Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:26:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013322.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_SRR6013322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:26:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,657,640
Mapped reads	1,176,274 / 70.96%
Unmapped reads	481,366 / 29.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,392 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	59,465 / 3.59%
Duplication rate	4.36%
Clipped reads	790,871 / 47.71%

2.2. ACGT Content

Number/percentage of A's	20,378,570 / 28.71%
Number/percentage of C's	11,964,282 / 16.86%
Number/percentage of T's	21,938,066 / 30.91%
Number/percentage of G's	16,667,479 / 23.48%
Number/percentage of N's	24,634 / 0.03%
GC Percentage	40.34%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.1998

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

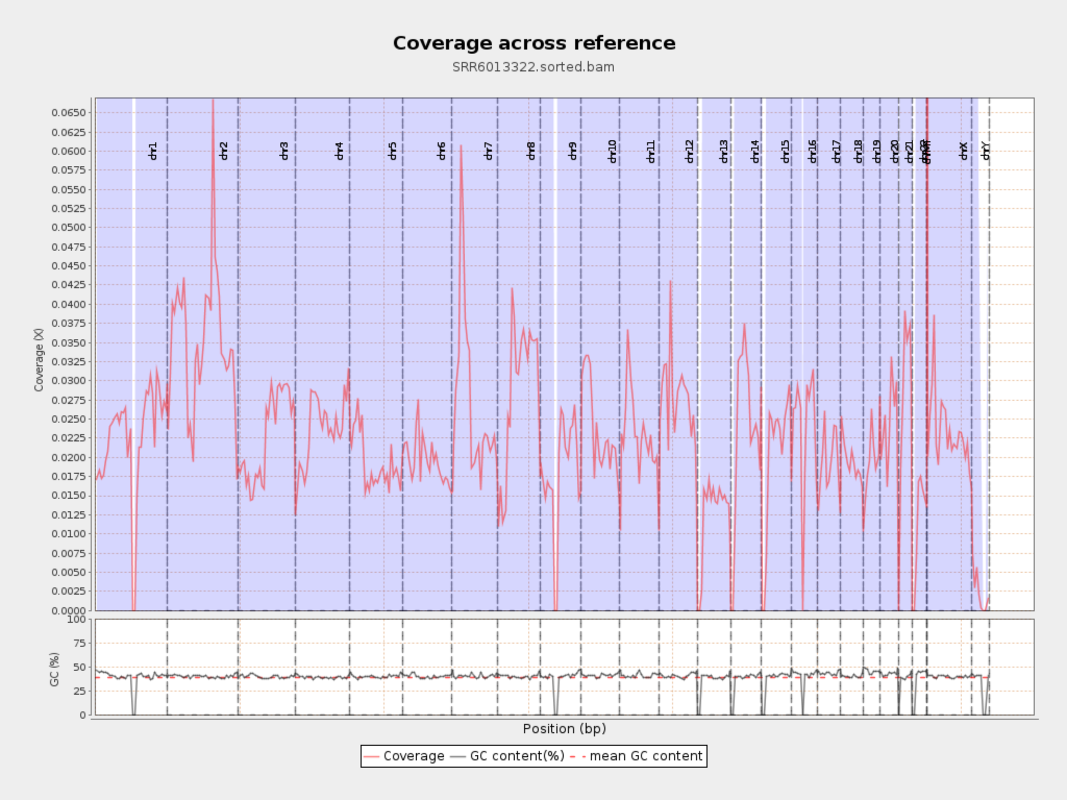
General error rate	1.12%
Mismatches	787,359
Insertions	4,625
Mapped reads with at least one insertion	0.39%
Deletions	18,771
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.04%

2.6. Chromosome stats

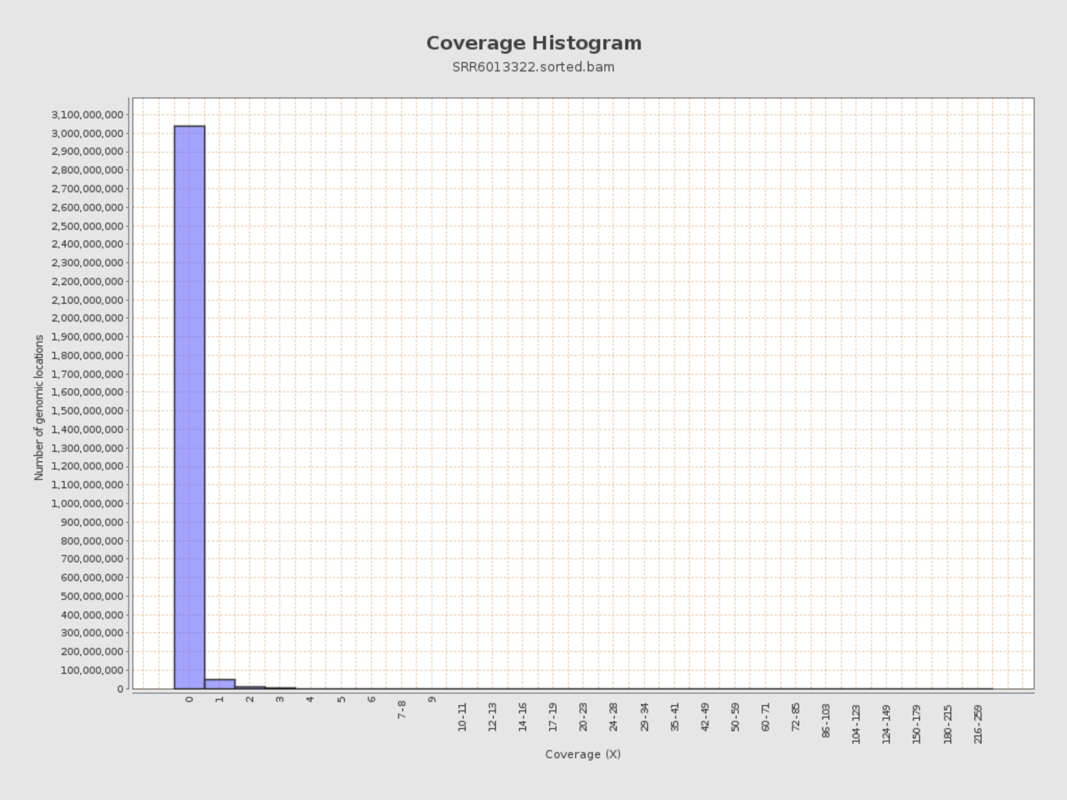
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5596668	0.0225	0.2464
chr2	243199373	8651475	0.0356	0.2399
chr3	198022430	4493314	0.0227	0.1745
chr4	191154276	4509337	0.0236	0.1824
chr5	180915260	3468776	0.0192	0.1618
chr6	171115067	3382780	0.0198	0.1787
chr7	159138663	4343689	0.0273	0.2854

chr8	146364022	4242824	0.029	0.2515
chr9	141213431	2540526	0.018	0.1716
chr10	135534747	3229618	0.0238	0.1942
chr11	135006516	3118879	0.0231	0.1947
chr12	133851895	3739190	0.0279	0.1962
chr13	115169878	1434835	0.0125	0.1286
chr14	107349540	2532996	0.0236	0.181
chr15	102531392	2062068	0.0201	0.176
chr16	90354753	2117665	0.0234	0.1805
chr17	81195210	1570106	0.0193	0.1678
chr18	78077248	1539086	0.0197	0.2204
chr19	59128983	1157718	0.0196	0.1906
chr20	63025520	1530909	0.0243	0.1821
chr21	48129895	1366232	0.0284	0.2011
chr22	51304566	578166	0.0113	0.1207
chrMT	16571	11760	0.7097	1.0764
chrX	155270560	3648443	0.0235	0.1845
chrY	59373566	136687	0.0023	0.0557

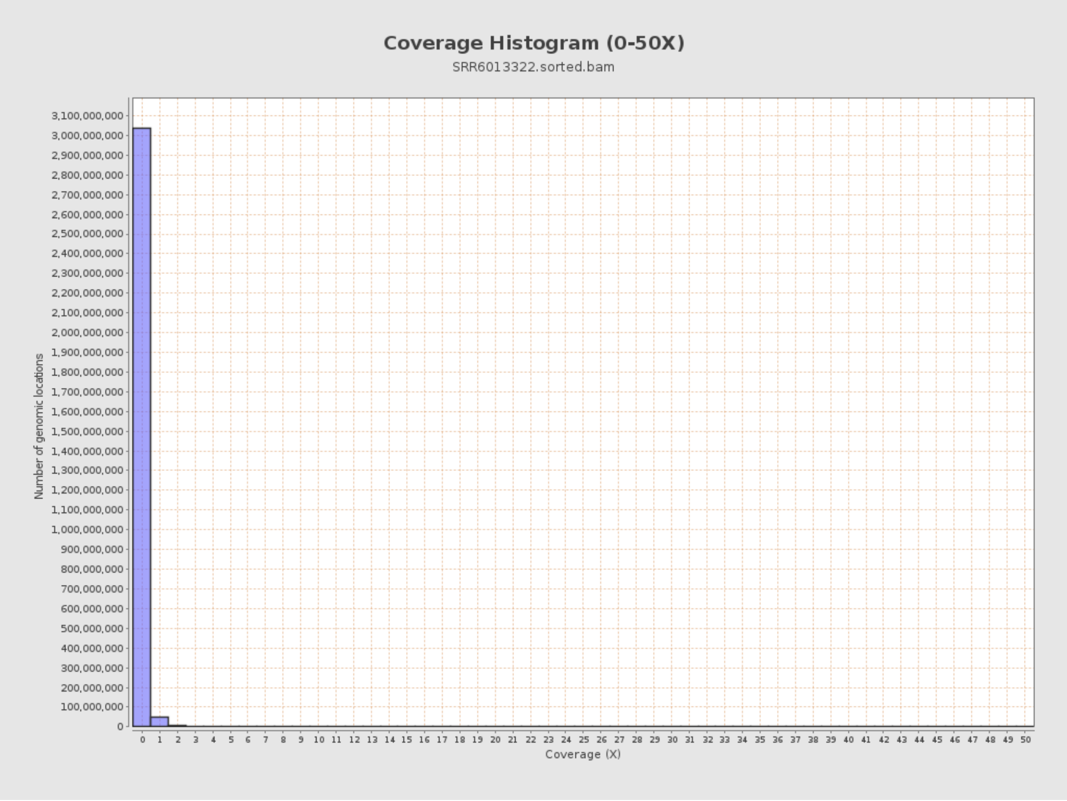
3. Results : Coverage across reference



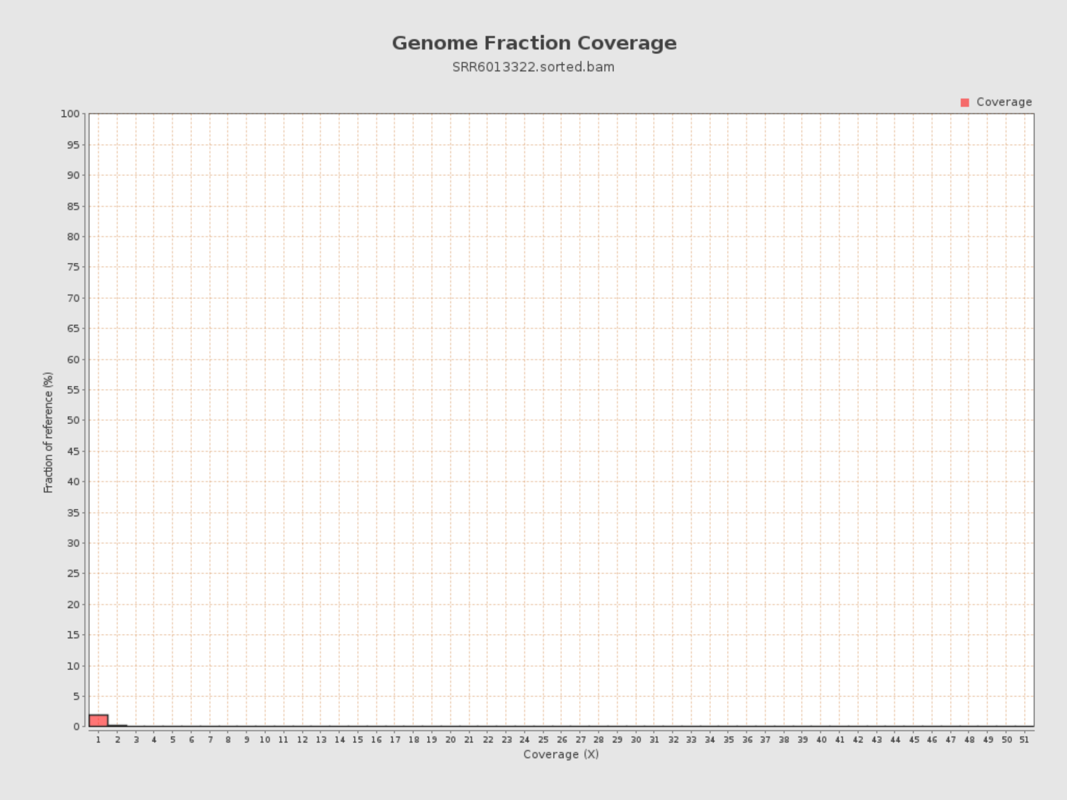
4. Results : Coverage Histogram



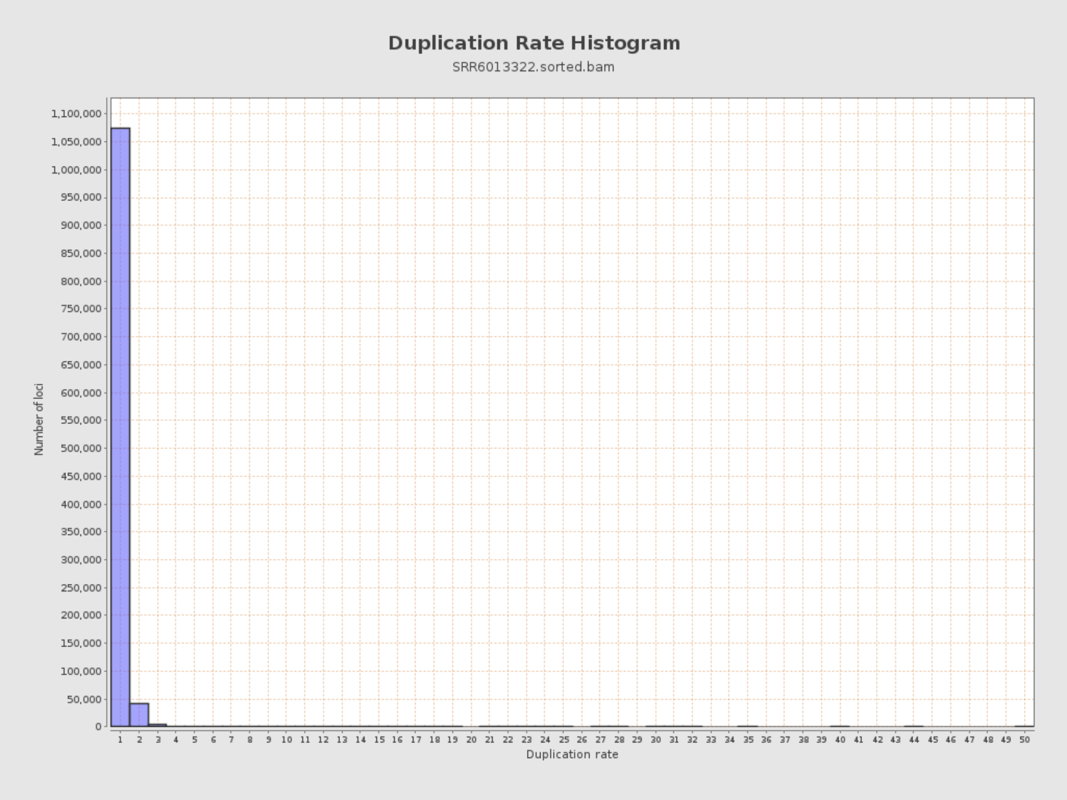
5. Results : Coverage Histogram (0-50X)



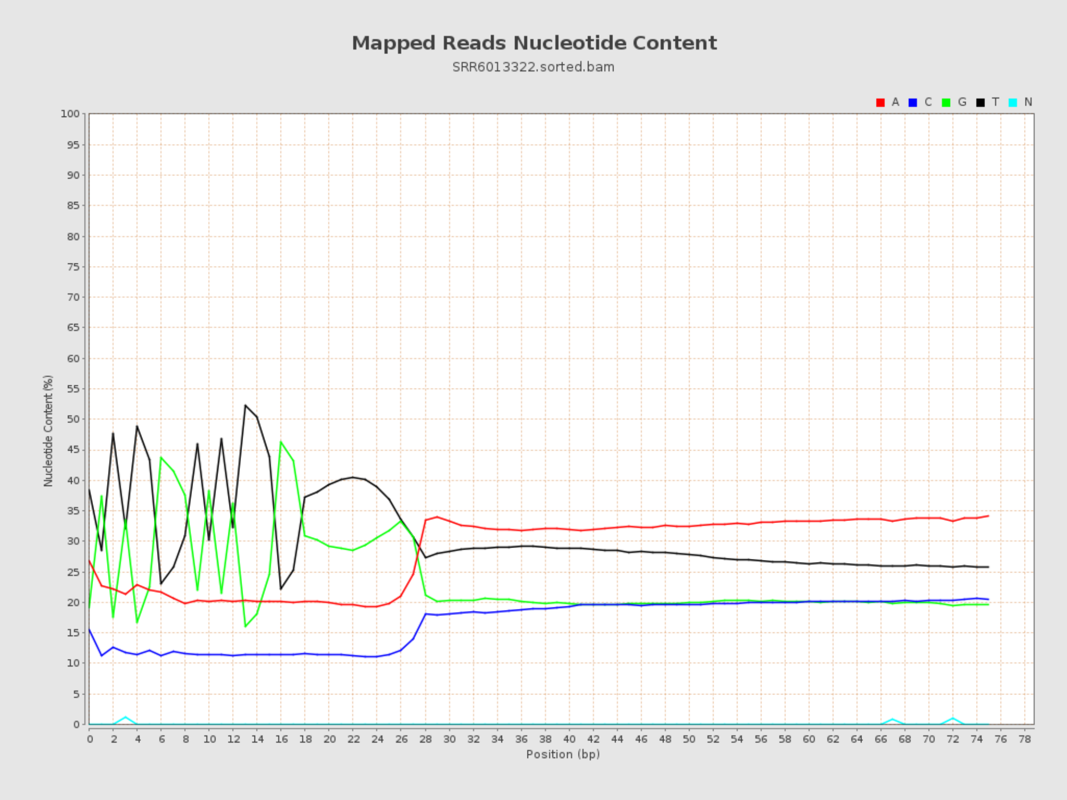
6. Results : Genome Fraction Coverage



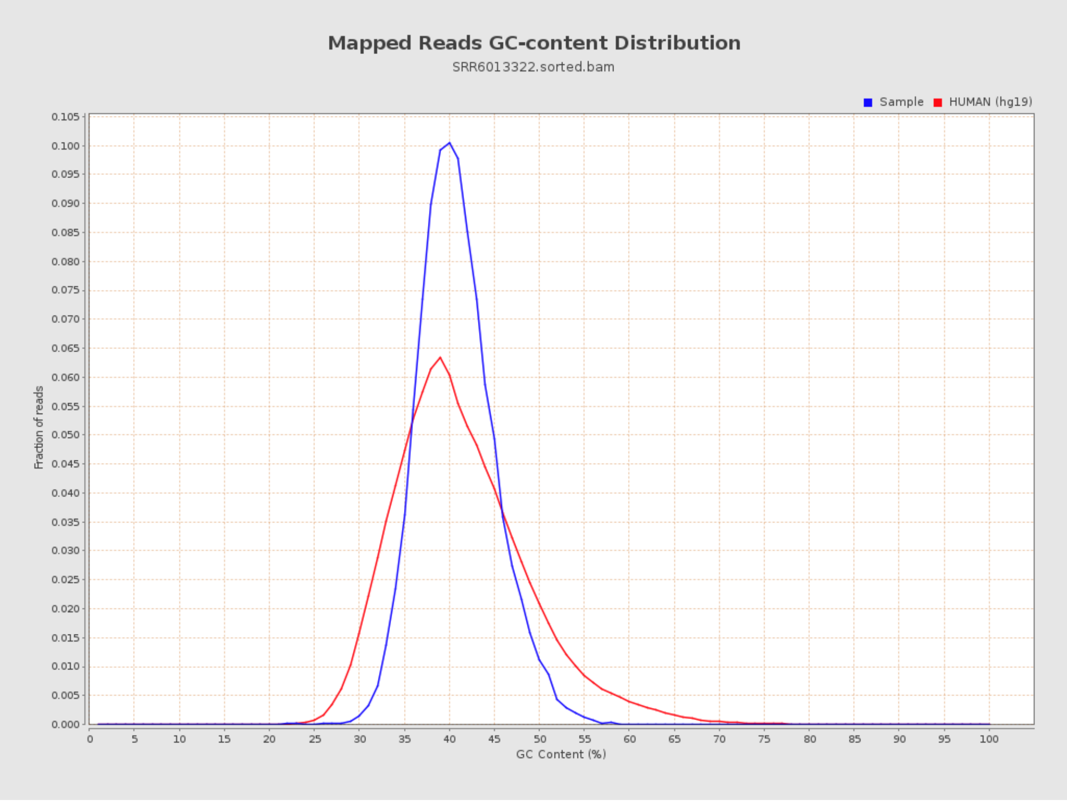
7. Results : Duplication Rate Histogram



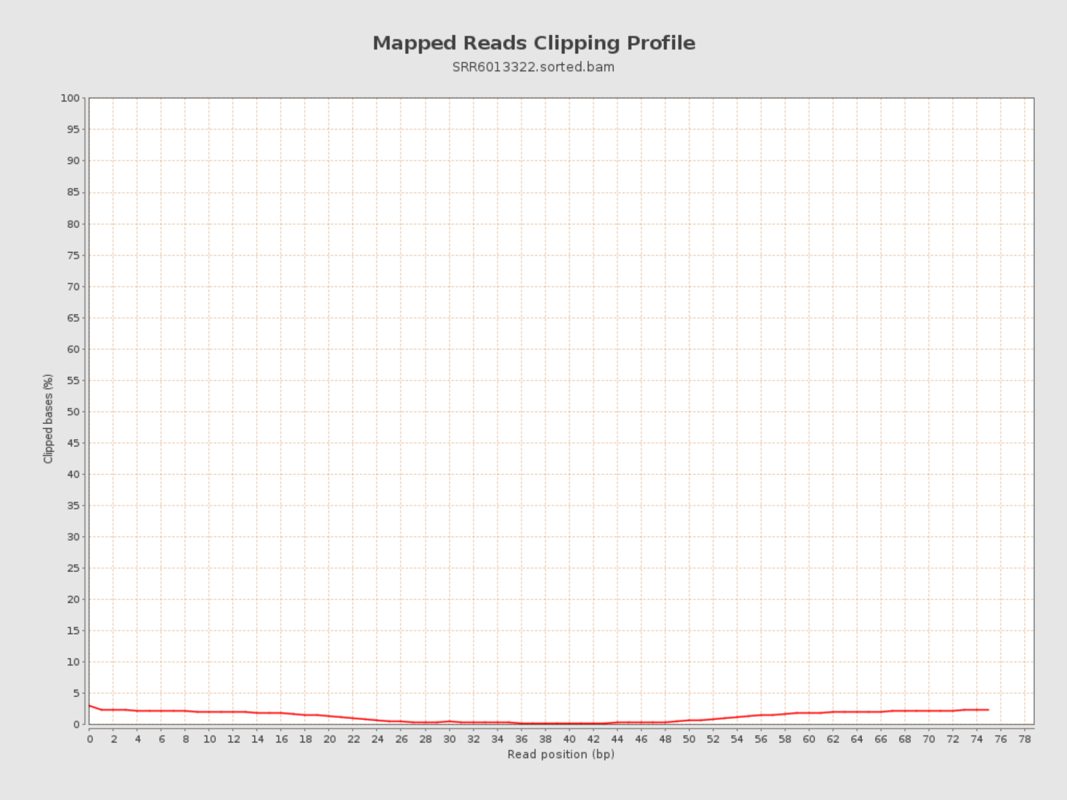
8. Results : Mapped Reads Nucleotide Content



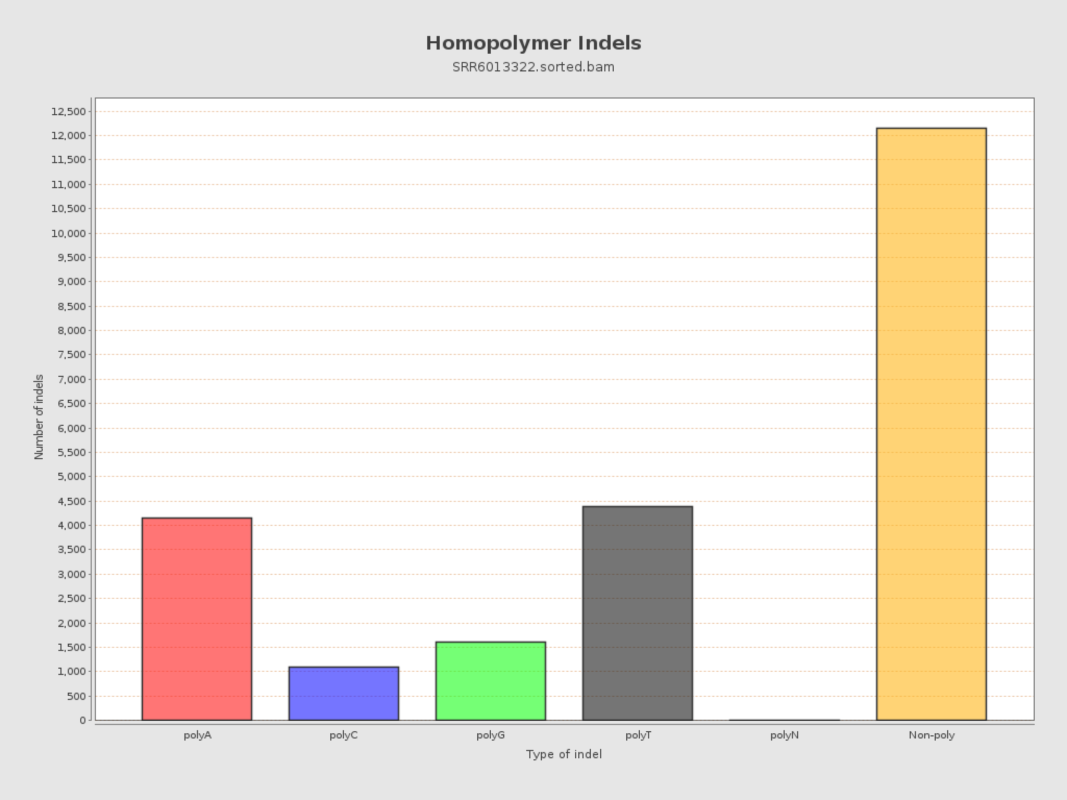
9. Results : Mapped Reads GC-content Distribution



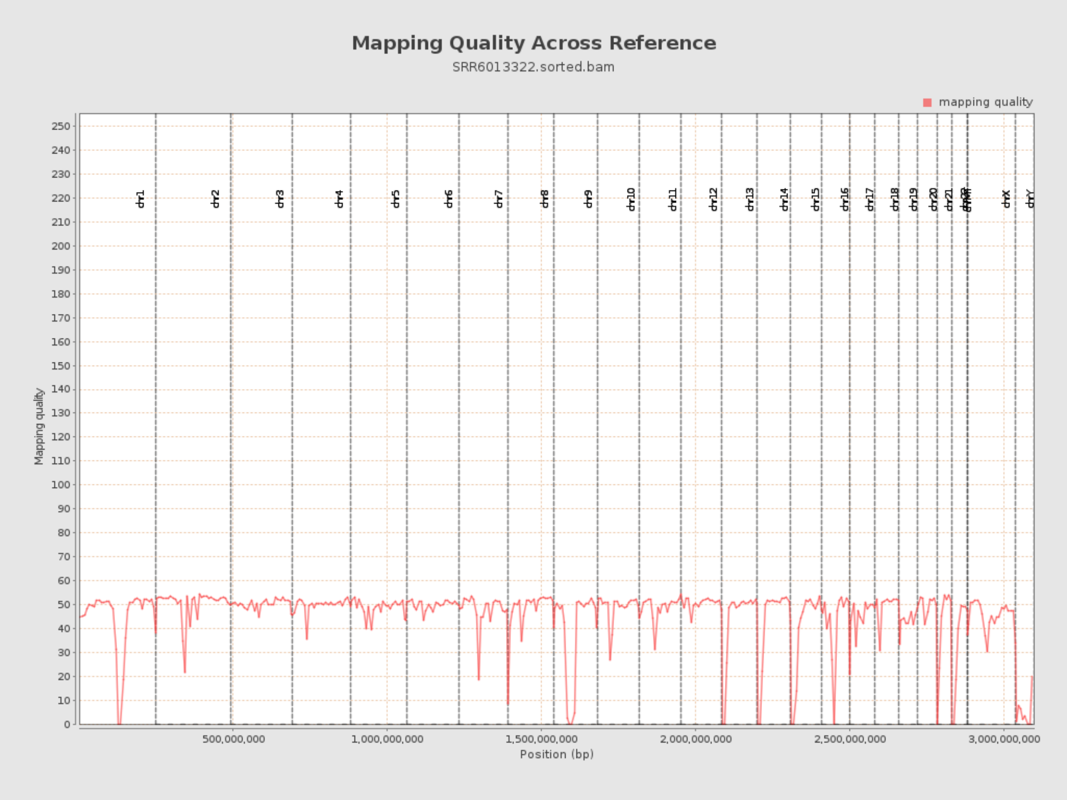
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram