Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:32:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818975.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_SRR1818975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:32:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,489,507
Mapped reads	1,452,253 / 97.5%
Unmapped reads	37,254 / 2.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,536 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	571,396 / 38.36%
Duplication rate	33.26%
Clipped reads	1,458,188 / 97.9%

2.2. ACGT Content

Number/percentage of A's	38,392,669 / 28.59%
Number/percentage of C's	27,568,708 / 20.53%
Number/percentage of T's	39,123,407 / 29.14%
Number/percentage of G's	29,186,499 / 21.74%
Number/percentage of N's	6,234 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.5484

2.4. Mapping Quality

Mean Mapping Quality	49.19

2.5. Mismatches and indels

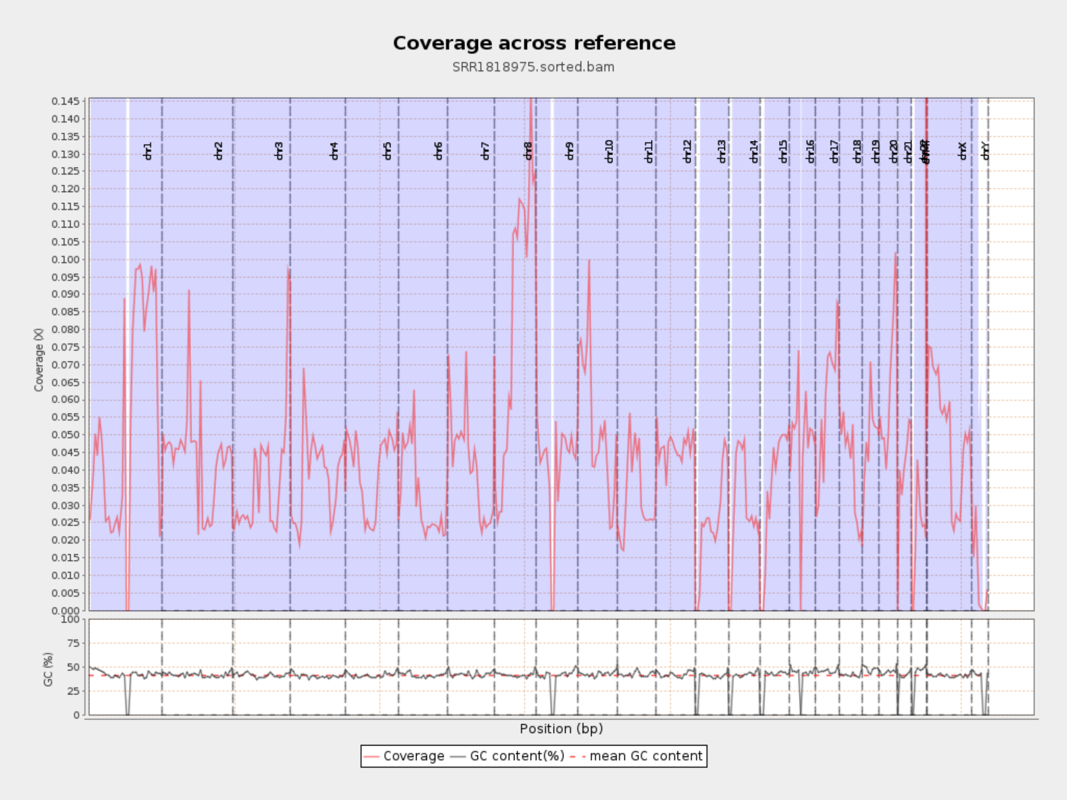
General error rate	0.68%
Mismatches	865,523
Insertions	22,108
Mapped reads with at least one insertion	1.48%
Deletions	43,291
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.79%

2.6. Chromosome stats

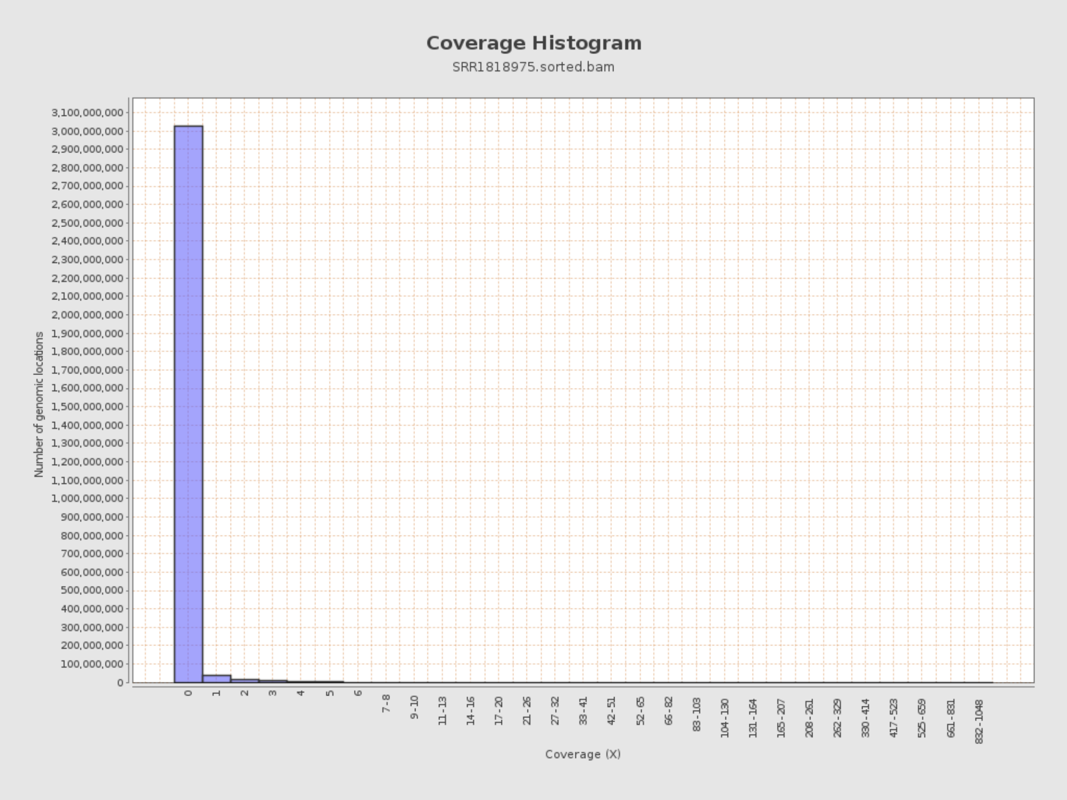
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13491941	0.0541	0.9812
chr2	243199373	10613833	0.0436	0.7413
chr3	198022430	7247241	0.0366	0.3251
chr4	191154276	7307043	0.0382	0.384
chr5	180915260	7274911	0.0402	0.3457
chr6	171115067	5609132	0.0328	0.3692
chr7	159138663	6593929	0.0414	0.6189

chr8	146364022	12313659	0.0841	0.5489
chr9	141213431	5655838	0.0401	0.4873
chr10	135534747	7212748	0.0532	0.6701
chr11	135006516	4383402	0.0325	0.3667
chr12	133851895	6226906	0.0465	0.3709
chr13	115169878	2881828	0.025	0.2654
chr14	107349540	3178484	0.0296	0.3001
chr15	102531392	3556531	0.0347	0.3185
chr16	90354753	4367974	0.0483	0.6141
chr17	81195210	4862716	0.0599	0.4647
chr18	78077248	3205558	0.0411	0.6008
chr19	59128983	2924911	0.0495	0.904
chr20	63025520	4036618	0.064	0.4628
chr21	48129895	1916125	0.0398	0.3812
chr22	51304566	1080420	0.0211	0.27
chrMT	16571	28841	1.7405	2.7808
chrX	155270560	7866864	0.0507	0.4312
chrY	59373566	521401	0.0088	0.5405

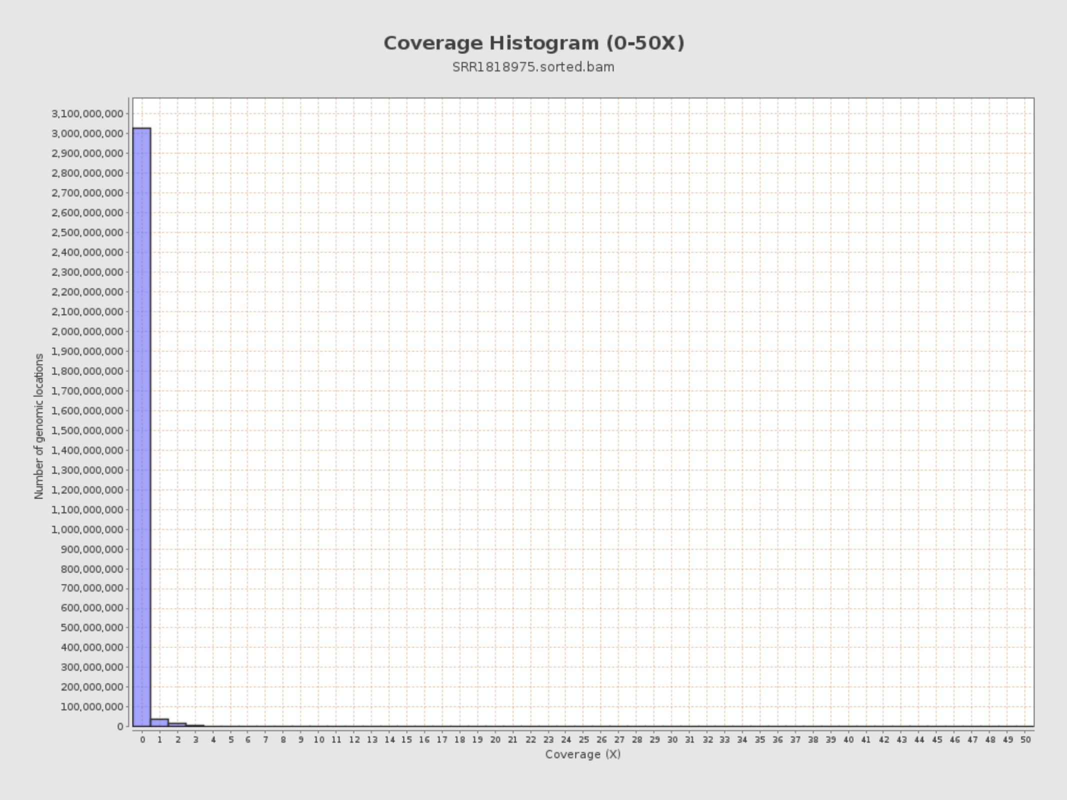
3. Results : Coverage across reference



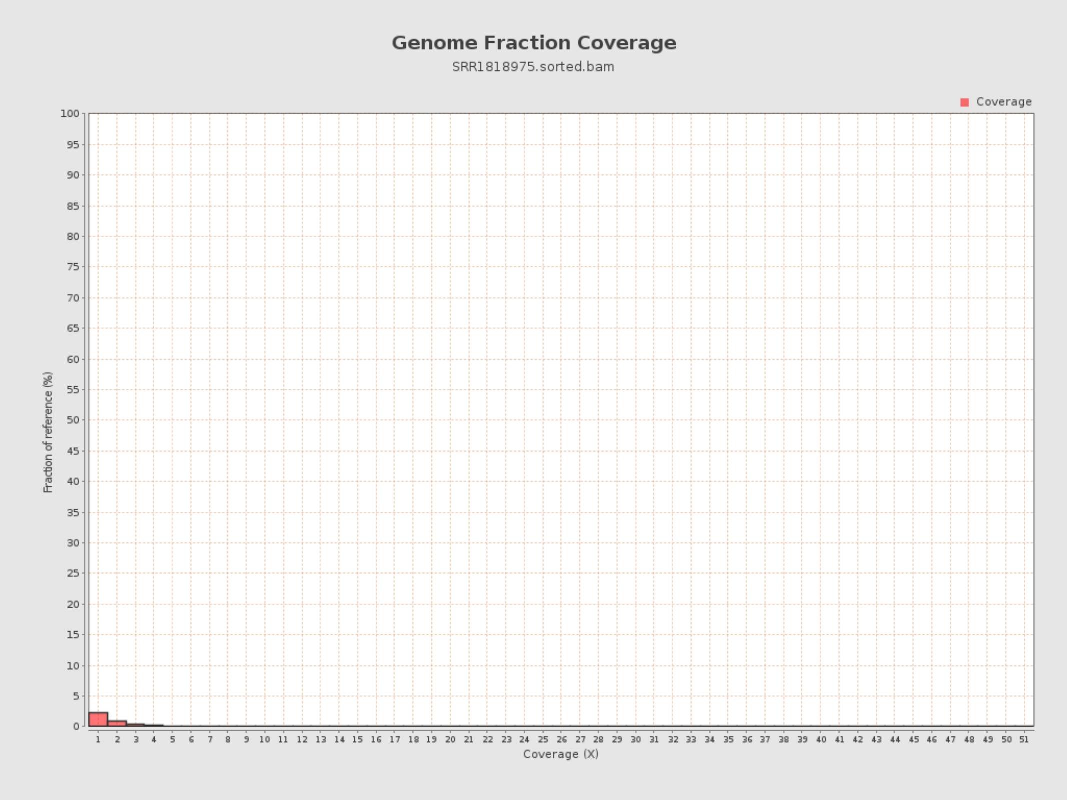
4. Results : Coverage Histogram



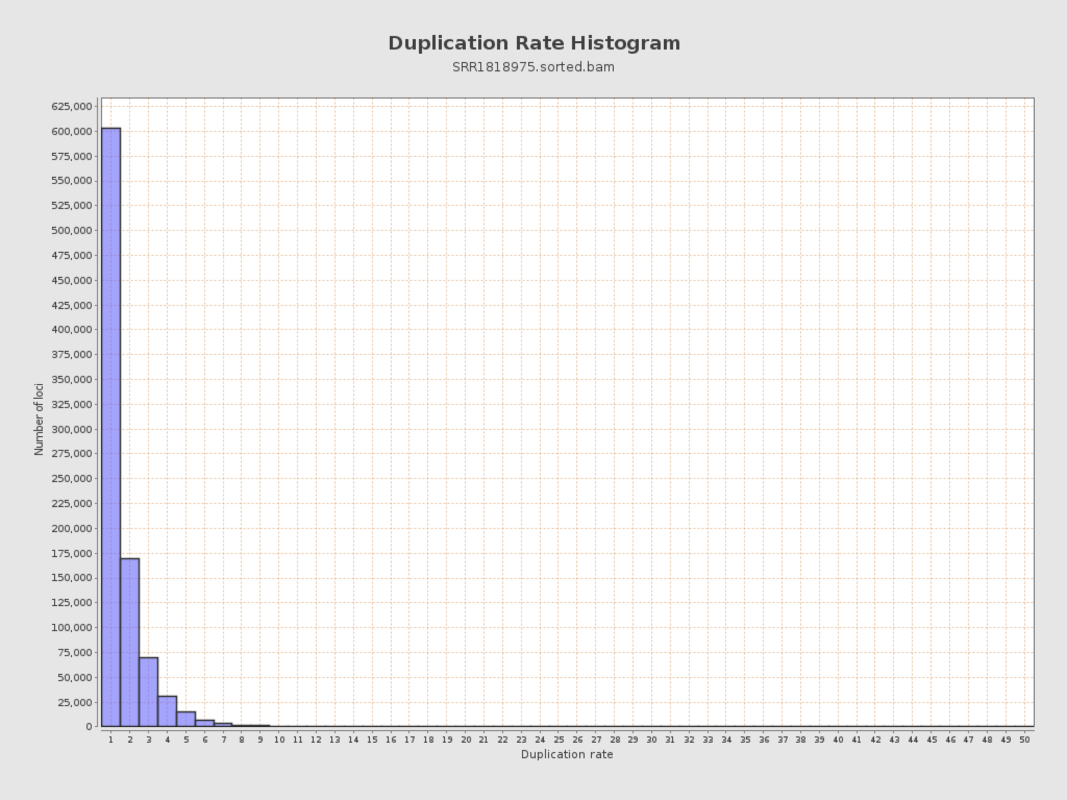
5. Results : Coverage Histogram (0-50X)



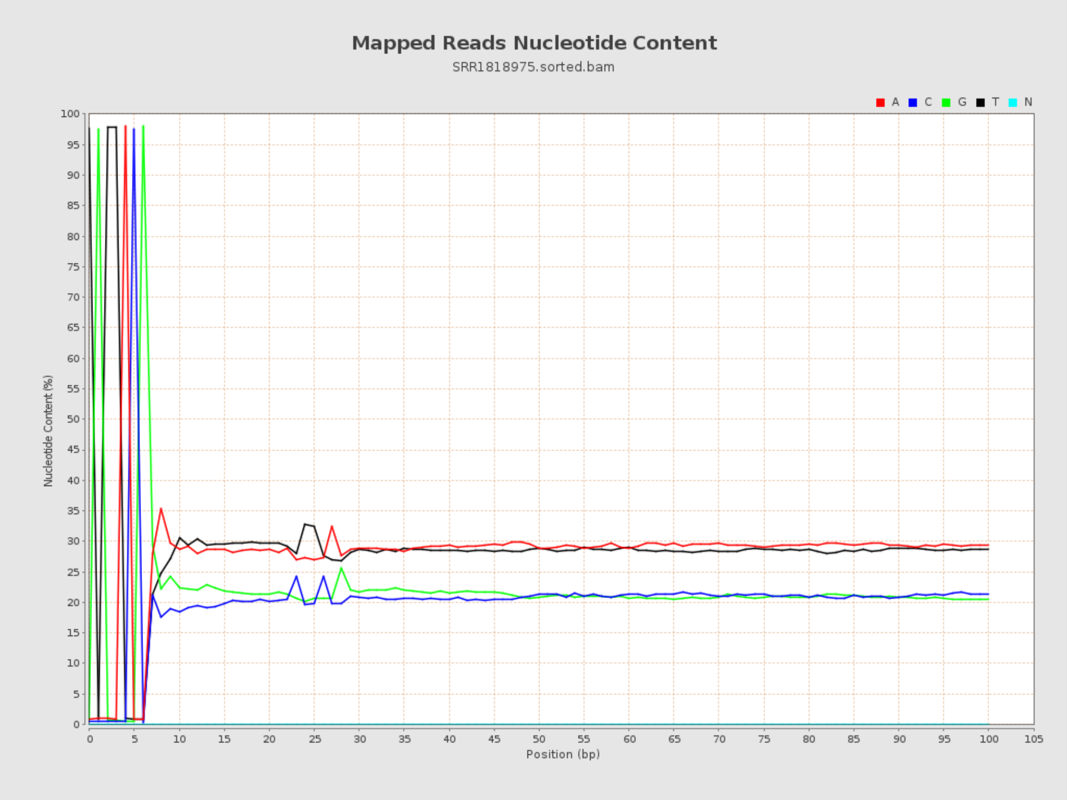
6. Results : Genome Fraction Coverage



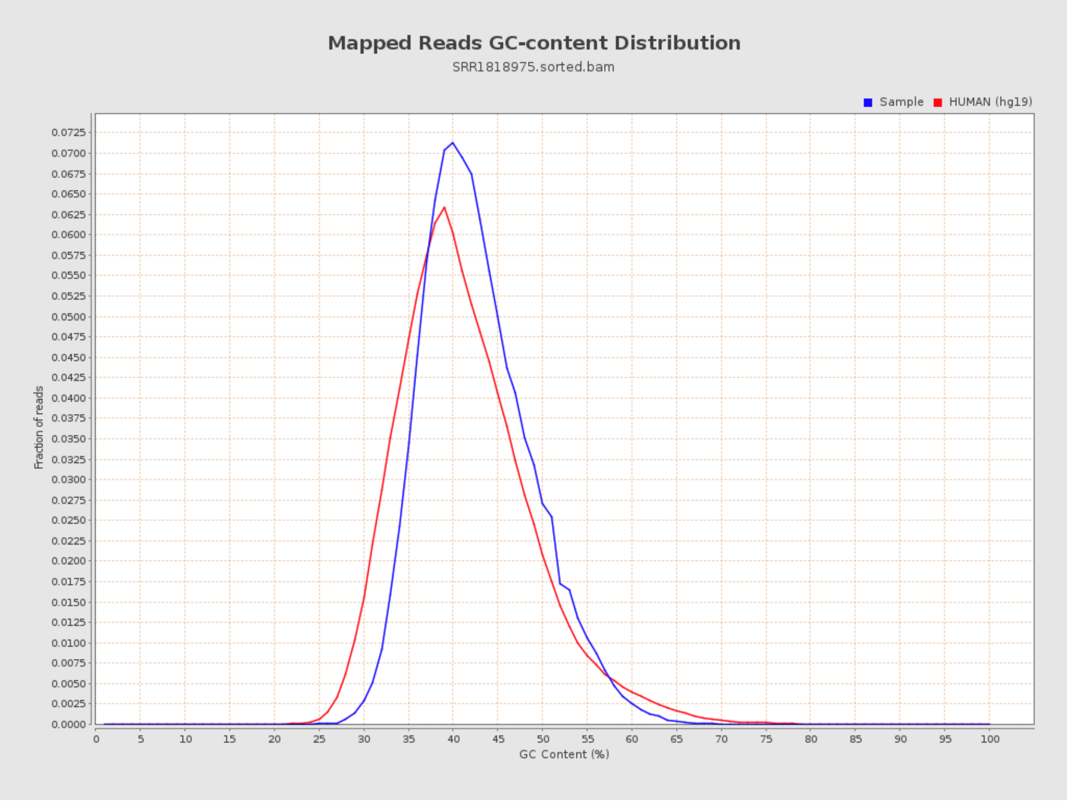
7. Results : Duplication Rate Histogram



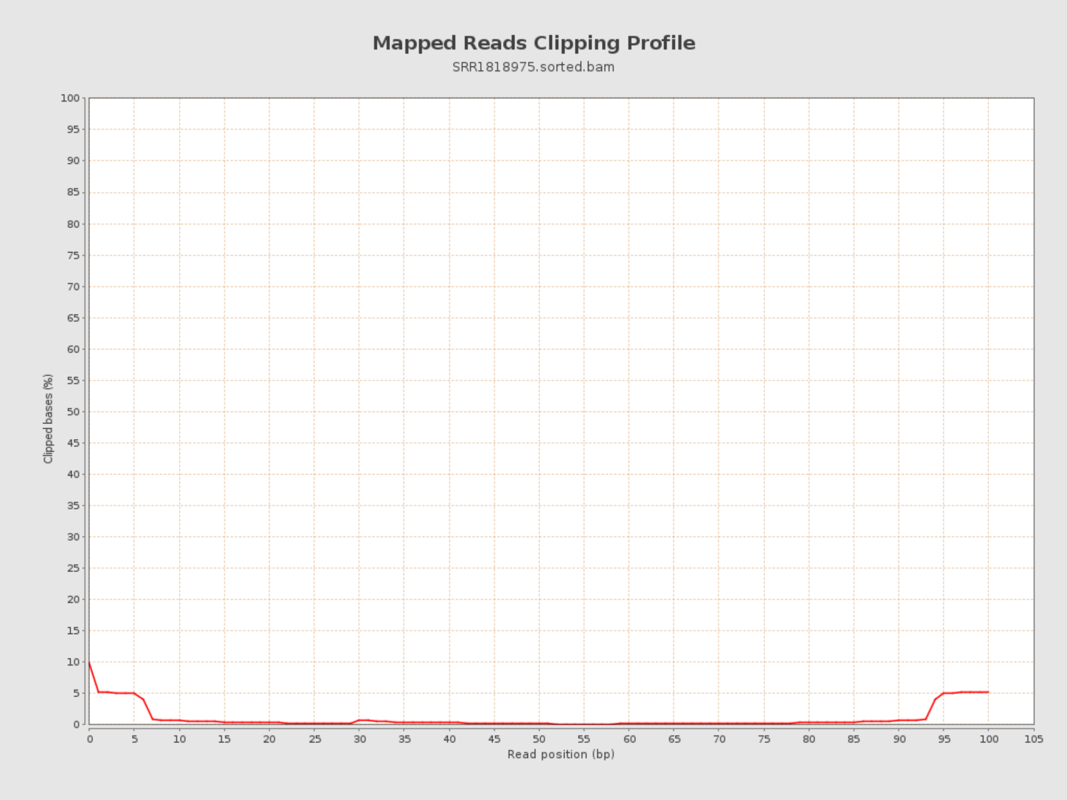
8. Results : Mapped Reads Nucleotide Content



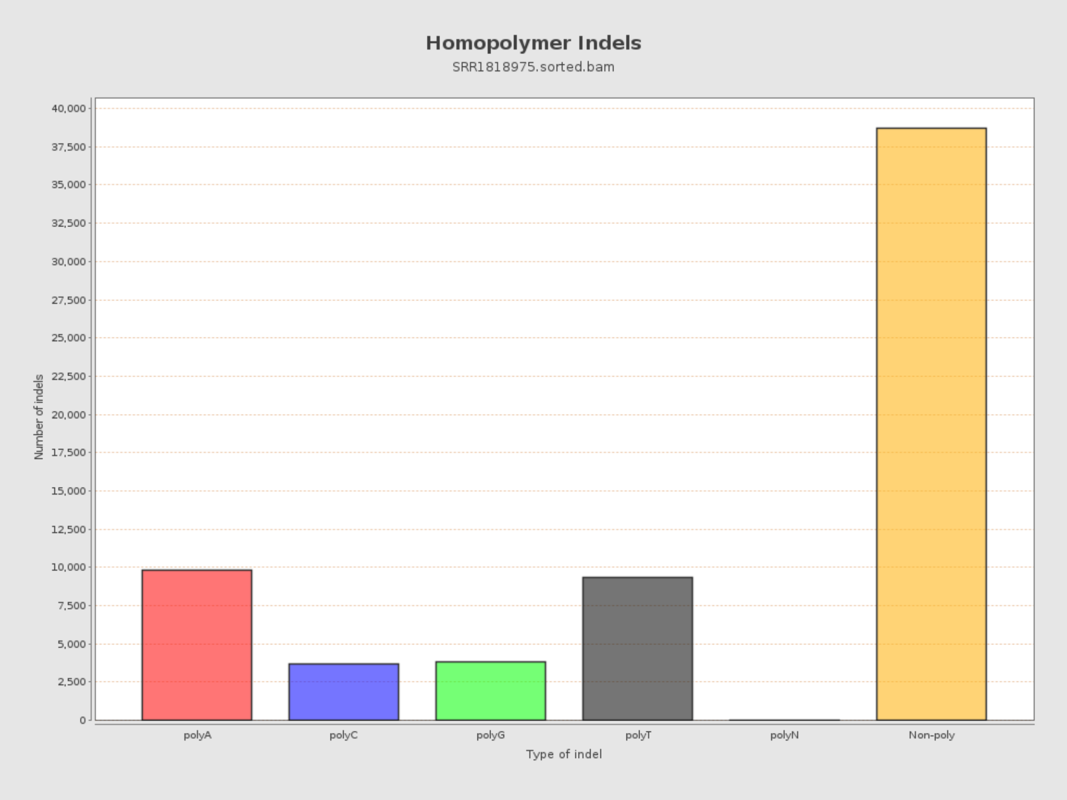
9. Results : Mapped Reads GC-content Distribution



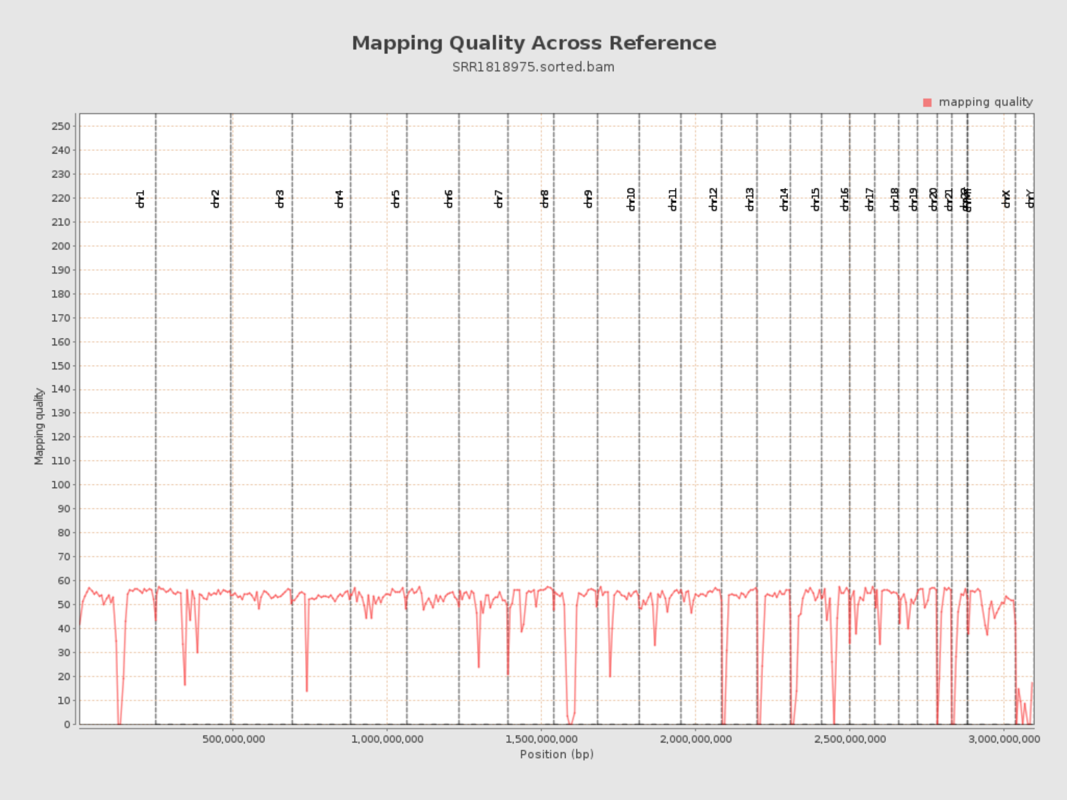
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram