Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:06:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083618.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_SRR3083618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:06:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,909
Mapped reads	1,349,879 / 88.41%
Unmapped reads	177,030 / 11.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,423 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	66,412 / 4.35%
Duplication rate	4.23%
Clipped reads	628,955 / 41.19%

2.2. ACGT Content

Number/percentage of A's	24,034,686 / 26.9%
Number/percentage of C's	16,620,764 / 18.6%
Number/percentage of T's	28,169,051 / 31.53%
Number/percentage of G's	20,520,802 / 22.97%
Number/percentage of N's	4,312 / 0%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2641

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

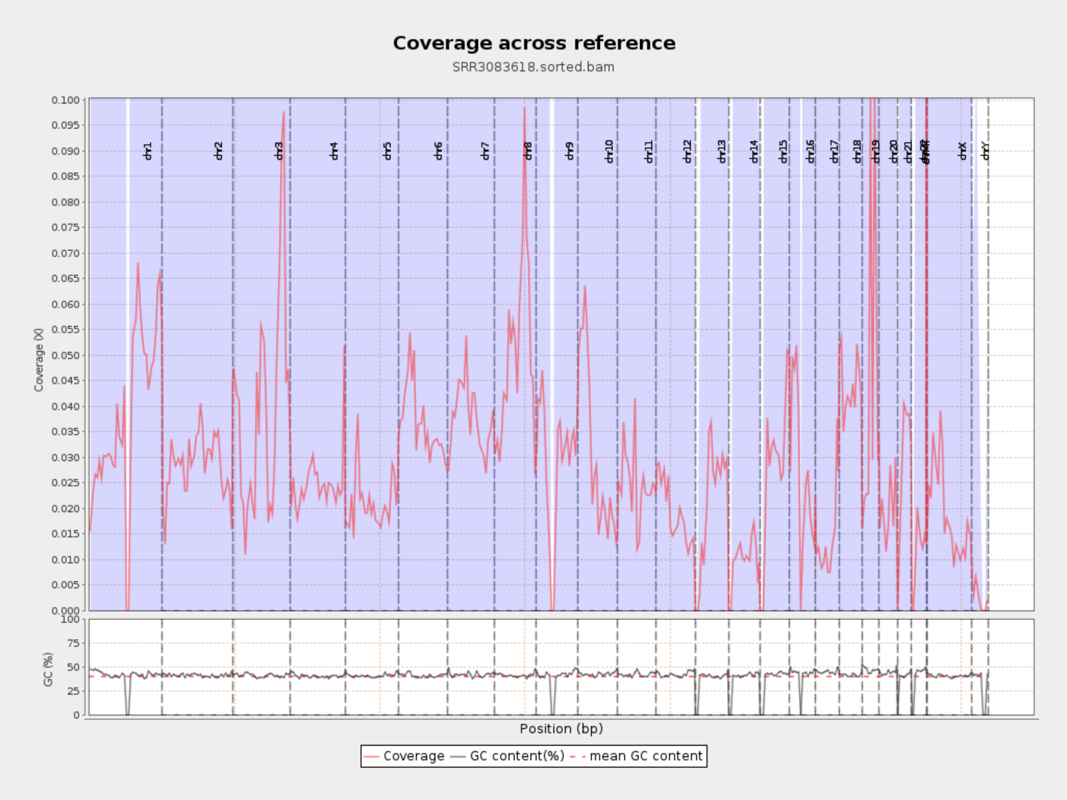
General error rate	0.71%
Mismatches	623,234
Insertions	6,533
Mapped reads with at least one insertion	0.48%
Deletions	20,118
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.54%

2.6. Chromosome stats

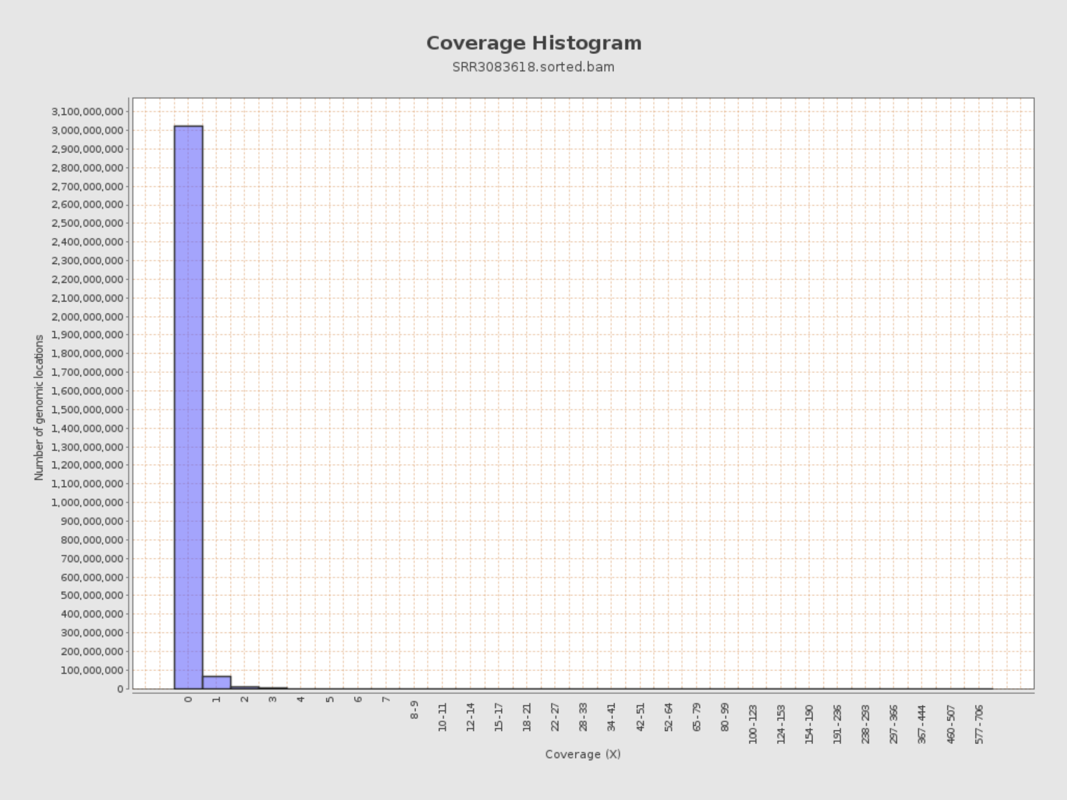
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9560607	0.0384	0.4733
chr2	243199373	6951529	0.0286	0.362
chr3	198022430	7800449	0.0394	0.2325
chr4	191154276	4777834	0.025	0.1849
chr5	180915260	3849580	0.0213	0.1691
chr6	171115067	6302060	0.0368	0.2499
chr7	159138663	6026604	0.0379	0.3705

chr8	146364022	7449600	0.0509	0.3069
chr9	141213431	4098421	0.029	0.2119
chr10	135534747	4258952	0.0314	0.2373
chr11	135006516	3326309	0.0246	0.1882
chr12	133851895	2547339	0.019	0.1602
chr13	115169878	2472023	0.0215	0.1695
chr14	107349540	1070043	0.01	0.116
chr15	102531392	2871267	0.028	0.1981
chr16	90354753	2460961	0.0272	0.1943
chr17	81195210	1152250	0.0142	0.1399
chr18	78077248	3435845	0.044	0.2807
chr19	59128983	2653669	0.0449	0.374
chr20	63025520	1253442	0.0199	0.1631
chr21	48129895	1390009	0.0289	0.199
chr22	51304566	564867	0.011	0.1192
chrMT	16571	5802	0.3501	0.7476
chrX	155270560	2963846	0.0191	0.1644
chrY	59373566	139041	0.0023	0.0593

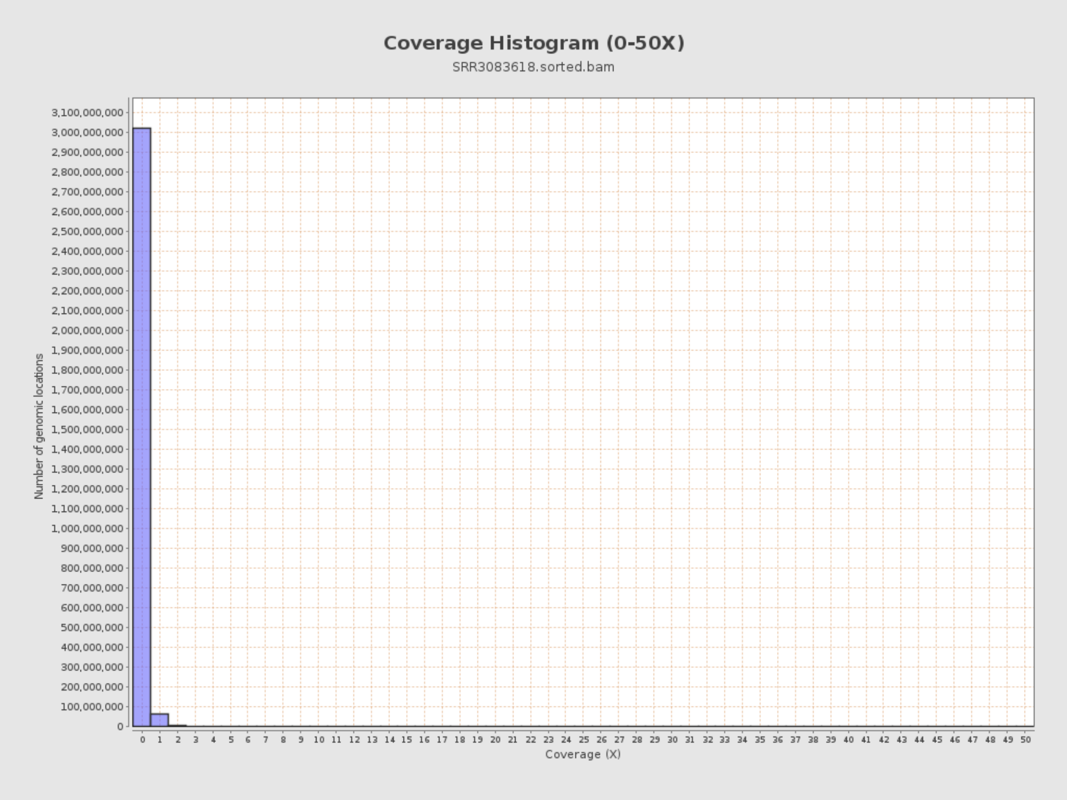
3. Results : Coverage across reference



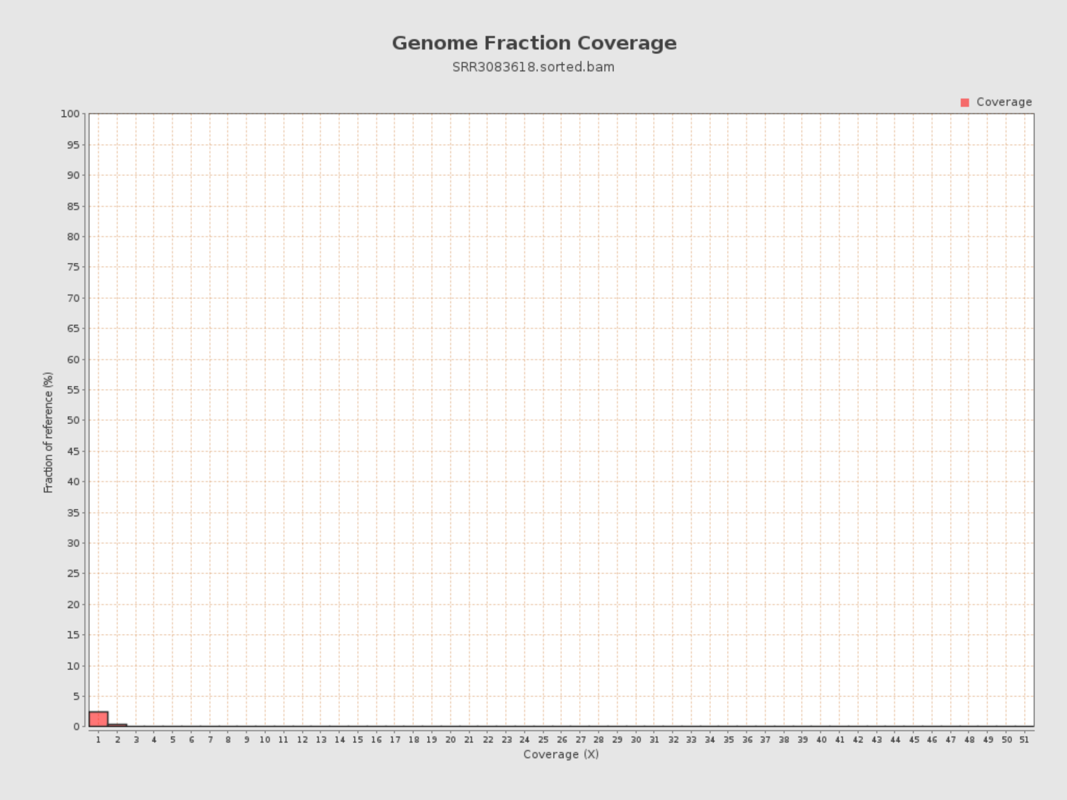
4. Results : Coverage Histogram



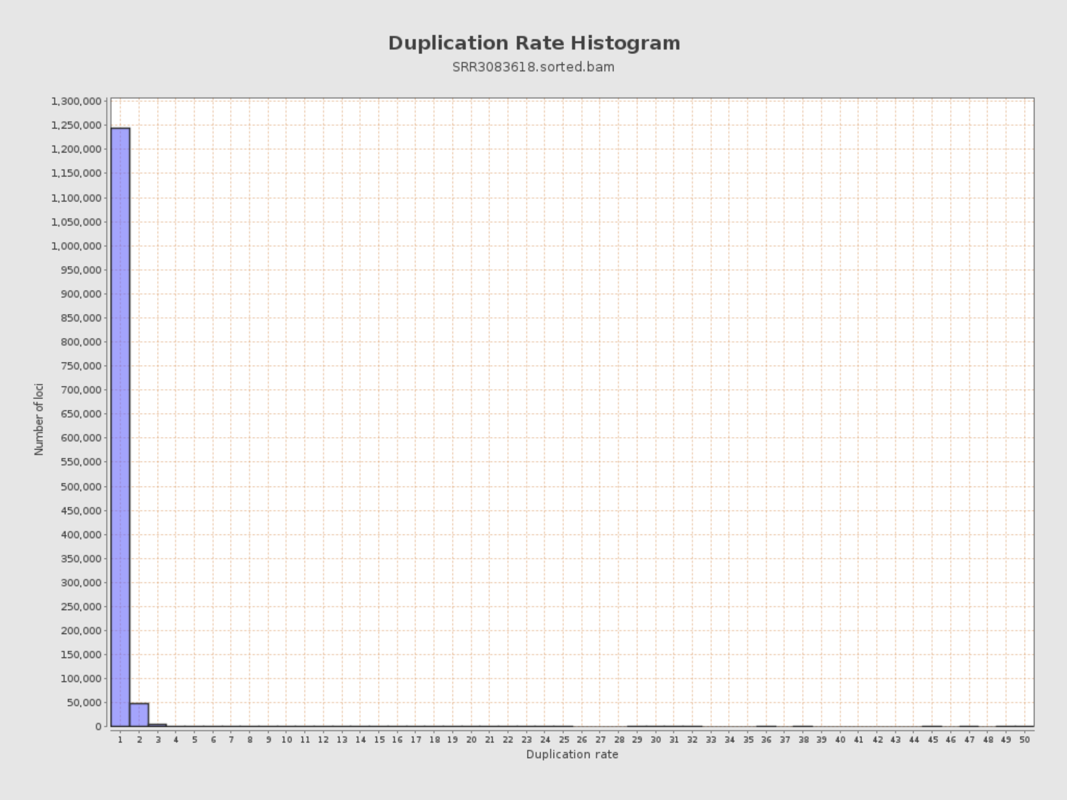
5. Results : Coverage Histogram (0-50X)



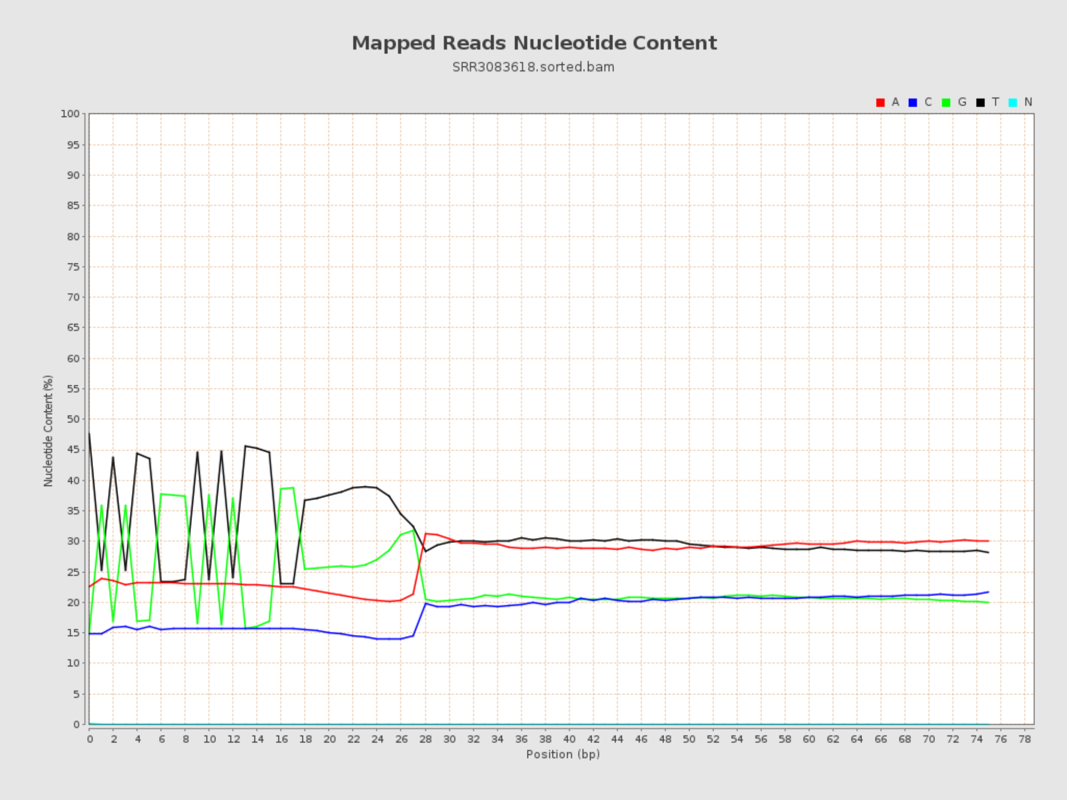
6. Results : Genome Fraction Coverage



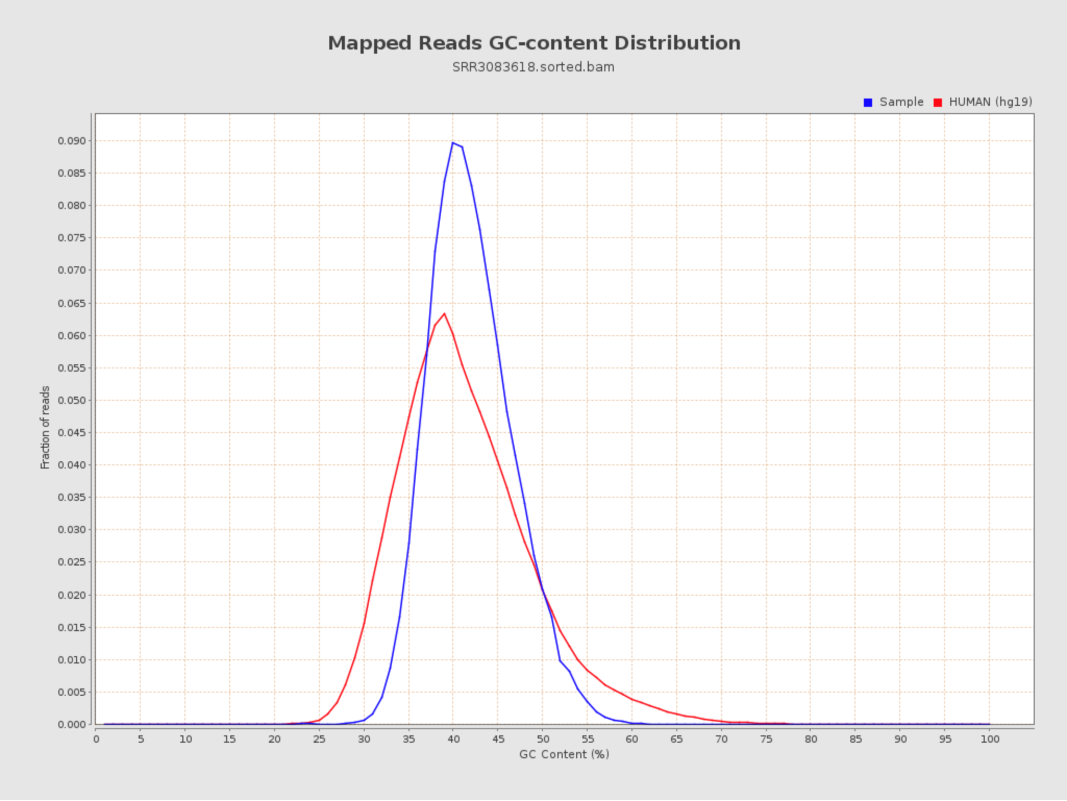
7. Results : Duplication Rate Histogram



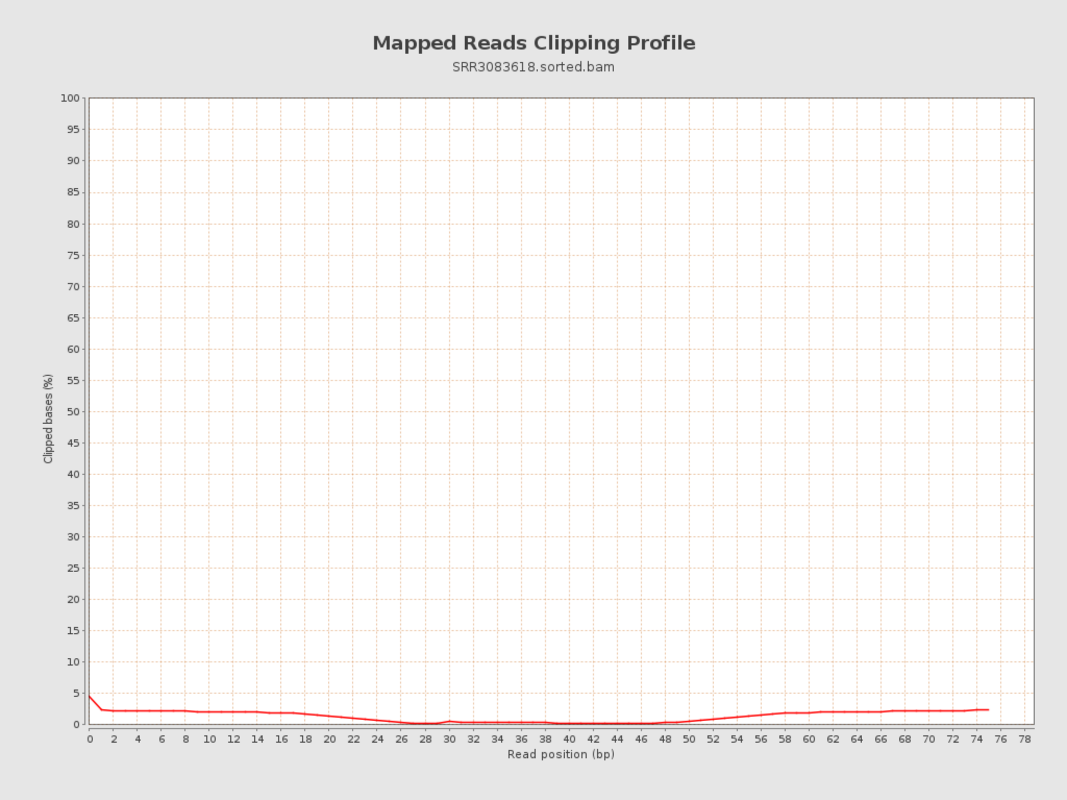
8. Results : Mapped Reads Nucleotide Content



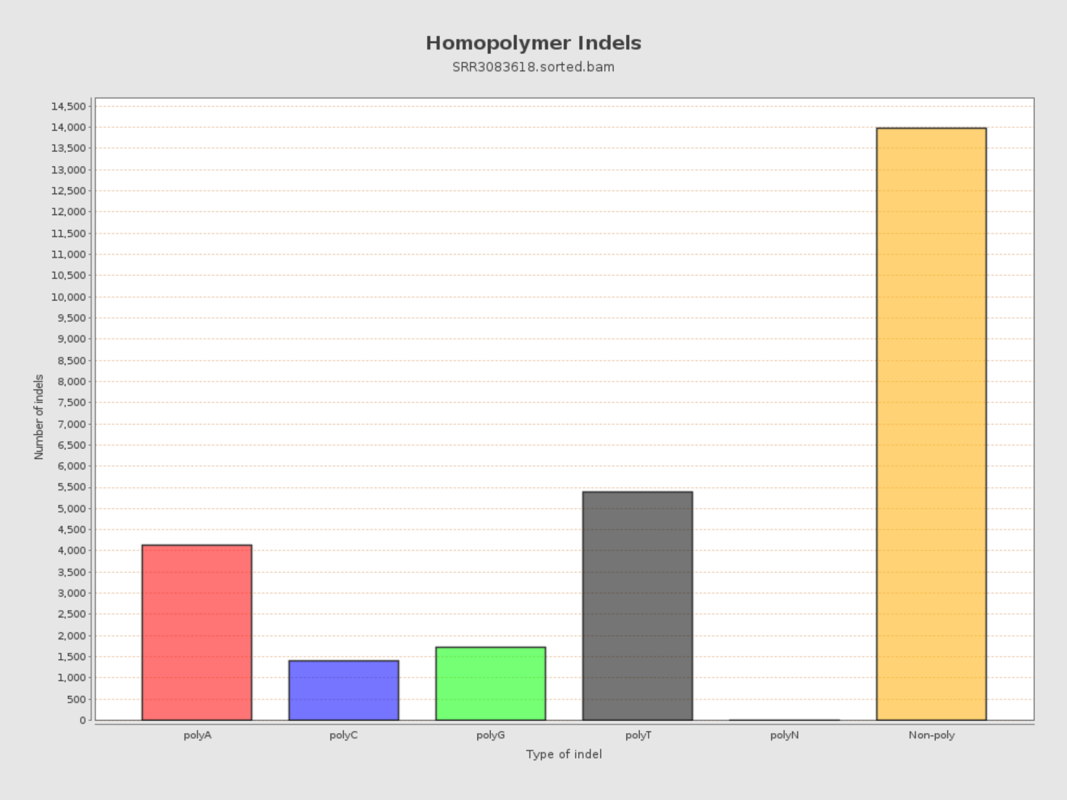
9. Results : Mapped Reads GC-content Distribution



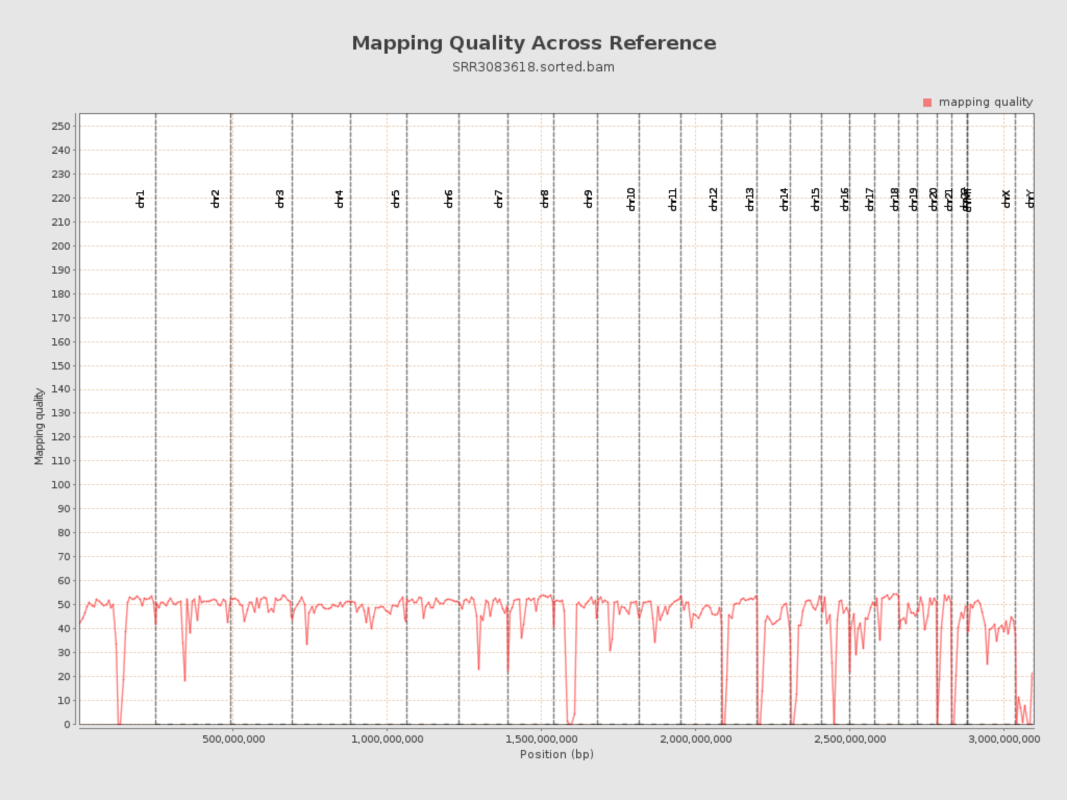
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram