Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:17:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089597.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_SRR089597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:17:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,268,481
Mapped reads	18,828,749 / 80.92%
Unmapped reads	4,439,732 / 19.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	634 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,029,085 / 8.72%
Duplication rate	8.03%
Clipped reads	2,900,501 / 12.47%

2.2. ACGT Content

Number/percentage of A's	269,593,184 / 30.77%
Number/percentage of C's	181,176,415 / 20.68%
Number/percentage of T's	234,977,200 / 26.82%
Number/percentage of G's	189,763,858 / 21.66%
Number/percentage of N's	652,607 / 0.07%
GC Percentage	42.34%

2.3. Coverage

Mean	0.2831

Standard Deviation	1.4495

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Mismatches and indels

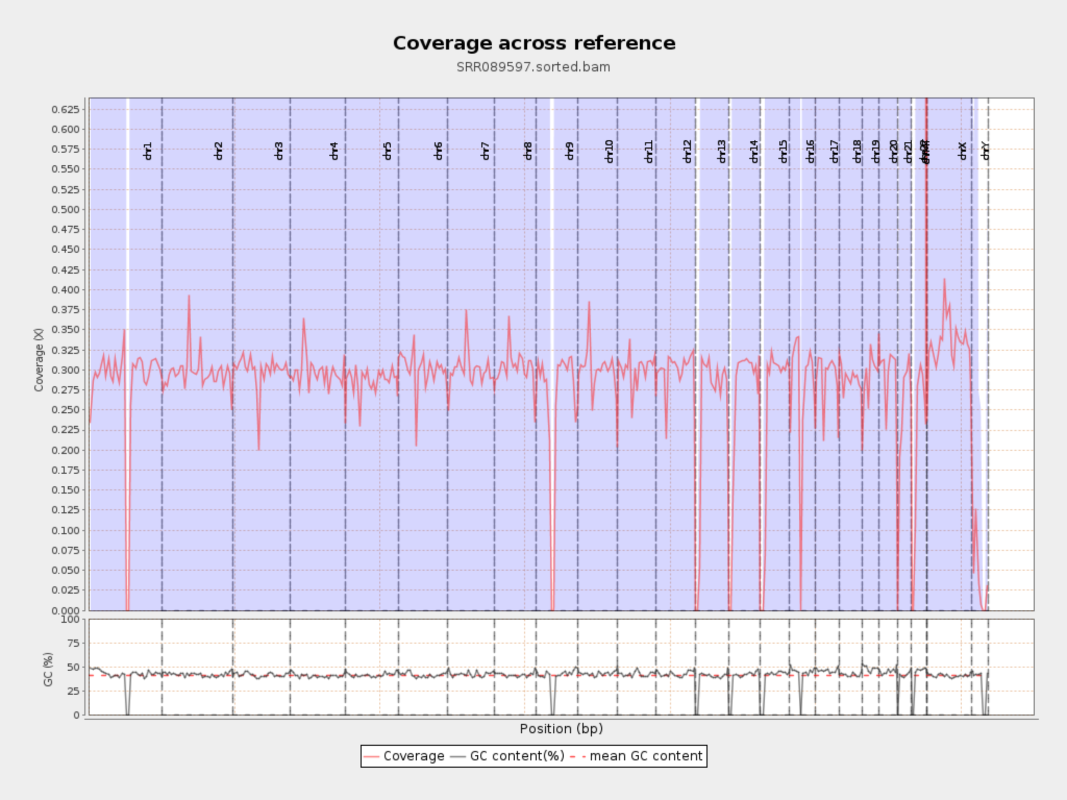
General error rate	0.54%
Mismatches	4,716,534
Insertions	36,685
Mapped reads with at least one insertion	0.19%
Deletions	113,171
Mapped reads with at least one deletion	0.6%
Homopolymer indels	43.47%

2.6. Chromosome stats

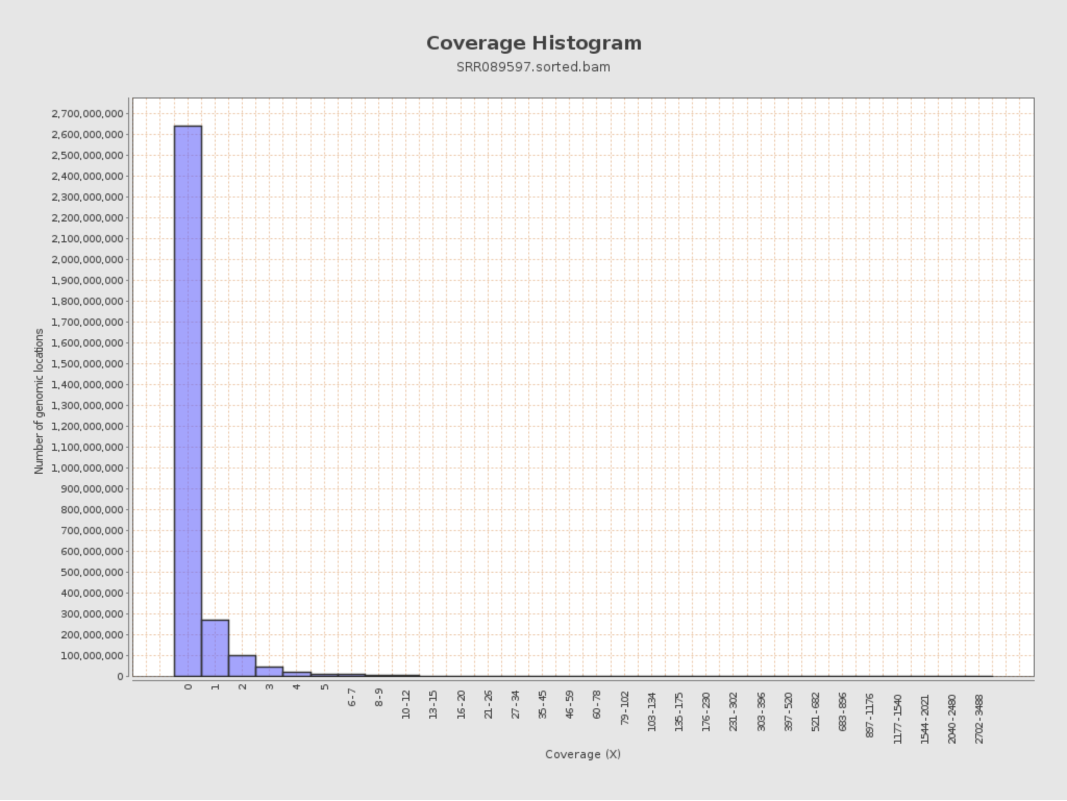
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	70006653	0.2809	2.0596
chr2	243199373	72326902	0.2974	1.7406
chr3	198022430	59188806	0.2989	0.9767
chr4	191154276	56799037	0.2971	1.0737
chr5	180915260	51897654	0.2869	0.9599
chr6	171115067	51486455	0.3009	1.1764
chr7	159138663	48019245	0.3017	1.9533

chr8	146364022	44412263	0.3034	2.2016
chr9	141213431	36415129	0.2579	1.3778
chr10	135534747	41095820	0.3032	1.5182
chr11	135006516	40422747	0.2994	1.4133
chr12	133851895	40116019	0.2997	1.0347
chr13	115169878	28167874	0.2446	0.8876
chr14	107349540	27259601	0.2539	1.1038
chr15	102531392	25112370	0.2449	0.8874
chr16	90354753	24953825	0.2762	1.0759
chr17	81195210	23513529	0.2896	1.1432
chr18	78077248	22633025	0.2899	2.1632
chr19	59128983	17396194	0.2942	1.9474
chr20	63025520	18631078	0.2956	1.0564
chr21	48129895	11554052	0.2401	1.1112
chr22	51304566	10111164	0.1971	0.7979
chrMT	16571	404368	24.4021	20.1464
chrX	155270560	51839521	0.3339	1.3229
chrY	59373566	2568284	0.0433	0.6952

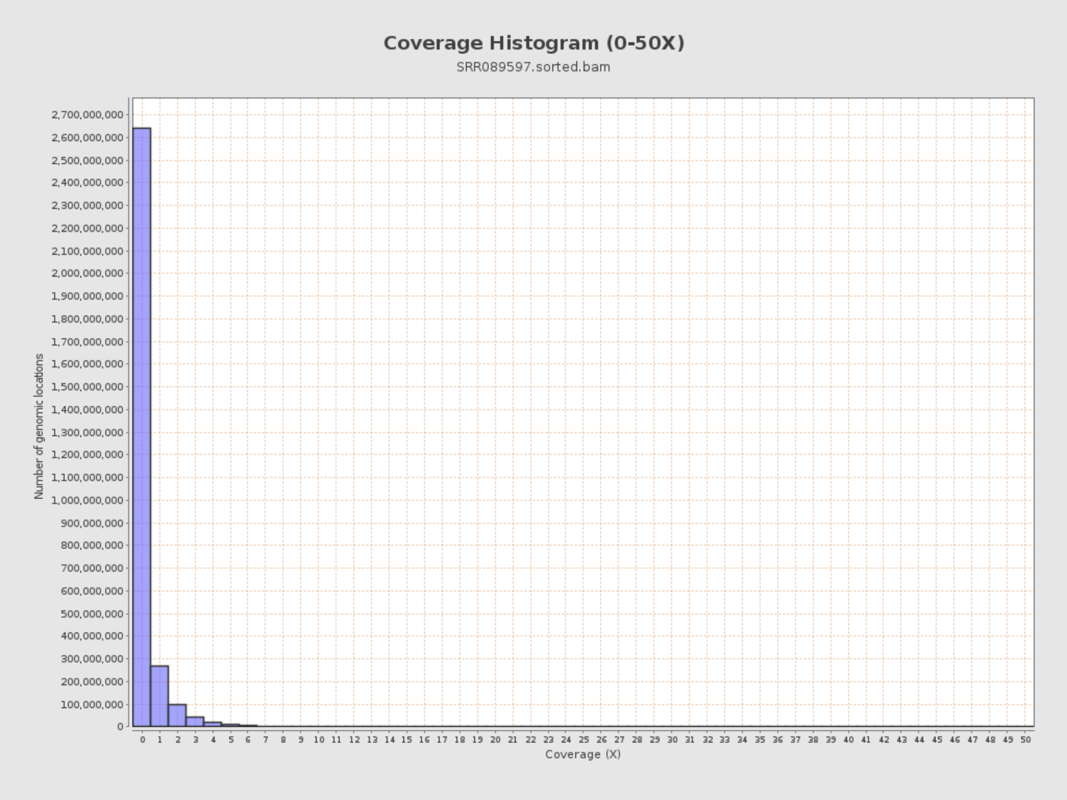
3. Results : Coverage across reference



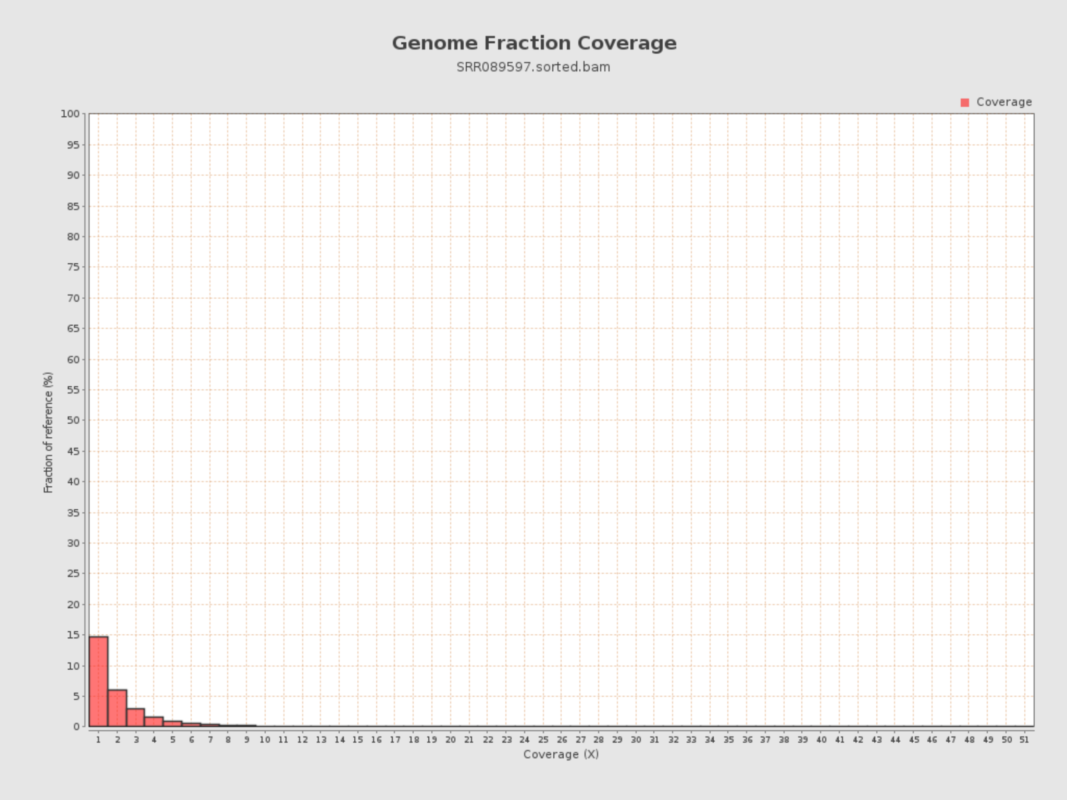
4. Results : Coverage Histogram



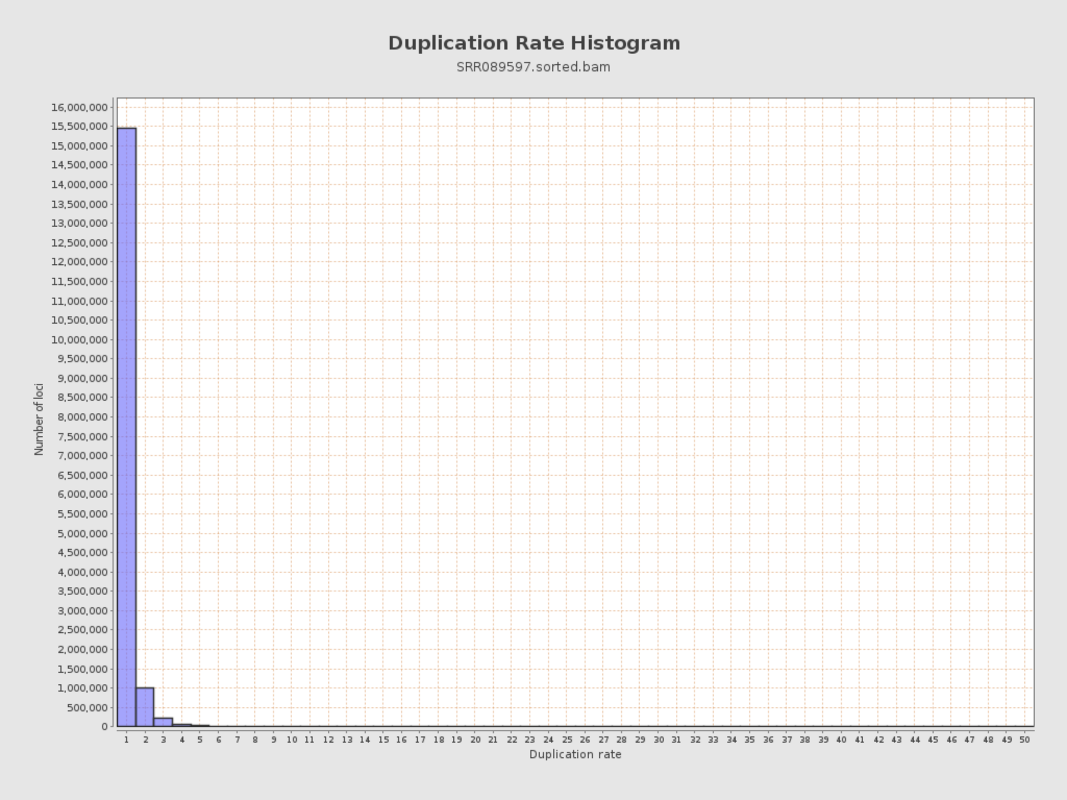
5. Results : Coverage Histogram (0-50X)



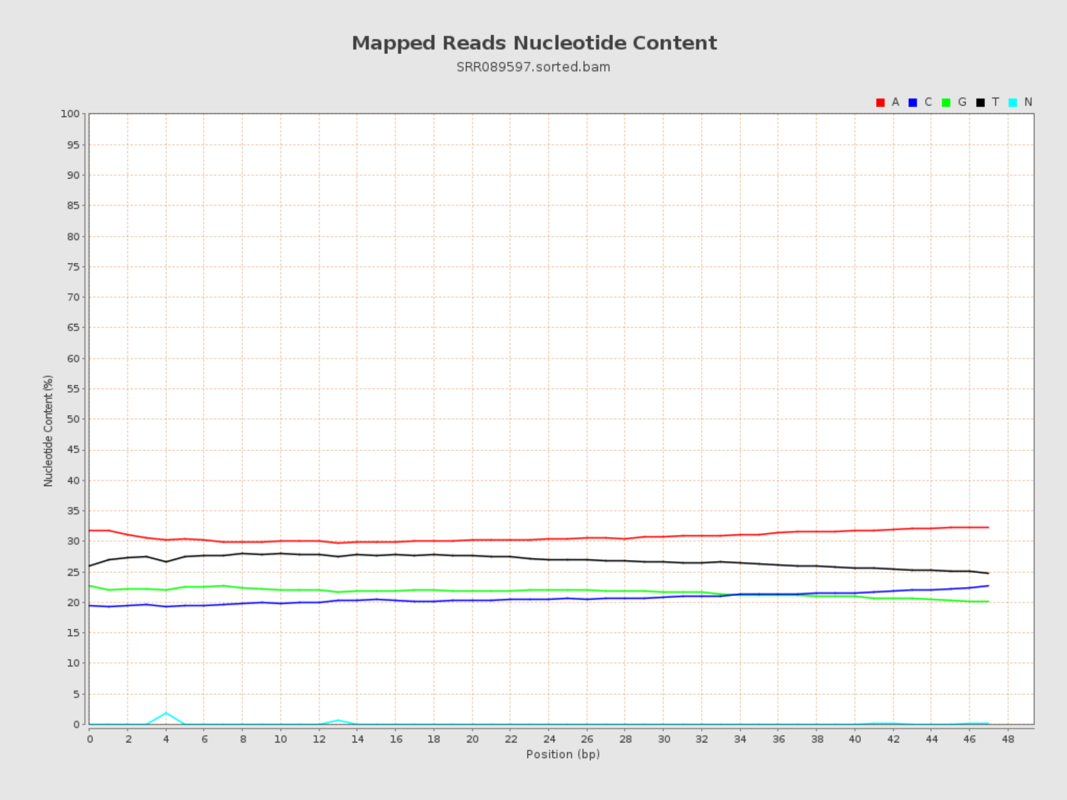
6. Results : Genome Fraction Coverage



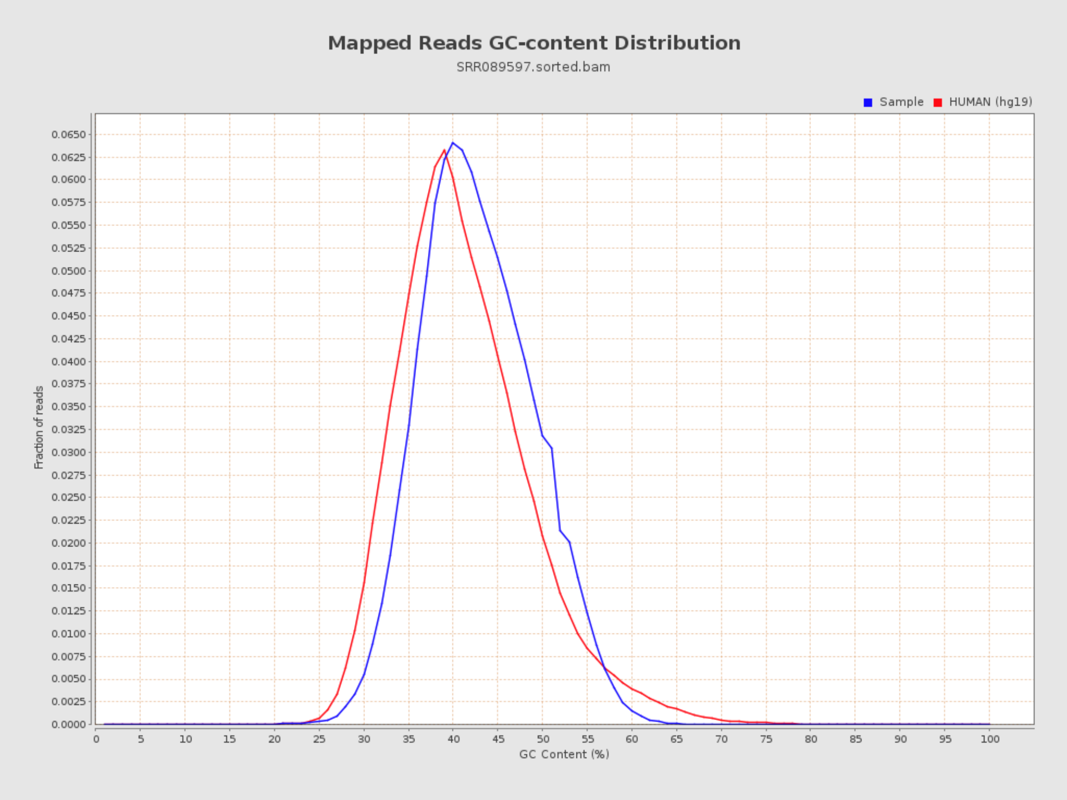
7. Results : Duplication Rate Histogram



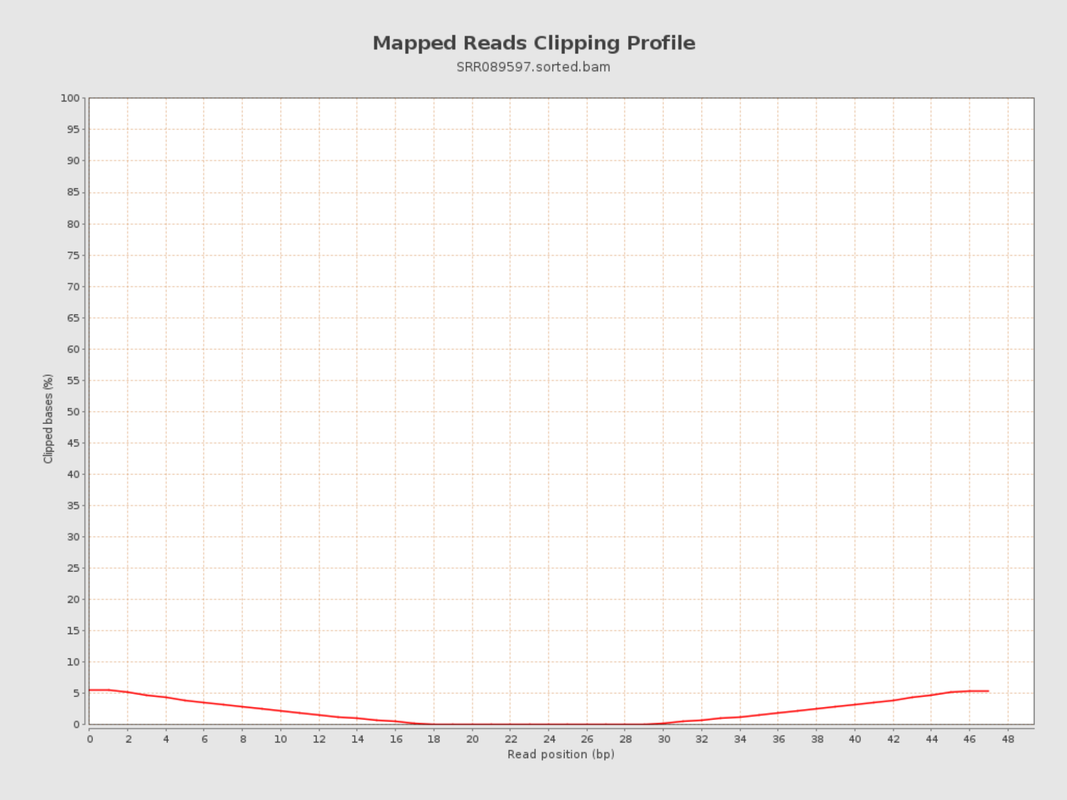
8. Results : Mapped Reads Nucleotide Content



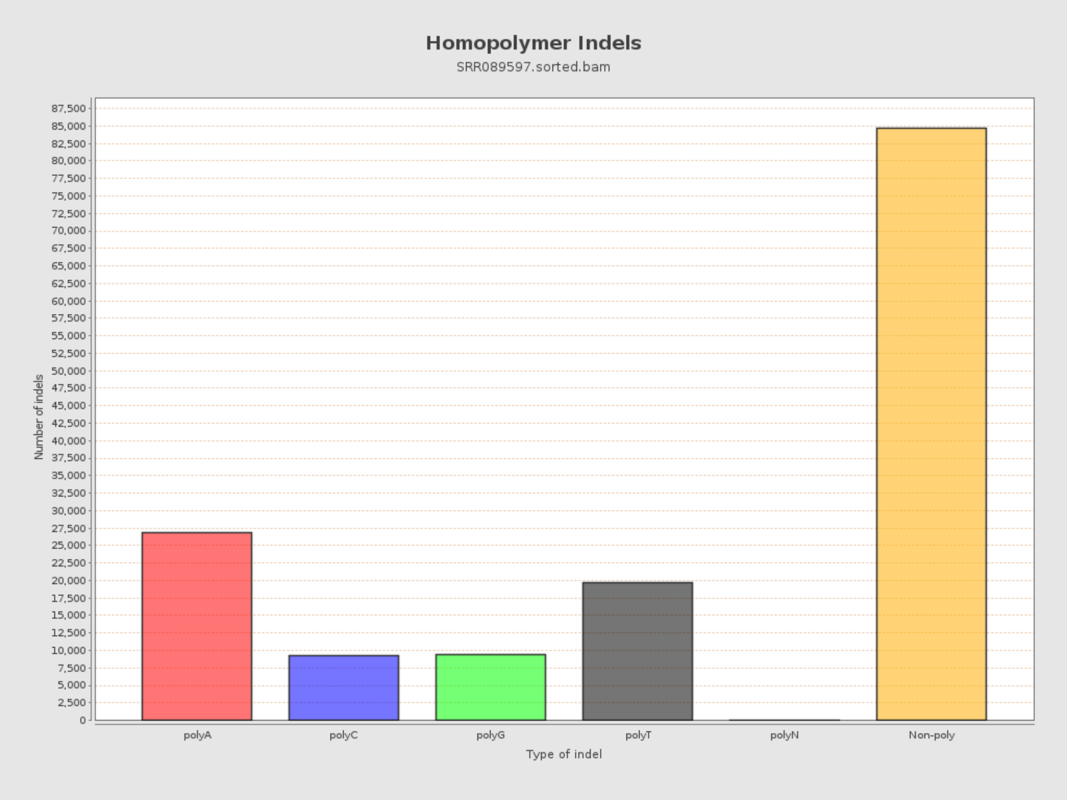
9. Results : Mapped Reads GC-content Distribution



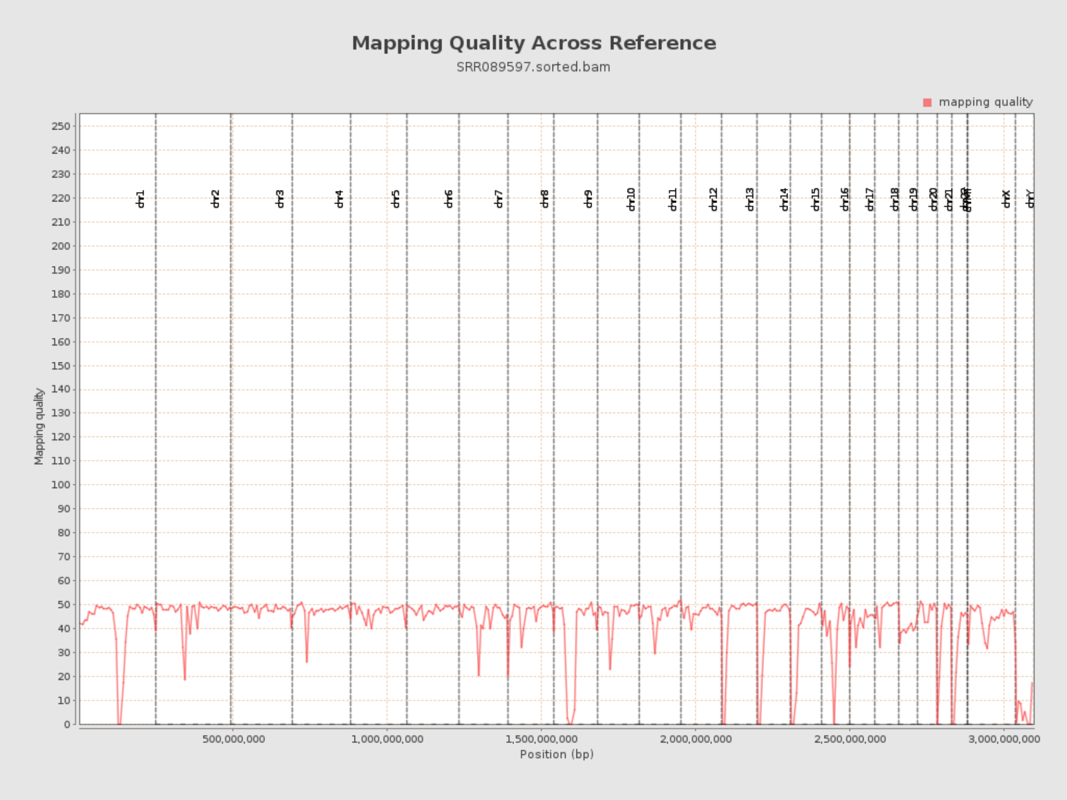
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram