Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 04:19:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063592.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_SRR6063592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 04:19:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,960,148
Mapped reads	1,423,038 / 72.6%
Unmapped reads	537,110 / 27.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,140 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	204,539 / 10.43%
Duplication rate	9.8%
Clipped reads	704,762 / 35.95%

2.2. ACGT Content

Number/percentage of A's	26,191,082 / 28.13%
Number/percentage of C's	16,855,391 / 18.1%
Number/percentage of T's	29,965,758 / 32.18%
Number/percentage of G's	20,095,301 / 21.58%
Number/percentage of N's	2,512 / 0%
GC Percentage	39.68%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.9337

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

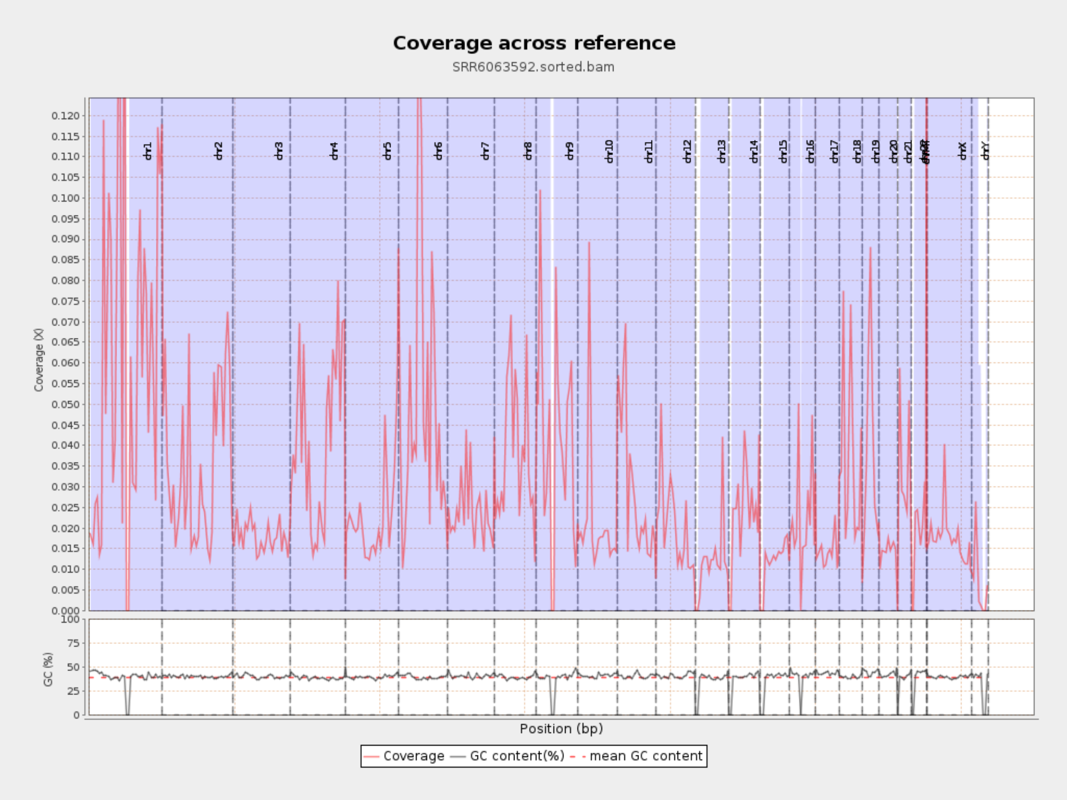
General error rate	0.94%
Mismatches	859,756
Insertions	9,244
Mapped reads with at least one insertion	0.64%
Deletions	25,239
Mapped reads with at least one deletion	1.75%
Homopolymer indels	45.47%

2.6. Chromosome stats

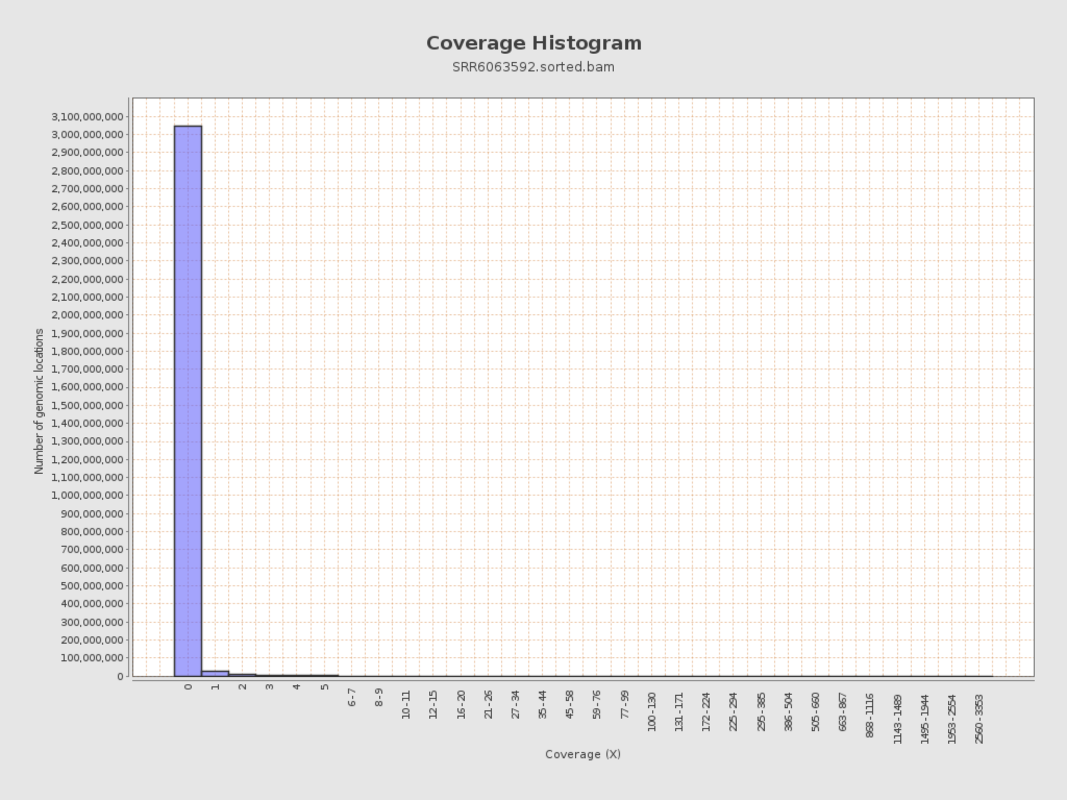
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15458712	0.062	2.7666
chr2	243199373	8649094	0.0356	0.5957
chr3	198022430	3527464	0.0178	0.2359
chr4	191154276	7975105	0.0417	0.3978
chr5	180915260	4092798	0.0226	0.2663
chr6	171115067	8483714	0.0496	0.4029
chr7	159138663	3804412	0.0239	0.4804

chr8	146364022	5620933	0.0384	0.6059
chr9	141213431	5915461	0.0419	0.6279
chr10	135534747	2847501	0.021	0.5634
chr11	135006516	4019409	0.0298	0.5396
chr12	133851895	2753418	0.0206	0.2484
chr13	115169878	1364661	0.0118	0.1815
chr14	107349540	2465166	0.023	0.2916
chr15	102531392	1223564	0.0119	0.2191
chr16	90354753	2034041	0.0225	0.3984
chr17	81195210	1119299	0.0138	0.1976
chr18	78077248	2868786	0.0367	1.7058
chr19	59128983	2376268	0.0402	1.2754
chr20	63025520	909674	0.0144	0.2199
chr21	48129895	1570027	0.0326	0.3423
chr22	51304566	931230	0.0182	0.2121
chrMT	16571	3628	0.2189	0.6912
chrX	155270560	2754519	0.0177	0.2892
chrY	59373566	383641	0.0065	0.2097

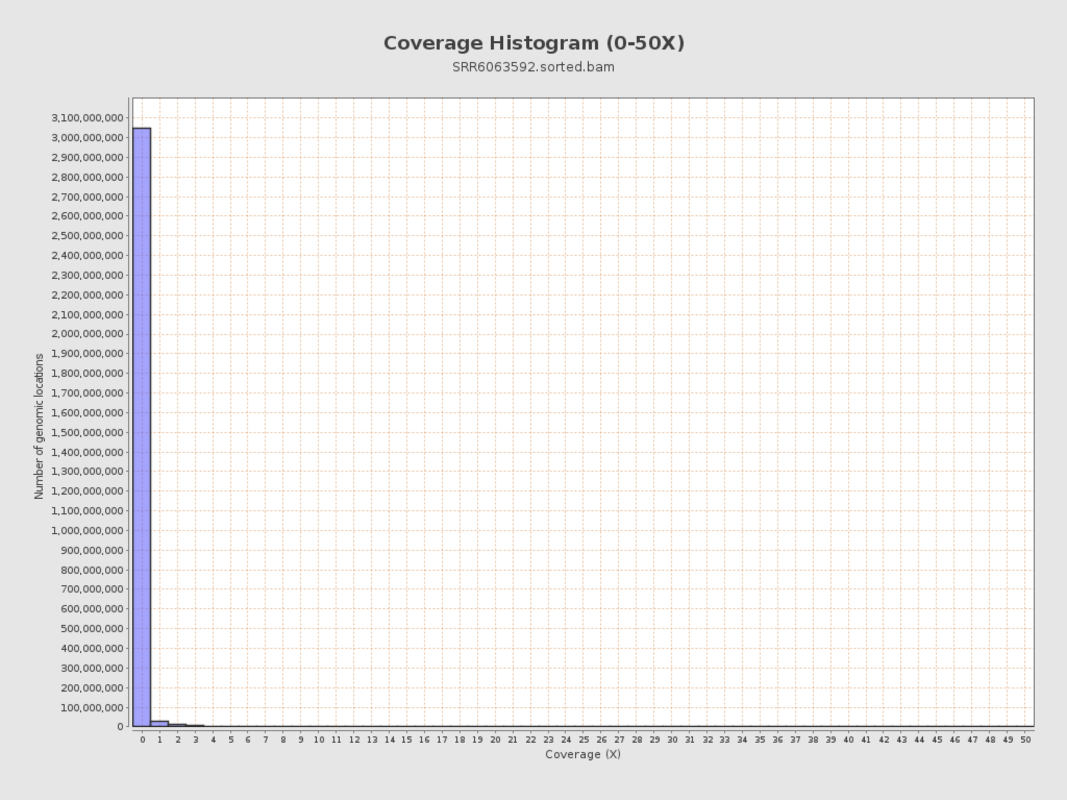
3. Results : Coverage across reference



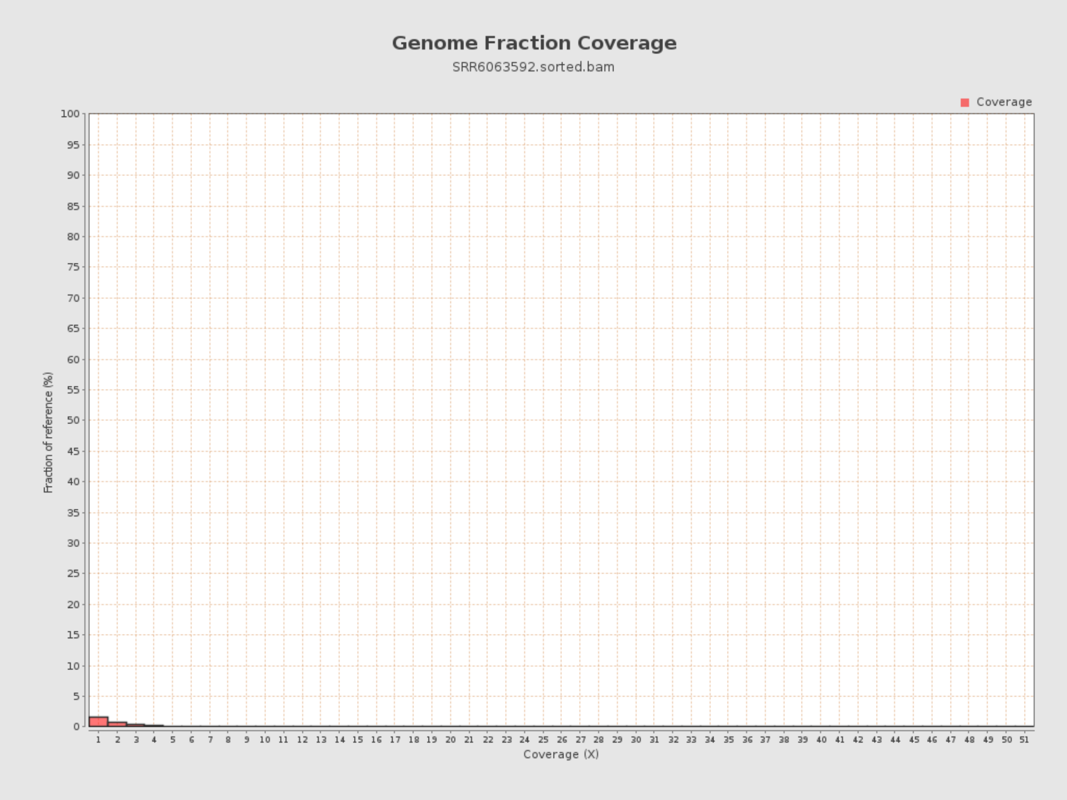
4. Results : Coverage Histogram



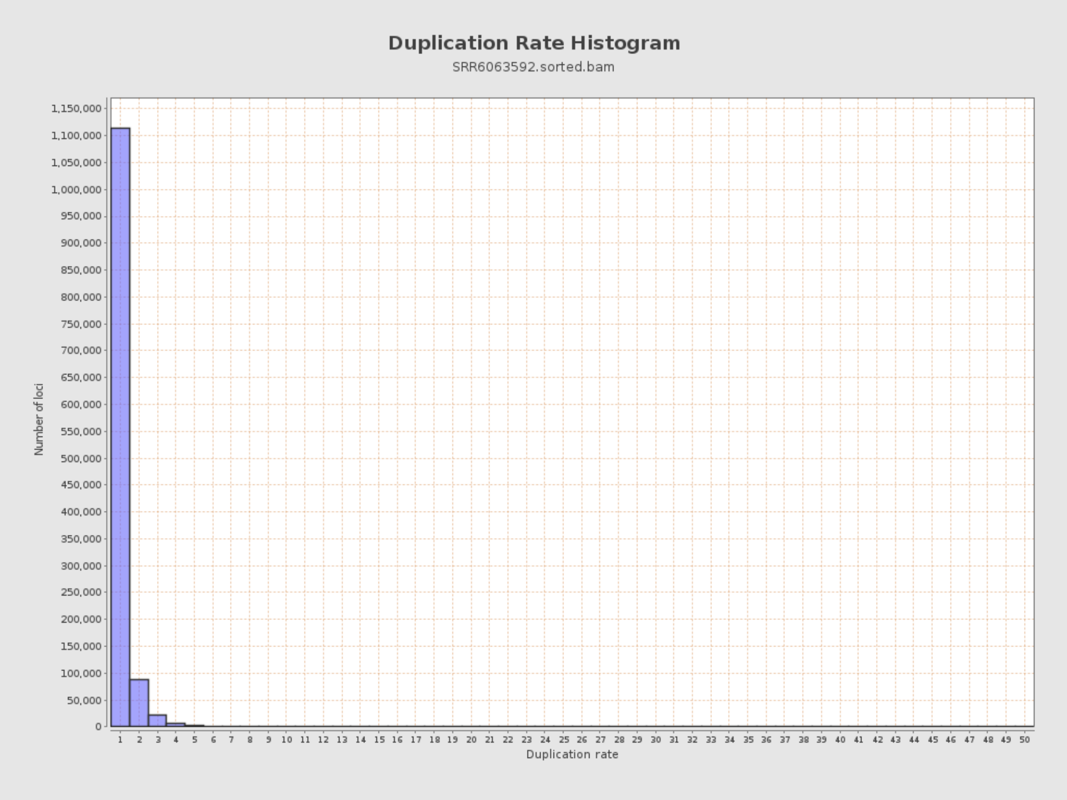
5. Results : Coverage Histogram (0-50X)



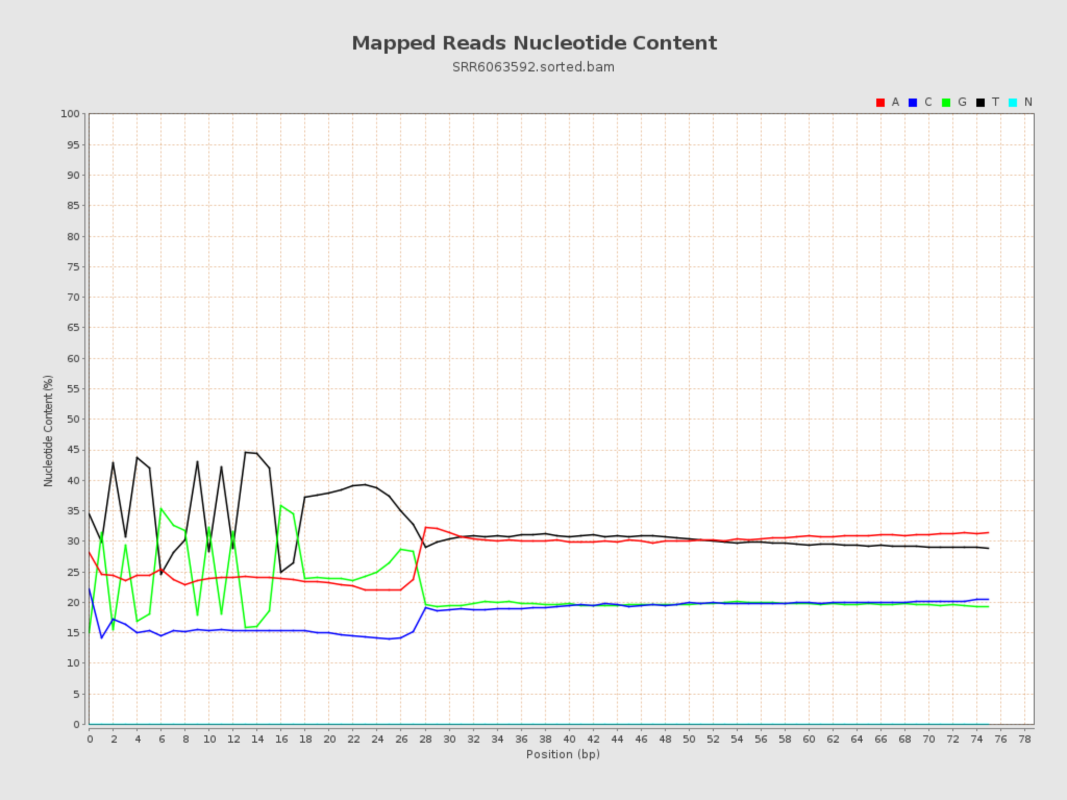
6. Results : Genome Fraction Coverage



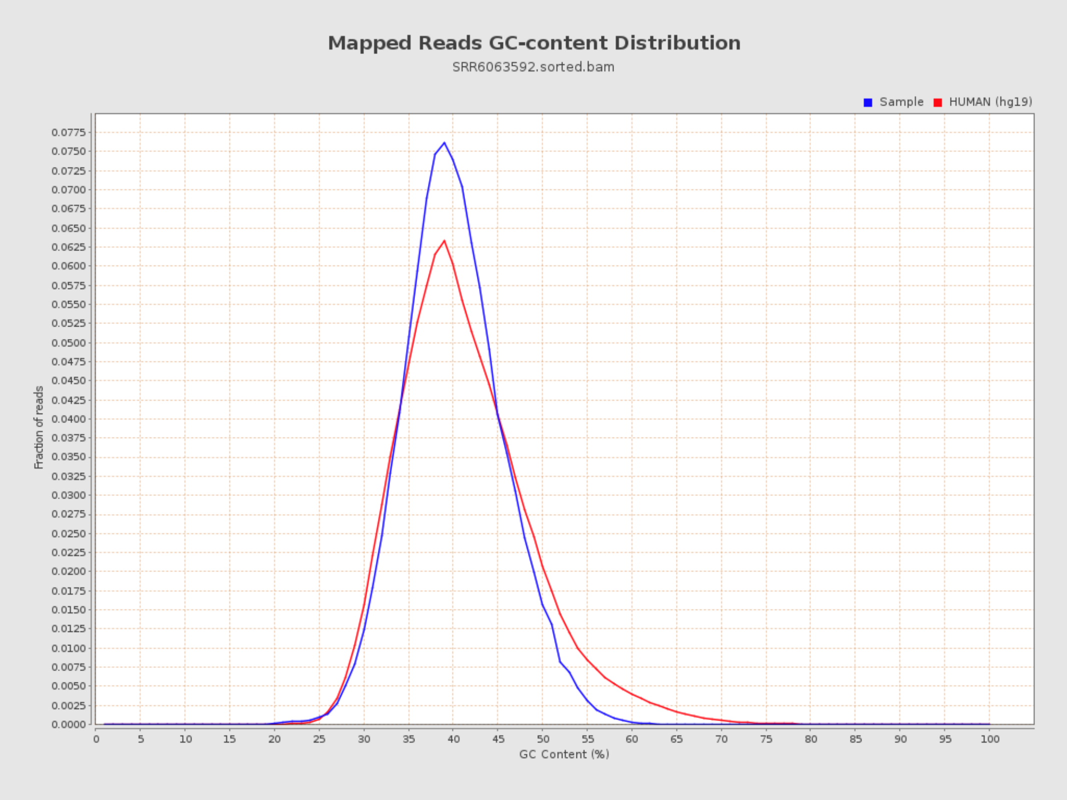
7. Results : Duplication Rate Histogram



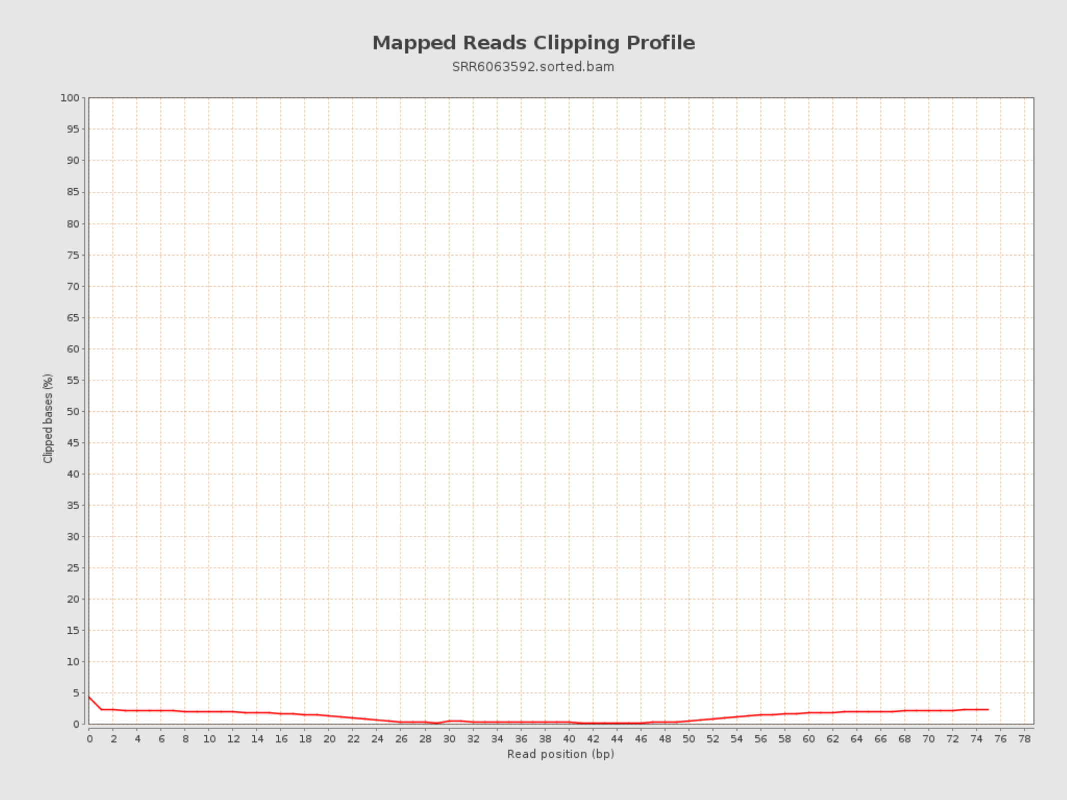
8. Results : Mapped Reads Nucleotide Content



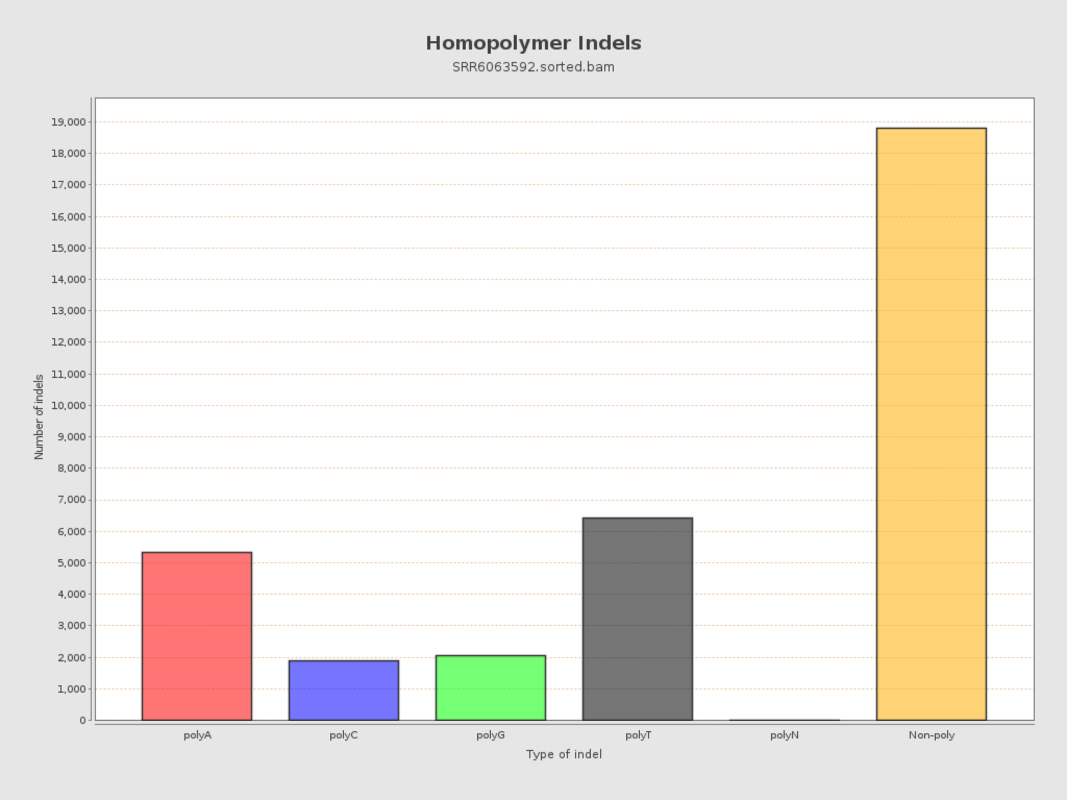
9. Results : Mapped Reads GC-content Distribution



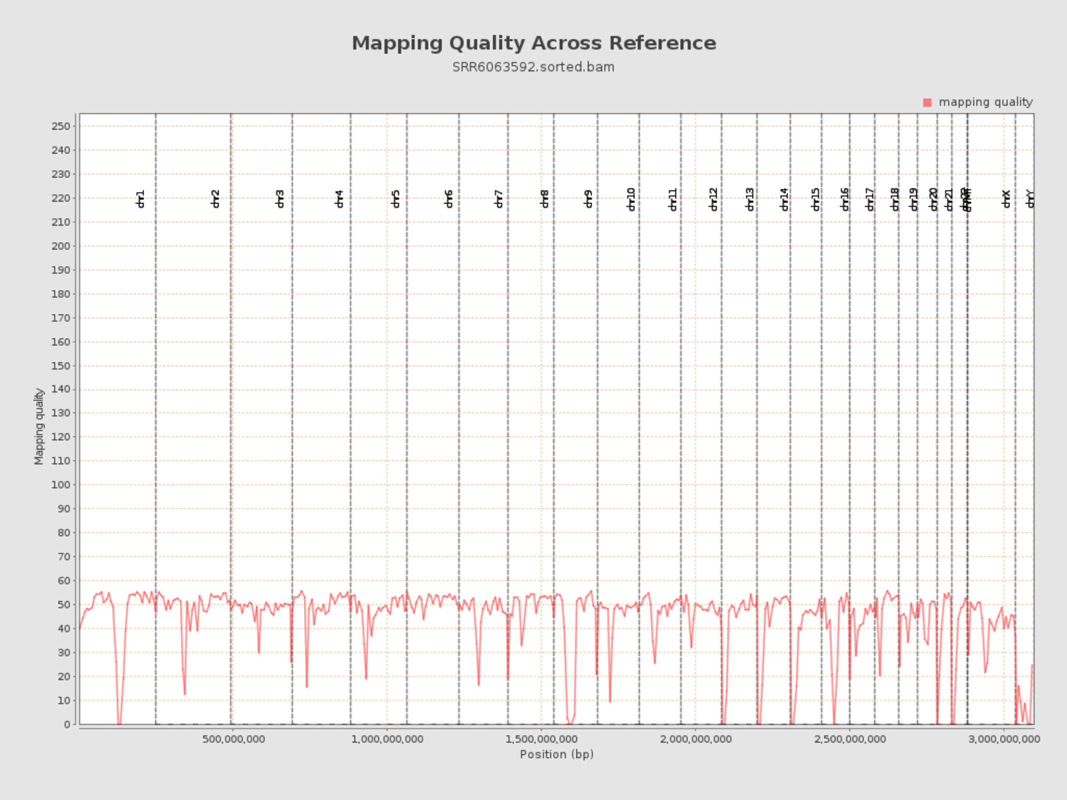
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram