Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:23:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013362.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_SRR6013362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013362.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:23:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,036,938
Mapped reads	1,772,664 / 87.03%
Unmapped reads	264,274 / 12.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,712 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	99,708 / 4.89%
Duplication rate	4.44%
Clipped reads	744,157 / 36.53%

2.2. ACGT Content

Number/percentage of A's	33,761,068 / 28.25%
Number/percentage of C's	21,864,955 / 18.3%
Number/percentage of T's	38,295,642 / 32.05%
Number/percentage of G's	25,553,591 / 21.38%
Number/percentage of N's	25,336 / 0.02%
GC Percentage	39.68%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3681

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

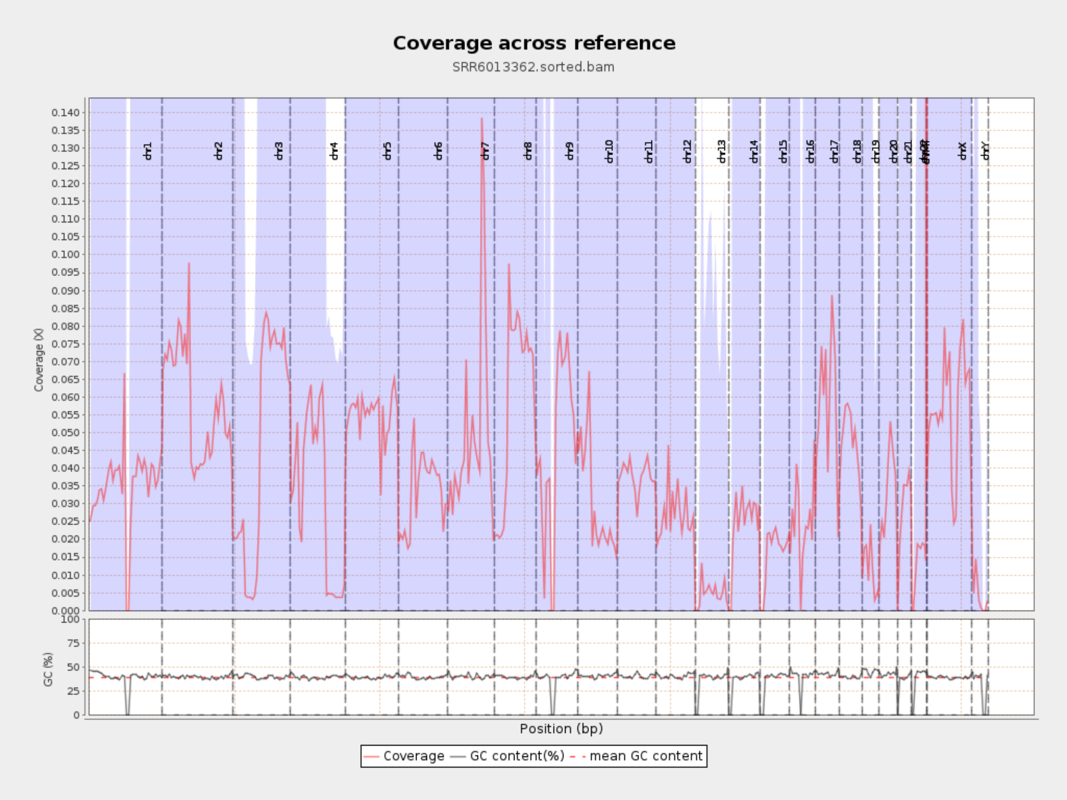
General error rate	0.82%
Mismatches	960,468
Insertions	9,030
Mapped reads with at least one insertion	0.51%
Deletions	29,061
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.53%

2.6. Chromosome stats

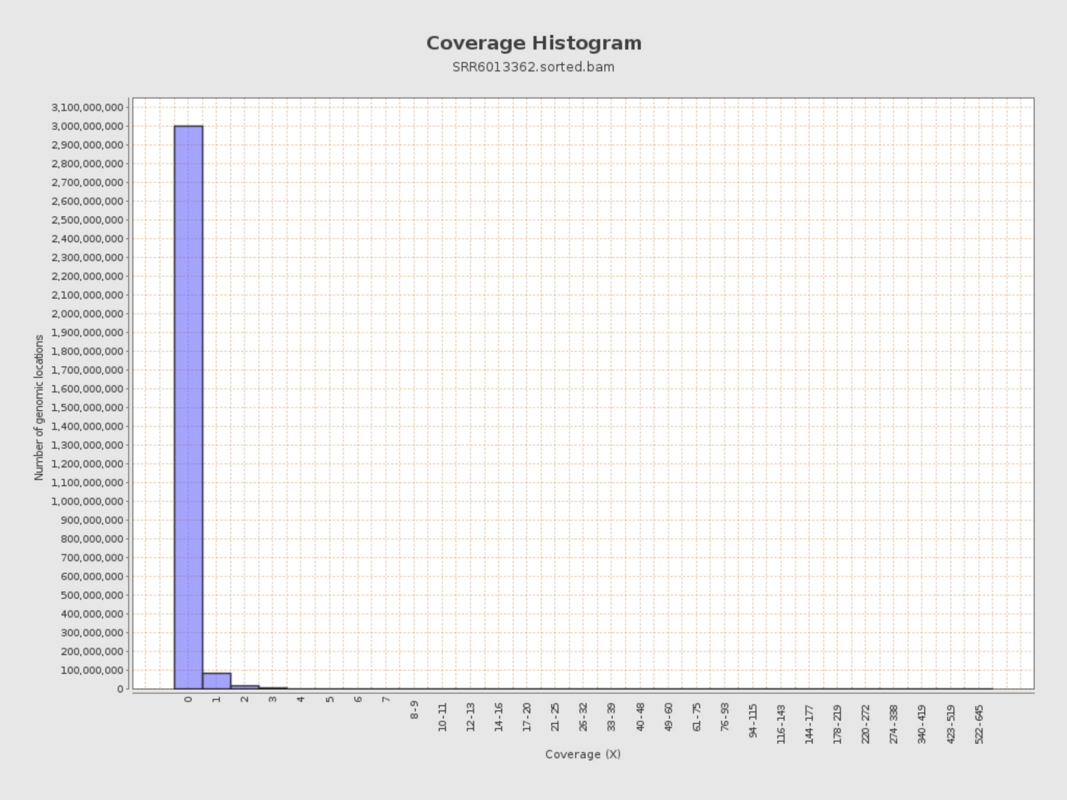
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8734620	0.035	0.6011
chr2	243199373	14296854	0.0588	0.5305
chr3	198022430	9055852	0.0457	0.2553
chr4	191154276	6006305	0.0314	0.254
chr5	180915260	9972990	0.0551	0.2789
chr6	171115067	5728016	0.0335	0.2765
chr7	159138663	8105114	0.0509	0.515

chr8	146364022	8777765	0.06	0.4269
chr9	141213431	6546581	0.0464	0.3931
chr10	135534747	4151029	0.0306	0.3685
chr11	135006516	5051535	0.0374	0.2771
chr12	133851895	3600461	0.0269	0.2013
chr13	115169878	570064	0.0049	0.0834
chr14	107349540	2578227	0.024	0.2007
chr15	102531392	1647330	0.0161	0.1496
chr16	90354753	2279868	0.0252	0.2102
chr17	81195210	4716272	0.0581	0.3614
chr18	78077248	3734558	0.0478	0.5355
chr19	59128983	721395	0.0122	0.4965
chr20	63025520	2135819	0.0339	0.2238
chr21	48129895	1368061	0.0284	0.2336
chr22	51304566	664677	0.013	0.1301
chrMT	16571	32735	1.9754	1.8349
chrX	155270560	8813522	0.0568	0.3191
chrY	59373566	260823	0.0044	0.1509

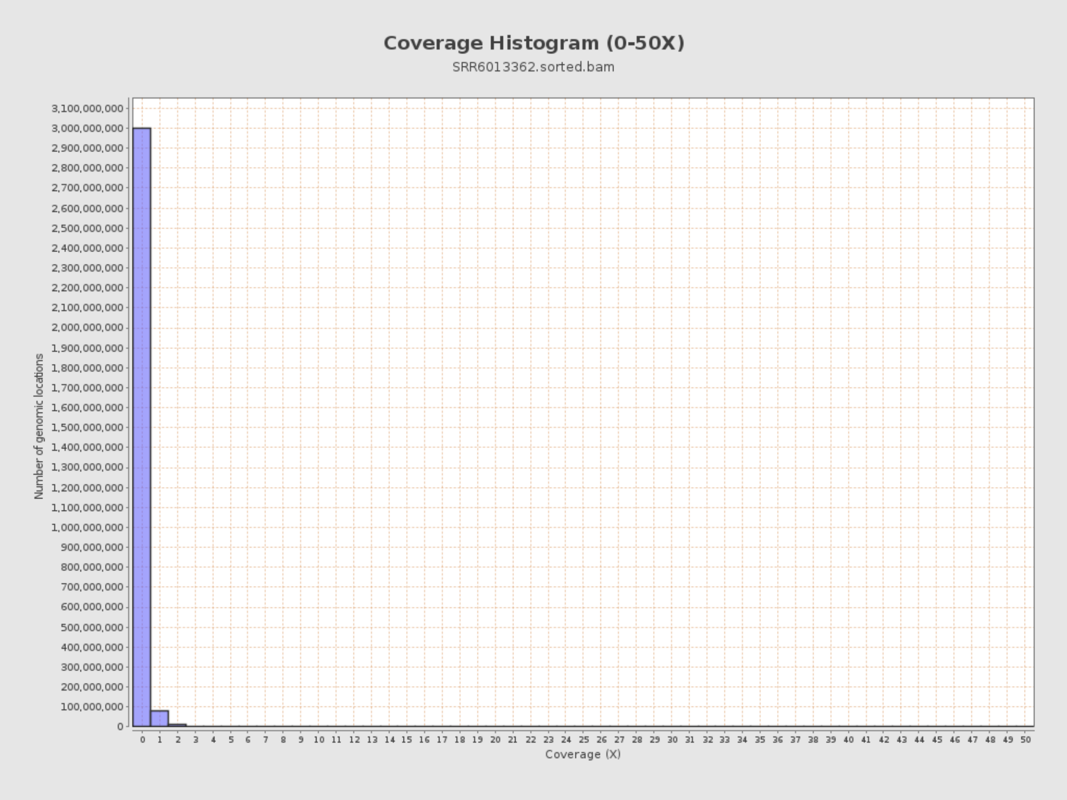
3. Results : Coverage across reference



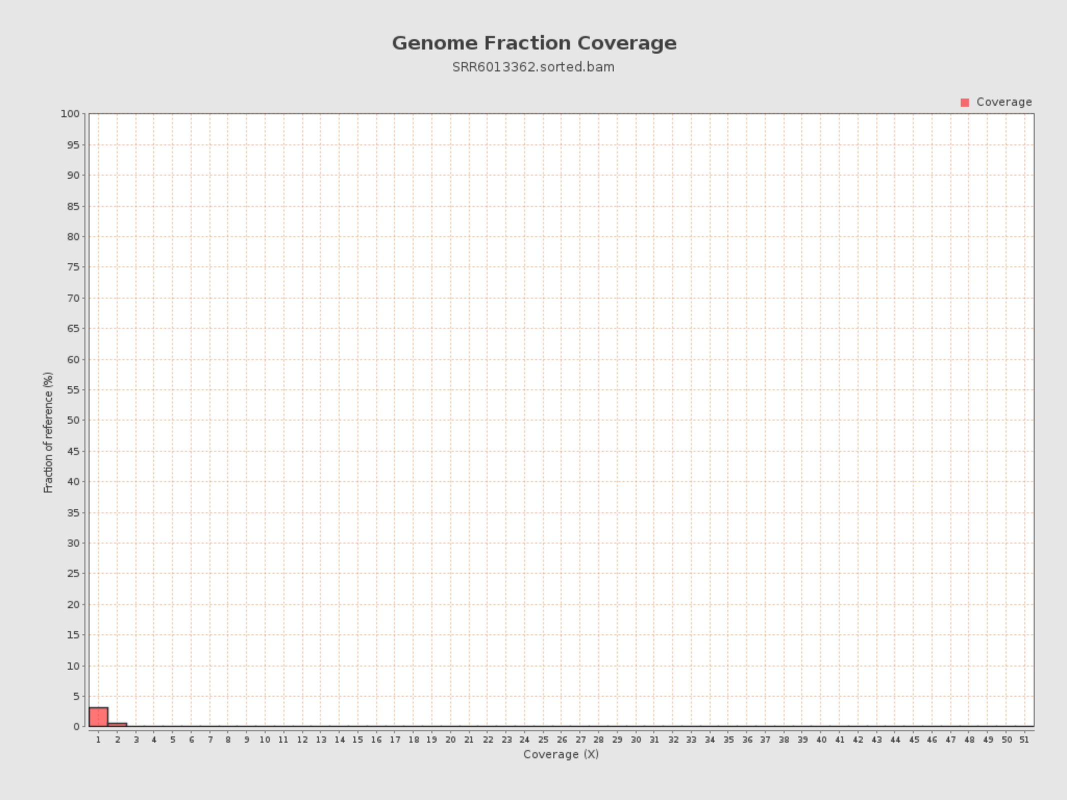
4. Results : Coverage Histogram



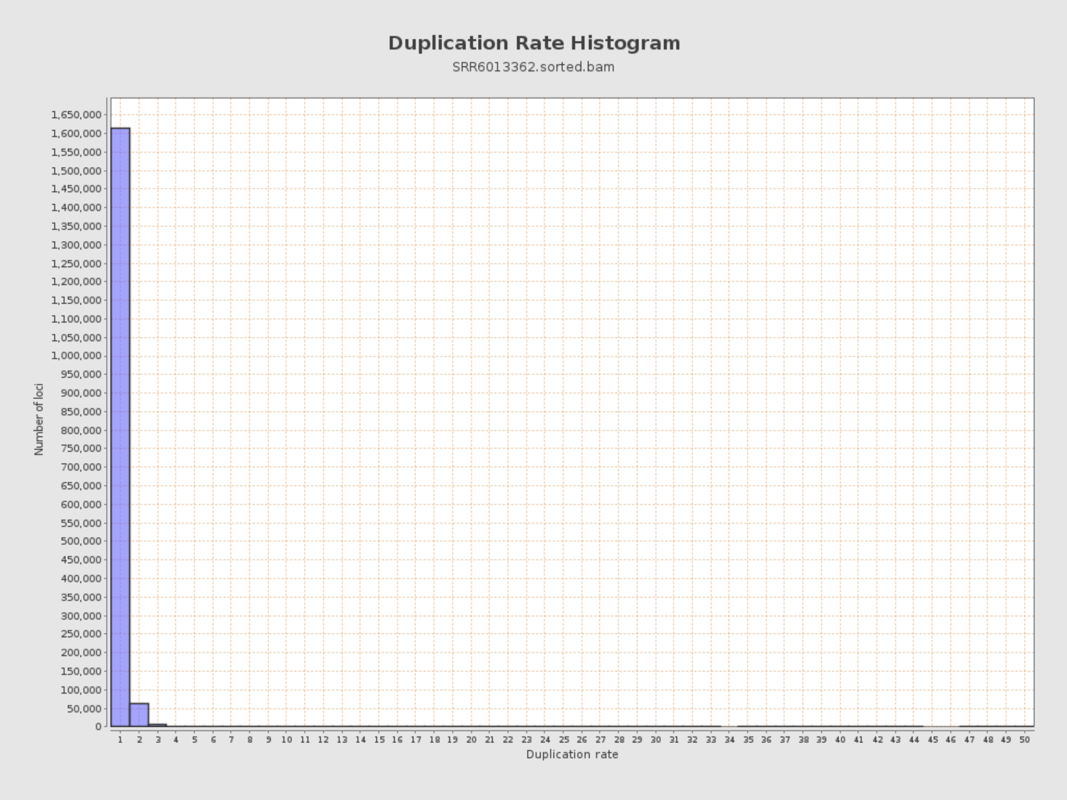
5. Results : Coverage Histogram (0-50X)



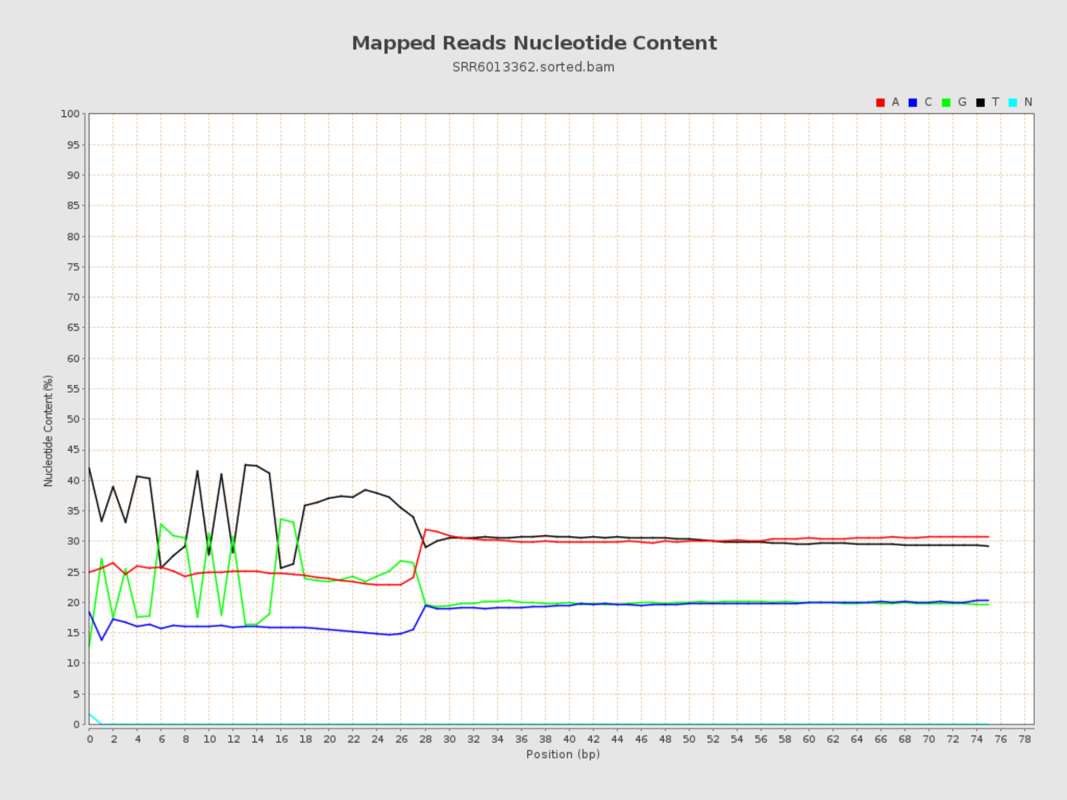
6. Results : Genome Fraction Coverage



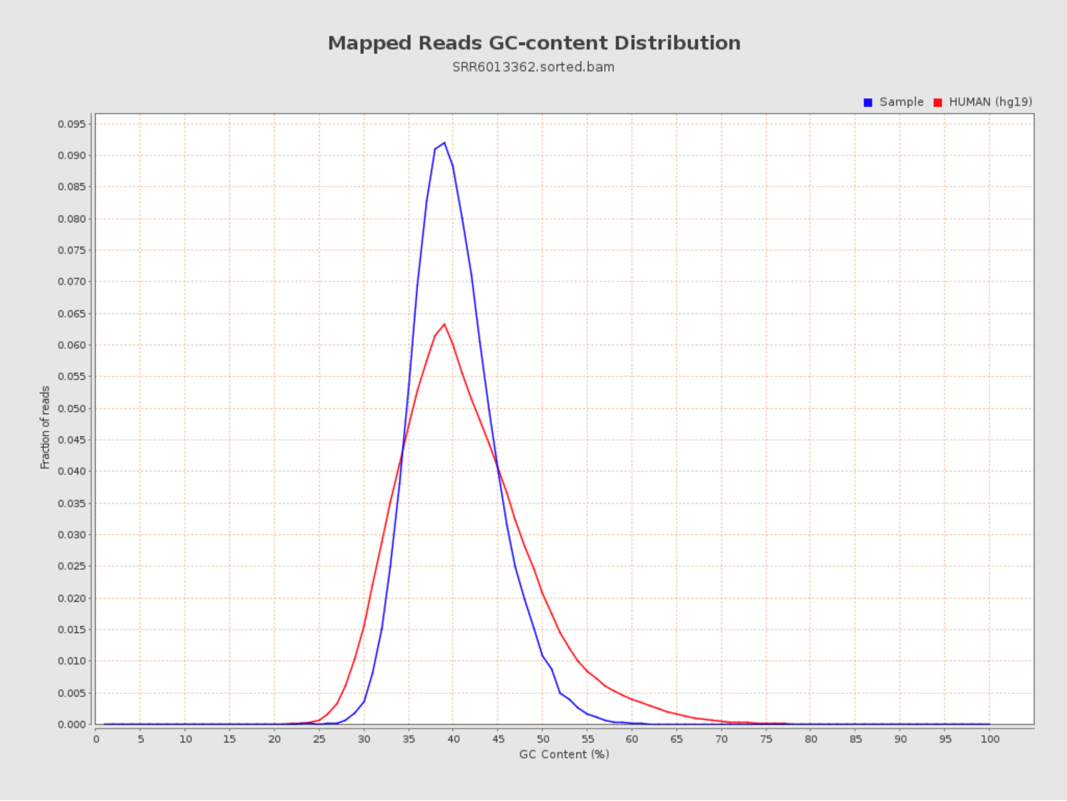
7. Results : Duplication Rate Histogram



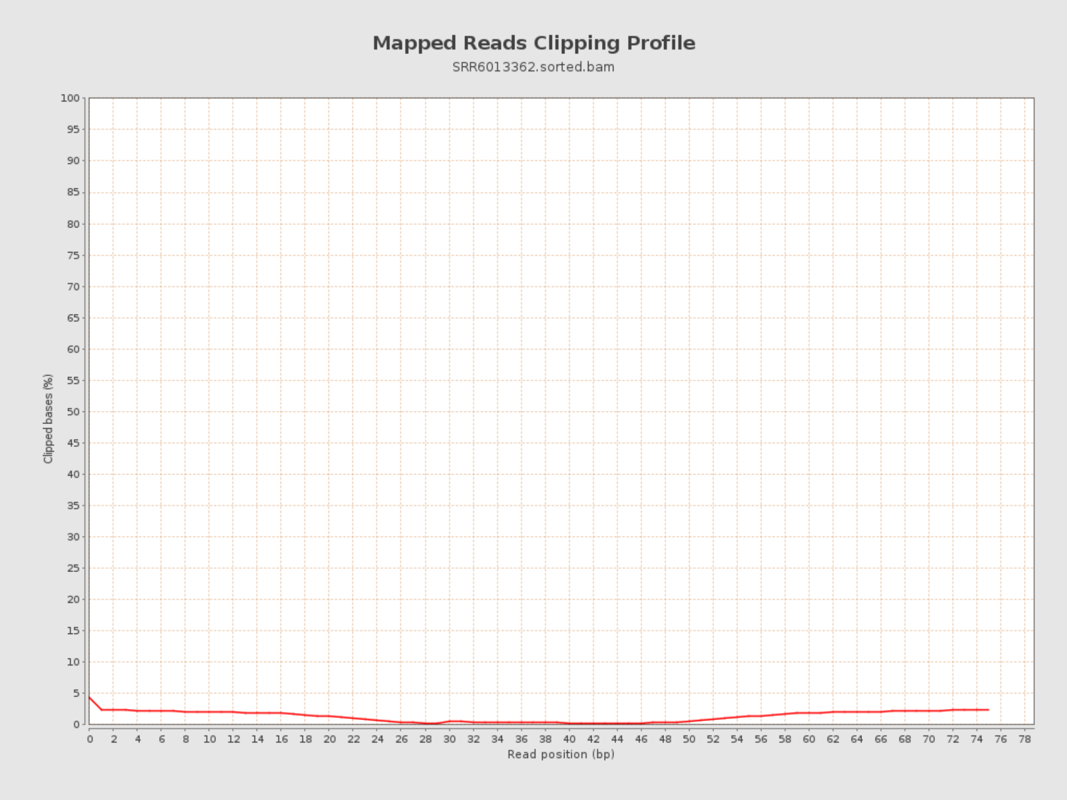
8. Results : Mapped Reads Nucleotide Content



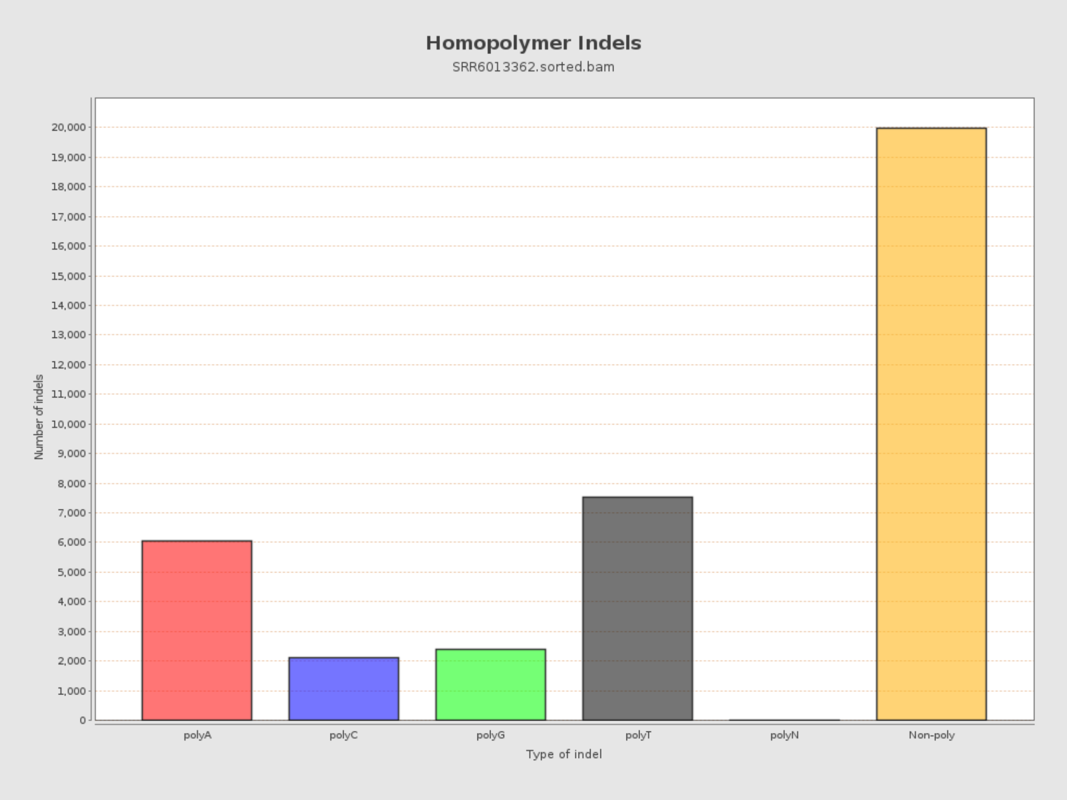
9. Results : Mapped Reads GC-content Distribution



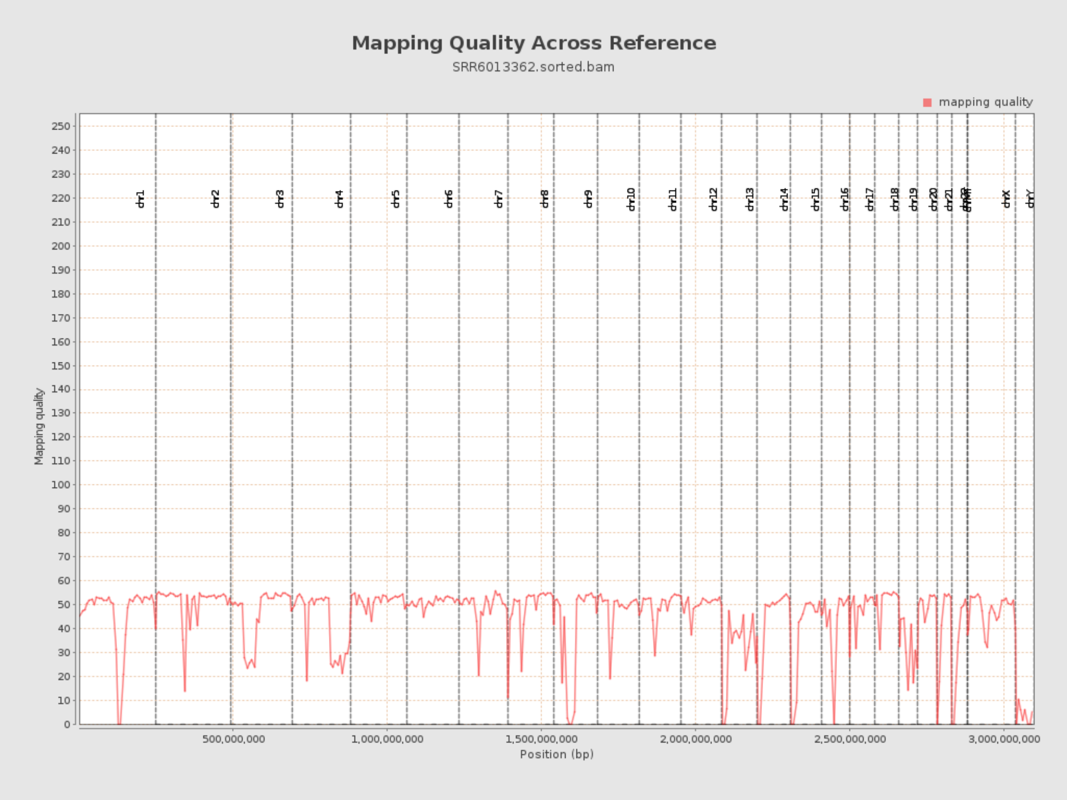
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram