Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:33:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089599.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_SRR089599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:33:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,656,684
Mapped reads	5,328,887 / 69.6%
Unmapped reads	2,327,797 / 30.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	206 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,637,889 / 21.39%
Duplication rate	22.88%
Clipped reads	881,546 / 11.51%

2.2. ACGT Content

Number/percentage of A's	80,462,278 / 32.48%
Number/percentage of C's	47,903,166 / 19.34%
Number/percentage of T's	62,761,943 / 25.34%
Number/percentage of G's	56,555,593 / 22.83%
Number/percentage of N's	30,591 / 0.01%
GC Percentage	42.17%

2.3. Coverage

Mean	0.08

Standard Deviation	0.7813

2.4. Mapping Quality

Mean Mapping Quality	41.1

2.5. Mismatches and indels

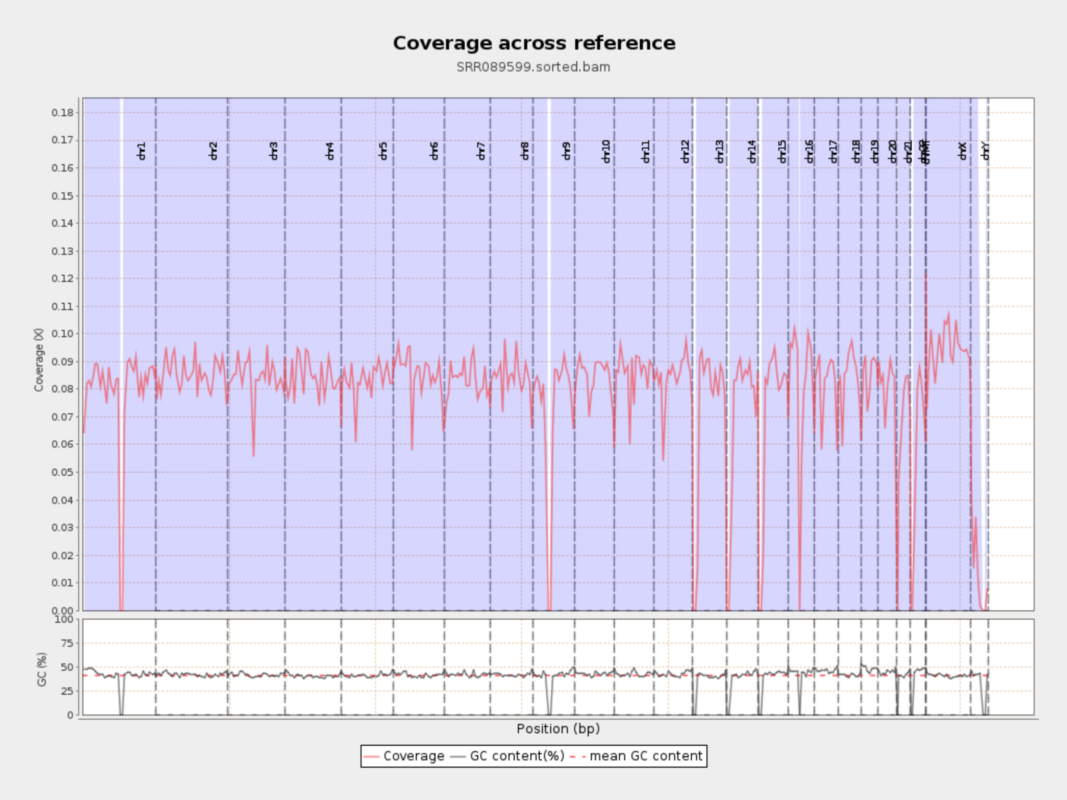
General error rate	0.93%
Mismatches	2,273,081
Insertions	13,982
Mapped reads with at least one insertion	0.26%
Deletions	33,450
Mapped reads with at least one deletion	0.63%
Homopolymer indels	41.13%

2.6. Chromosome stats

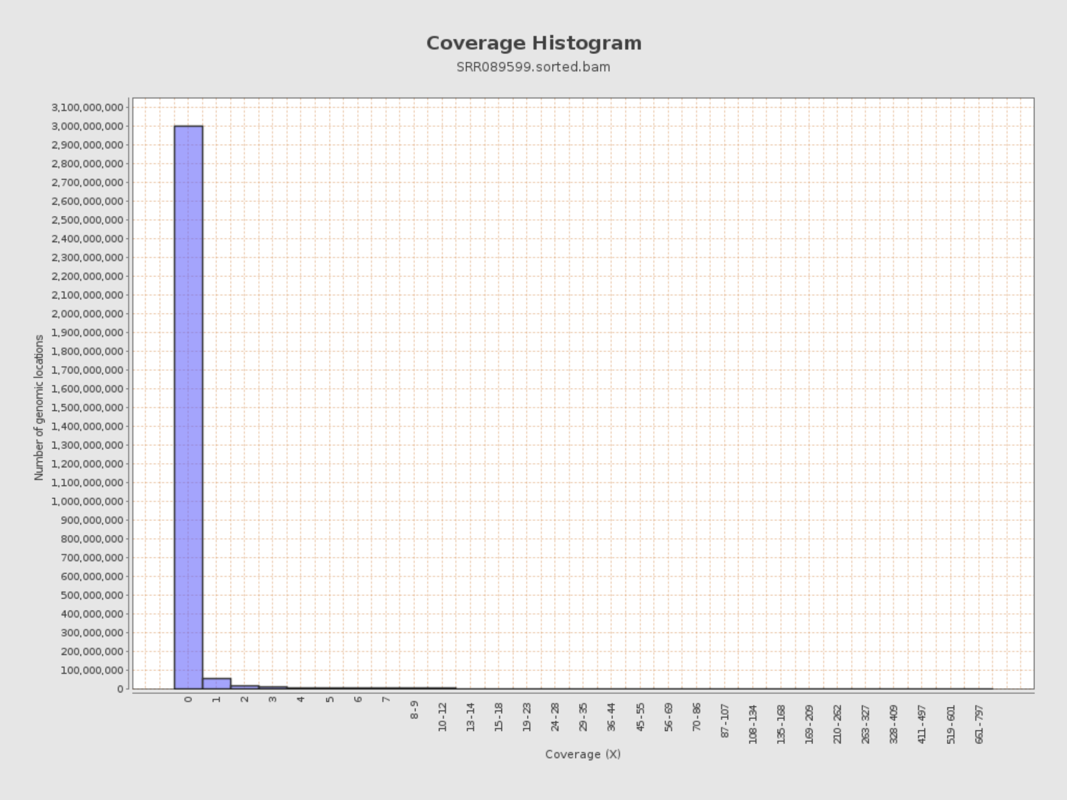
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19485859	0.0782	0.8166
chr2	243199373	20810888	0.0856	0.8764
chr3	198022430	16672391	0.0842	0.7671
chr4	191154276	16163540	0.0846	0.7831
chr5	180915260	15075374	0.0833	0.763
chr6	171115067	14636563	0.0855	0.8199
chr7	159138663	13253843	0.0833	0.8419

chr8	146364022	12358795	0.0844	0.8742
chr9	141213431	10113202	0.0716	0.7119
chr10	135534747	11509138	0.0849	0.7818
chr11	135006516	11559684	0.0856	0.8365
chr12	133851895	11339292	0.0847	0.7749
chr13	115169878	8184810	0.0711	0.7186
chr14	107349540	7554277	0.0704	0.7182
chr15	102531392	7052798	0.0688	0.6868
chr16	90354753	7193751	0.0796	0.7305
chr17	81195210	6736766	0.083	0.7481
chr18	78077248	6590990	0.0844	0.8027
chr19	59128983	4992342	0.0844	0.7672
chr20	63025520	5125600	0.0813	0.7334
chr21	48129895	3121666	0.0649	0.6729
chr22	51304566	2834608	0.0553	0.5948
chrMT	16571	2023	0.1221	1.3051
chrX	155270560	14638608	0.0943	0.8353
chrY	59373566	756827	0.0127	0.2682

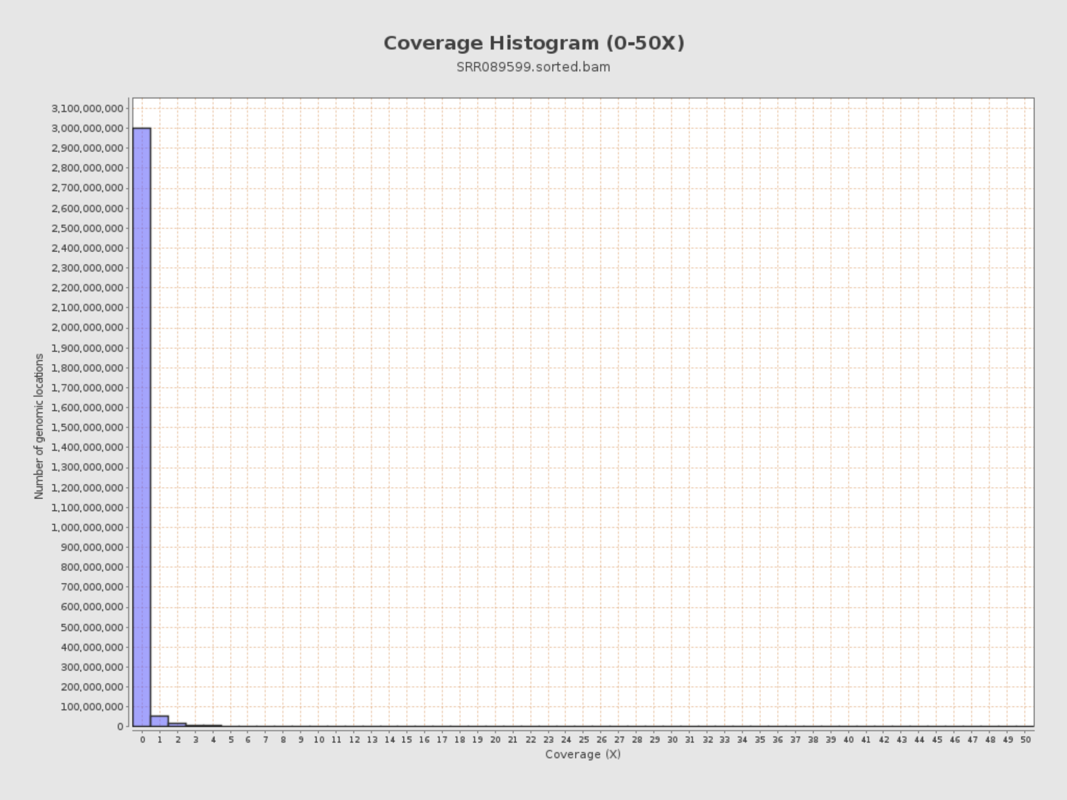
3. Results : Coverage across reference



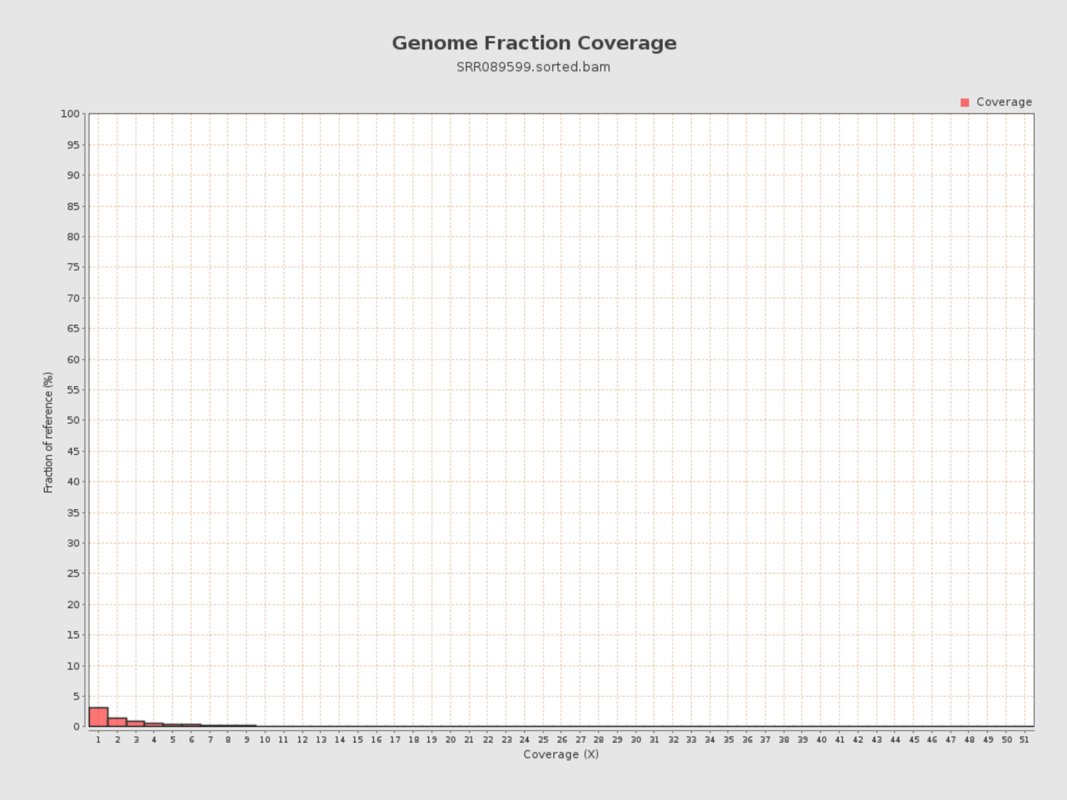
4. Results : Coverage Histogram



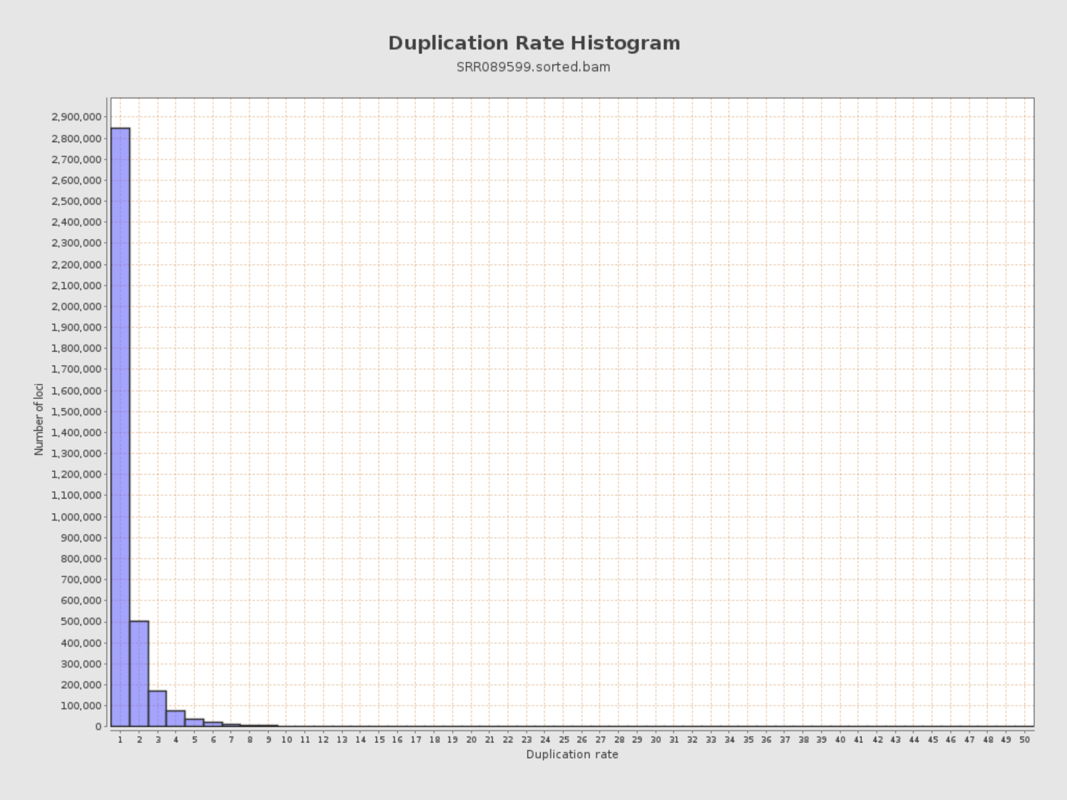
5. Results : Coverage Histogram (0-50X)



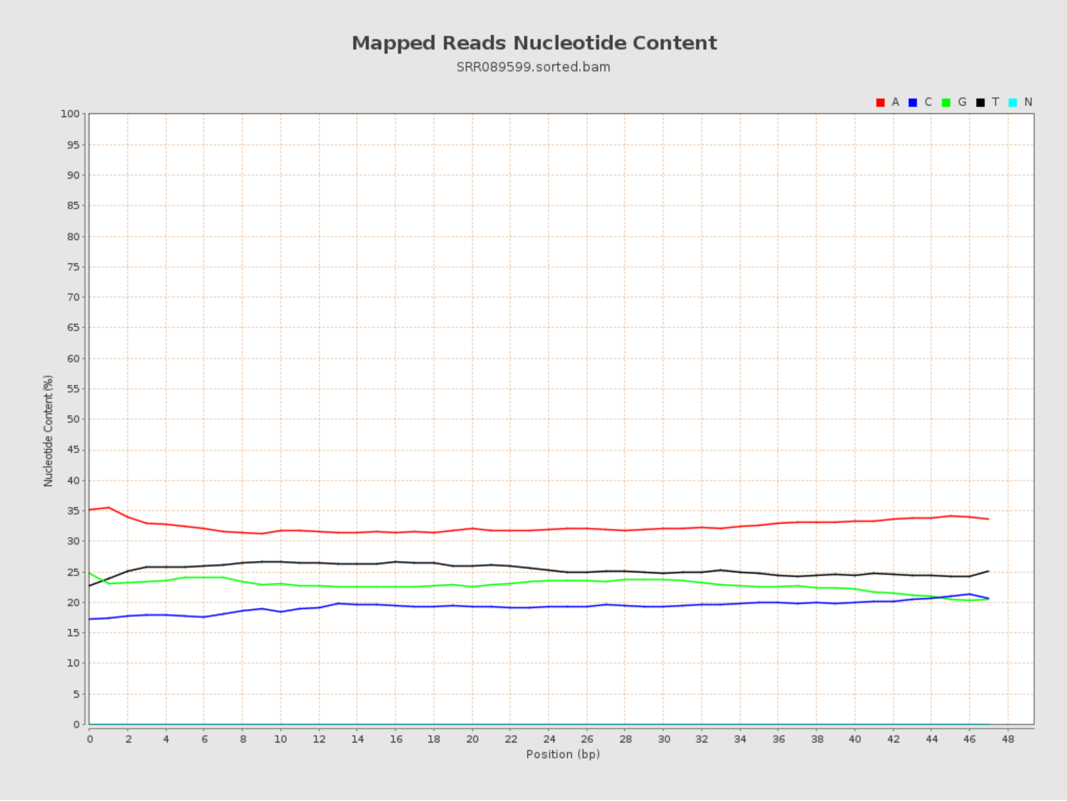
6. Results : Genome Fraction Coverage



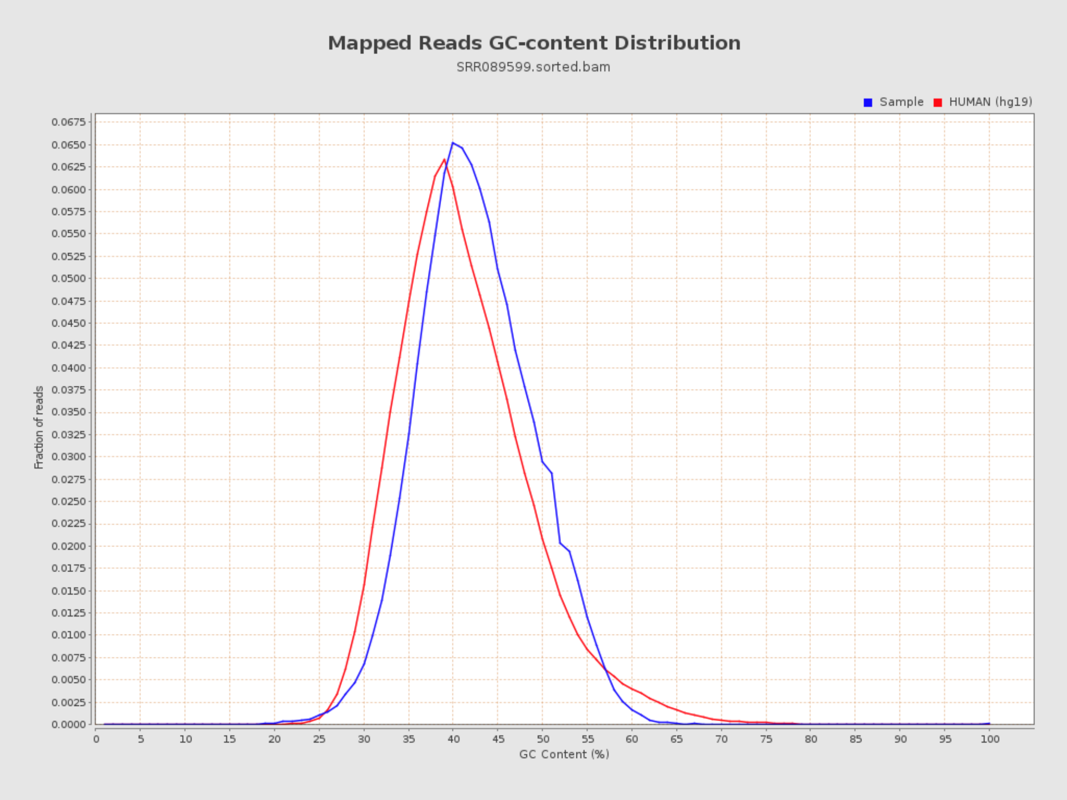
7. Results : Duplication Rate Histogram



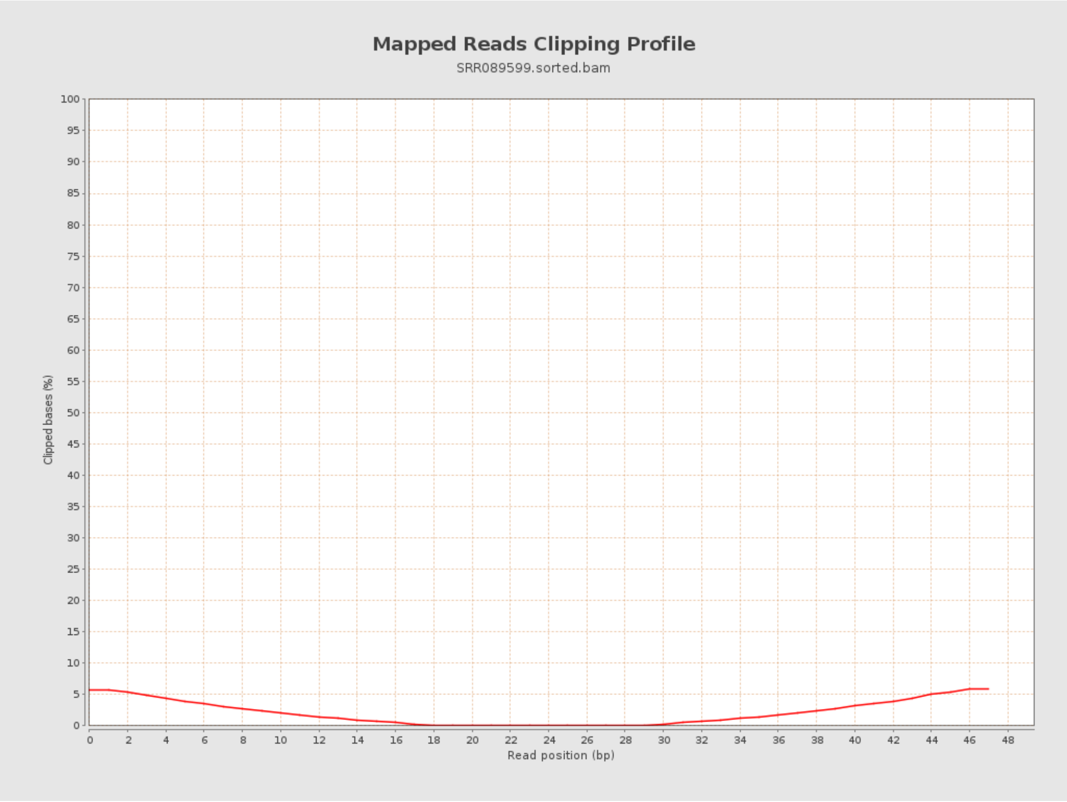
8. Results : Mapped Reads Nucleotide Content



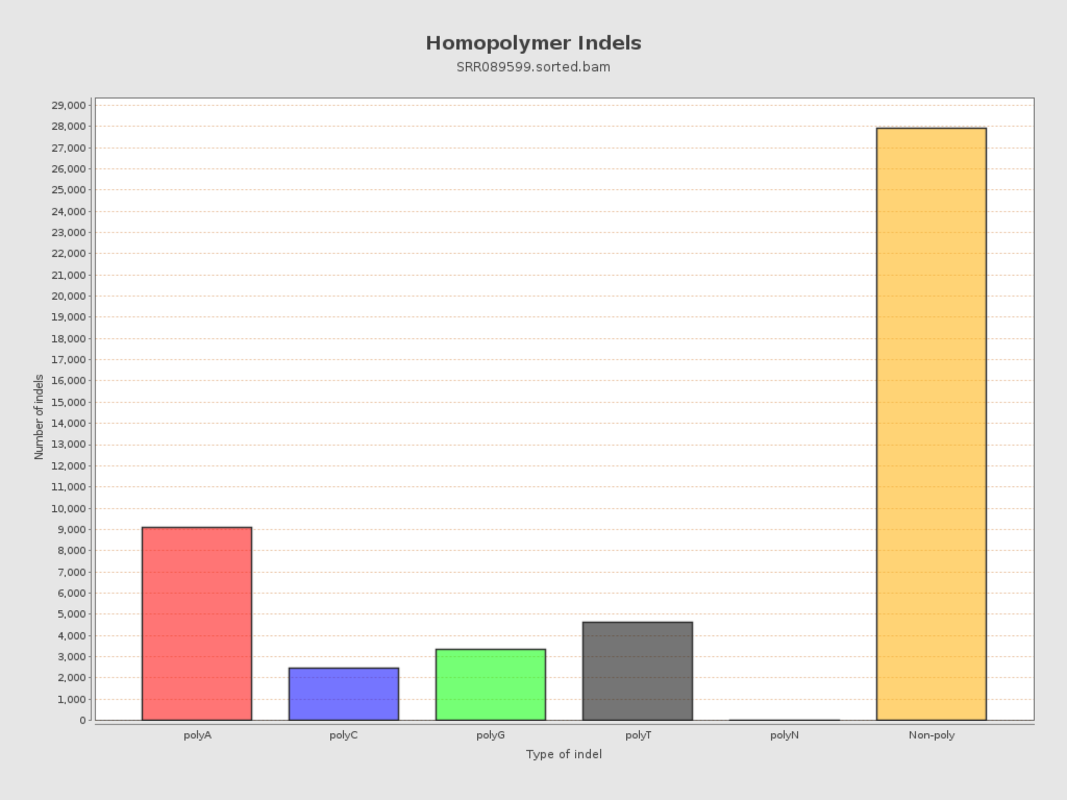
9. Results : Mapped Reads GC-content Distribution



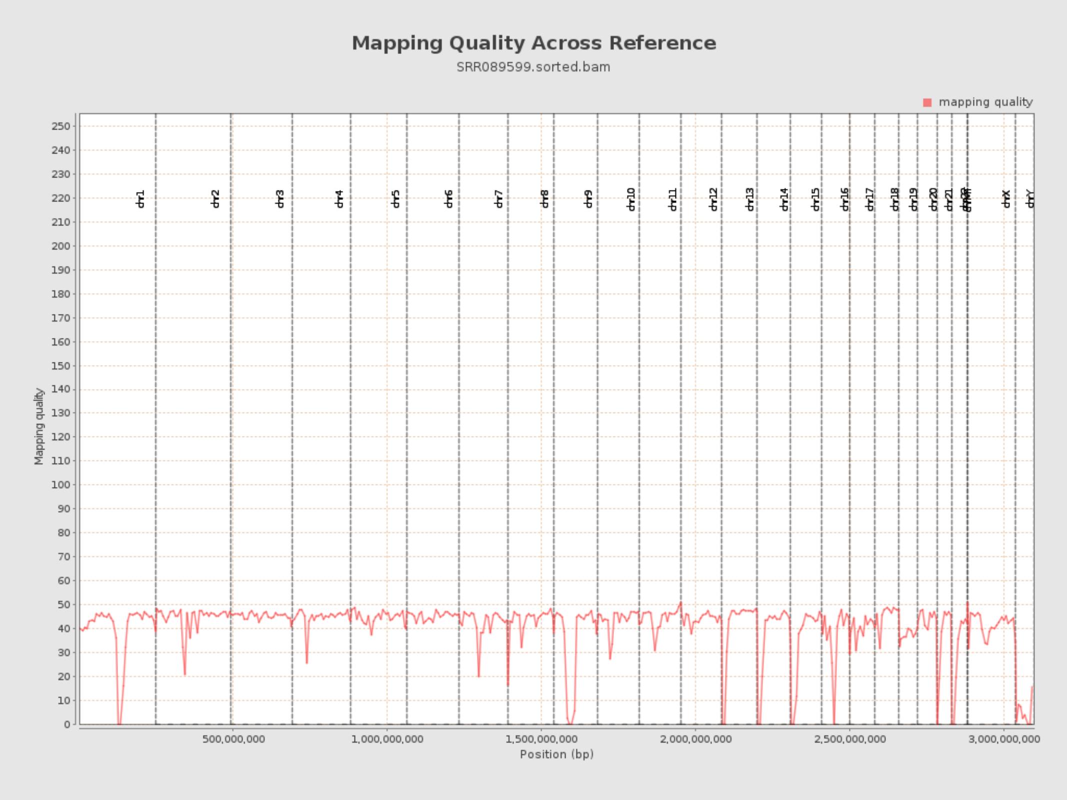
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram