Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013319.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_SRR6013319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:18:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,903,496
Mapped reads	1,658,798 / 87.14%
Unmapped reads	244,698 / 12.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,599 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	175,507 / 9.22%
Duplication rate	8.52%
Clipped reads	878,634 / 46.16%

2.2. ACGT Content

Number/percentage of A's	29,366,235 / 27.42%
Number/percentage of C's	19,253,593 / 17.98%
Number/percentage of T's	34,575,614 / 32.28%
Number/percentage of G's	23,896,021 / 22.31%
Number/percentage of N's	12,347 / 0.01%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3895

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

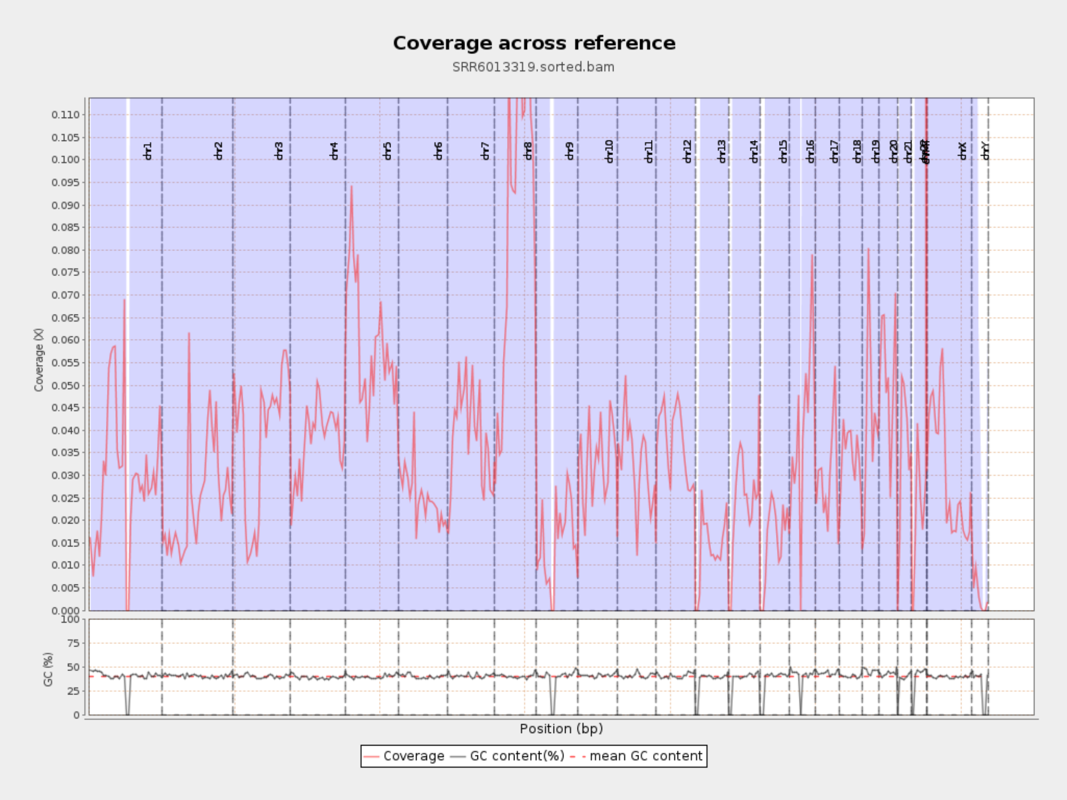
General error rate	0.81%
Mismatches	851,176
Insertions	6,960
Mapped reads with at least one insertion	0.42%
Deletions	38,152
Mapped reads with at least one deletion	2.27%
Homopolymer indels	44.05%

2.6. Chromosome stats

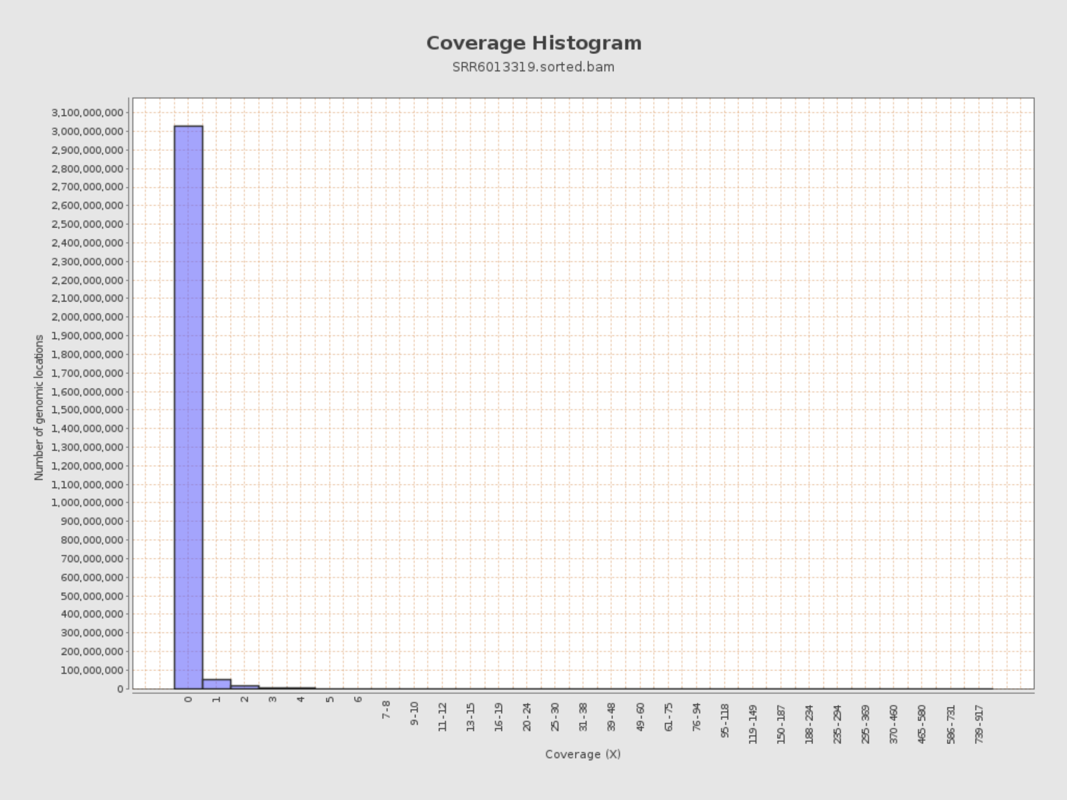
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7474392	0.03	0.7852
chr2	243199373	6042997	0.0248	0.3859
chr3	198022430	7705393	0.0389	0.2815
chr4	191154276	7173112	0.0375	0.2789
chr5	180915260	10775473	0.0596	0.3535
chr6	171115067	4322776	0.0253	0.2869
chr7	159138663	6268192	0.0394	0.4111

chr8	146364022	13155361	0.0899	0.5509
chr9	141213431	2203611	0.0156	0.2749
chr10	135534747	4582233	0.0338	0.3626
chr11	135006516	4403224	0.0326	0.3256
chr12	133851895	4969816	0.0371	0.2773
chr13	115169878	1587835	0.0138	0.1659
chr14	107349540	2540207	0.0237	0.2222
chr15	102531392	1632941	0.0159	0.1791
chr16	90354753	3719600	0.0412	0.2953
chr17	81195210	2355491	0.029	0.2654
chr18	78077248	2689102	0.0344	0.4869
chr19	59128983	2545060	0.043	0.5571
chr20	63025520	3345204	0.0531	0.332
chr21	48129895	1655849	0.0344	0.2695
chr22	51304566	1028353	0.02	0.1948
chrMT	16571	19450	1.1737	2.2708
chrX	155270560	4759418	0.0307	0.2773
chrY	59373566	215107	0.0036	0.0949

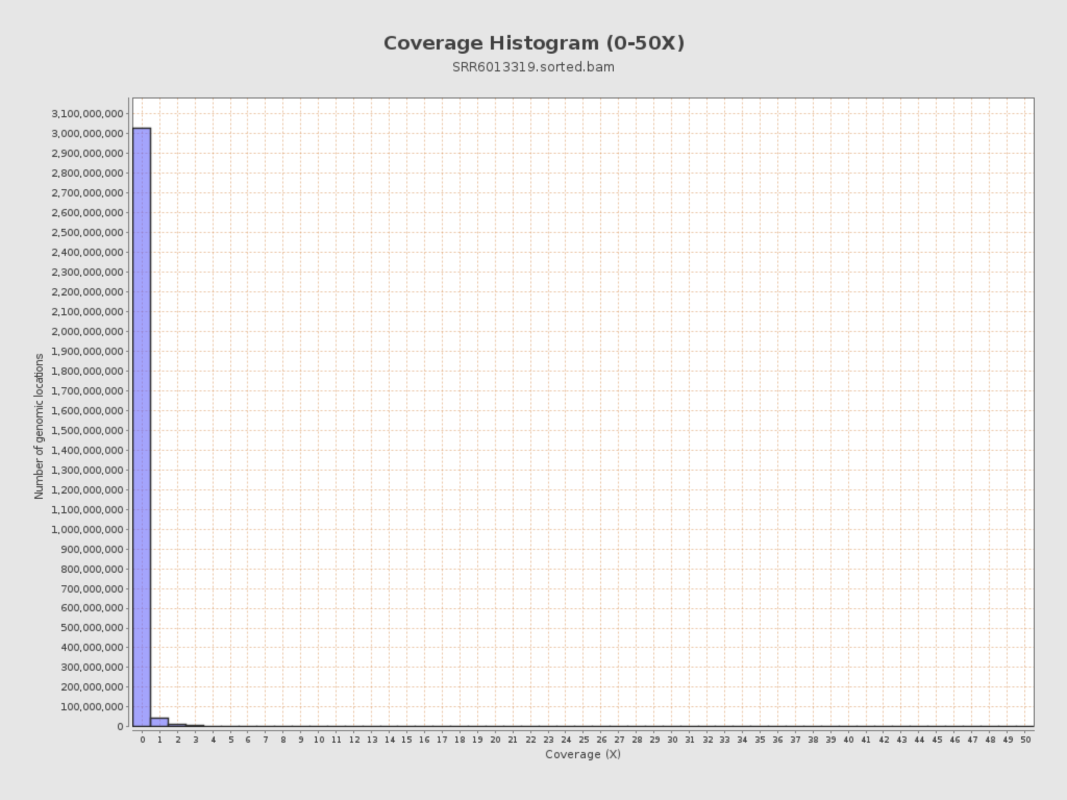
3. Results : Coverage across reference



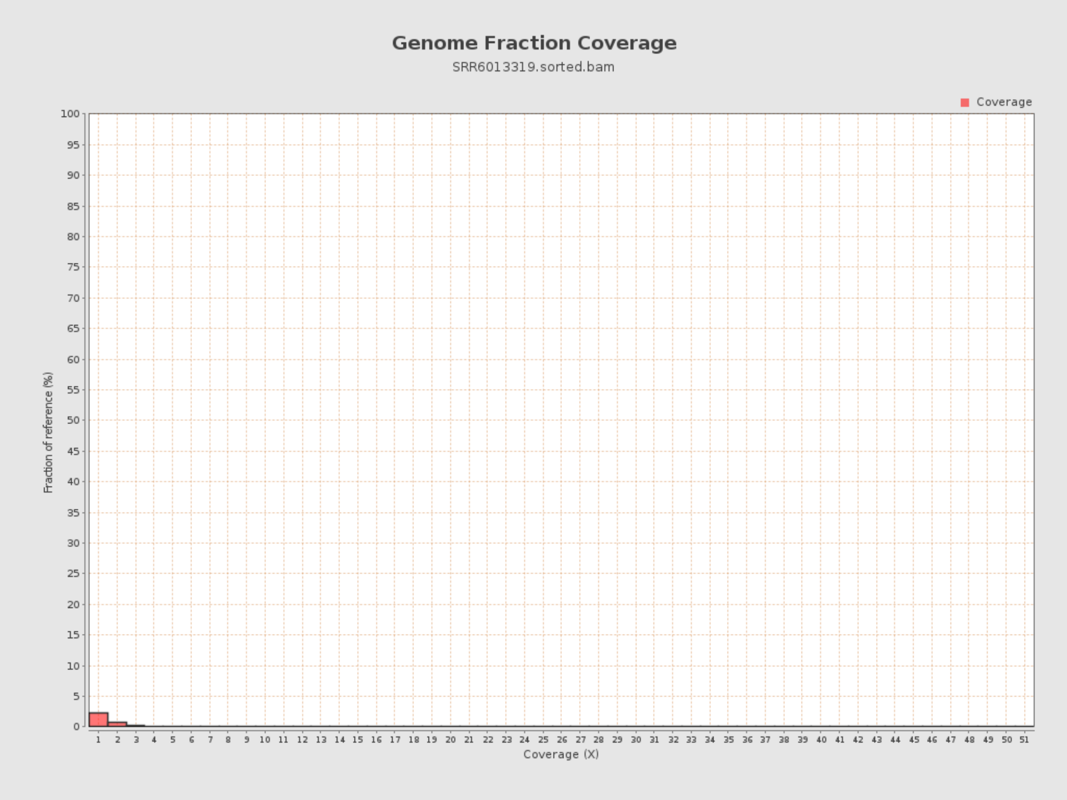
4. Results : Coverage Histogram



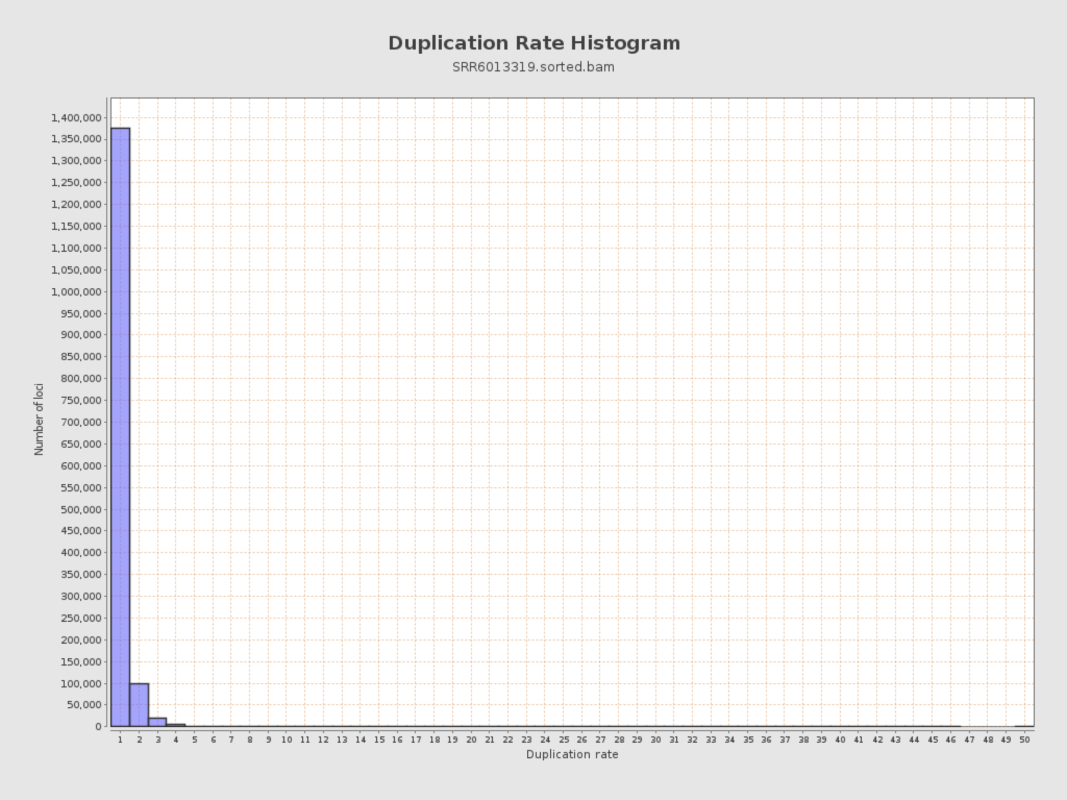
5. Results : Coverage Histogram (0-50X)



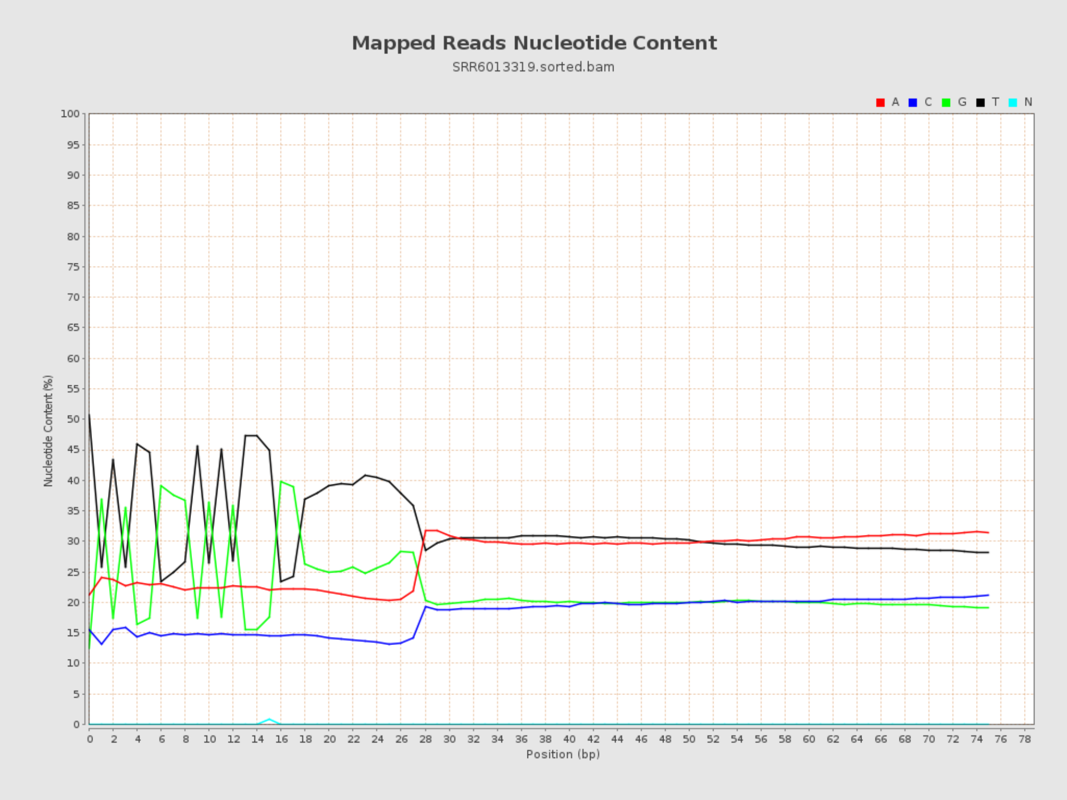
6. Results : Genome Fraction Coverage



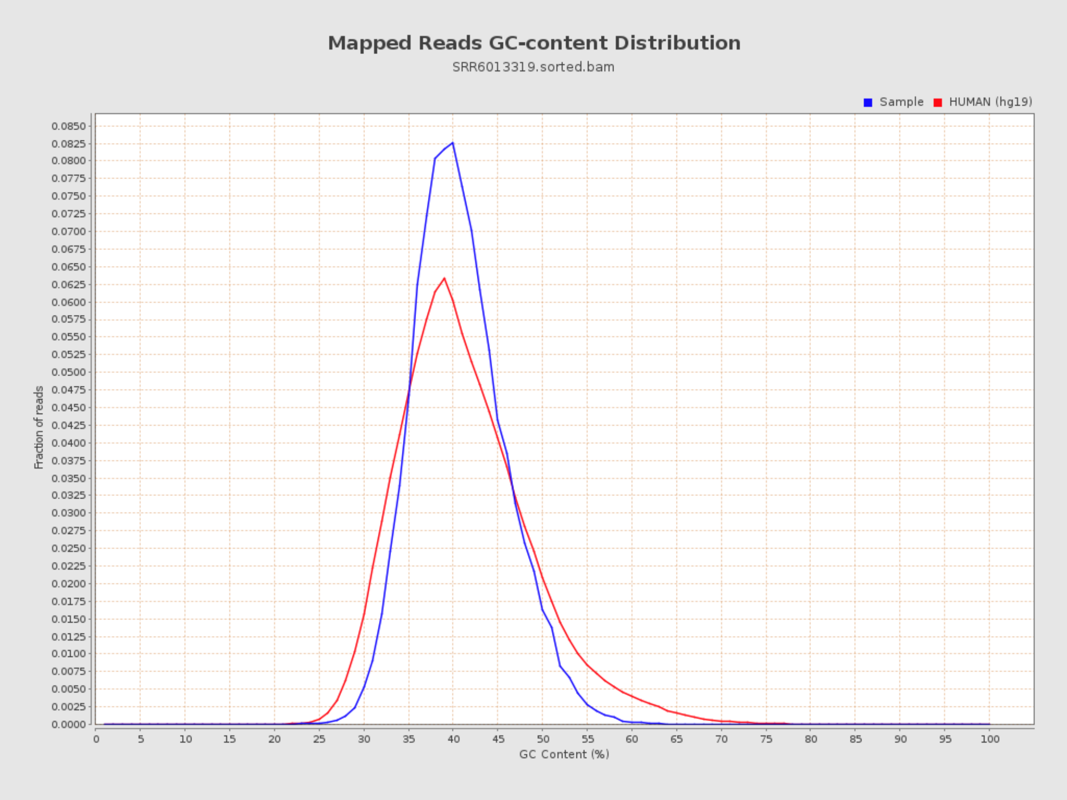
7. Results : Duplication Rate Histogram



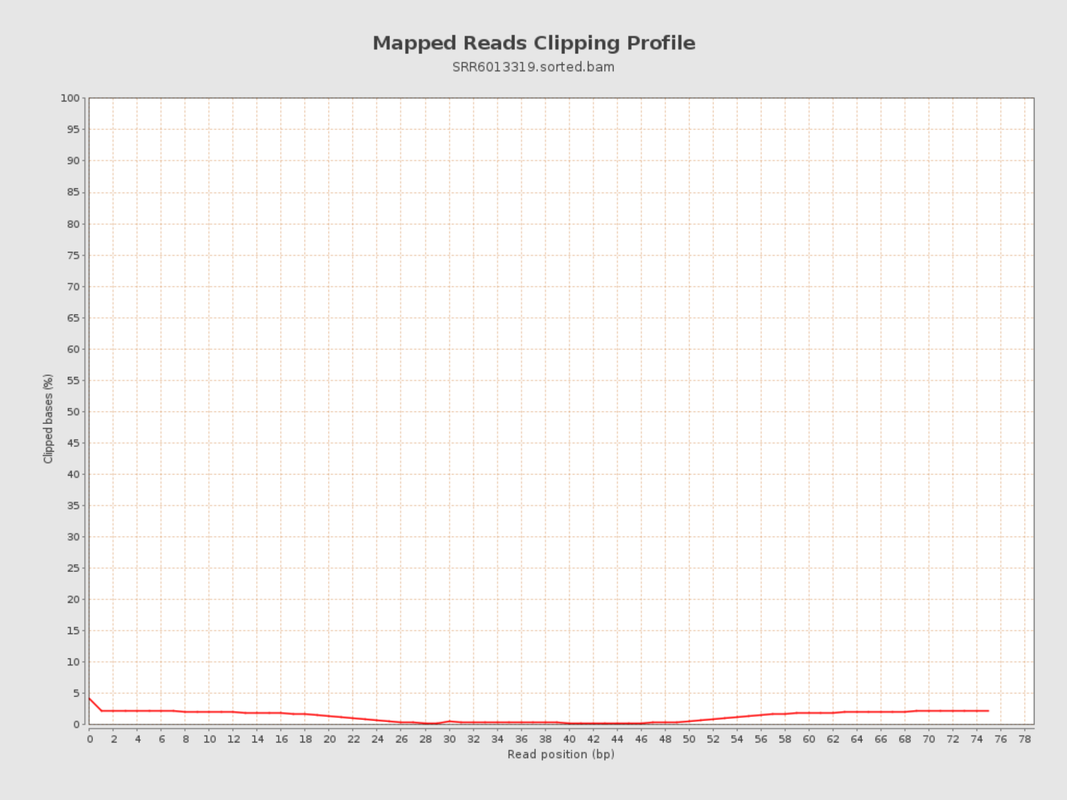
8. Results : Mapped Reads Nucleotide Content



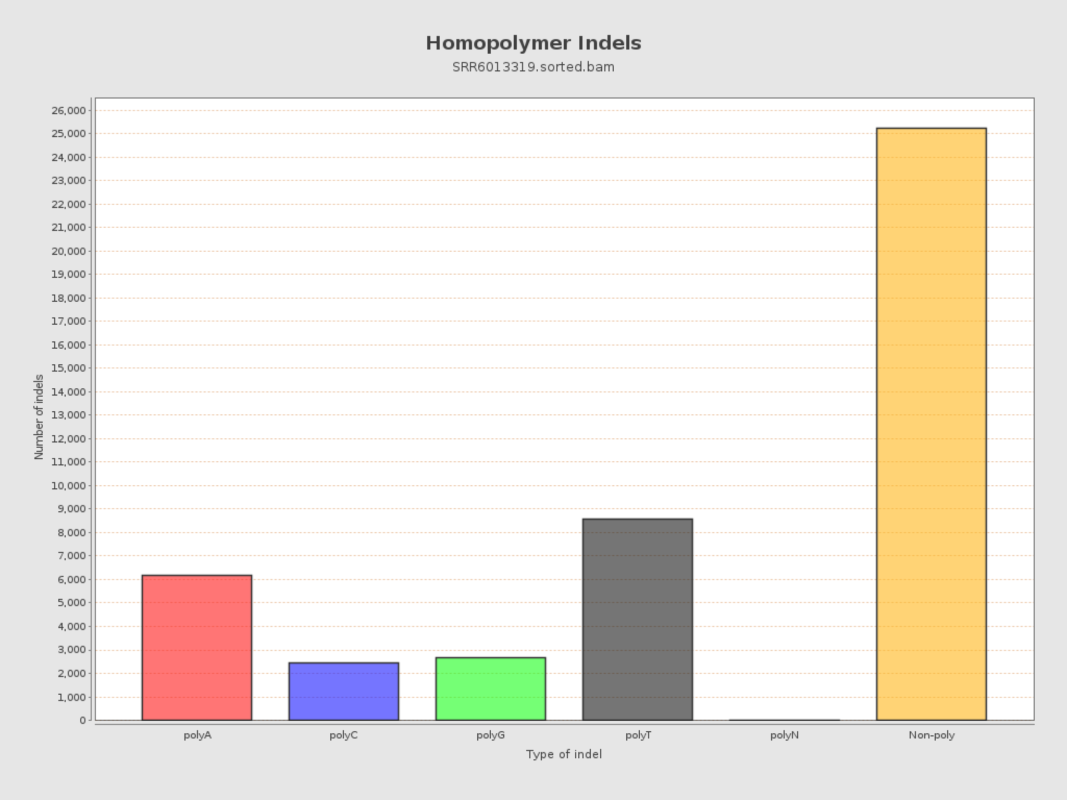
9. Results : Mapped Reads GC-content Distribution



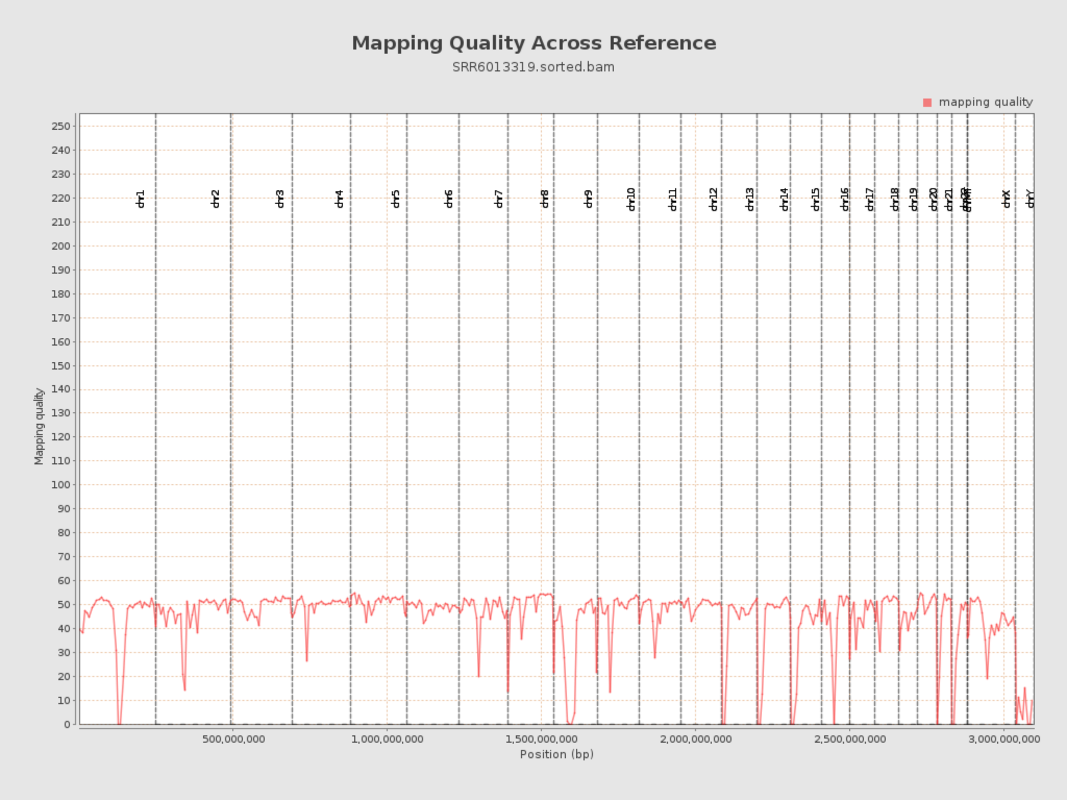
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram