Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 17:48:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR619719.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR619719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 17:48:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR619719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,643,235
Mapped reads	3,546,110 / 24.22%
Unmapped reads	11,097,125 / 75.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	770,389 / 5.26%
Duplication rate	13.23%
Clipped reads	1,484,245 / 10.14%

2.2. ACGT Content

Number/percentage of A's	36,128,251 / 23.97%
Number/percentage of C's	24,967,802 / 16.56%
Number/percentage of T's	55,469,294 / 36.8%
Number/percentage of G's	34,173,409 / 22.67%
Number/percentage of N's	9,091 / 0.01%
GC Percentage	39.23%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.5743

2.4. Mapping Quality

Mean Mapping Quality	42.89

2.5. Mismatches and indels

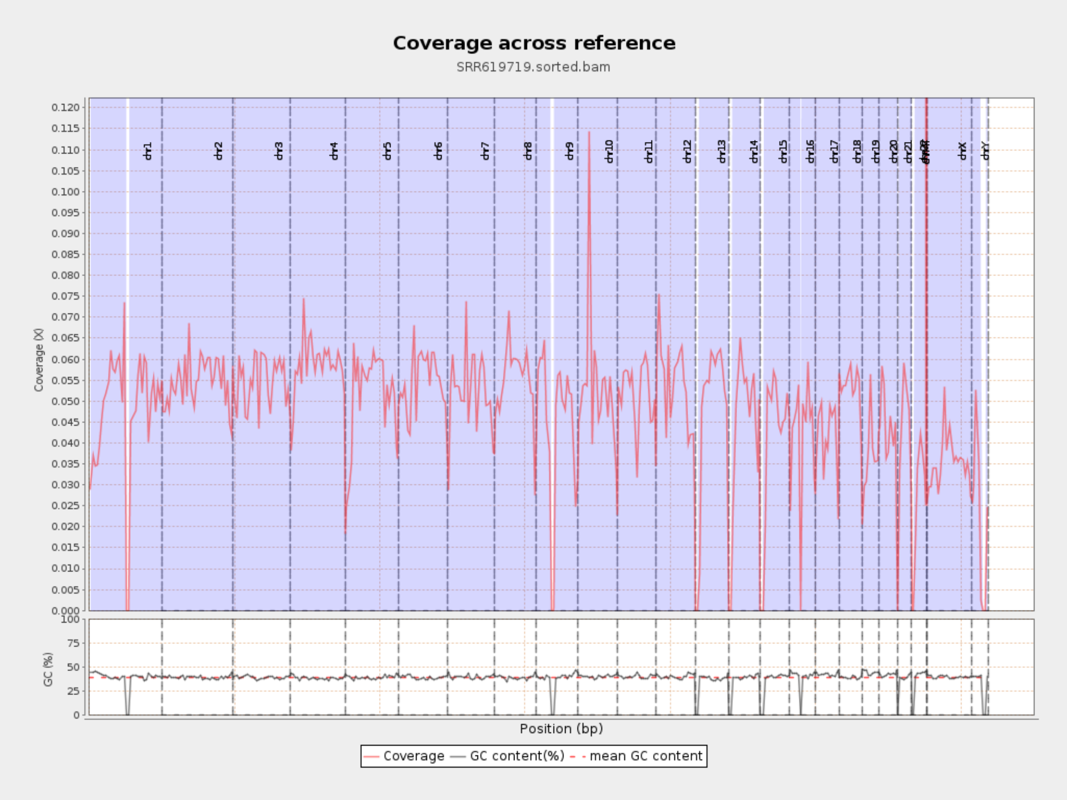
General error rate	0.91%
Mismatches	1,358,703
Insertions	11,048
Mapped reads with at least one insertion	0.31%
Deletions	27,049
Mapped reads with at least one deletion	0.76%
Homopolymer indels	44.19%

2.6. Chromosome stats

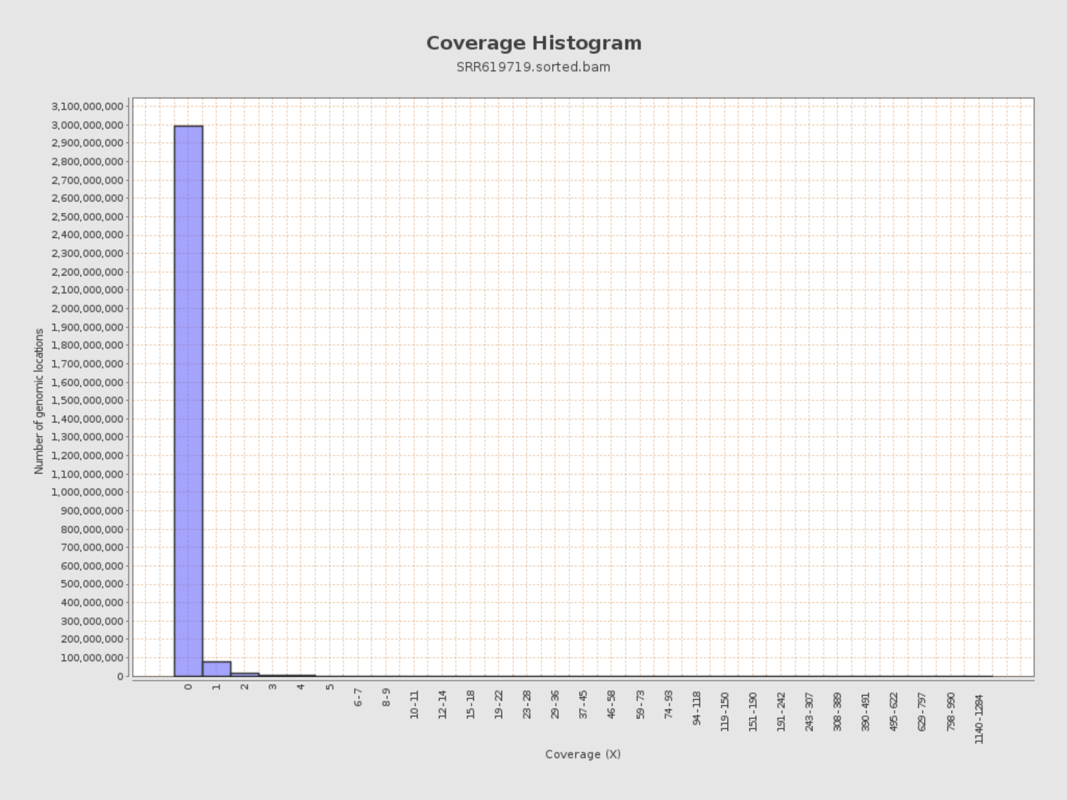
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11888838	0.0477	0.7549
chr2	243199373	13295411	0.0547	0.5875
chr3	198022430	10854809	0.0548	0.4779
chr4	191154276	11211772	0.0587	0.5584
chr5	180915260	9346368	0.0517	0.4553
chr6	171115067	9349772	0.0546	0.4979
chr7	159138663	8432610	0.053	0.7818

chr8	146364022	8093687	0.0553	0.8881
chr9	141213431	6341679	0.0449	0.5158
chr10	135534747	7287852	0.0538	0.6775
chr11	135006516	6948926	0.0515	0.6375
chr12	133851895	7233002	0.054	0.4565
chr13	115169878	5350858	0.0465	0.4385
chr14	107349540	4664548	0.0435	0.3934
chr15	102531392	4138462	0.0404	0.3946
chr16	90354753	3775789	0.0418	0.3891
chr17	81195210	3321593	0.0409	0.4099
chr18	78077248	4200364	0.0538	0.7772
chr19	59128983	2207357	0.0373	0.5258
chr20	63025520	2764071	0.0439	0.4585
chr21	48129895	1988180	0.0413	0.4396
chr22	51304566	1300880	0.0254	0.2937
chrMT	16571	42822	2.5842	3.2073
chrX	155270560	5489203	0.0354	0.488
chrY	59373566	1257722	0.0212	0.2969

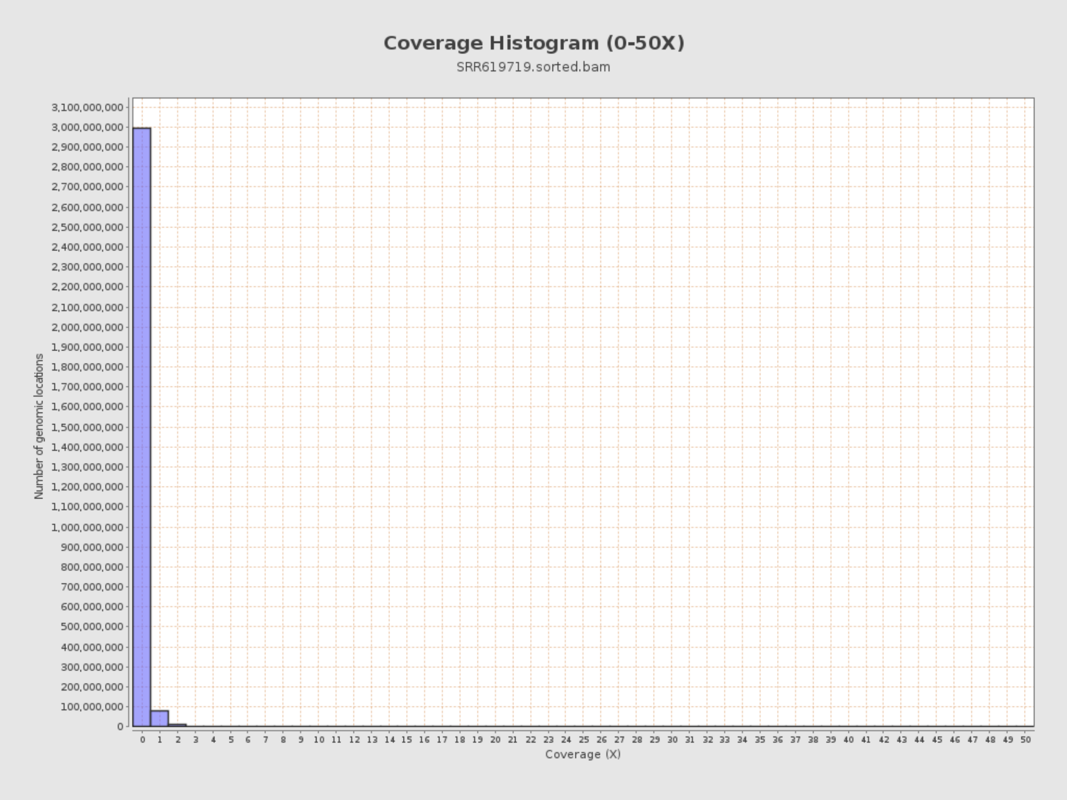
3. Results : Coverage across reference



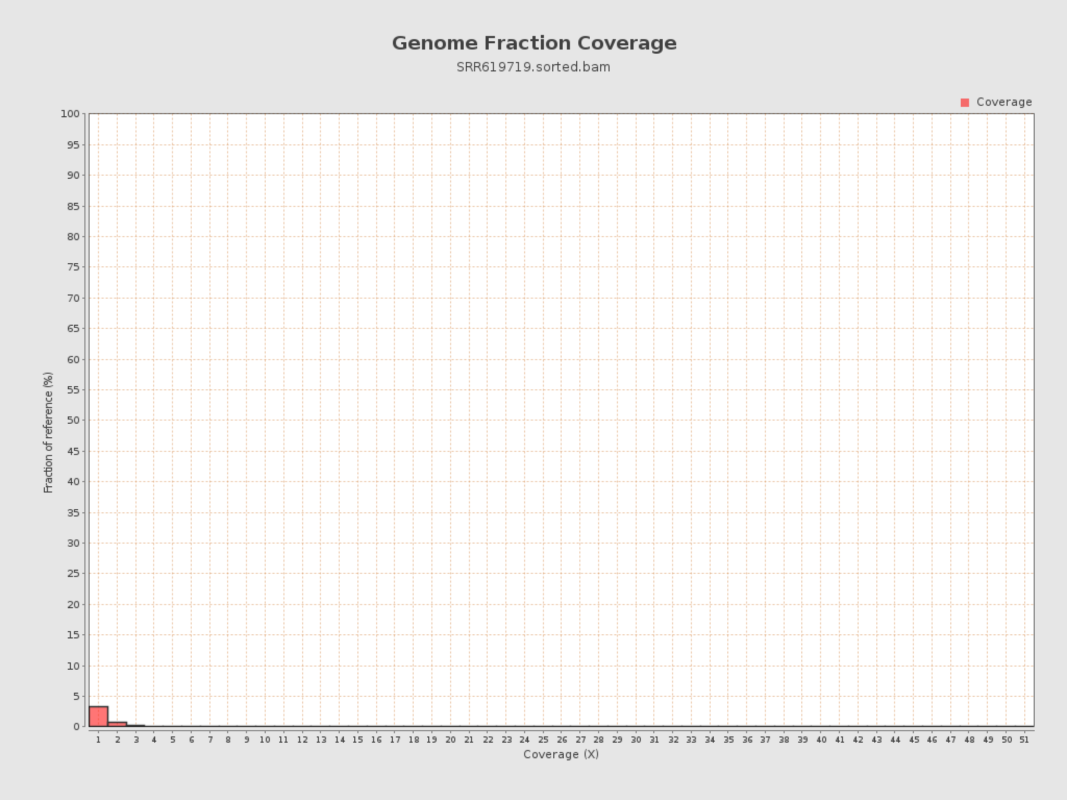
4. Results : Coverage Histogram



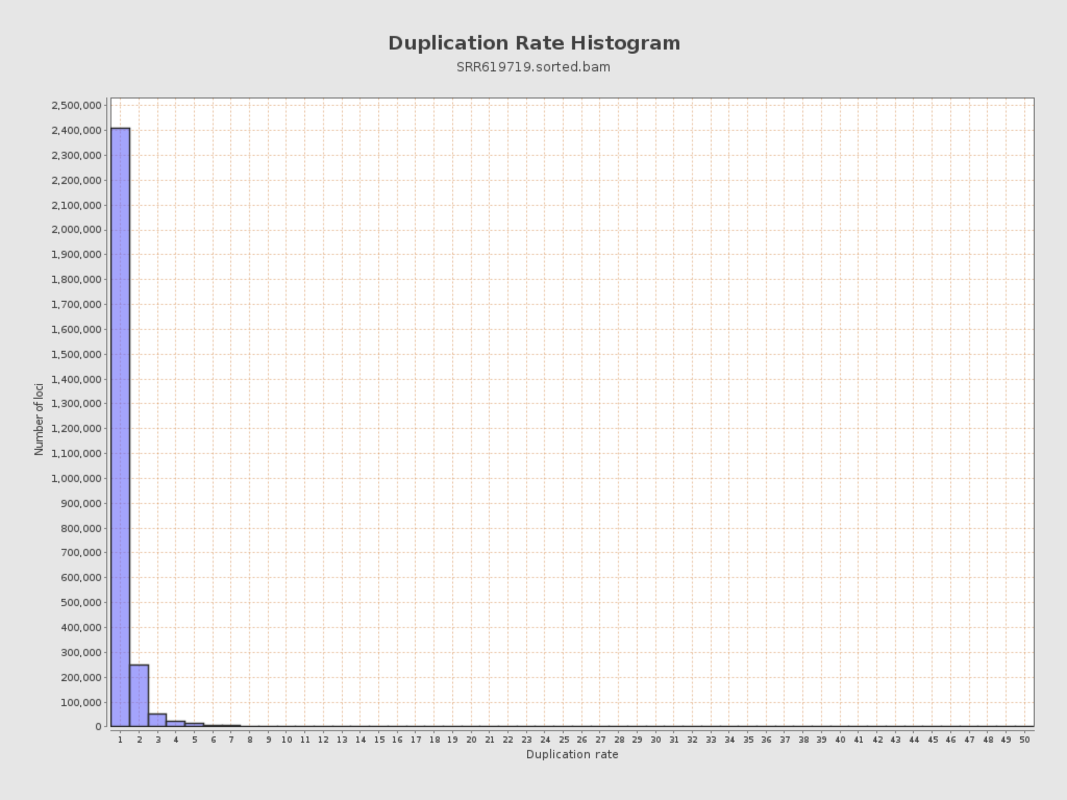
5. Results : Coverage Histogram (0-50X)



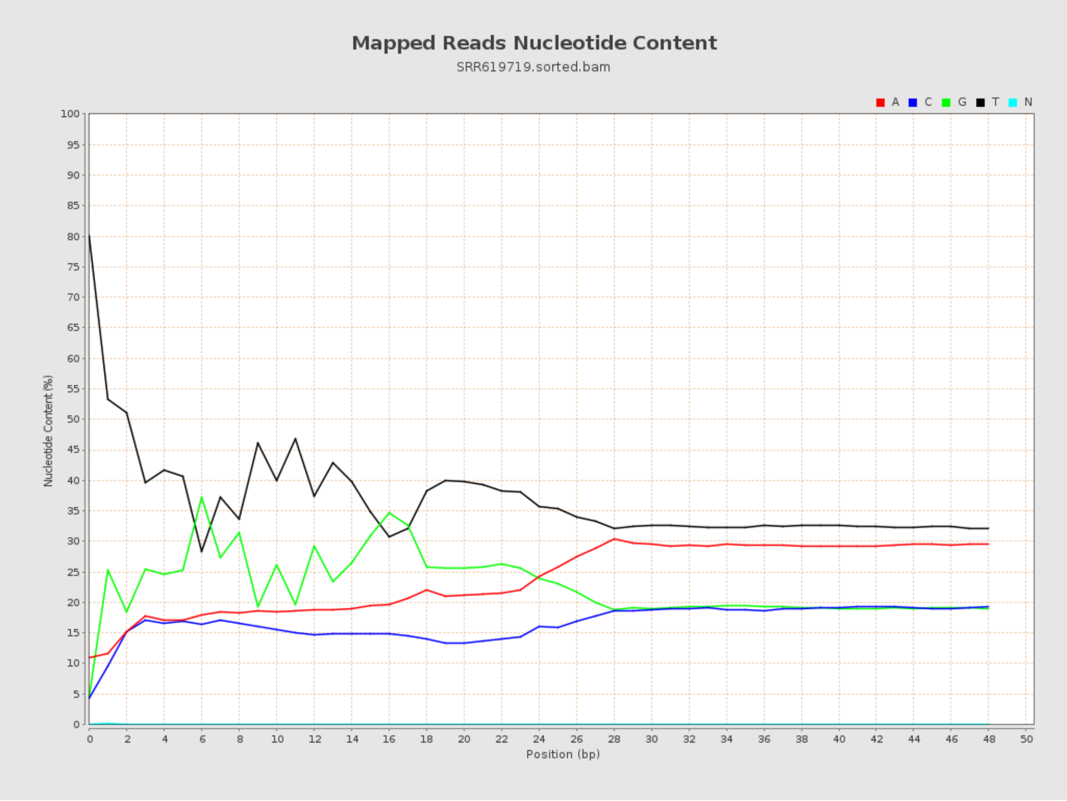
6. Results : Genome Fraction Coverage



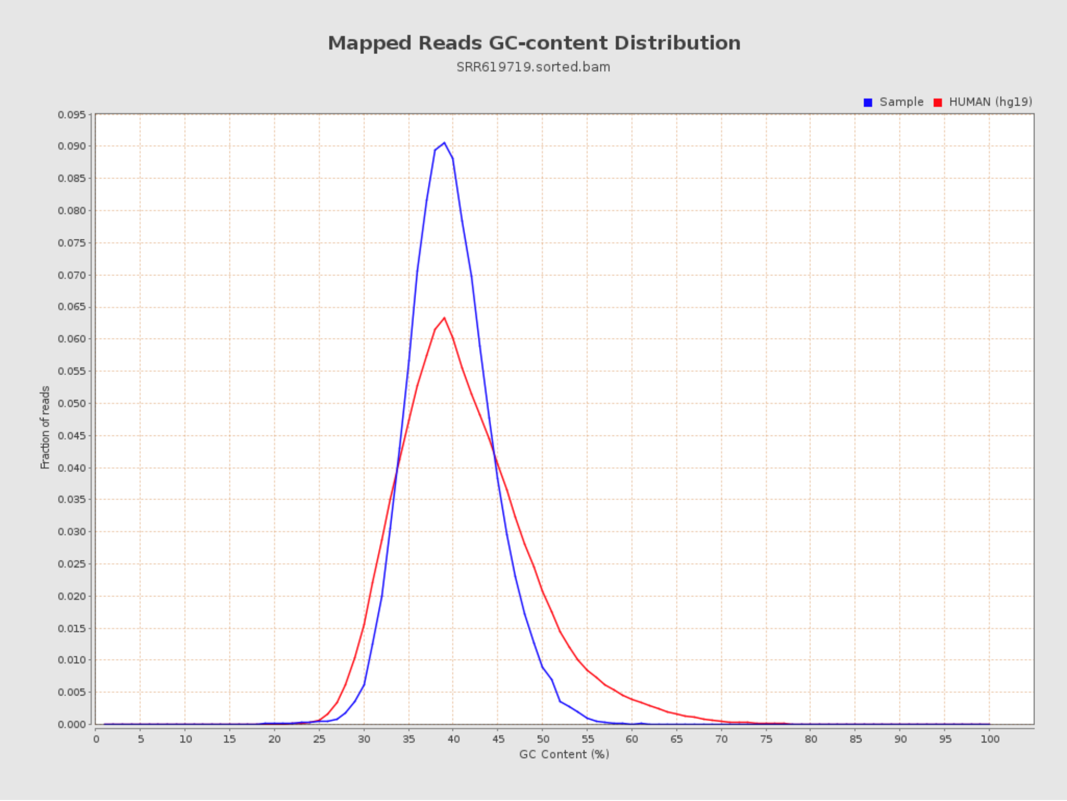
7. Results : Duplication Rate Histogram



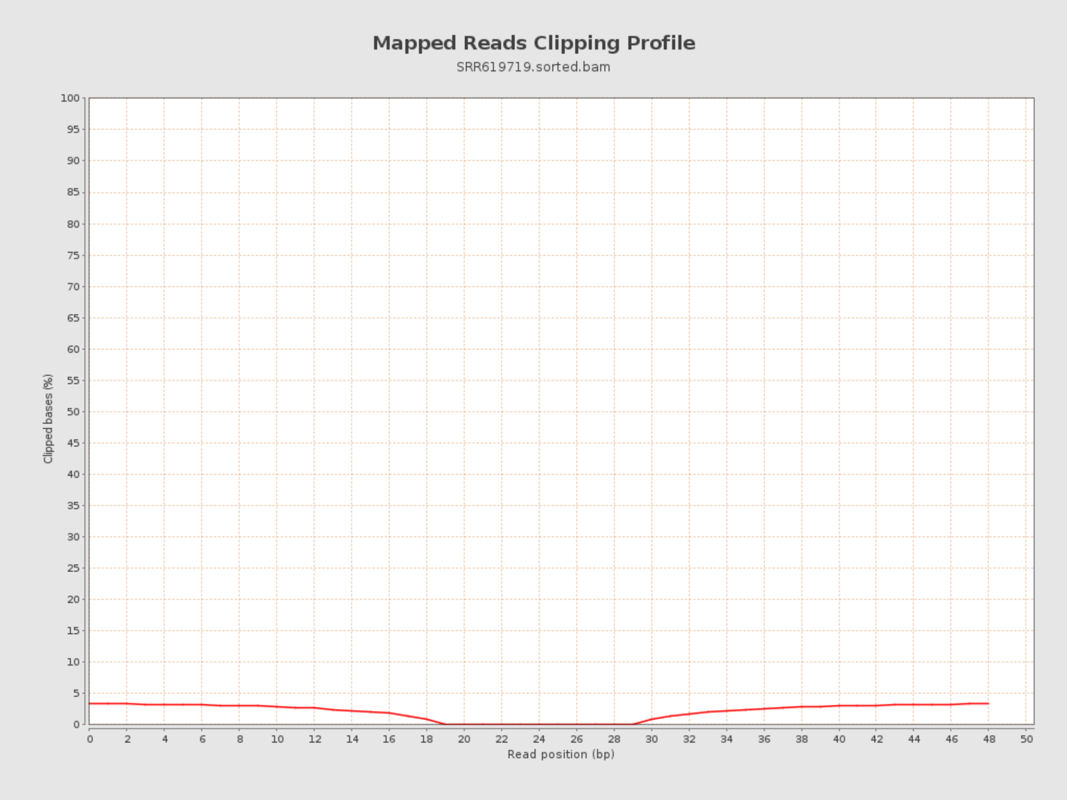
8. Results : Mapped Reads Nucleotide Content



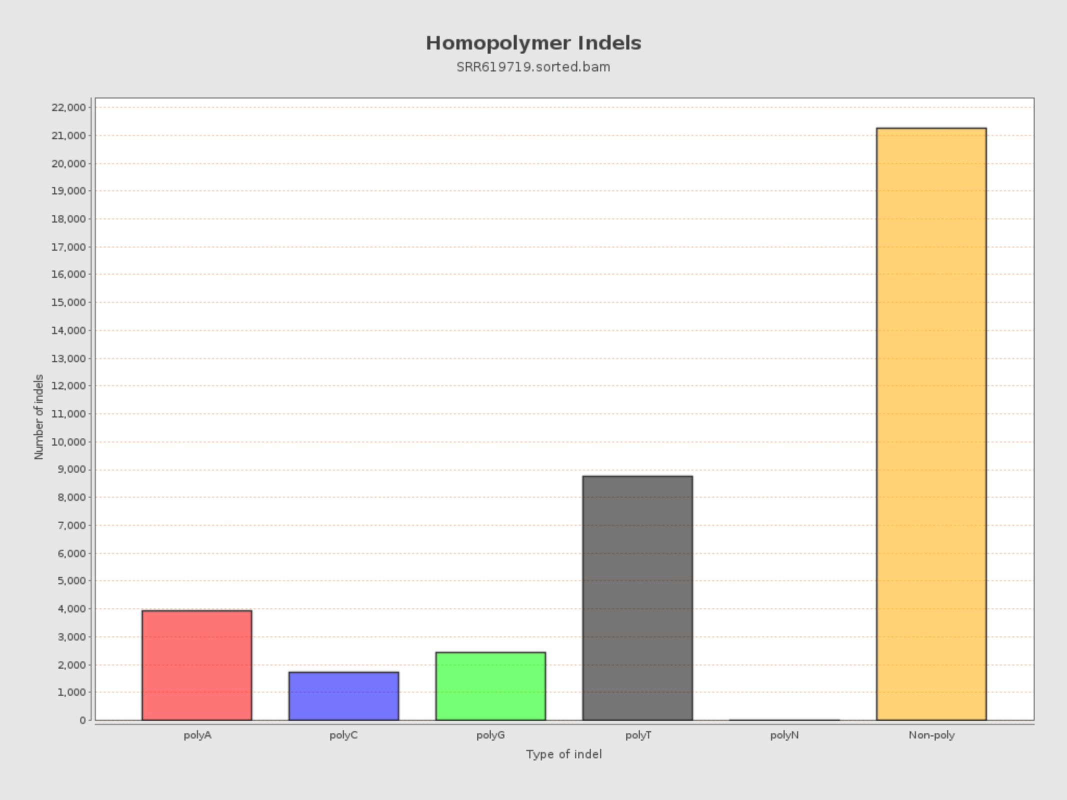
9. Results : Mapped Reads GC-content Distribution



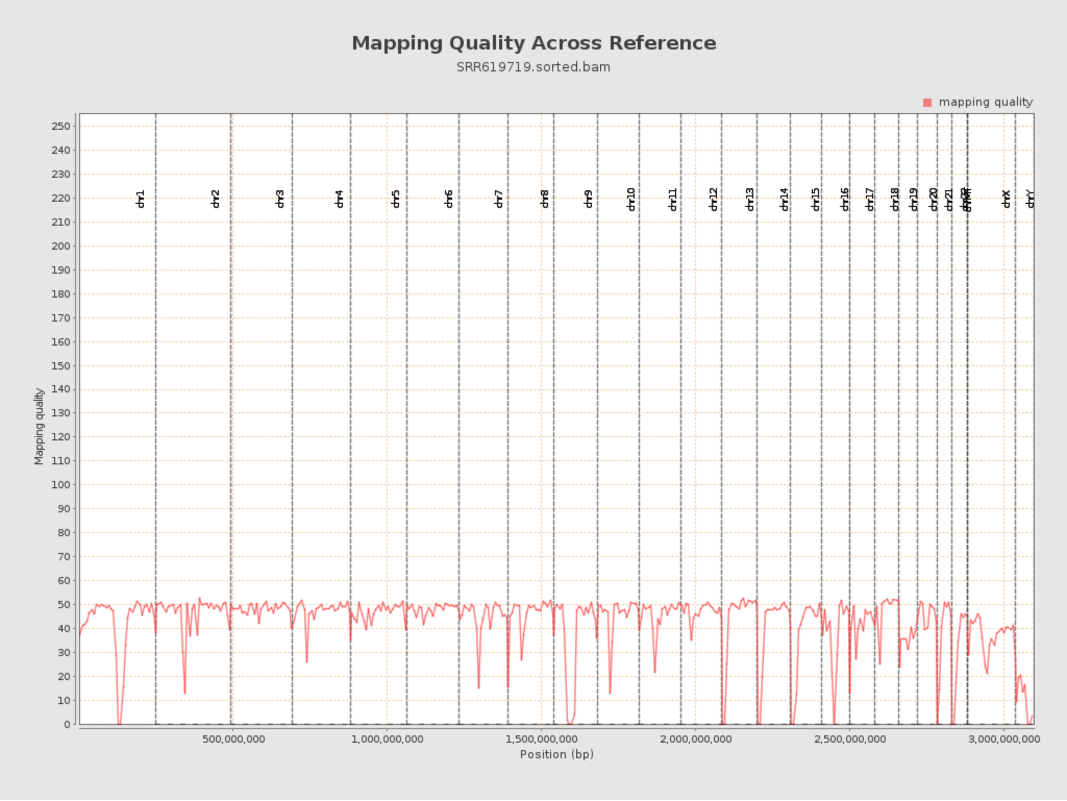
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram