Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:06:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083648.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_SRR3083648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:06:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,672,487
Mapped reads	1,285,713 / 76.87%
Unmapped reads	386,774 / 23.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,891 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	27,368 / 1.64%
Duplication rate	1.72%
Clipped reads	837,953 / 50.1%

2.2. ACGT Content

Number/percentage of A's	23,643,847 / 30.03%
Number/percentage of C's	15,051,903 / 19.11%
Number/percentage of T's	23,033,539 / 29.25%
Number/percentage of G's	17,005,544 / 21.6%
Number/percentage of N's	10,570 / 0.01%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2276

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

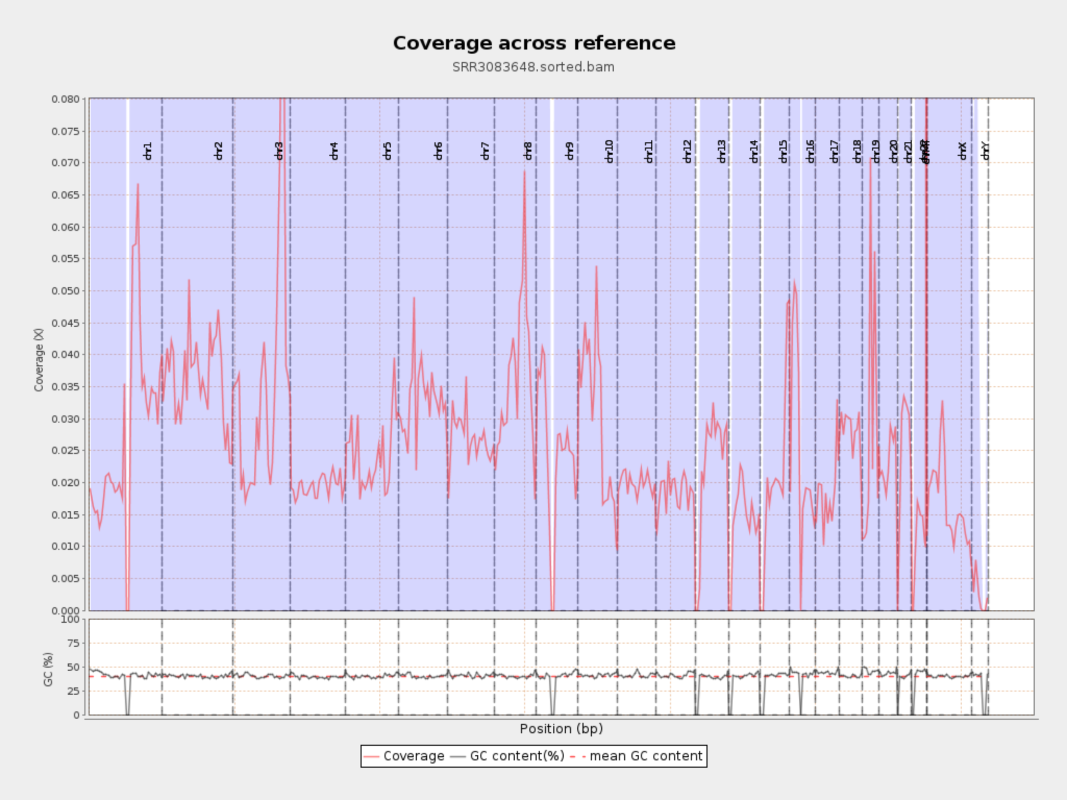
General error rate	0.91%
Mismatches	704,300
Insertions	5,748
Mapped reads with at least one insertion	0.44%
Deletions	16,336
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.77%

2.6. Chromosome stats

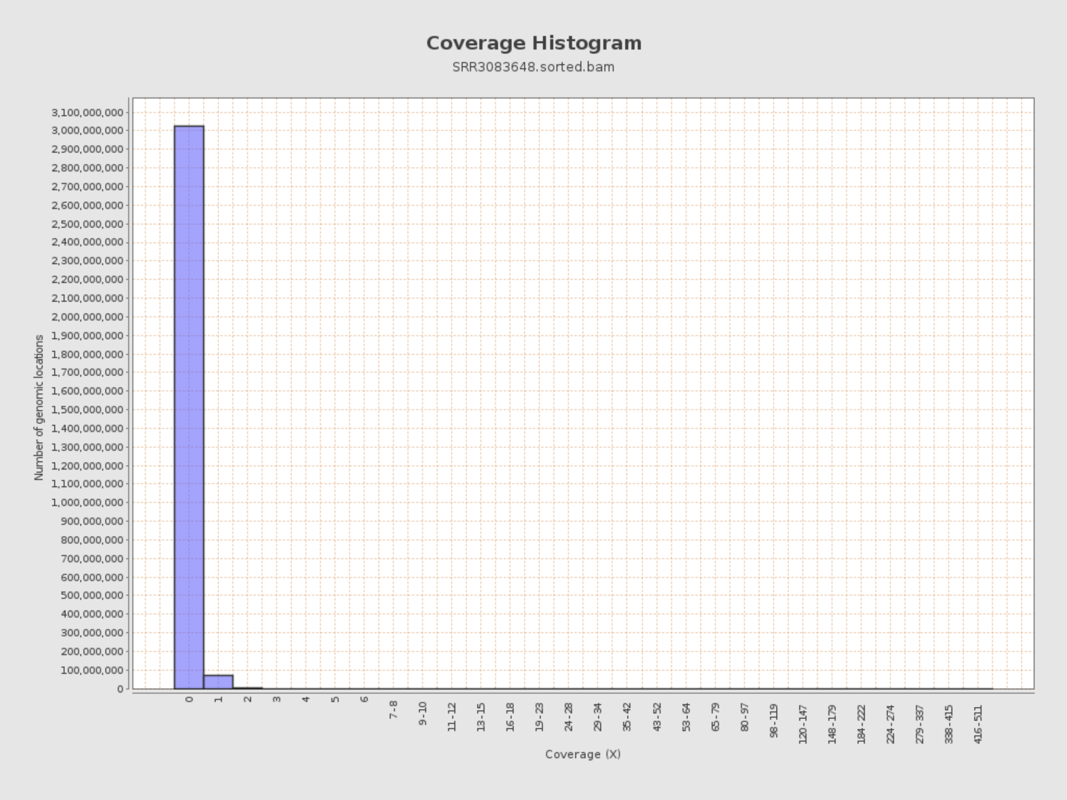
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6774949	0.0272	0.4512
chr2	243199373	8853110	0.0364	0.2415
chr3	198022430	7089836	0.0358	0.2015
chr4	191154276	3709140	0.0194	0.148
chr5	180915260	4382743	0.0242	0.1637
chr6	171115067	5641635	0.033	0.2123
chr7	159138663	4313481	0.0271	0.2461

chr8	146364022	5334659	0.0364	0.2834
chr9	141213431	3480824	0.0246	0.1859
chr10	135534747	4245605	0.0313	0.2401
chr11	135006516	2665062	0.0197	0.1656
chr12	133851895	2471228	0.0185	0.1435
chr13	115169878	2564237	0.0223	0.1571
chr14	107349540	1528663	0.0142	0.1271
chr15	102531392	2055881	0.0201	0.1492
chr16	90354753	2304104	0.0255	0.1736
chr17	81195210	1483018	0.0183	0.146
chr18	78077248	2208234	0.0283	0.2719
chr19	59128983	1688904	0.0286	0.3124
chr20	63025520	1456319	0.0231	0.1616
chr21	48129895	1201249	0.025	0.1689
chr22	51304566	533985	0.0104	0.1065
chrMT	16571	8583	0.518	0.7934
chrX	155270560	2628870	0.0169	0.1426
chrY	59373566	146632	0.0025	0.0611

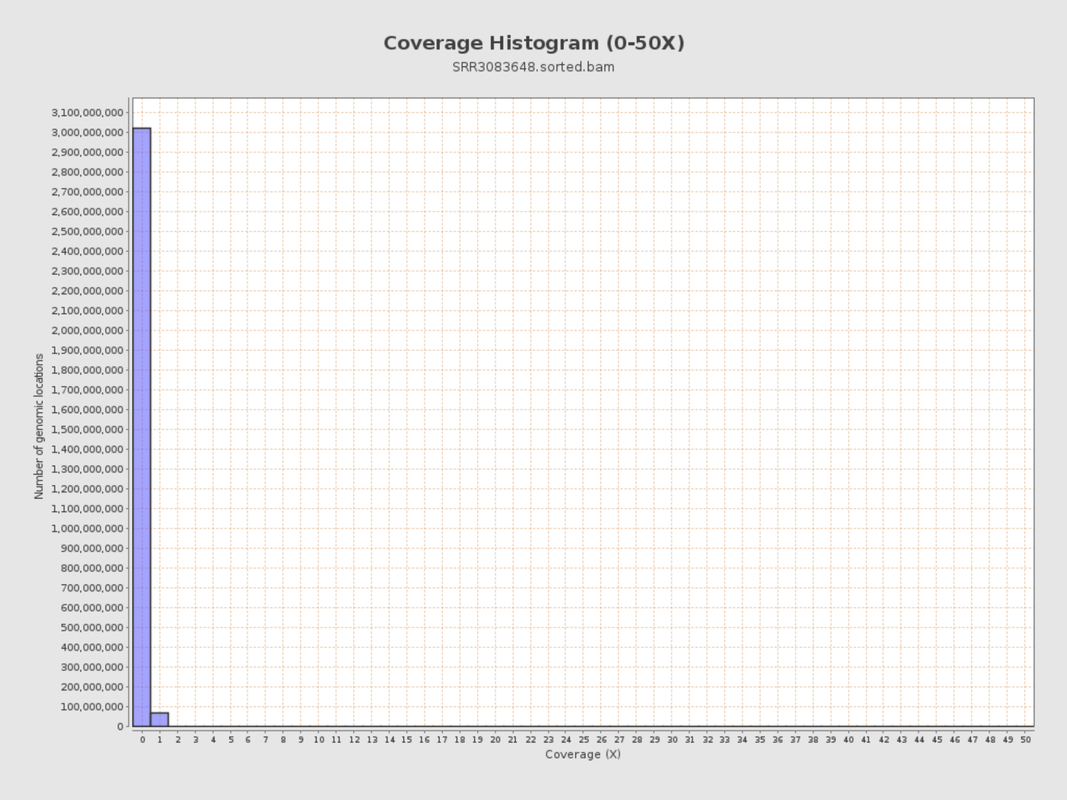
3. Results : Coverage across reference



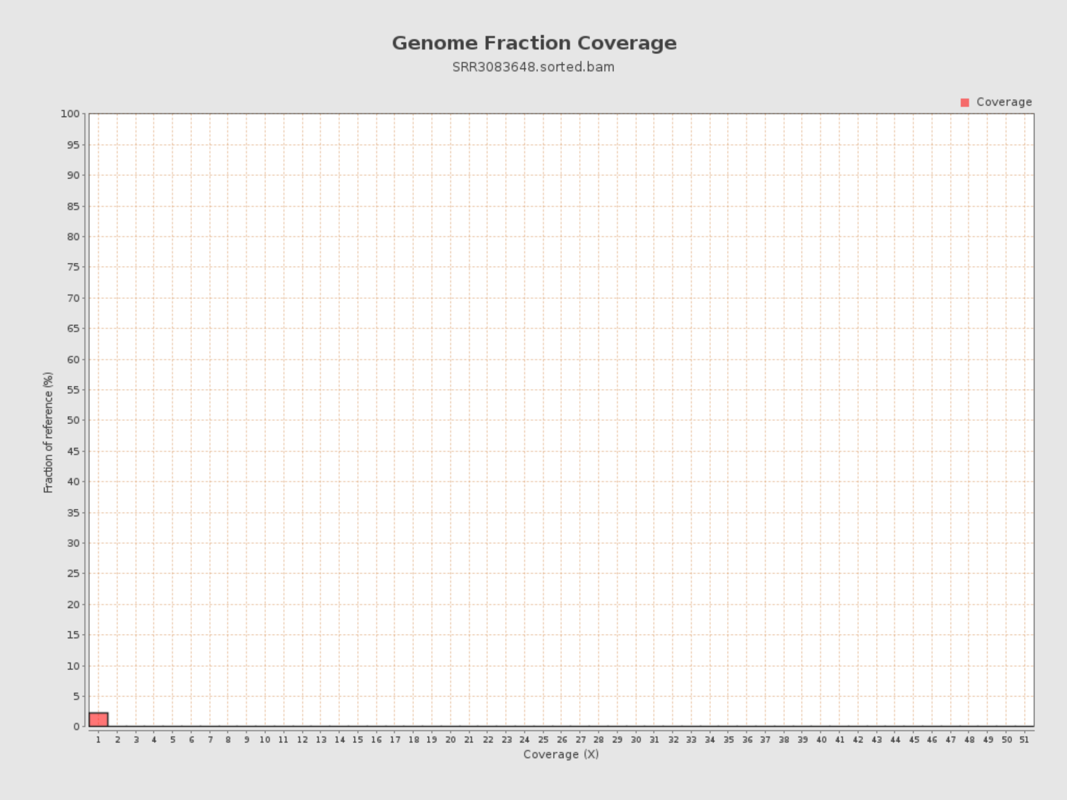
4. Results : Coverage Histogram



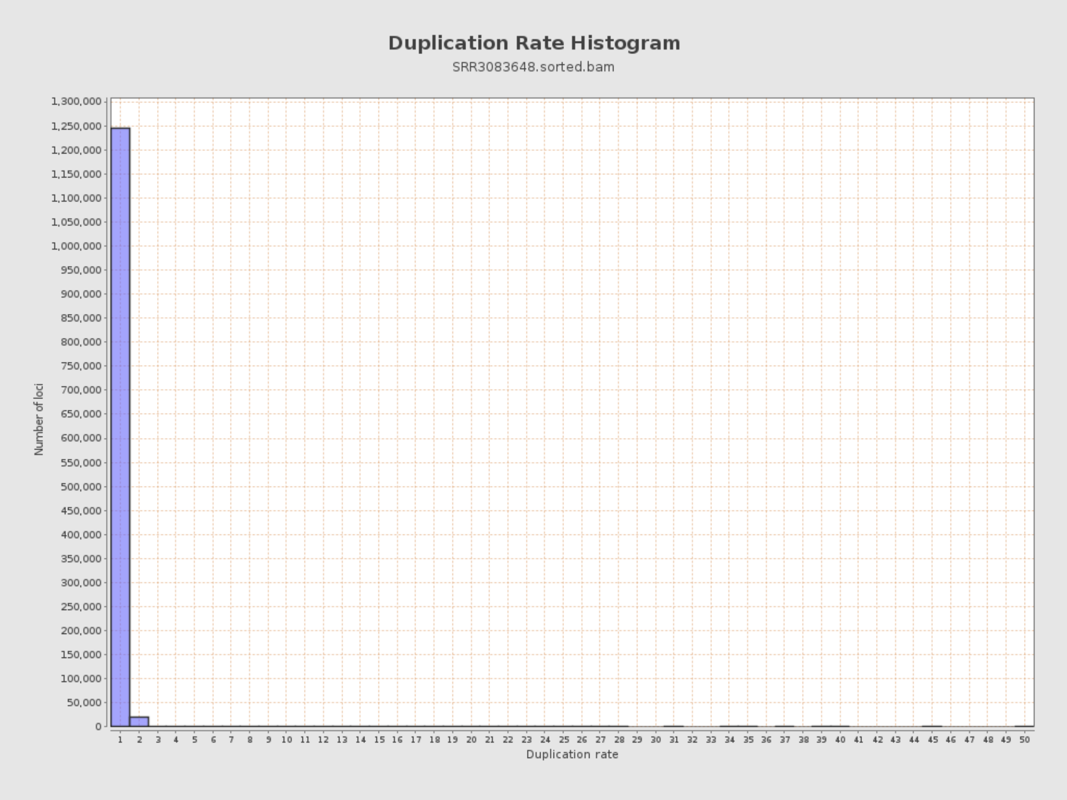
5. Results : Coverage Histogram (0-50X)



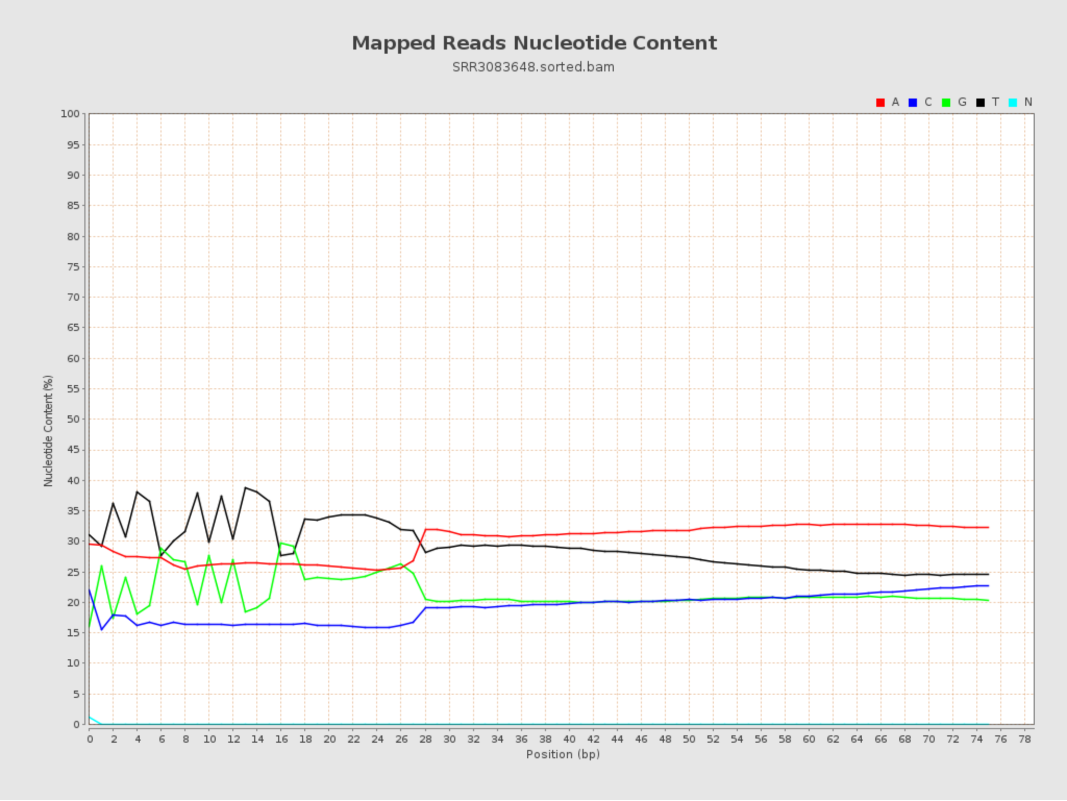
6. Results : Genome Fraction Coverage



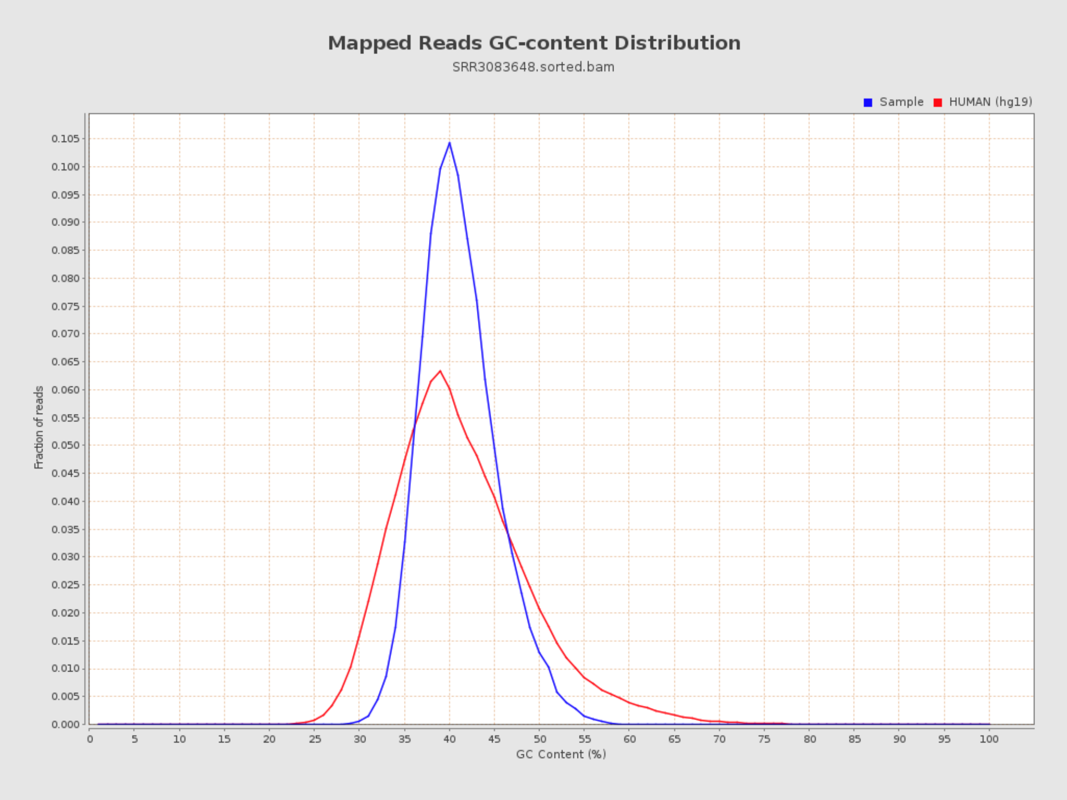
7. Results : Duplication Rate Histogram



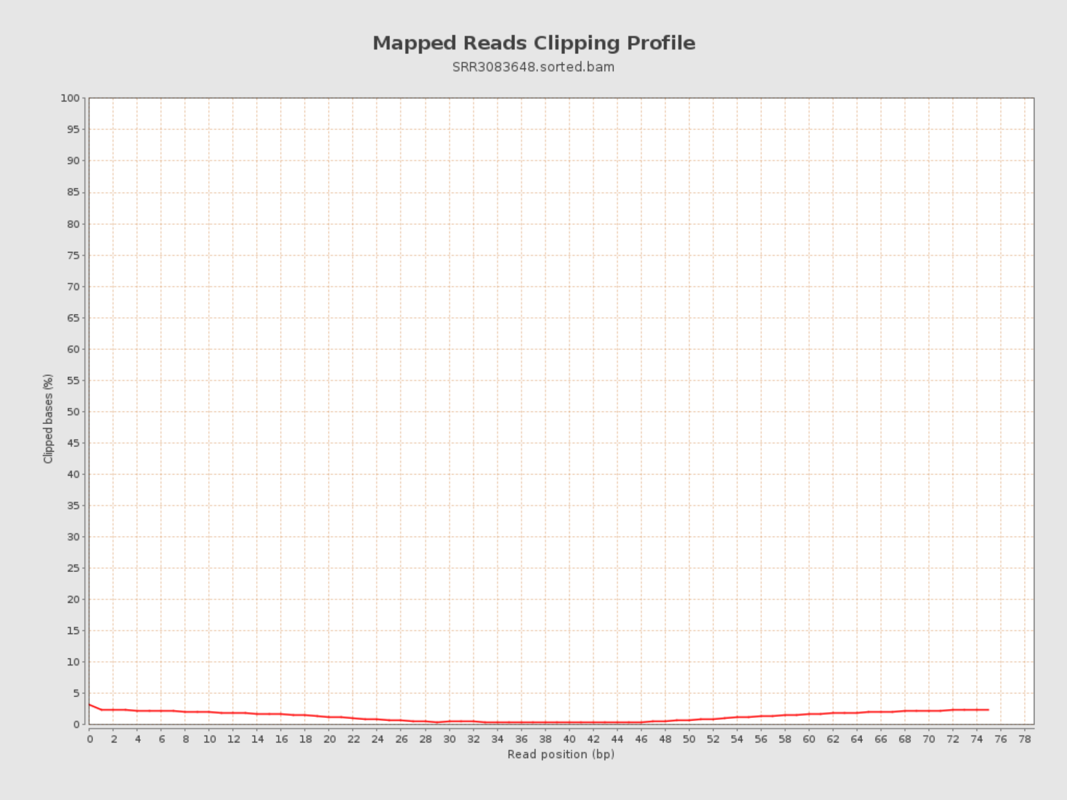
8. Results : Mapped Reads Nucleotide Content



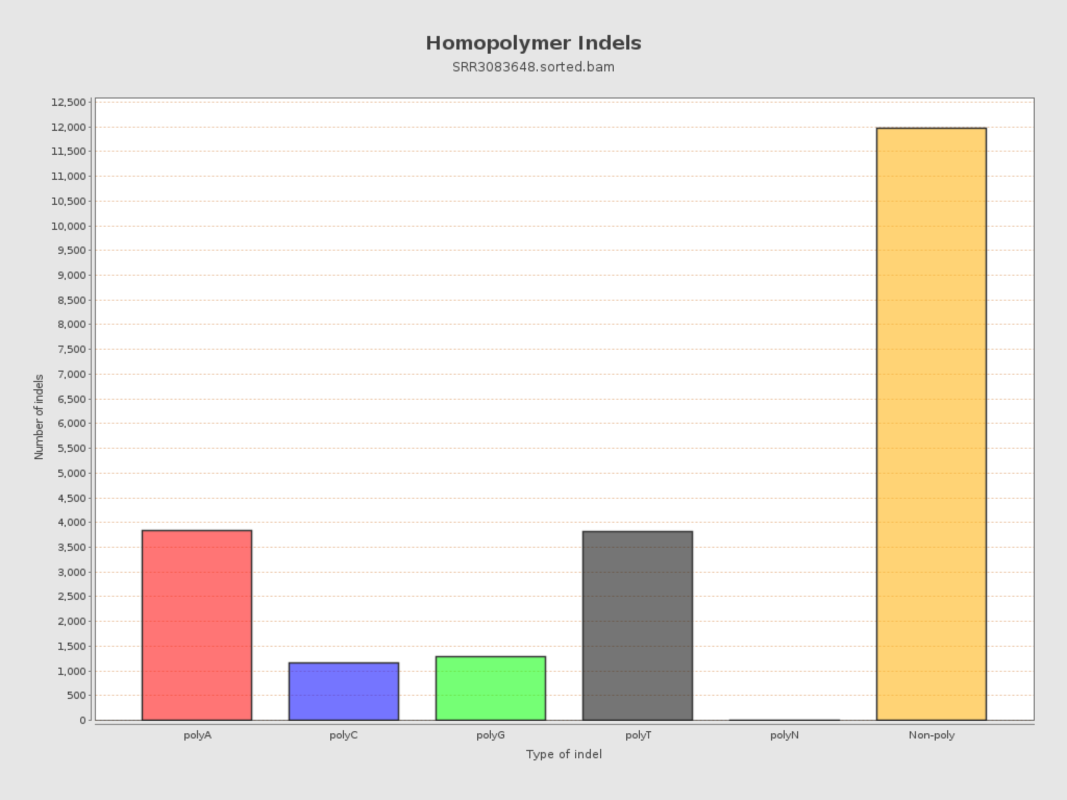
9. Results : Mapped Reads GC-content Distribution



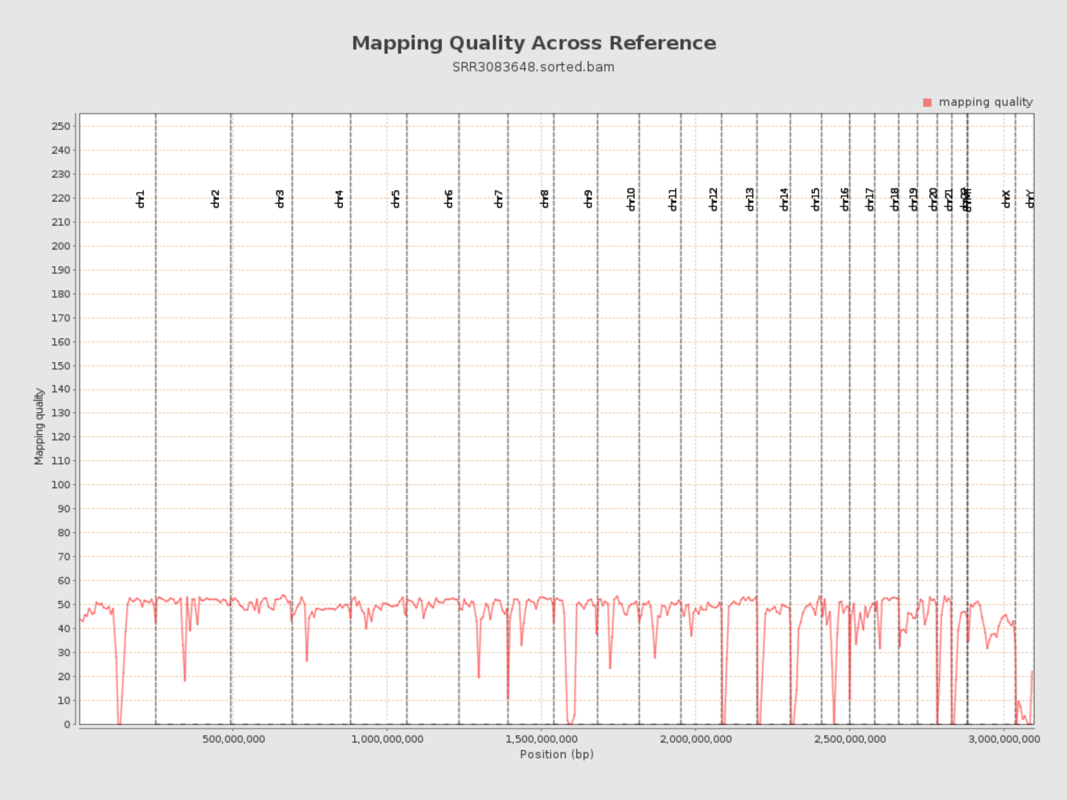
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram