Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:51:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013225.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_SRR6013225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,305,840
Mapped reads	1,119,071 / 85.7%
Unmapped reads	186,769 / 14.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,921 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	41,596 / 3.19%
Duplication rate	3.16%
Clipped reads	600,694 / 46%

2.2. ACGT Content

Number/percentage of A's	19,187,545 / 26.66%
Number/percentage of C's	12,891,660 / 17.91%
Number/percentage of T's	23,259,063 / 32.32%
Number/percentage of G's	16,628,465 / 23.11%
Number/percentage of N's	954 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2183

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

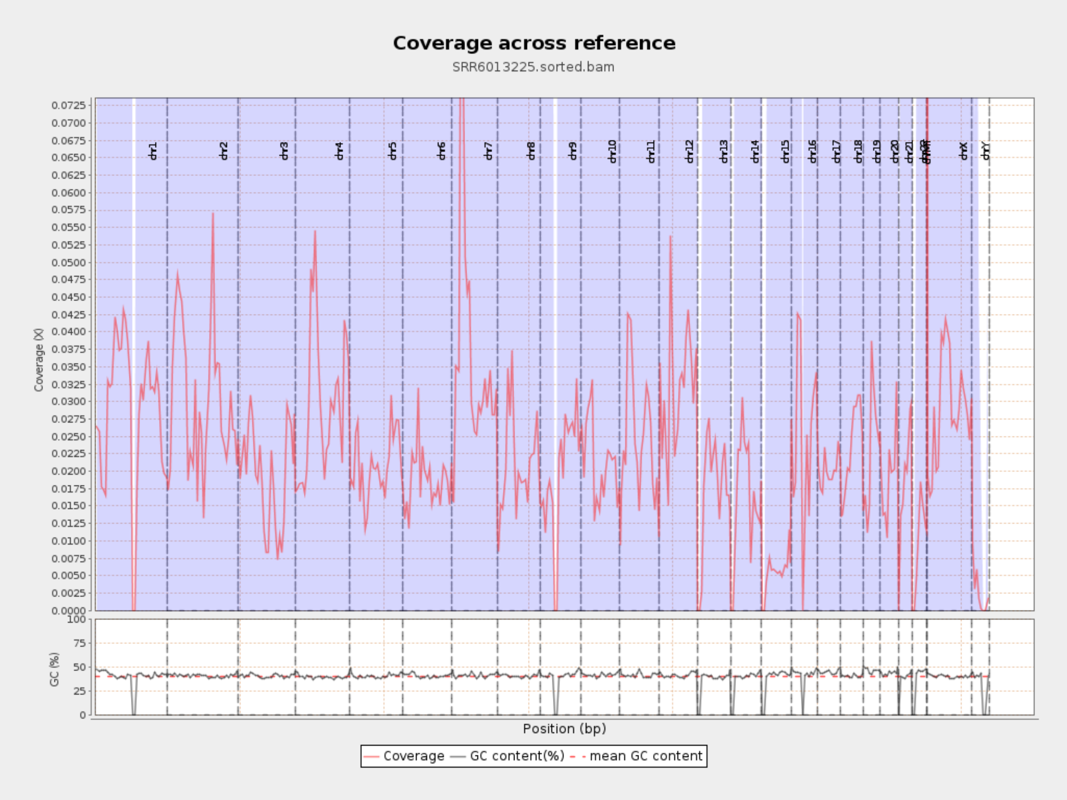
General error rate	0.74%
Mismatches	523,620
Insertions	4,667
Mapped reads with at least one insertion	0.41%
Deletions	18,720
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.59%

2.6. Chromosome stats

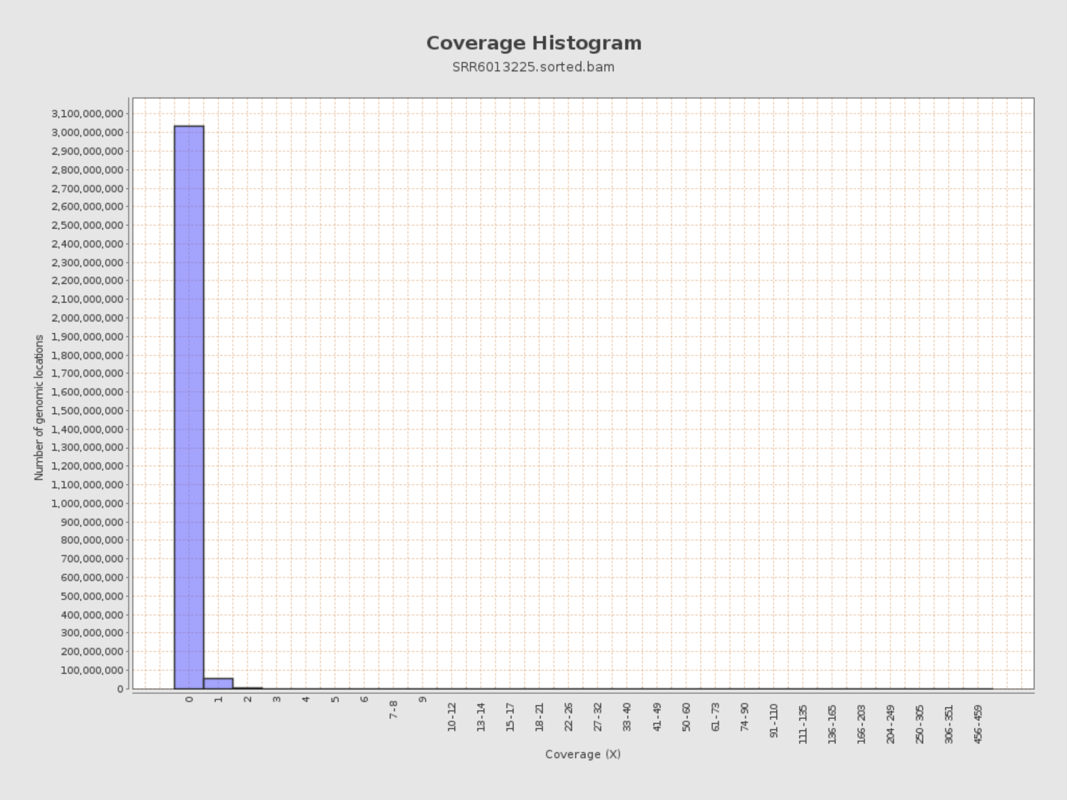
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7147534	0.0287	0.3366
chr2	243199373	7405149	0.0304	0.2798
chr3	198022430	3811008	0.0192	0.1544
chr4	191154276	5633860	0.0295	0.1939
chr5	180915260	3776605	0.0209	0.161
chr6	171115067	3215364	0.0188	0.1834
chr7	159138663	5959437	0.0374	0.3663

chr8	146364022	3094361	0.0211	0.2291
chr9	141213431	2725874	0.0193	0.173
chr10	135534747	2912520	0.0215	0.2032
chr11	135006516	3346743	0.0248	0.1902
chr12	133851895	4321193	0.0323	0.2013
chr13	115169878	1978022	0.0172	0.1459
chr14	107349540	1736191	0.0162	0.1464
chr15	102531392	559365	0.0055	0.0847
chr16	90354753	2171873	0.024	0.1774
chr17	81195210	1634543	0.0201	0.1643
chr18	78077248	1847708	0.0237	0.2355
chr19	59128983	1383179	0.0234	0.2492
chr20	63025520	1227059	0.0195	0.157
chr21	48129895	913110	0.019	0.1562
chr22	51304566	498571	0.0097	0.1084
chrMT	16571	29836	1.8005	1.6912
chrX	155270560	4521774	0.0291	0.2038
chrY	59373566	148358	0.0025	0.0596

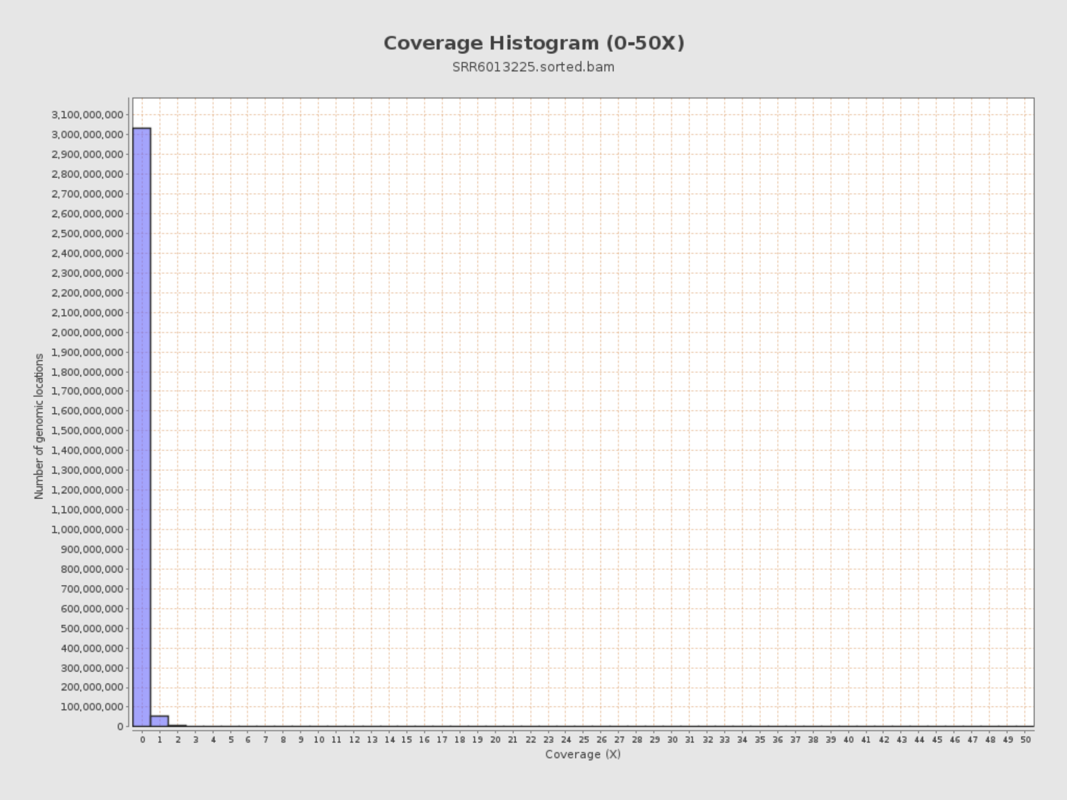
3. Results : Coverage across reference



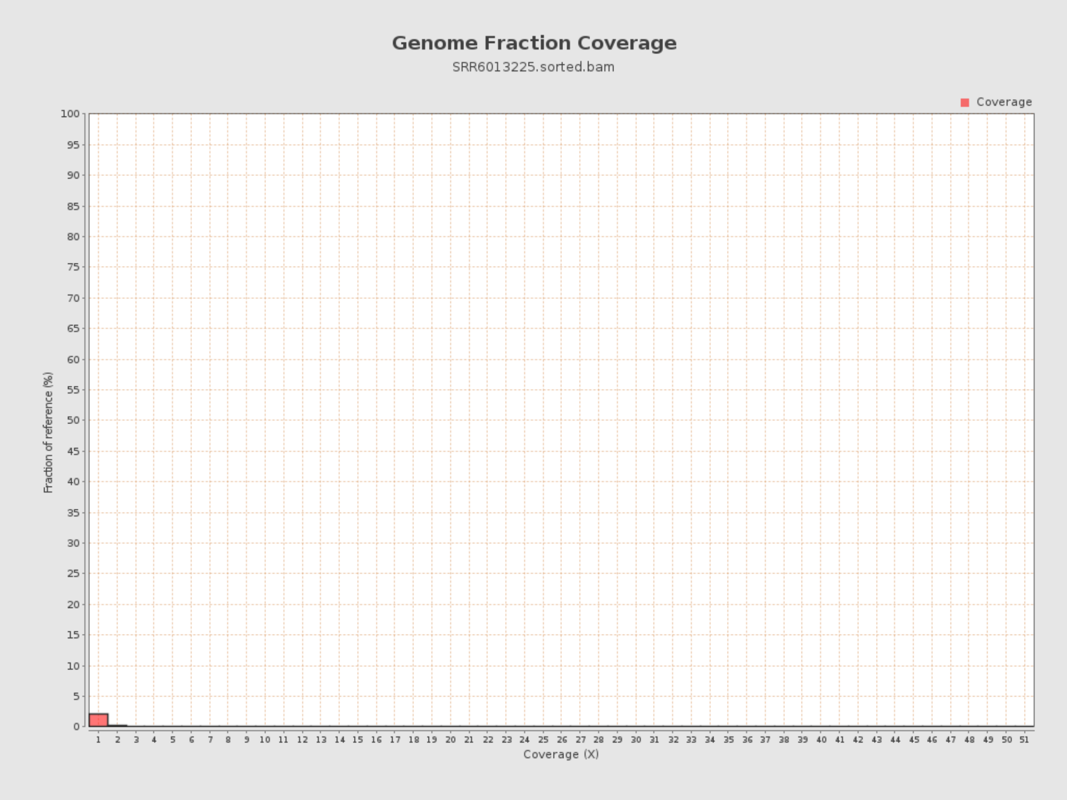
4. Results : Coverage Histogram



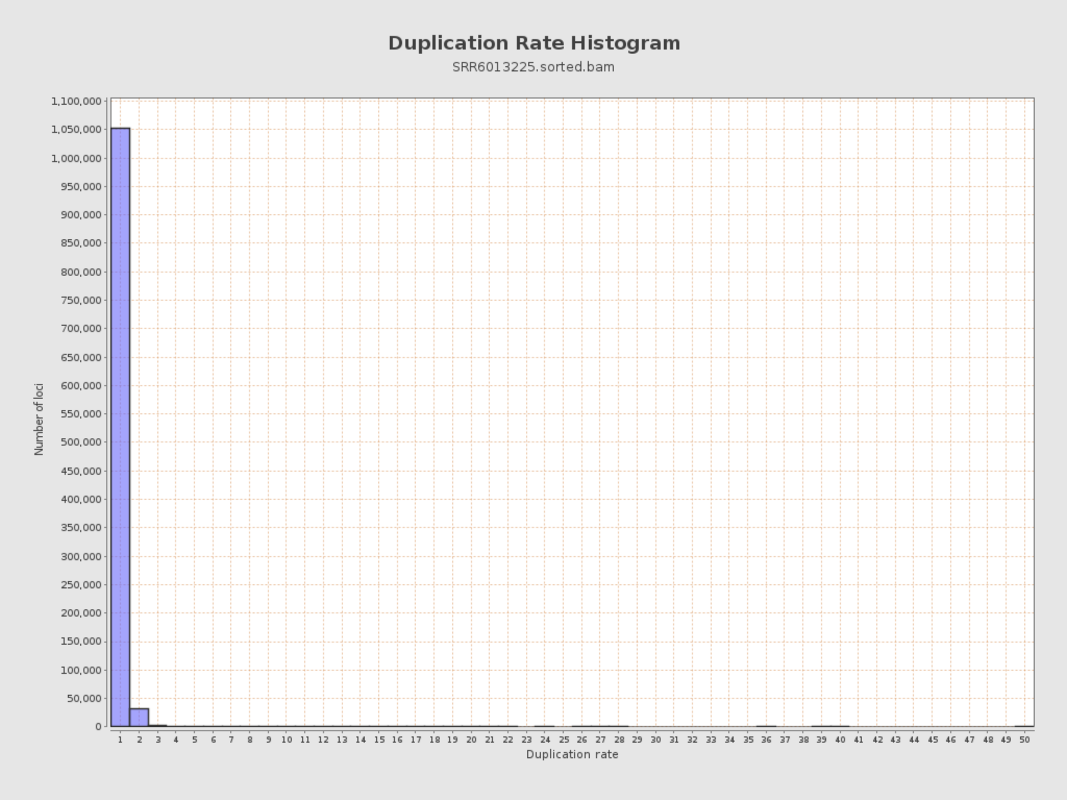
5. Results : Coverage Histogram (0-50X)



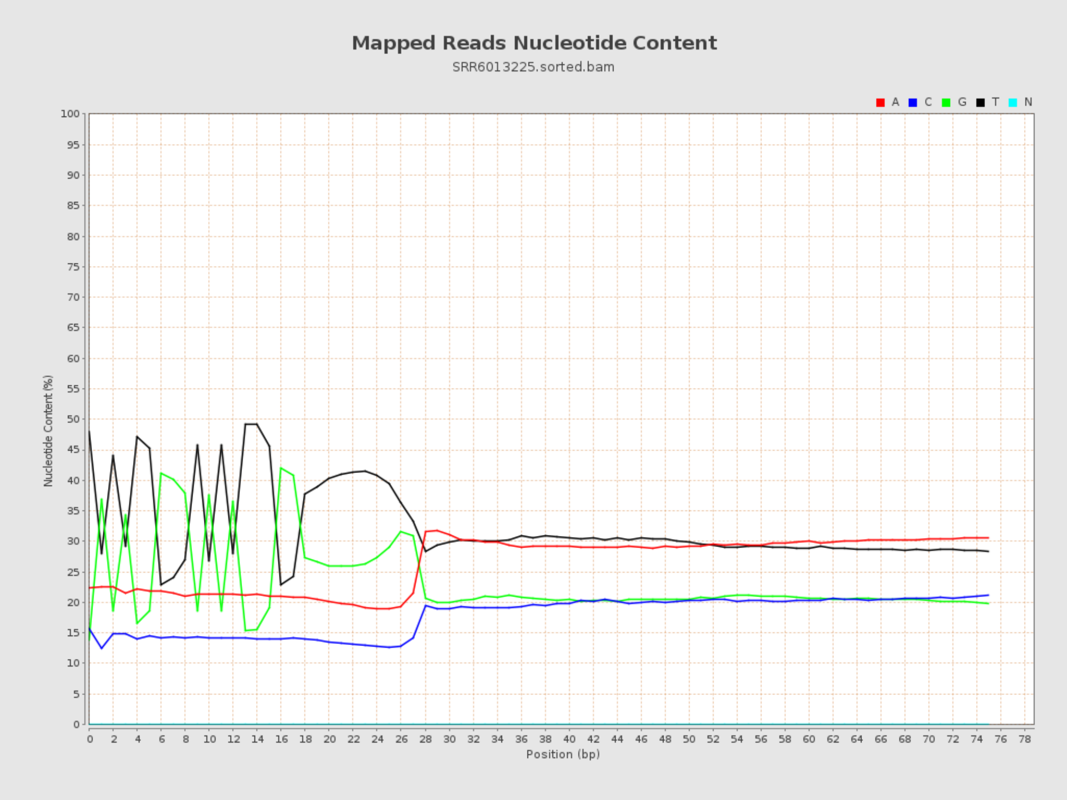
6. Results : Genome Fraction Coverage



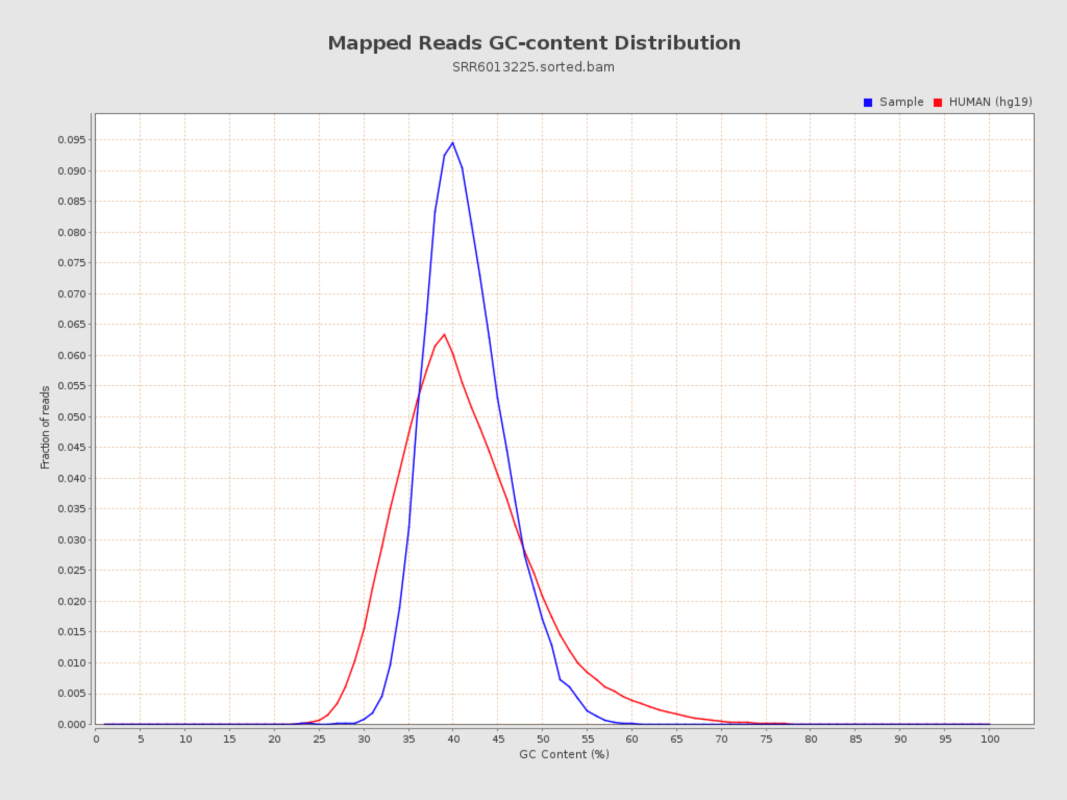
7. Results : Duplication Rate Histogram



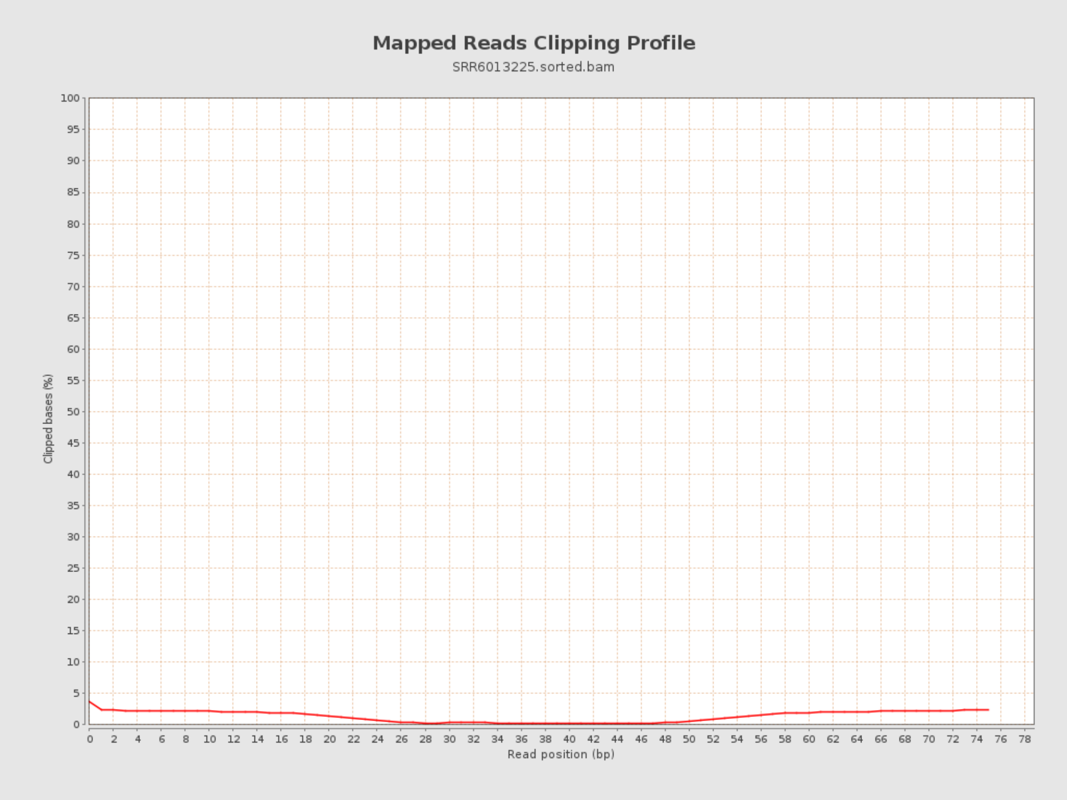
8. Results : Mapped Reads Nucleotide Content



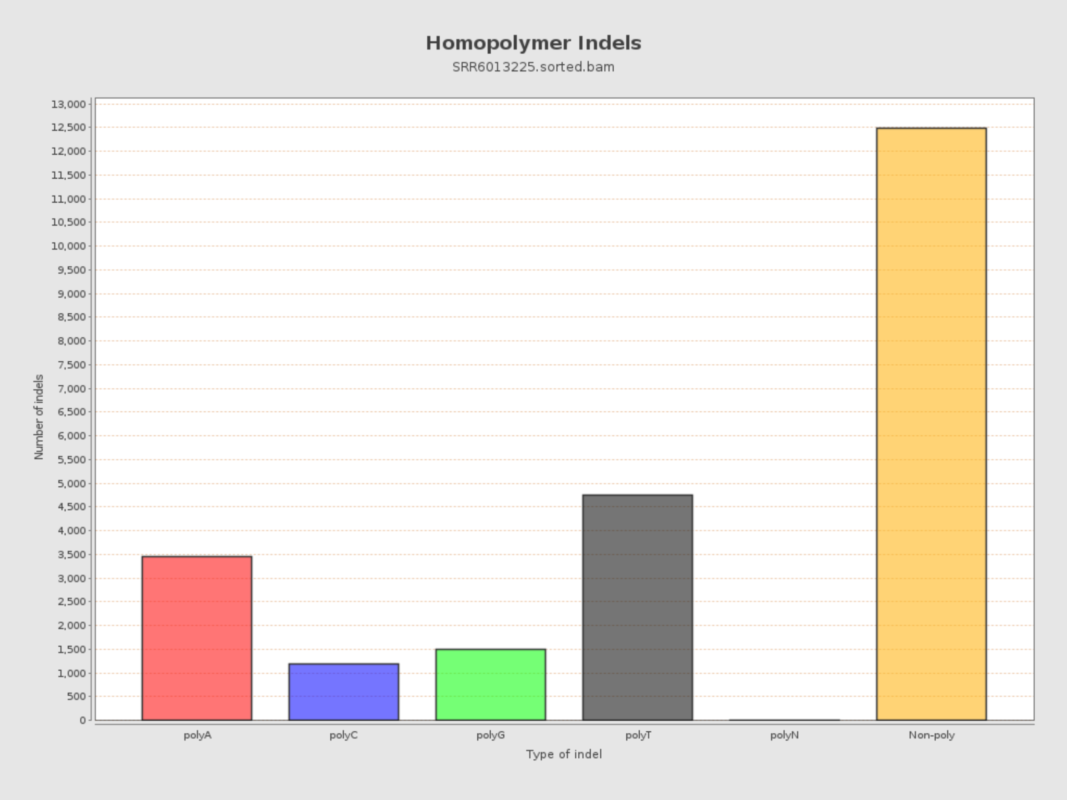
9. Results : Mapped Reads GC-content Distribution



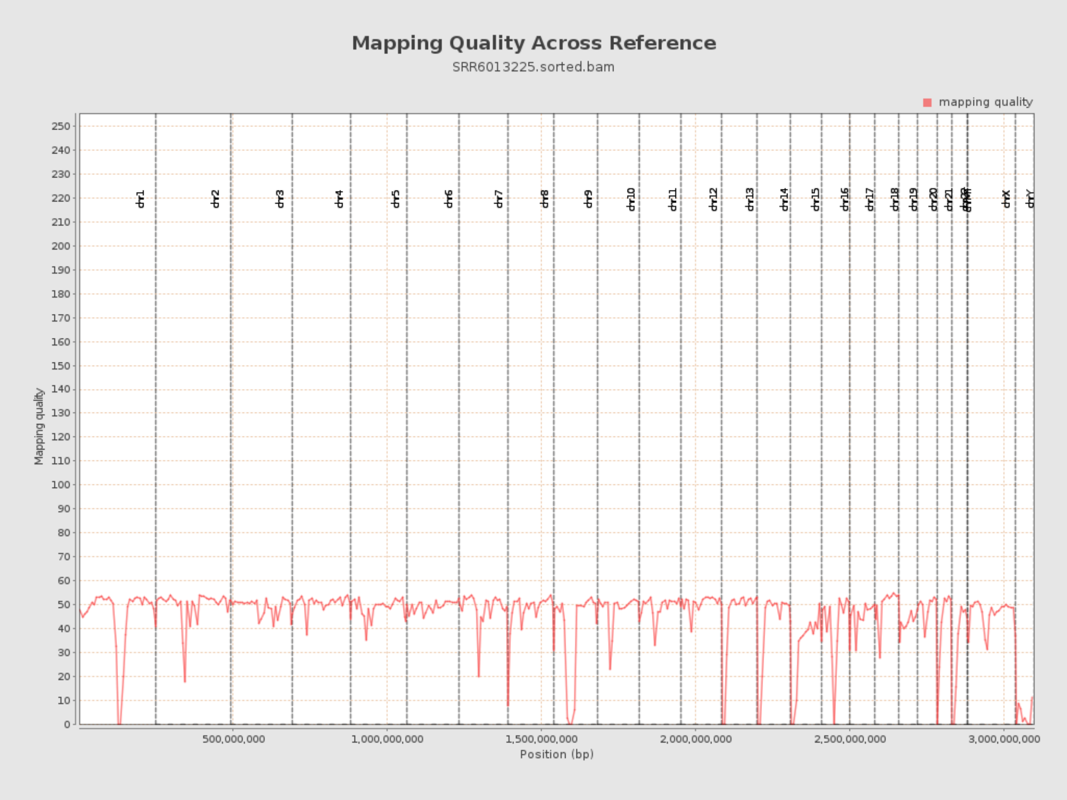
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram