.6035

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

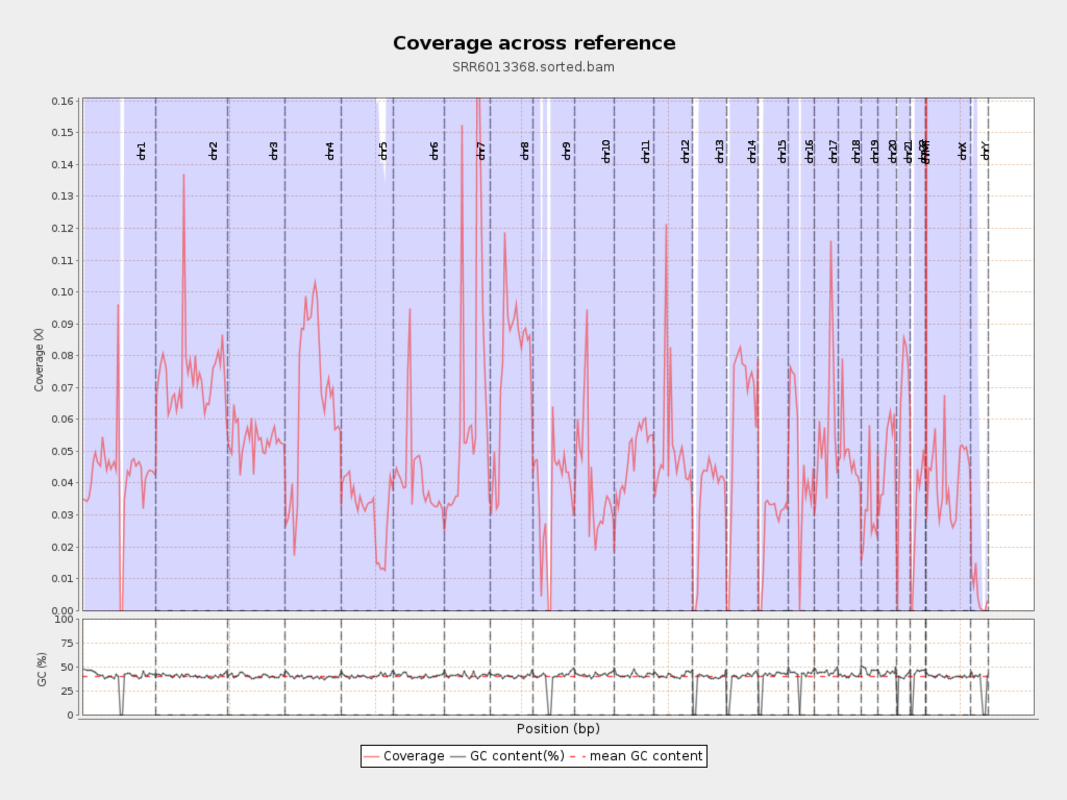
General error rate	0.83%
Mismatches	1,257,440
Insertions	11,158
Mapped reads with at least one insertion	0.48%
Deletions	35,693
Mapped reads with at least one deletion	1.53%
Homopolymer indels	45.63%

2.6. Chromosome stats

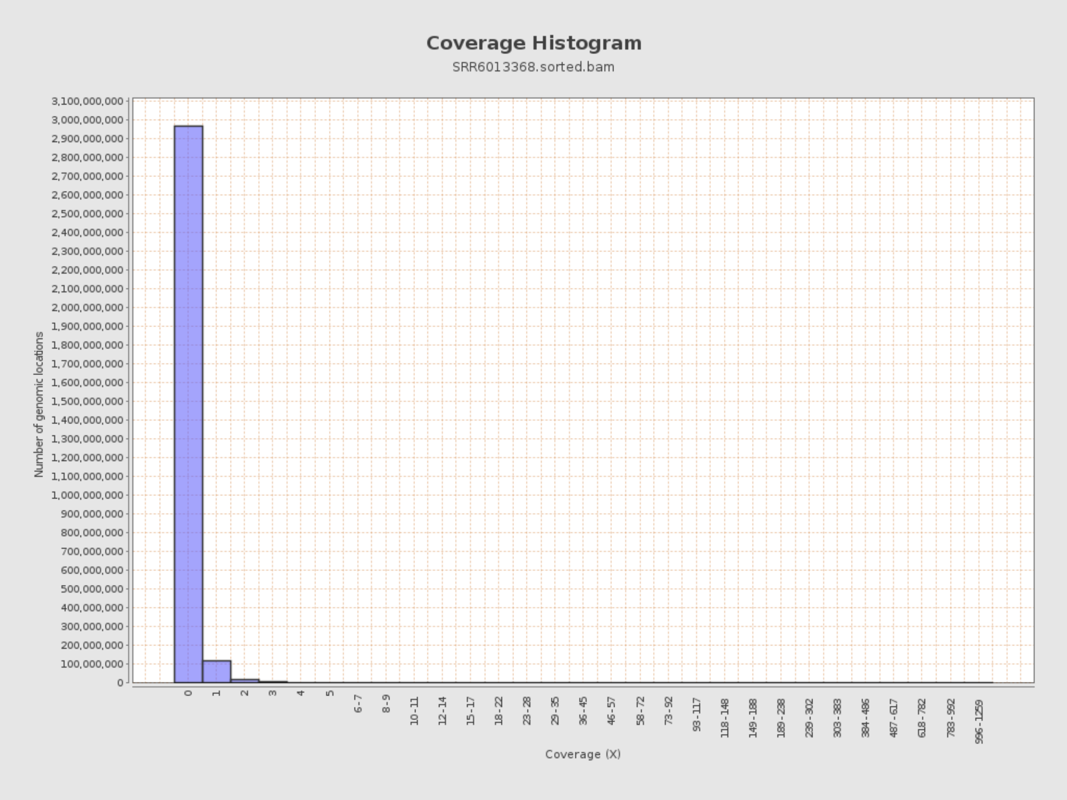
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10591416	0.0425	1.0076
chr2	243199373	18002702	0.074	0.7137
chr3	198022430	10613350	0.0536	0.2596
chr4	191154276	12944462	0.0677	0.3208
chr5	180915260	5690046	0.0315	0.2039
chr6	171115067	7332996	0.0429	0.388
chr7	159138663	10633812	0.0668	1.3875

chr8	146364022	11169070	0.0763	0.7172
chr9	141213431	4970911	0.0352	0.4959
chr10	135534747	5513761	0.0407	0.5832
chr11	135006516	6528897	0.0484	0.4221
chr12	133851895	6837555	0.0511	0.2698
chr13	115169878	4021413	0.0349	0.2108
chr14	107349540	6723968	0.0626	0.3154
chr15	102531392	2683187	0.0262	0.1889
chr16	90354753	4227172	0.0468	0.2985
chr17	81195210	4812582	0.0593	0.3128
chr18	78077248	3855667	0.0494	1.0875
chr19	59128983	1820592	0.0308	0.7345
chr20	63025520	3048262	0.0484	0.273
chr21	48129895	2972708	0.0618	0.294
chr22	51304566	1597143	0.0311	0.196
chrMT	16571	175251	10.5758	6.6103
chrX	155270560	6510700	0.0419	0.2913
chrY	59373566	296966	0.005	0.119

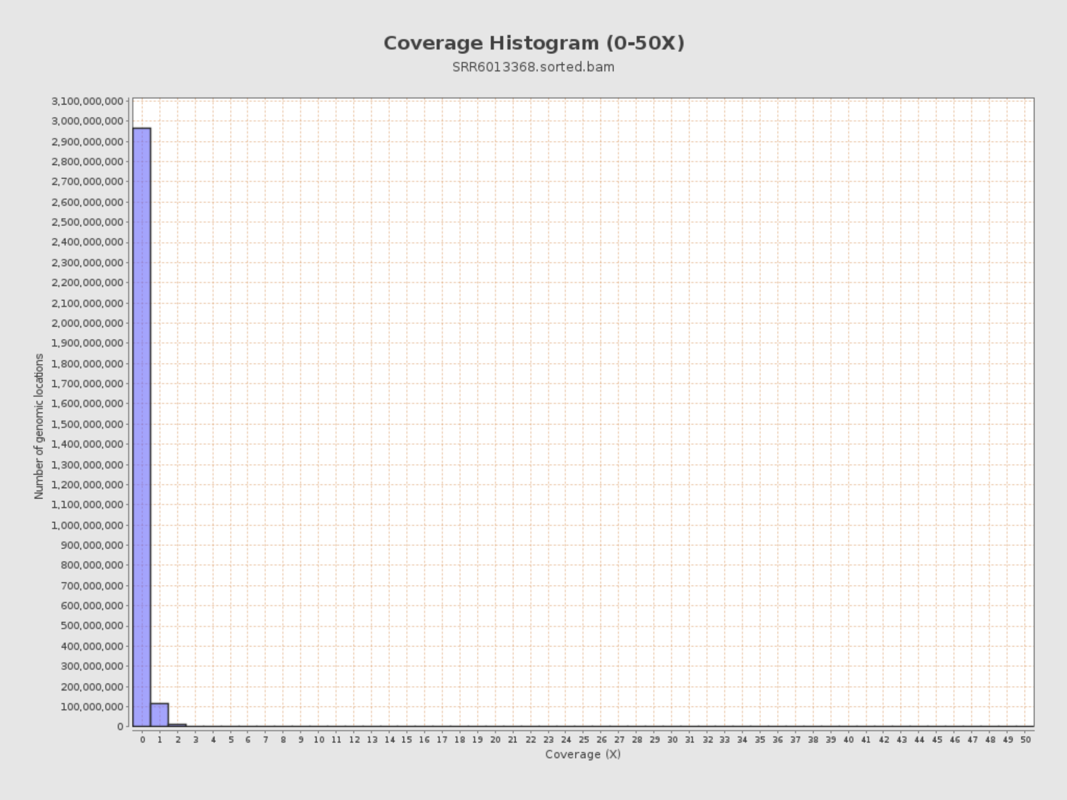
3. Results : Coverage across reference



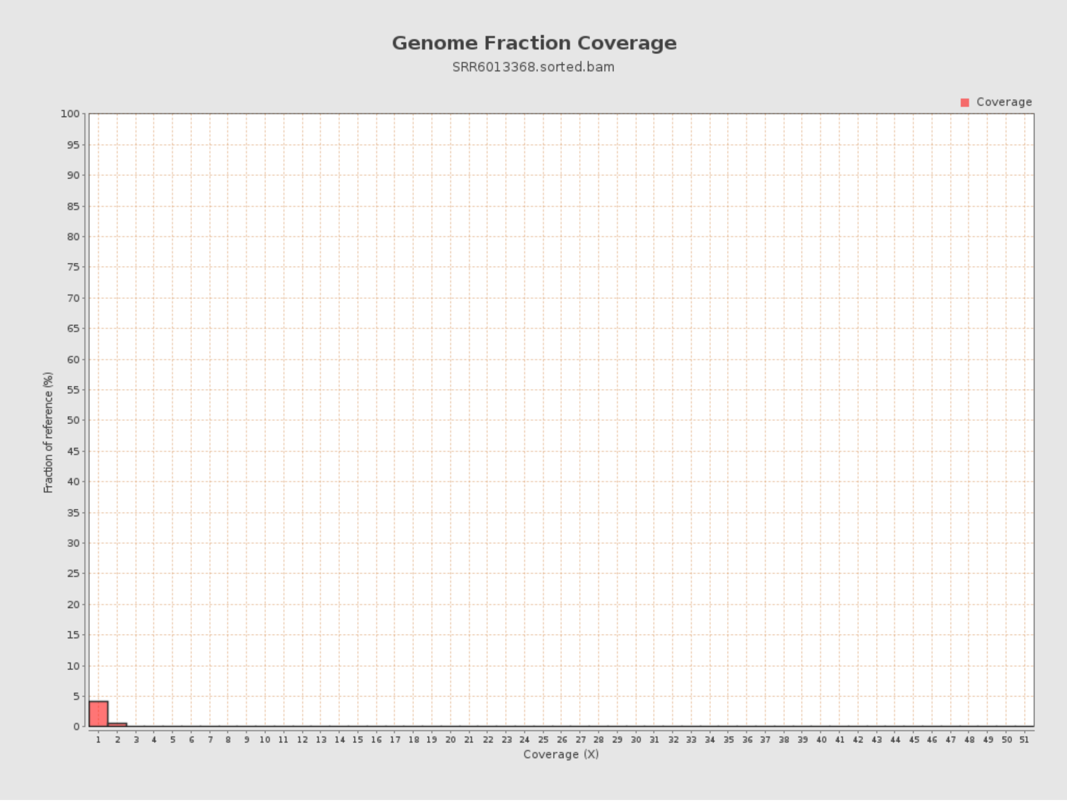
4. Results : Coverage Histogram



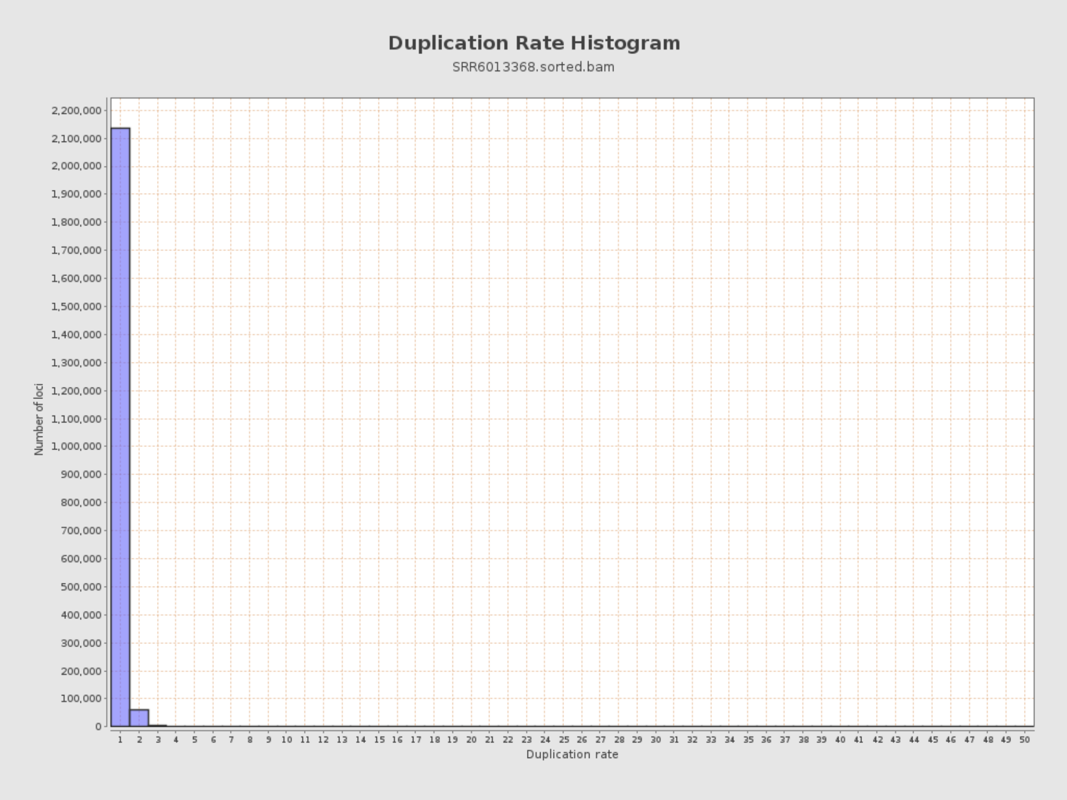
5. Results : Coverage Histogram (0-50X)



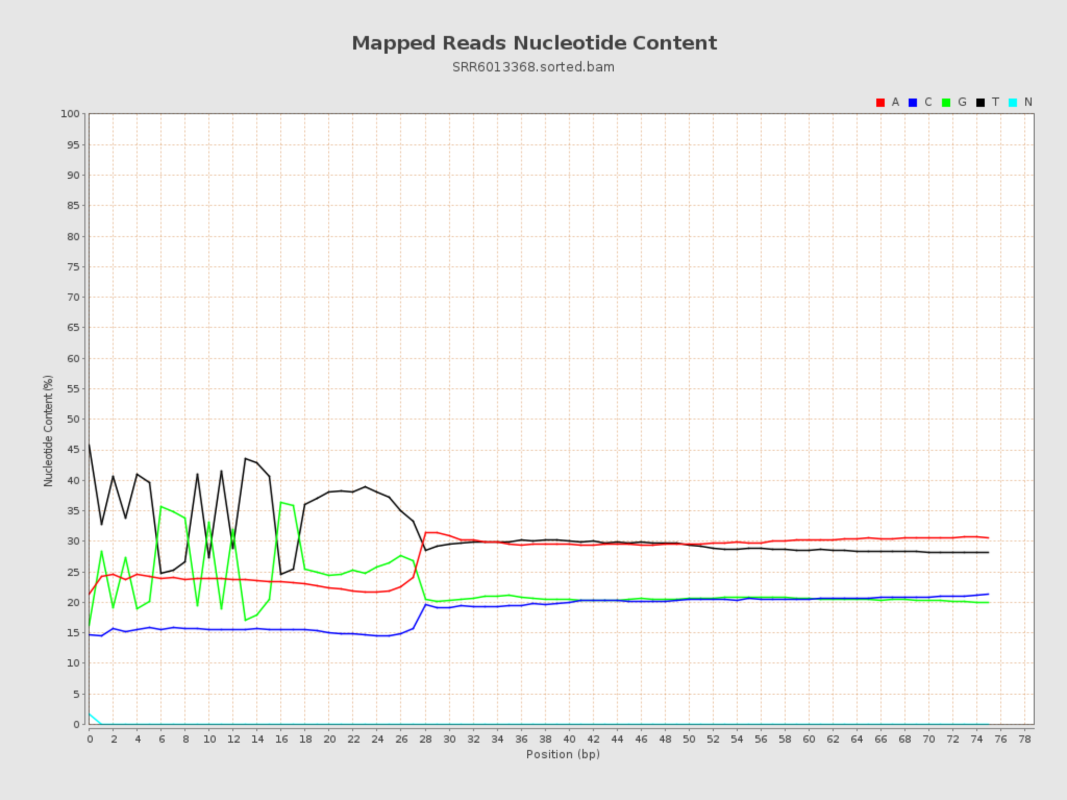
6. Results : Genome Fraction Coverage



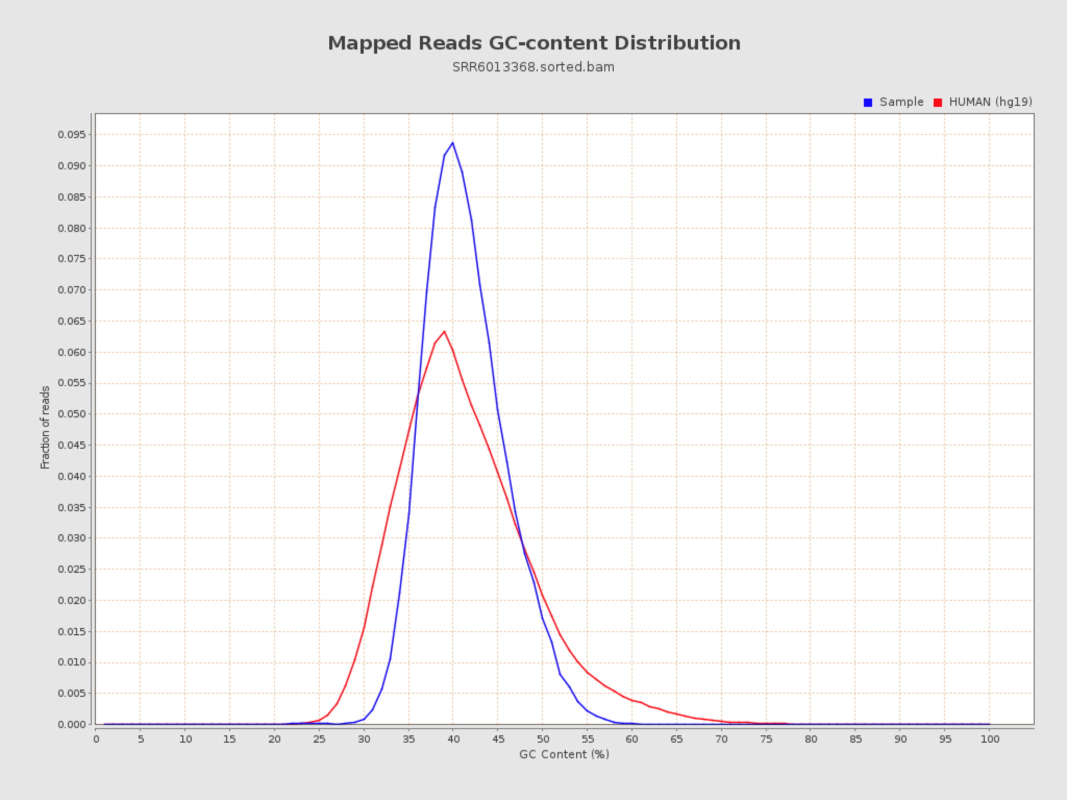
7. Results : Duplication Rate Histogram



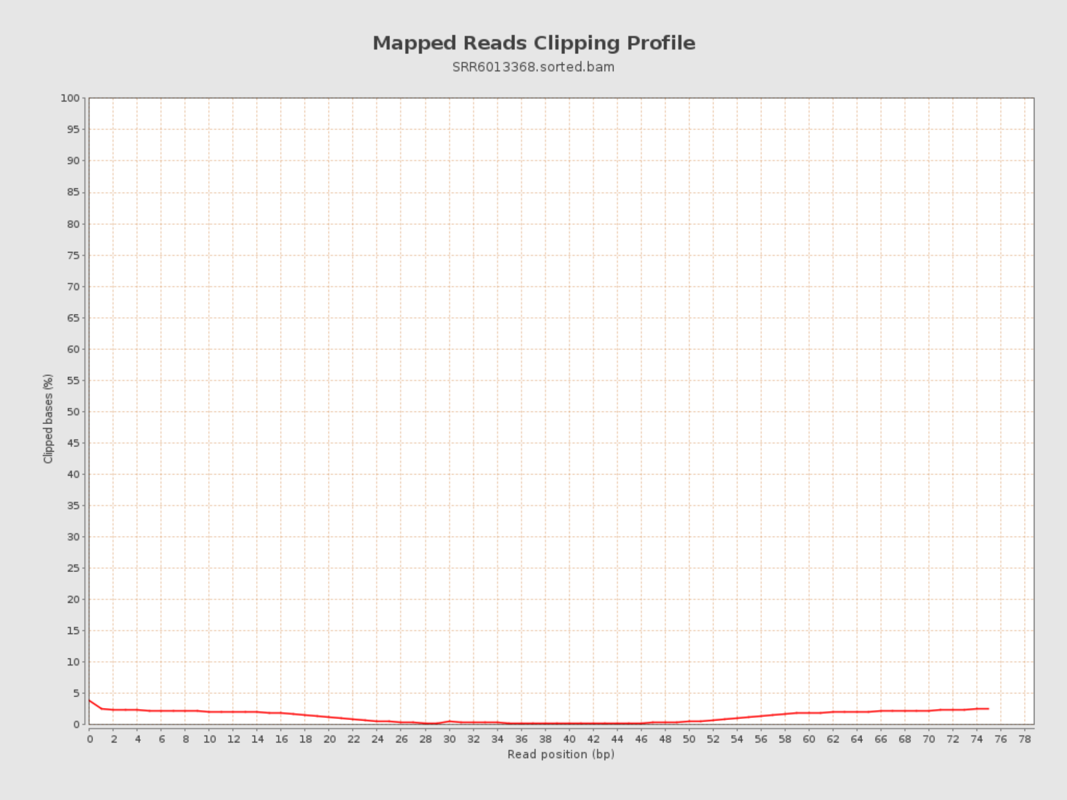
8. Results : Mapped Reads Nucleotide Content



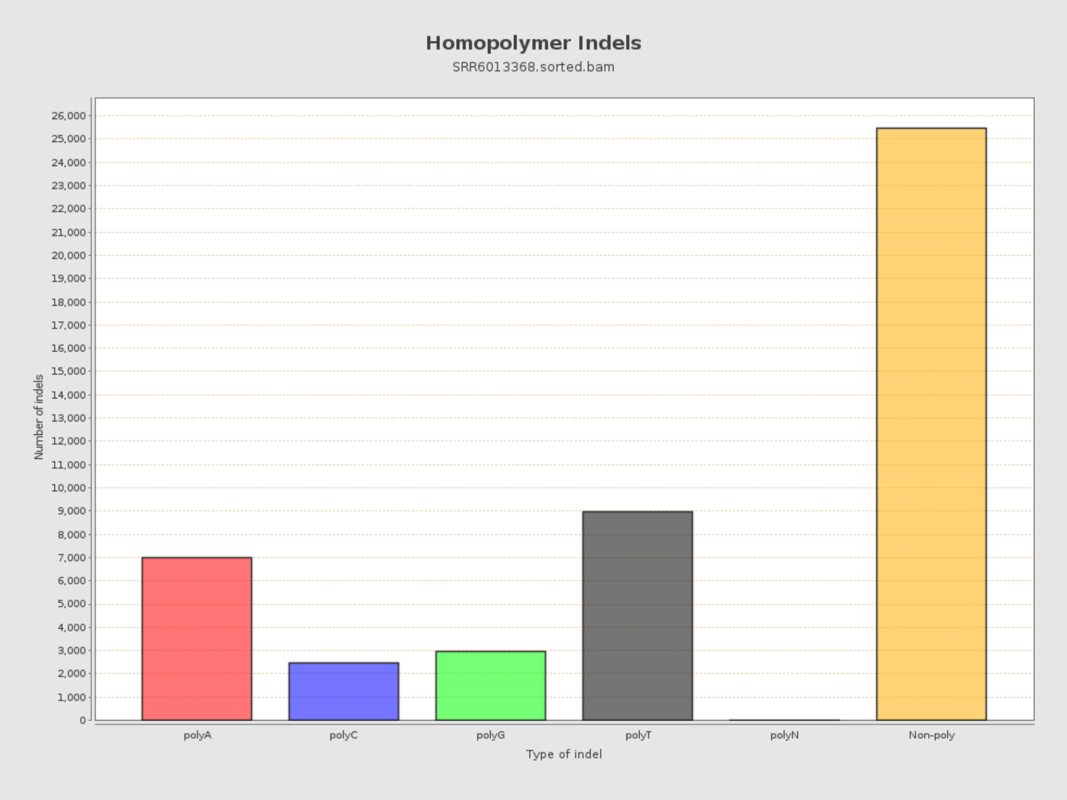
9. Results : Mapped Reads GC-content Distribution



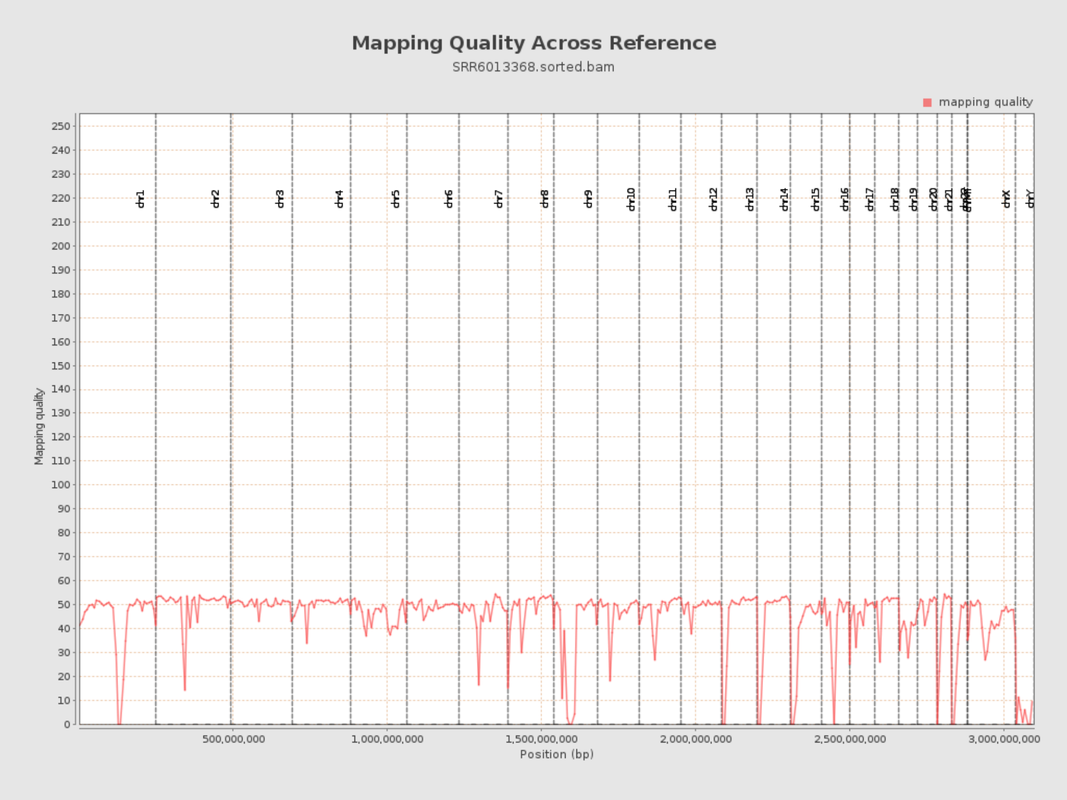
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram