Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:21:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013320.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_SRR6013320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:21:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,999,901
Mapped reads	1,207,562 / 60.38%
Unmapped reads	792,339 / 39.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,865 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	150,016 / 7.5%
Duplication rate	9.63%
Clipped reads	654,187 / 32.71%

2.2. ACGT Content

Number/percentage of A's	20,765,992 / 26.68%
Number/percentage of C's	14,941,883 / 19.19%
Number/percentage of T's	24,066,776 / 30.92%
Number/percentage of G's	18,064,340 / 23.2%
Number/percentage of N's	8,831 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.3133

2.4. Mapping Quality

Mean Mapping Quality	42.27

2.5. Mismatches and indels

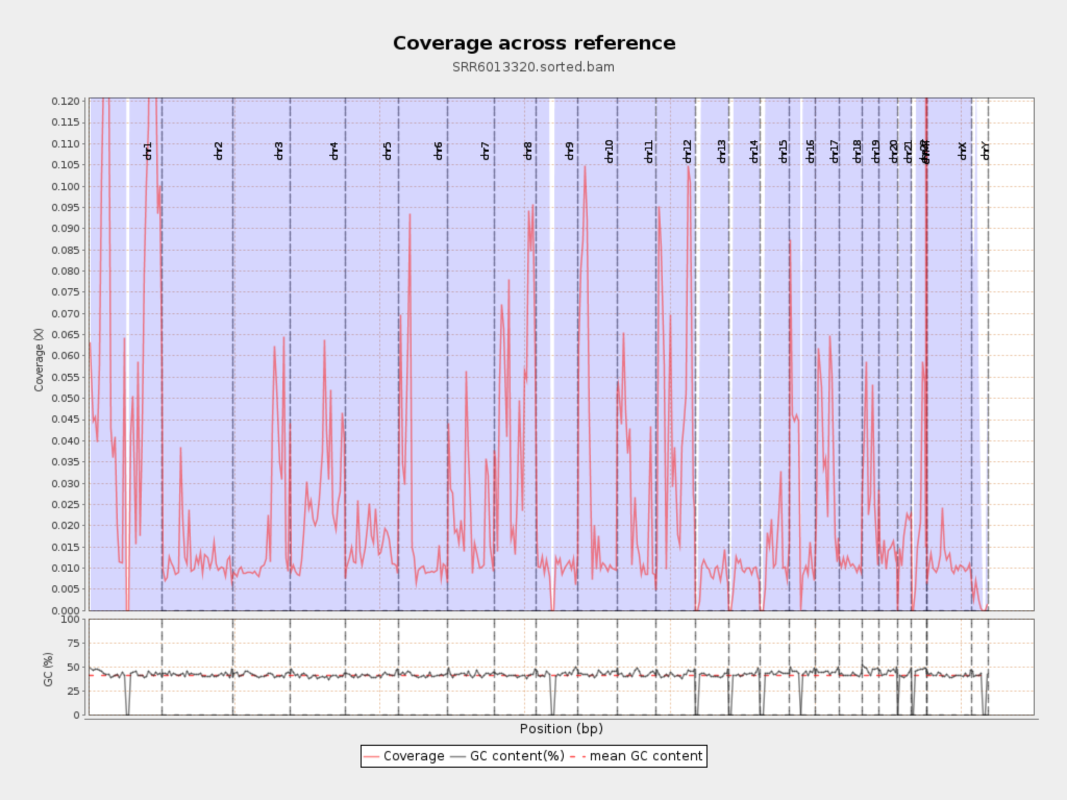
General error rate	0.83%
Mismatches	637,204
Insertions	5,006
Mapped reads with at least one insertion	0.41%
Deletions	25,801
Mapped reads with at least one deletion	2.11%
Homopolymer indels	44.36%

2.6. Chromosome stats

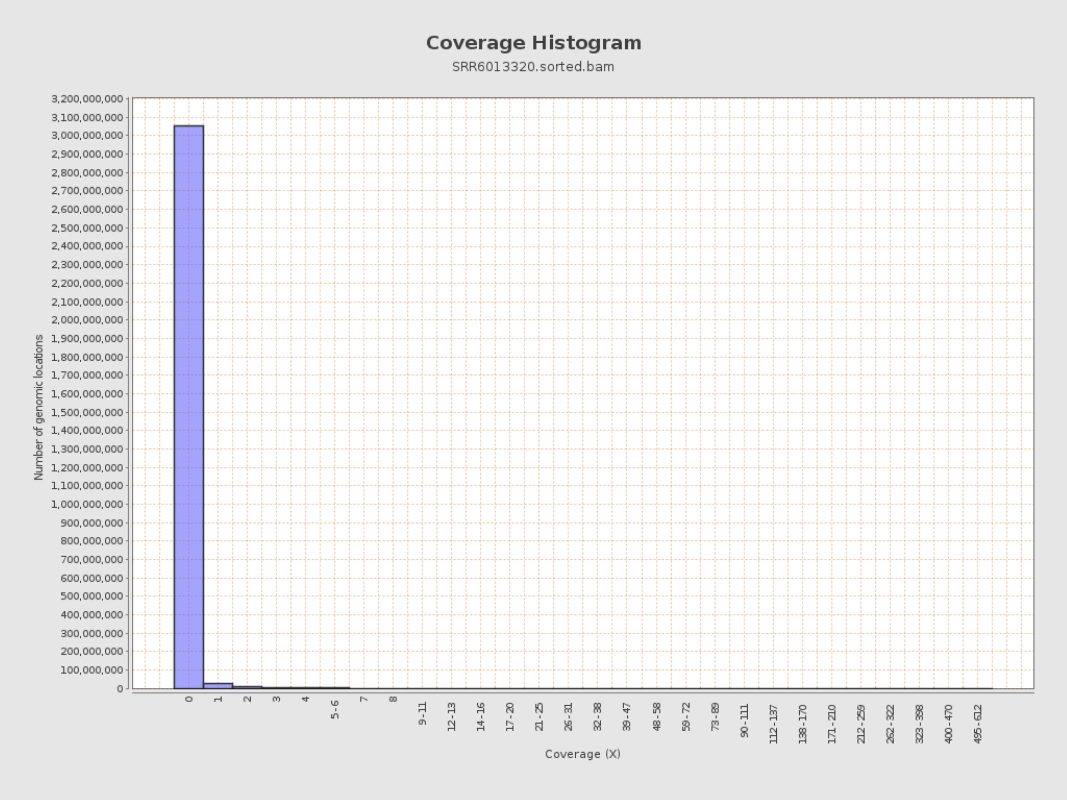
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16476114	0.0661	0.5814
chr2	243199373	3007028	0.0124	0.3116
chr3	198022430	3854984	0.0195	0.223
chr4	191154276	5024456	0.0263	0.2559
chr5	180915260	2789022	0.0154	0.1985
chr6	171115067	3672858	0.0215	0.2529
chr7	159138663	3493117	0.022	0.4594

chr8	146364022	7373096	0.0504	0.3957
chr9	141213431	1318190	0.0093	0.1614
chr10	135534747	4625582	0.0341	0.3712
chr11	135006516	3651012	0.027	0.2701
chr12	133851895	6558414	0.049	0.3629
chr13	115169878	943826	0.0082	0.1474
chr14	107349540	897260	0.0084	0.143
chr15	102531392	1317153	0.0128	0.1789
chr16	90354753	2301604	0.0255	0.2575
chr17	81195210	2979109	0.0367	0.3287
chr18	78077248	839828	0.0108	0.2013
chr19	59128983	1985414	0.0336	0.4021
chr20	63025520	868684	0.0138	0.1911
chr21	48129895	783863	0.0163	0.2094
chr22	51304566	1214527	0.0237	0.2629
chrMT	16571	27469	1.6577	2.3456
chrX	155270560	1758044	0.0113	0.1697
chrY	59373566	131802	0.0022	0.0664

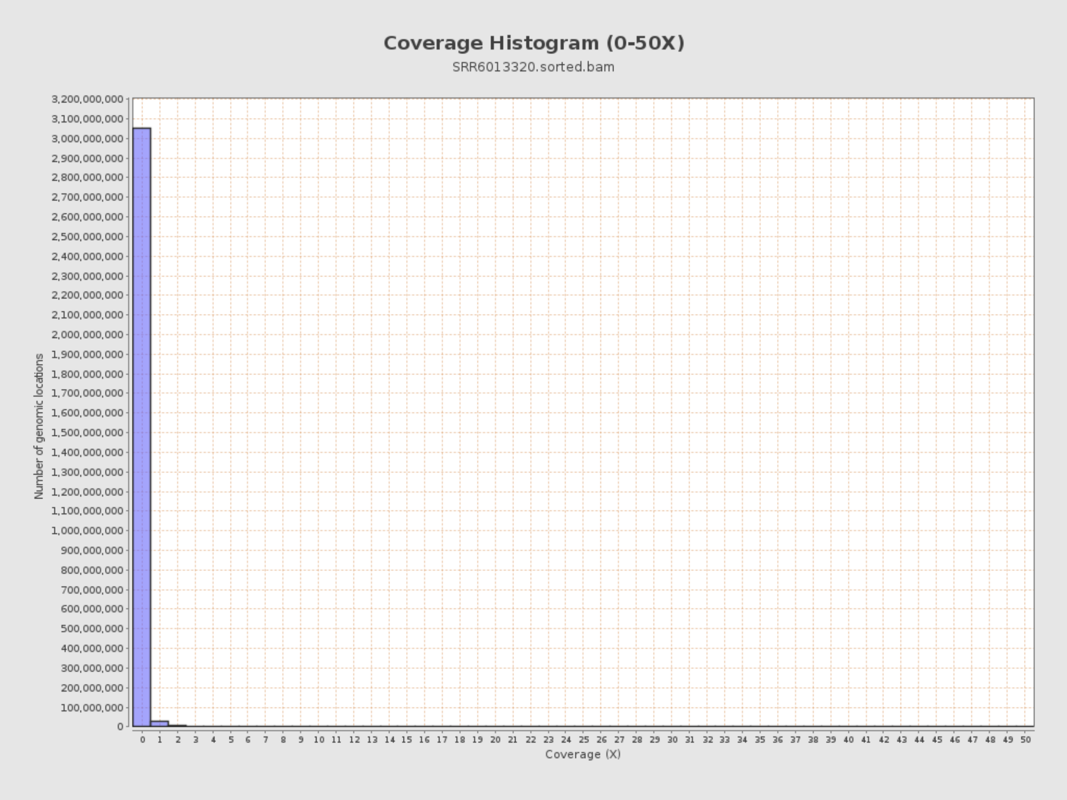
3. Results : Coverage across reference



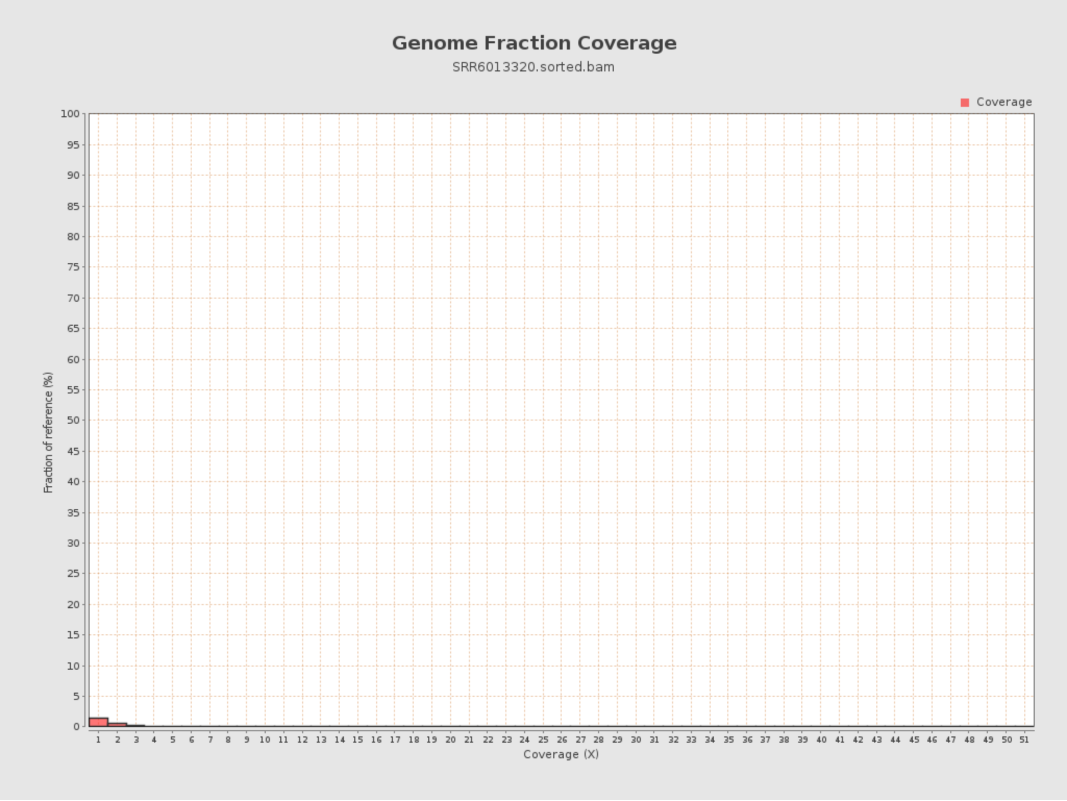
4. Results : Coverage Histogram



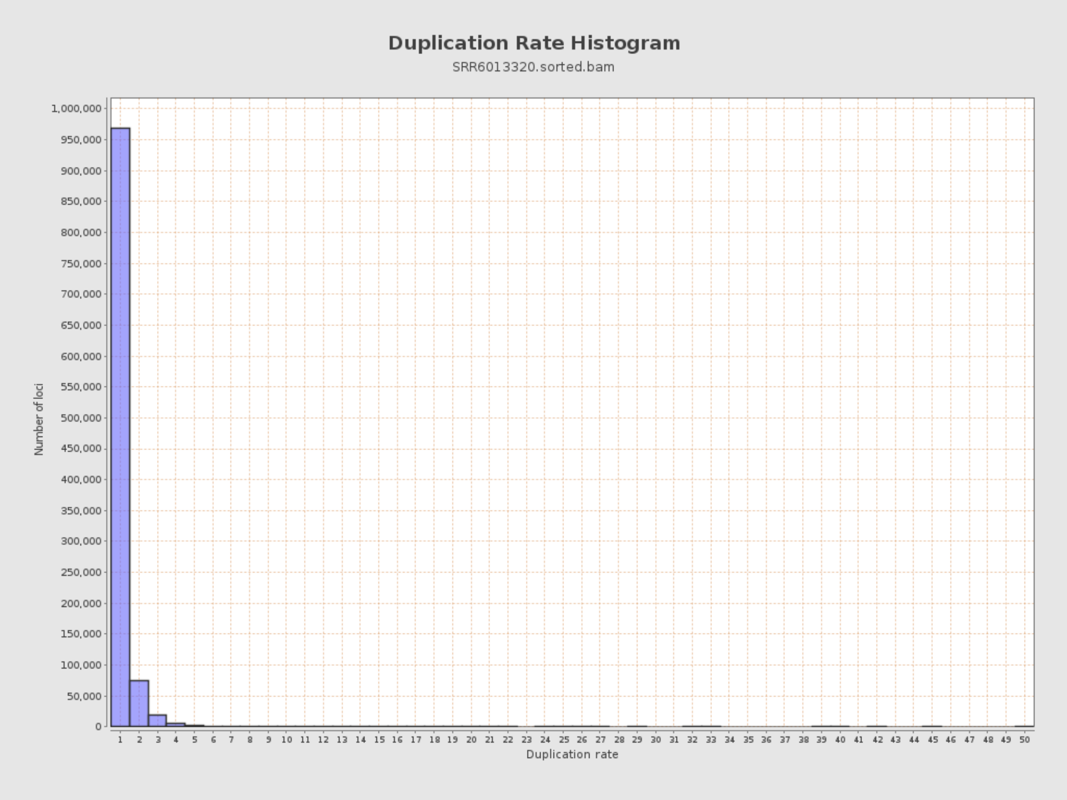
5. Results : Coverage Histogram (0-50X)



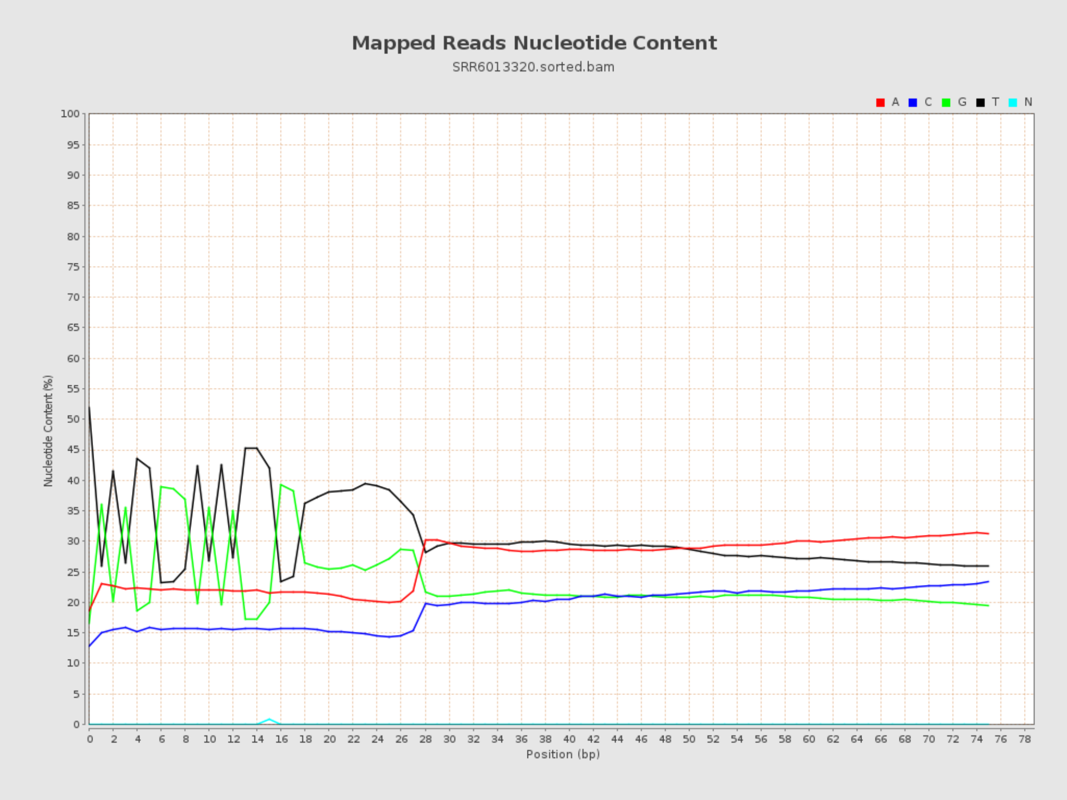
6. Results : Genome Fraction Coverage



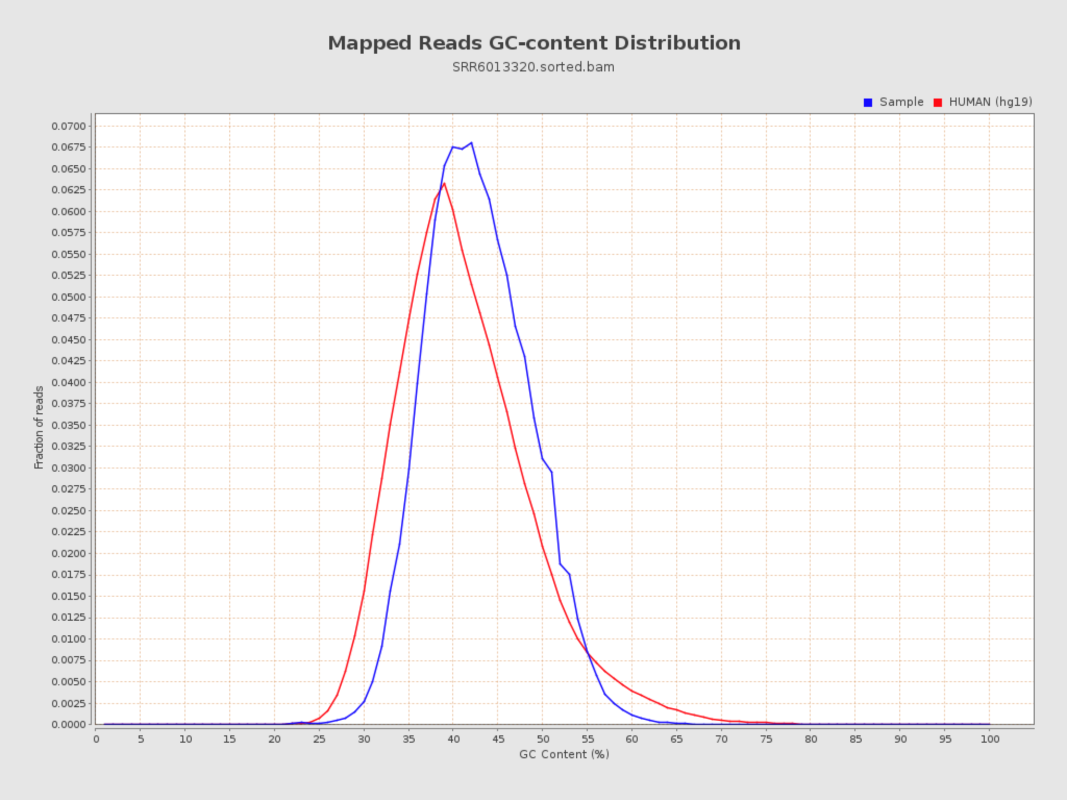
7. Results : Duplication Rate Histogram



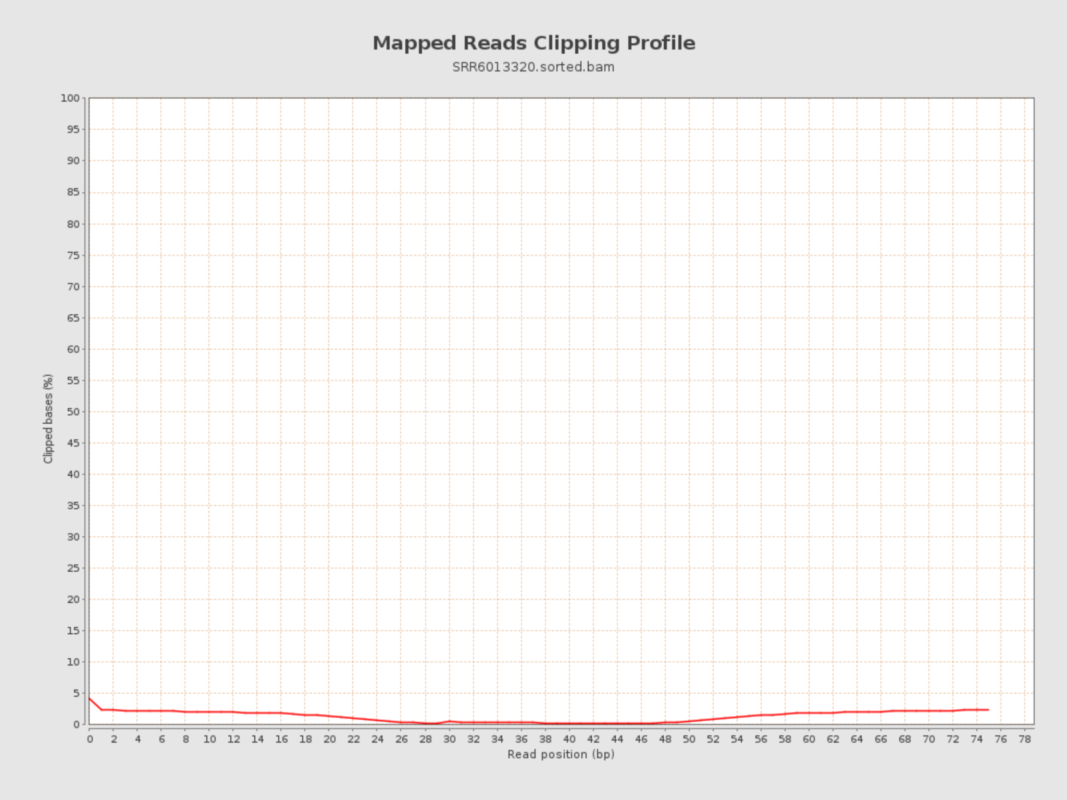
8. Results : Mapped Reads Nucleotide Content



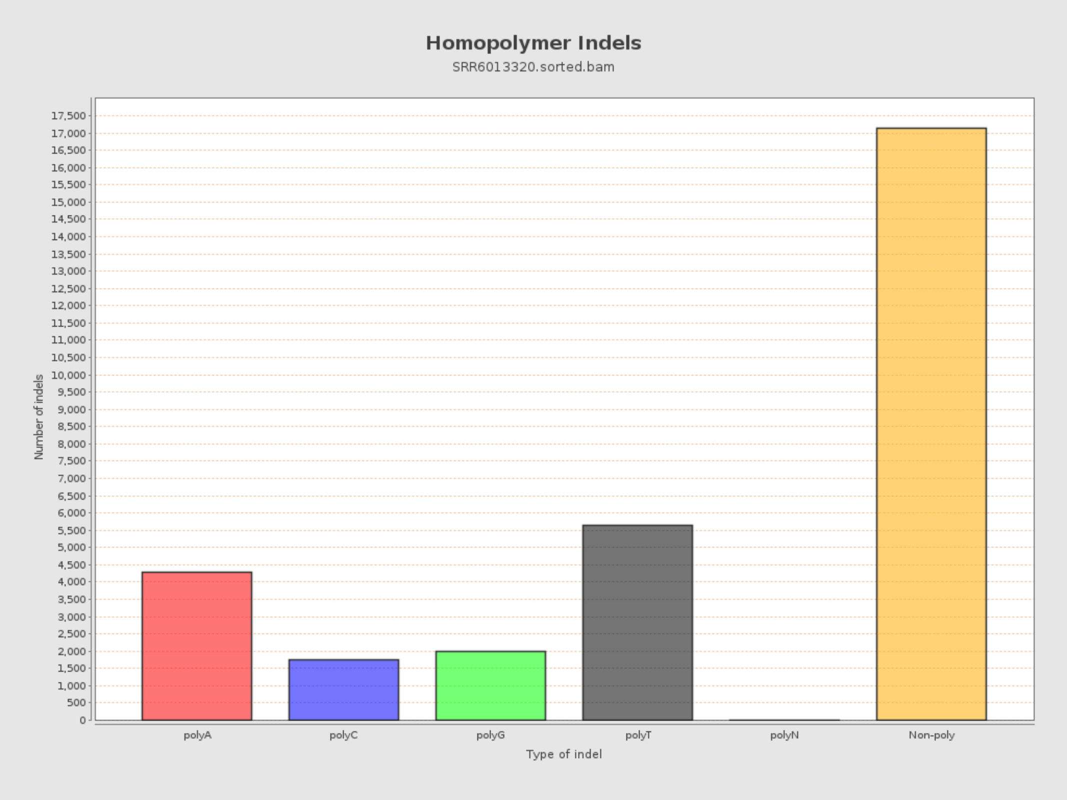
9. Results : Mapped Reads GC-content Distribution



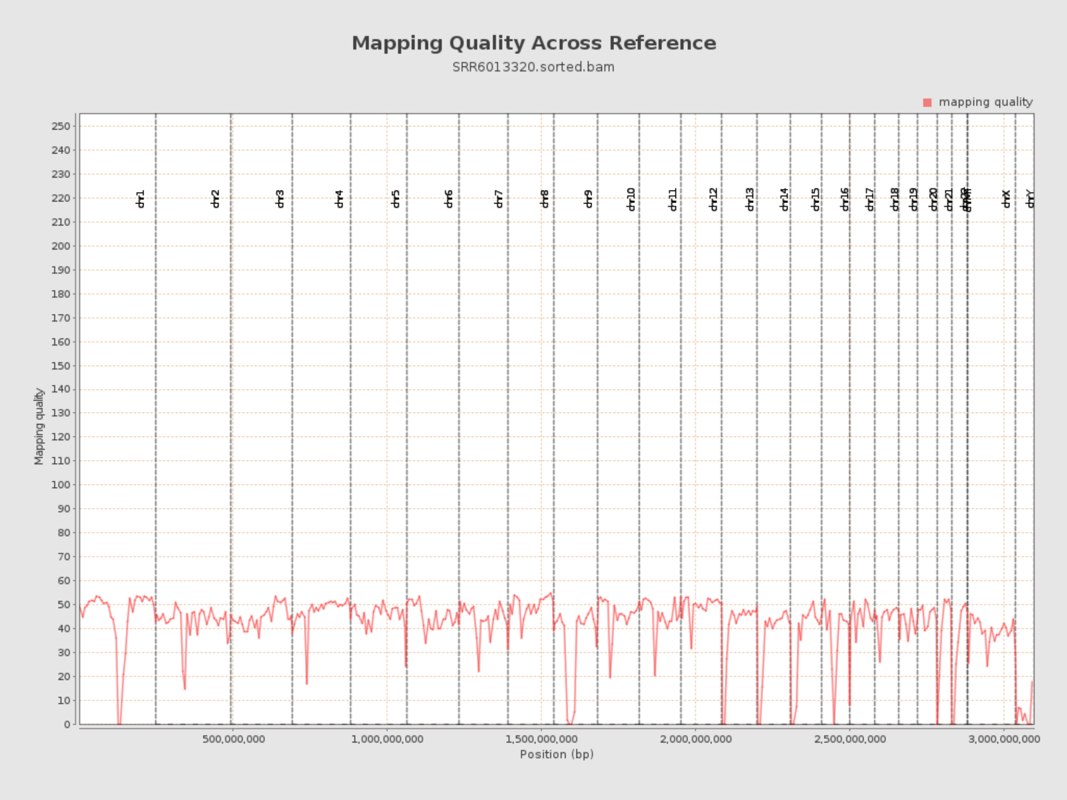
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram