Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:12:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083619.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_SRR3083619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083619.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:12:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,695,659
Mapped reads	1,501,090 / 88.53%
Unmapped reads	194,569 / 11.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,842 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	87,184 / 5.14%
Duplication rate	5%
Clipped reads	721,318 / 42.54%

2.2. ACGT Content

Number/percentage of A's	26,346,524 / 26.64%
Number/percentage of C's	18,624,662 / 18.83%
Number/percentage of T's	30,956,774 / 31.3%
Number/percentage of G's	22,966,008 / 23.22%
Number/percentage of N's	4,927 / 0%
GC Percentage	42.05%

2.3. Coverage

Mean	0.032

Standard Deviation	0.276

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

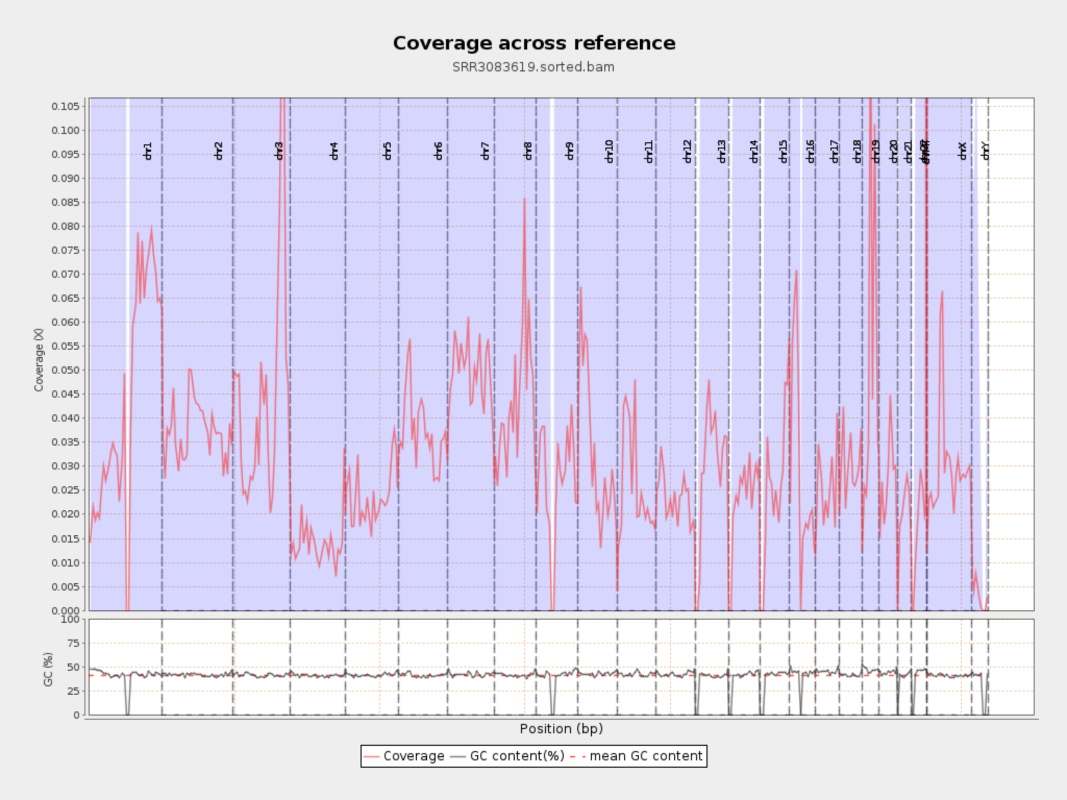
General error rate	0.71%
Mismatches	694,109
Insertions	7,074
Mapped reads with at least one insertion	0.47%
Deletions	22,085
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.88%

2.6. Chromosome stats

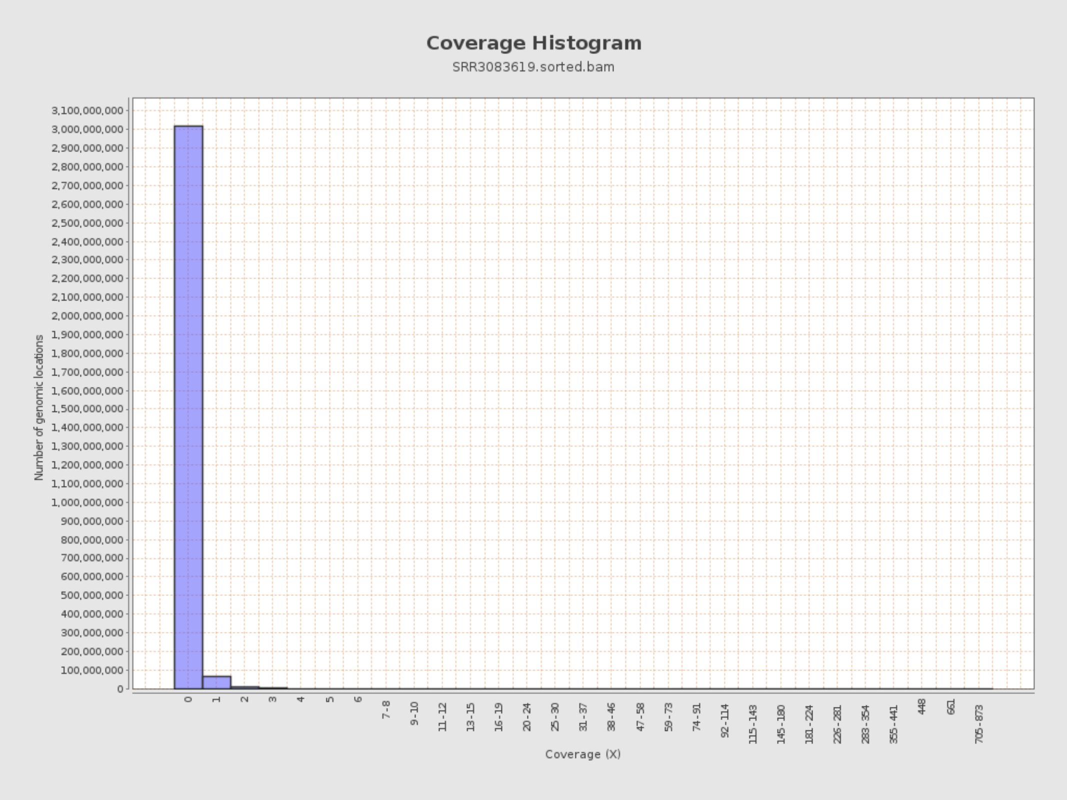
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10837440	0.0435	0.4544
chr2	243199373	9070093	0.0373	0.4332
chr3	198022430	9010259	0.0455	0.2616
chr4	191154276	2700094	0.0141	0.1472
chr5	180915260	4305803	0.0238	0.1851
chr6	171115067	6380452	0.0373	0.254
chr7	159138663	7926916	0.0498	0.3479

chr8	146364022	6452426	0.0441	0.2785
chr9	141213431	3838136	0.0272	0.2153
chr10	135534747	4560014	0.0336	0.2369
chr11	135006516	3530078	0.0261	0.2102
chr12	133851895	3133133	0.0234	0.1846
chr13	115169878	3410121	0.0296	0.2093
chr14	107349540	2446353	0.0228	0.1831
chr15	102531392	2613493	0.0255	0.2015
chr16	90354753	2737076	0.0303	0.2166
chr17	81195210	2124314	0.0262	0.195
chr18	78077248	2341644	0.03	0.297
chr19	59128983	3159929	0.0534	0.3824
chr20	63025520	1702348	0.027	0.1995
chr21	48129895	948450	0.0197	0.1697
chr22	51304566	833490	0.0162	0.1527
chrMT	16571	12993	0.7841	1.1175
chrX	155270560	4685840	0.0302	0.2142
chrY	59373566	173784	0.0029	0.0667

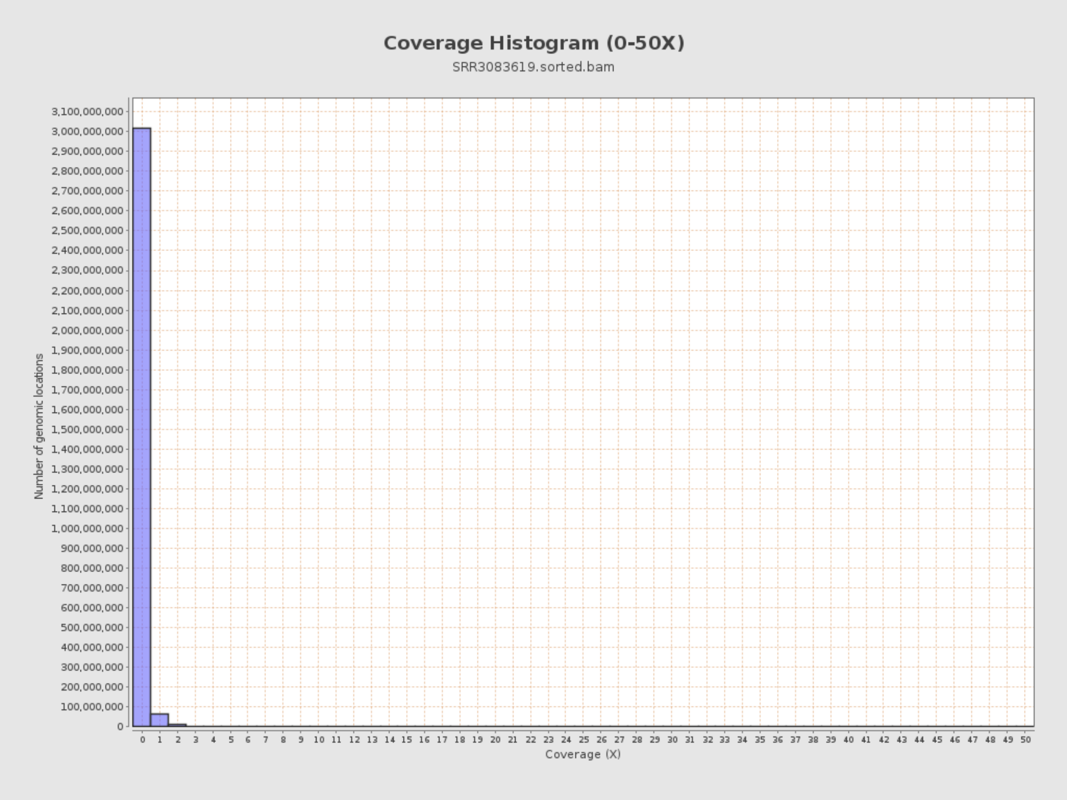
3. Results : Coverage across reference



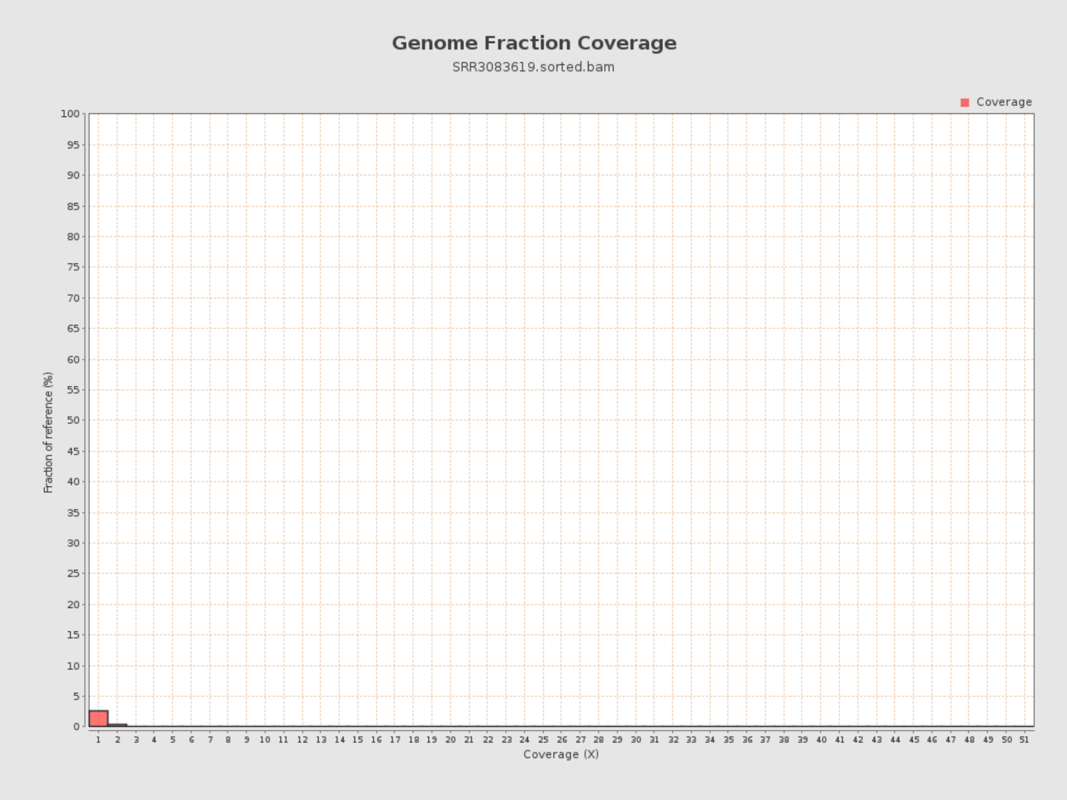
4. Results : Coverage Histogram



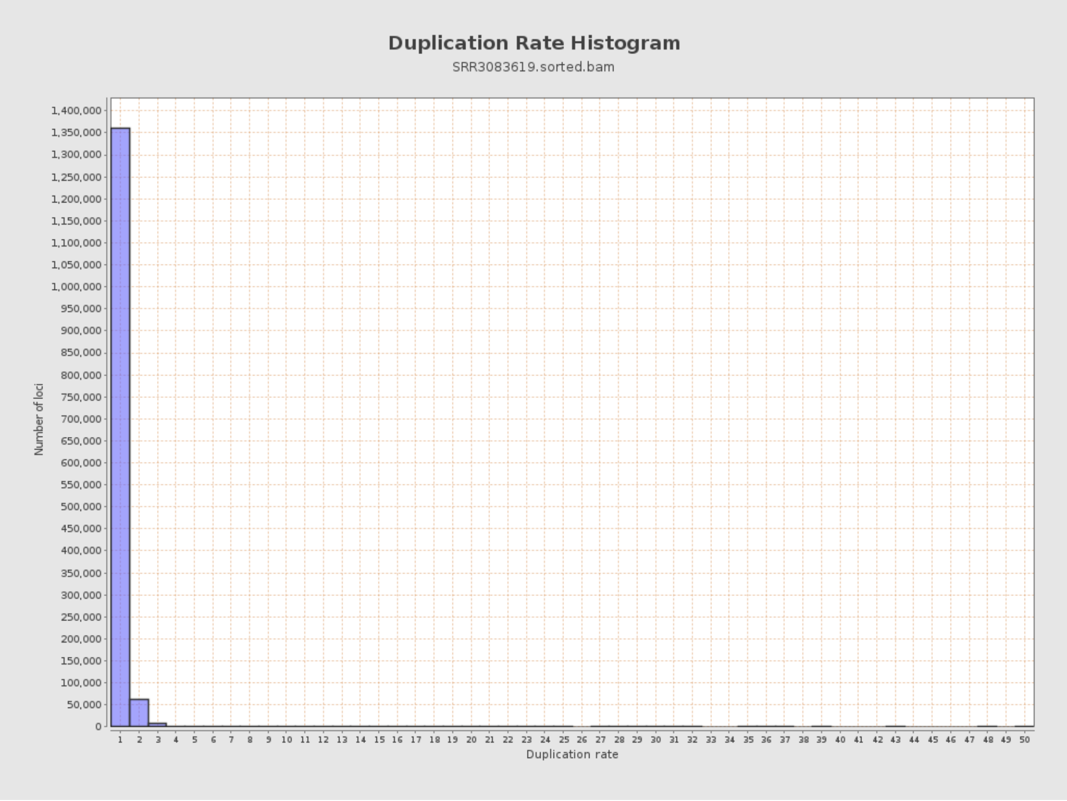
5. Results : Coverage Histogram (0-50X)



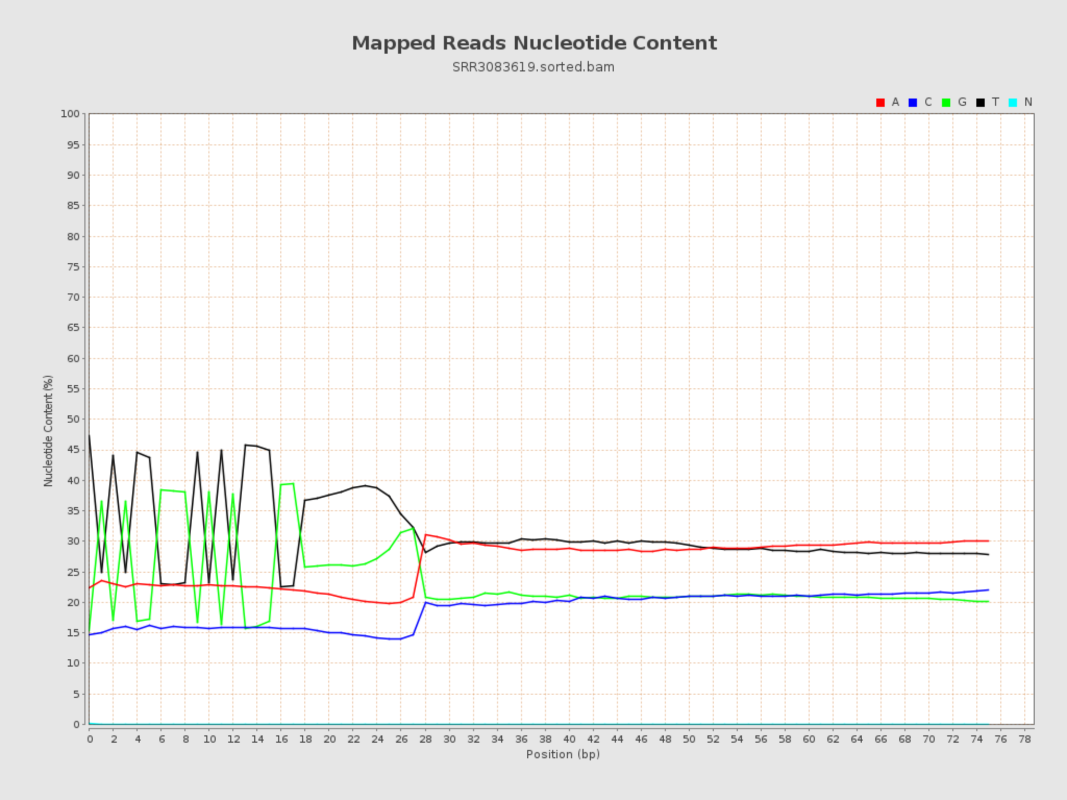
6. Results : Genome Fraction Coverage



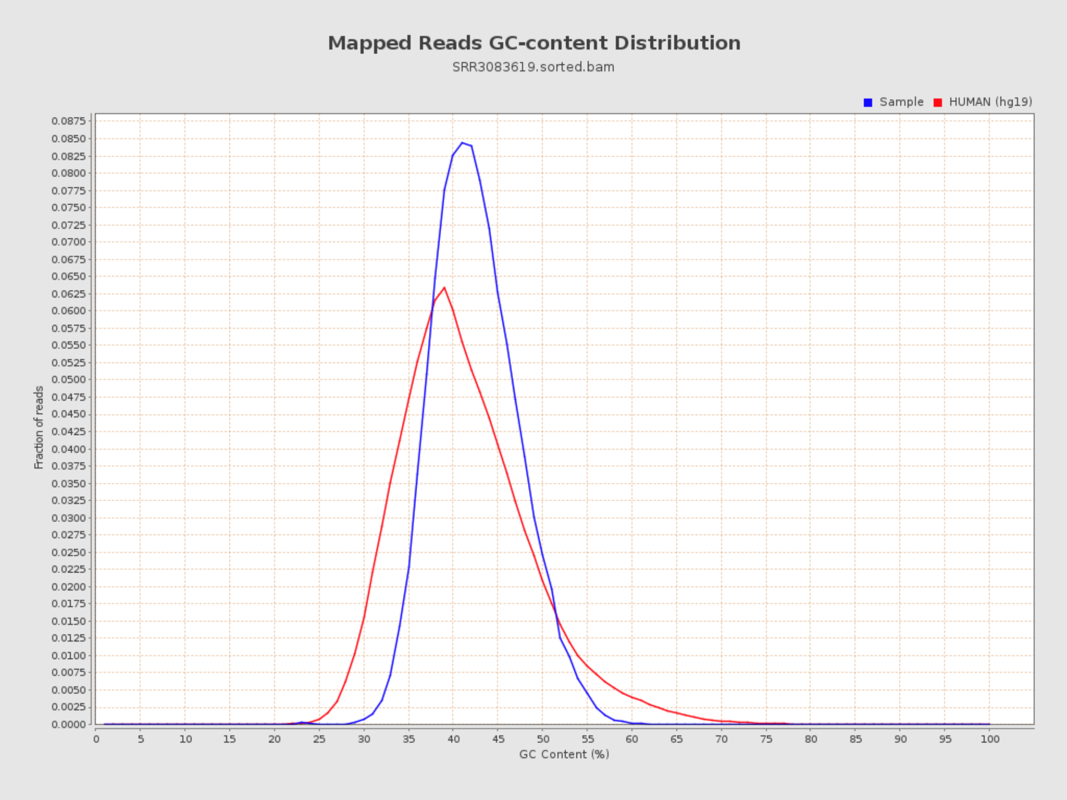
7. Results : Duplication Rate Histogram



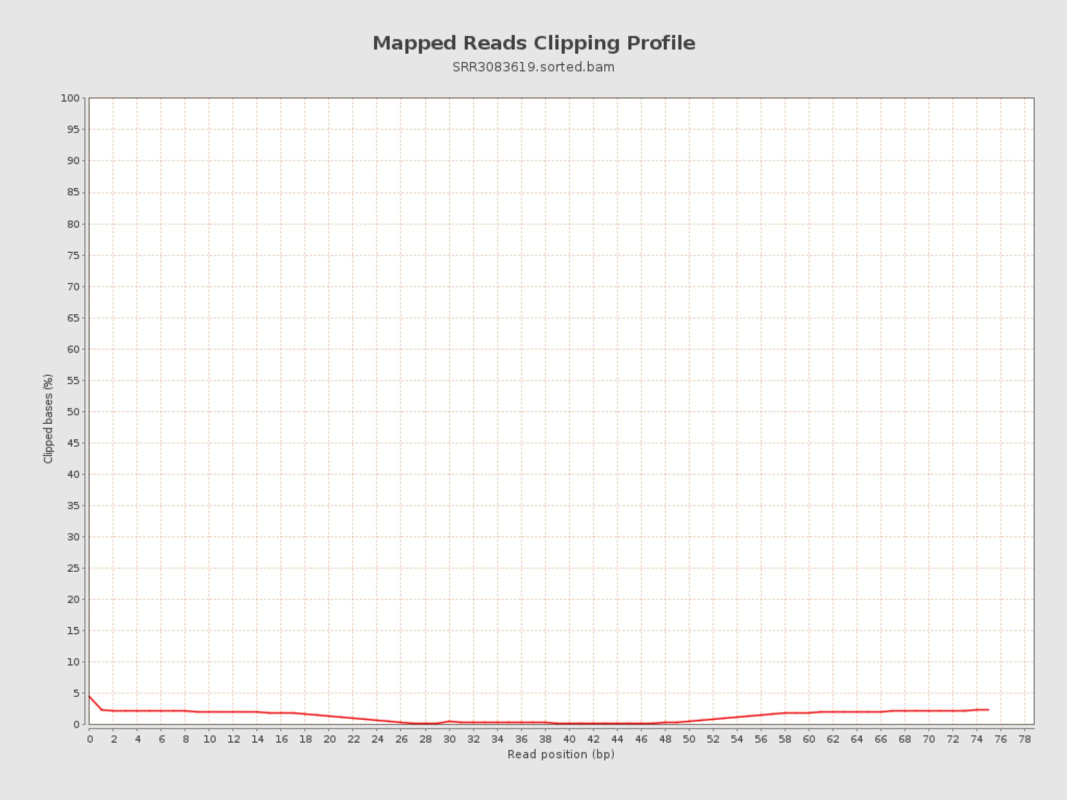
8. Results : Mapped Reads Nucleotide Content



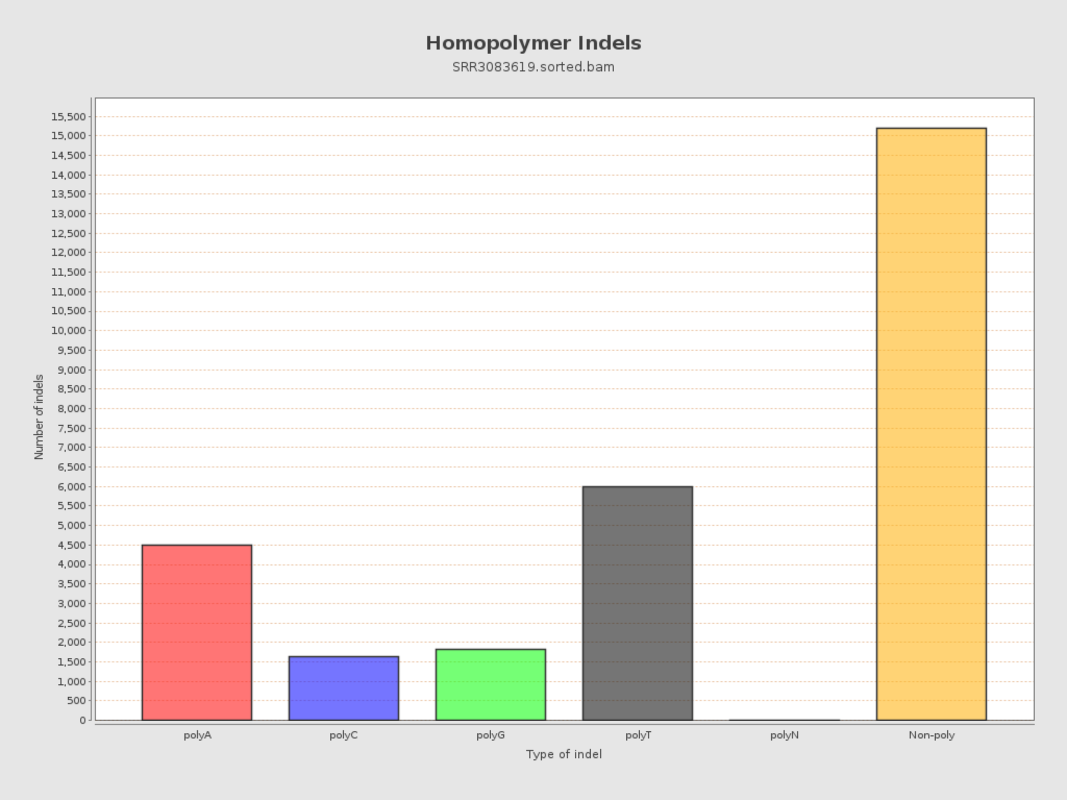
9. Results : Mapped Reads GC-content Distribution



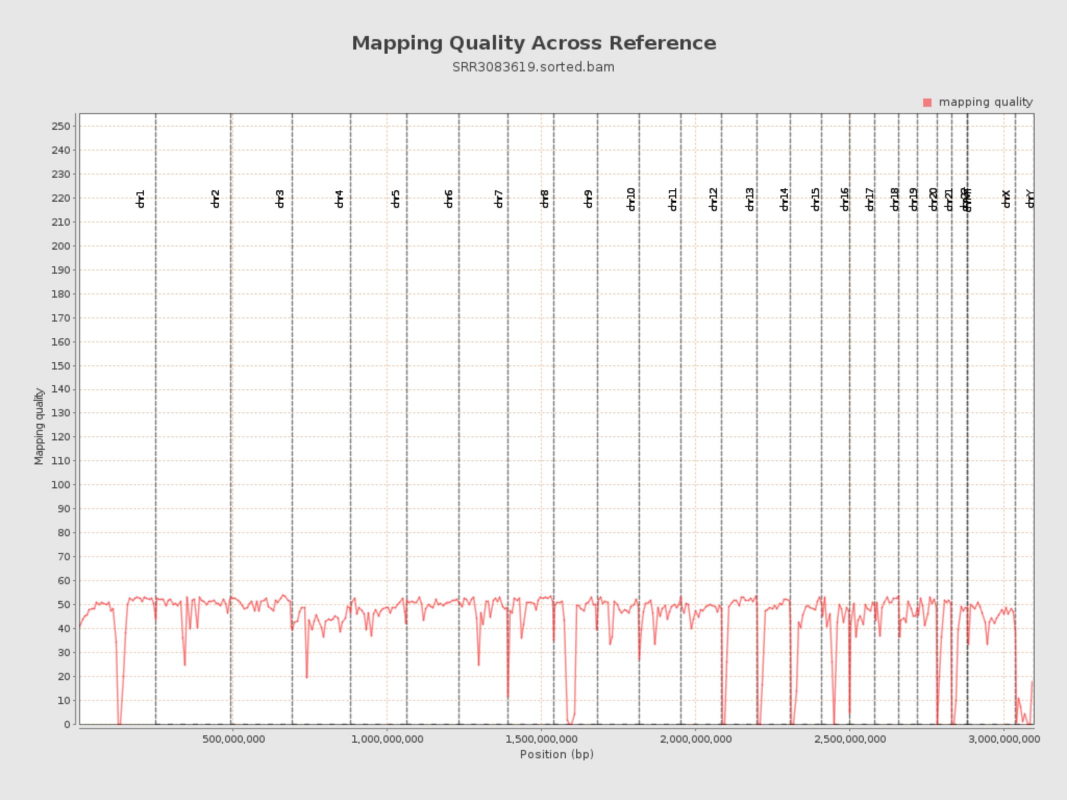
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram