Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 00:02:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089712.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_SRR089712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 00:02:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,431,281
Mapped reads	19,016,574 / 88.73%
Unmapped reads	2,414,707 / 11.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	135,440 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	5,469,888 / 25.52%
Duplication rate	14.93%
Clipped reads	8,346,162 / 38.94%

2.2. ACGT Content

Number/percentage of A's	336,909,295 / 26.65%
Number/percentage of C's	236,055,617 / 18.67%
Number/percentage of T's	395,878,632 / 31.32%
Number/percentage of G's	294,526,256 / 23.3%
Number/percentage of N's	699,280 / 0.06%
GC Percentage	41.97%

2.3. Coverage

Mean	0.4085

Standard Deviation	3.1031

2.4. Mapping Quality

Mean Mapping Quality	47.08

2.5. Mismatches and indels

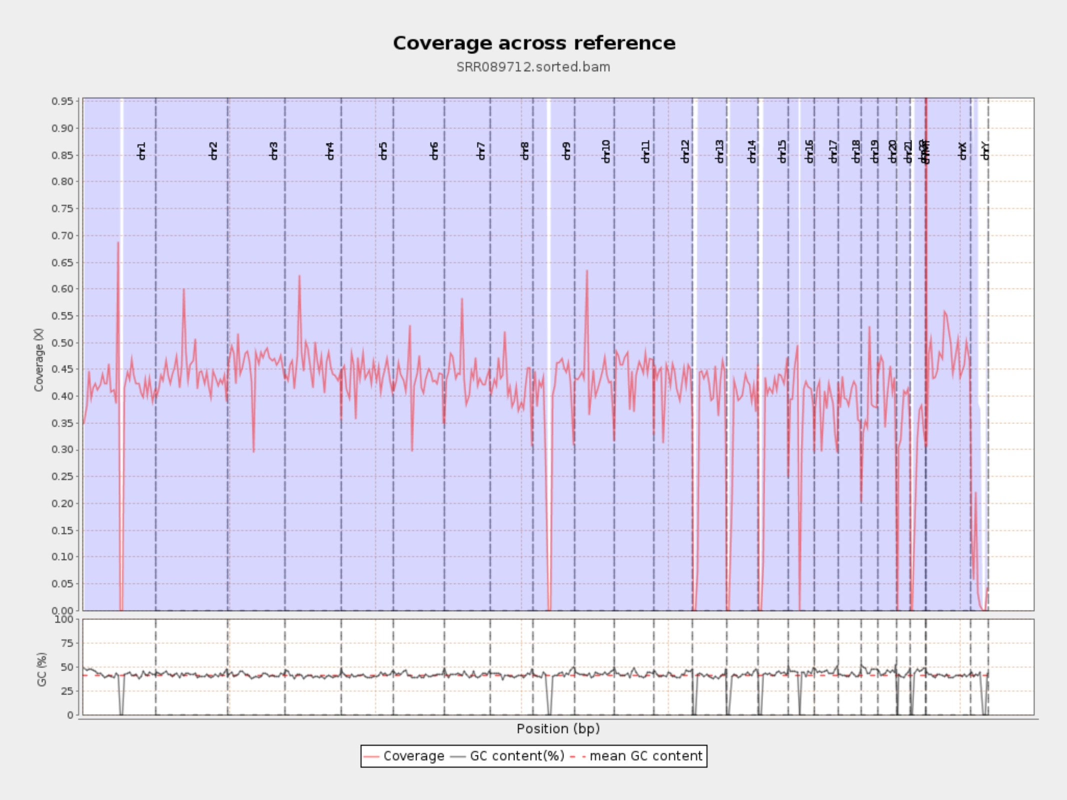
General error rate	0.71%
Mismatches	8,773,630
Insertions	85,626
Mapped reads with at least one insertion	0.45%
Deletions	252,017
Mapped reads with at least one deletion	1.31%
Homopolymer indels	47.18%

2.6. Chromosome stats

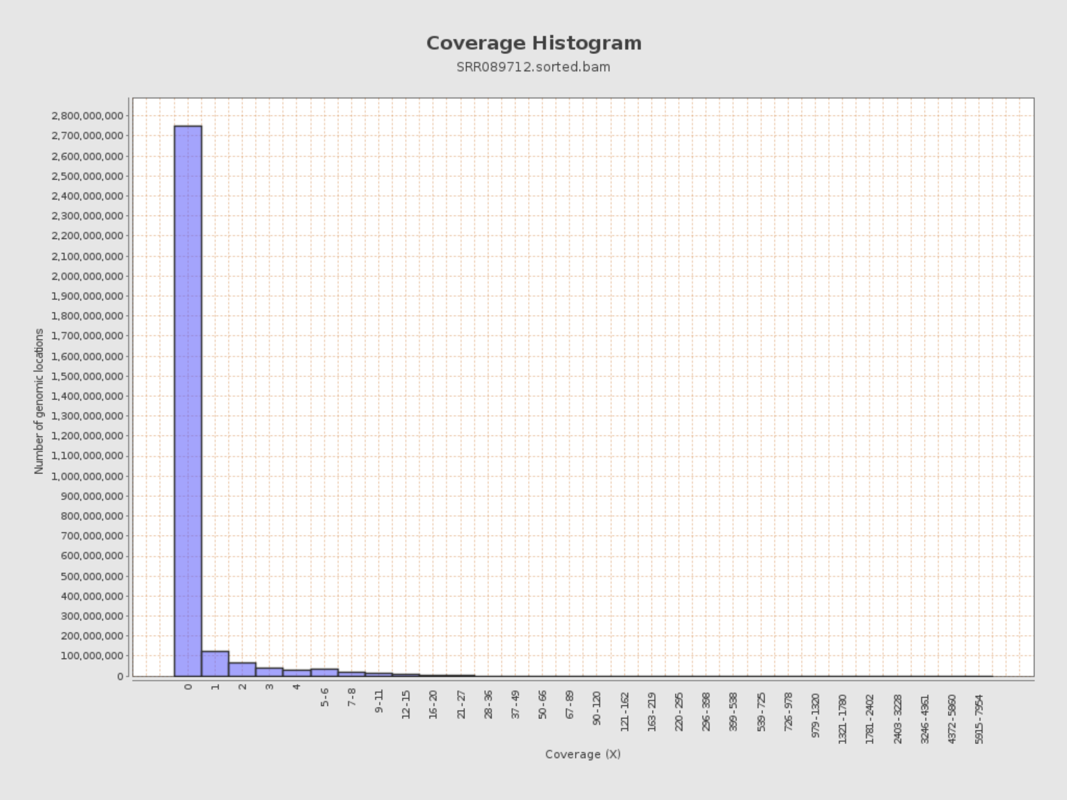
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	99801463	0.4004	6.4453
chr2	243199373	107976833	0.444	3.2639
chr3	198022430	91292789	0.461	1.8269
chr4	191154276	88245388	0.4616	2.1042
chr5	180915260	79300786	0.4383	1.7869
chr6	171115067	73794653	0.4313	2.1691
chr7	159138663	70248560	0.4414	3.6205

chr8	146364022	60960377	0.4165	4.8613
chr9	141213431	52772500	0.3737	2.376
chr10	135534747	59344319	0.4379	2.8054
chr11	135006516	60596346	0.4488	2.3353
chr12	133851895	57611447	0.4304	1.9565
chr13	115169878	41020875	0.3562	1.5886
chr14	107349540	36909217	0.3438	1.7272
chr15	102531392	35057269	0.3419	1.7939
chr16	90354753	32937008	0.3645	1.7843
chr17	81195210	30871074	0.3802	2.036
chr18	78077248	31174980	0.3993	4.5567
chr19	59128983	22462885	0.3799	3.7093
chr20	63025520	26623018	0.4224	1.925
chr21	48129895	15981697	0.3321	1.8767
chr22	51304566	12605465	0.2457	1.3866
chrMT	16571	110062	6.6418	9.8388
chrX	155270560	73278200	0.4719	1.99
chrY	59373566	3536388	0.0596	1.7597

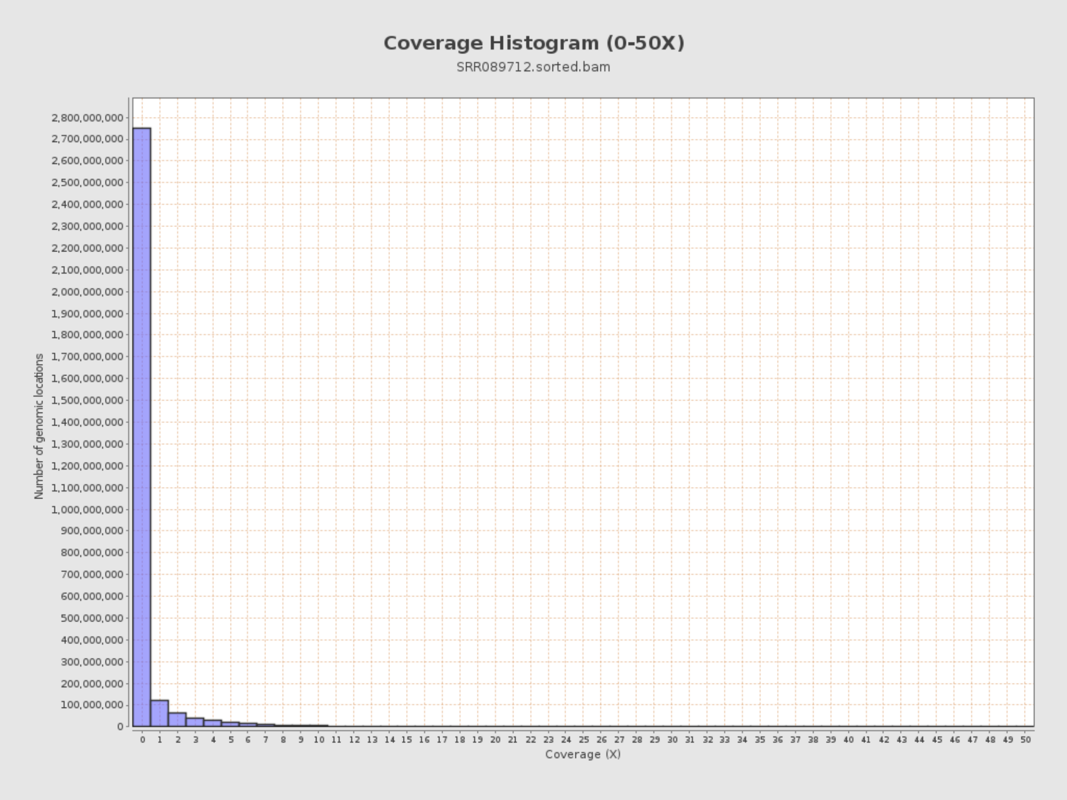
3. Results : Coverage across reference



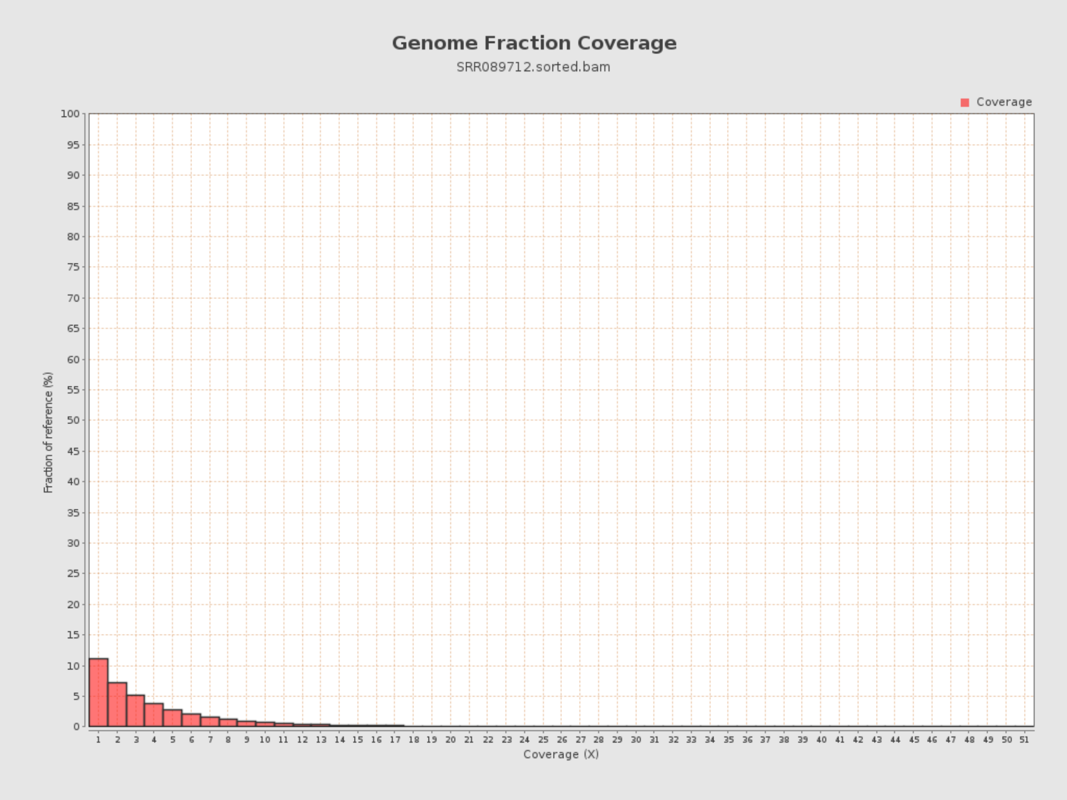
4. Results : Coverage Histogram



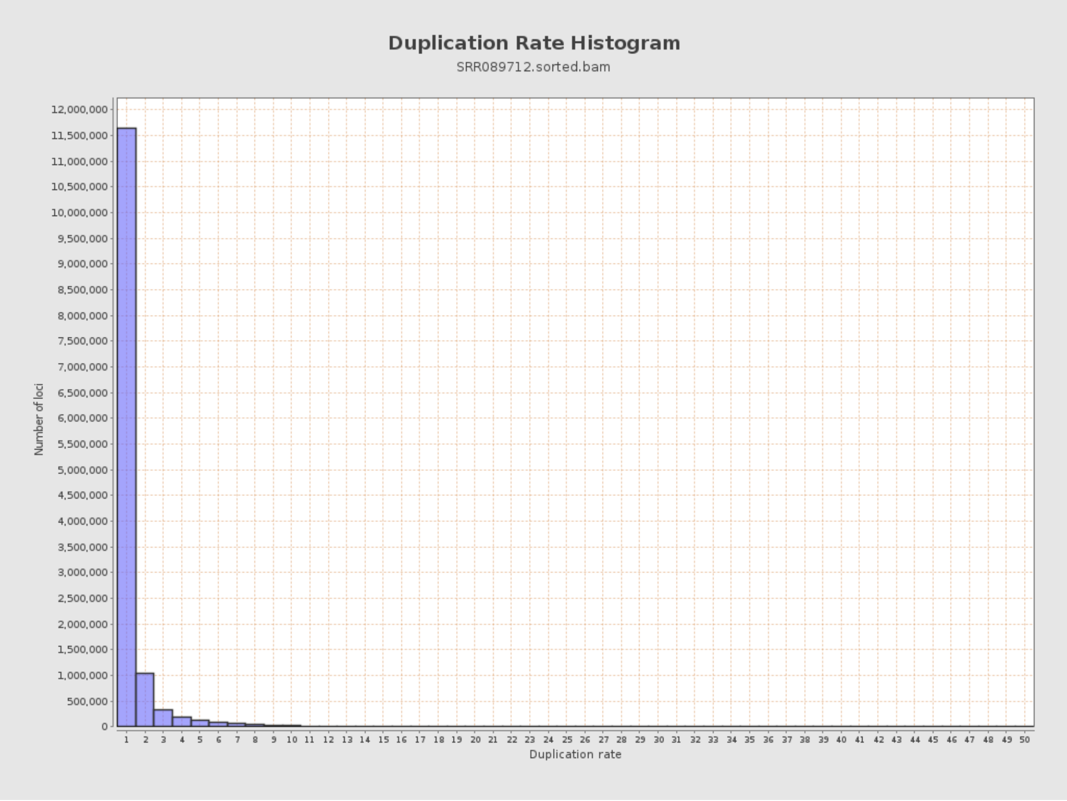
5. Results : Coverage Histogram (0-50X)



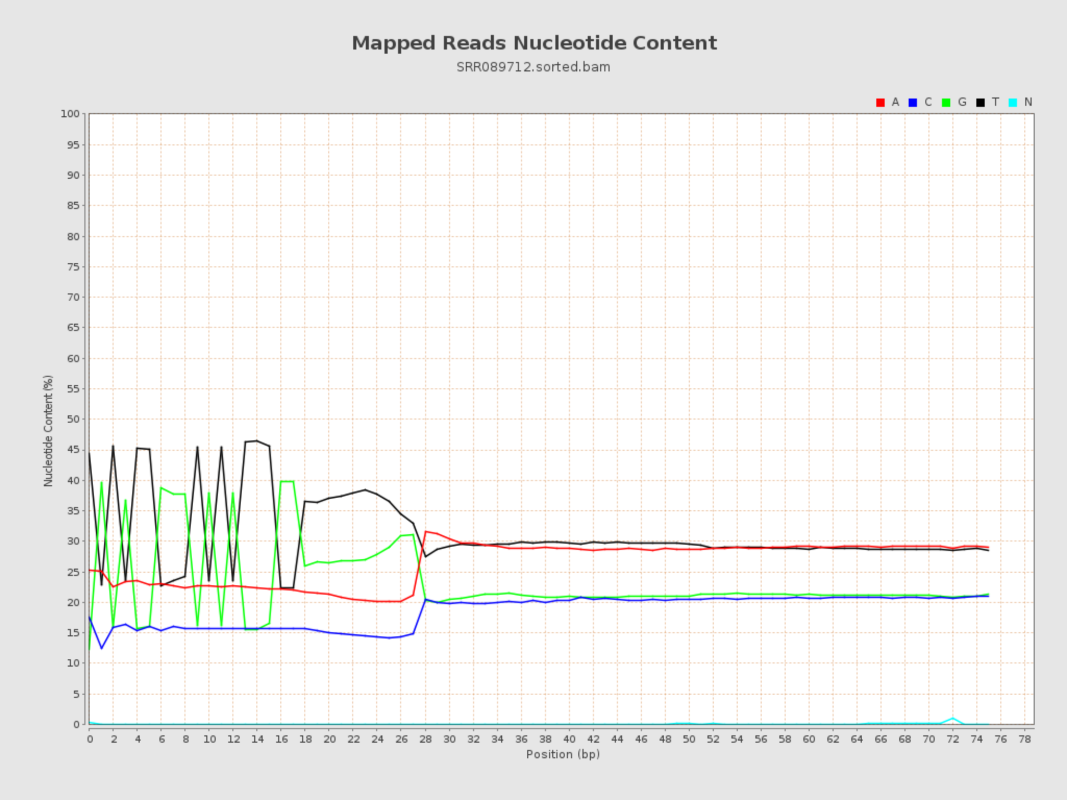
6. Results : Genome Fraction Coverage



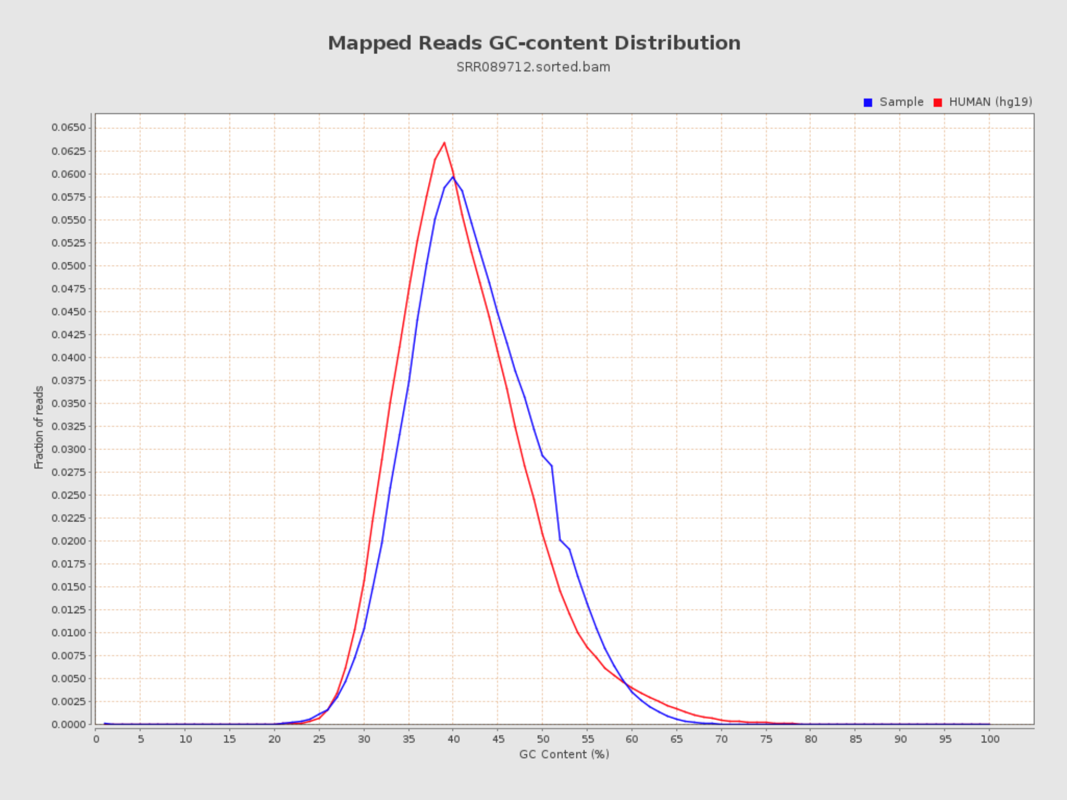
7. Results : Duplication Rate Histogram



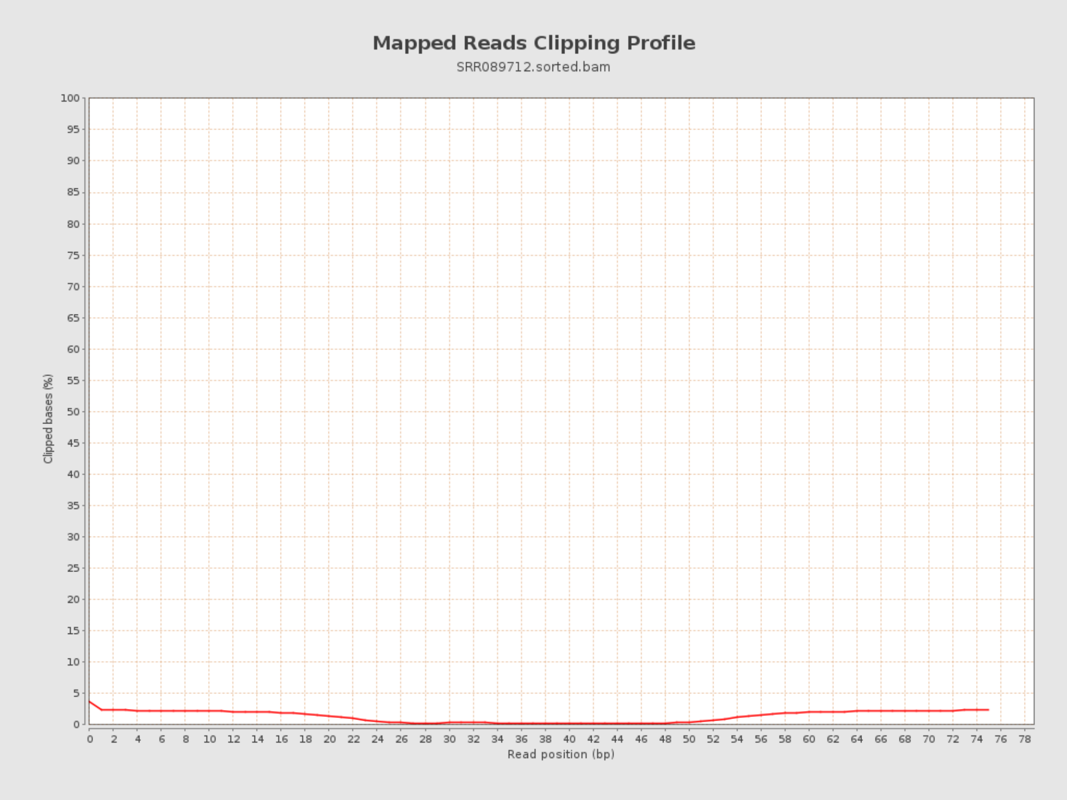
8. Results : Mapped Reads Nucleotide Content



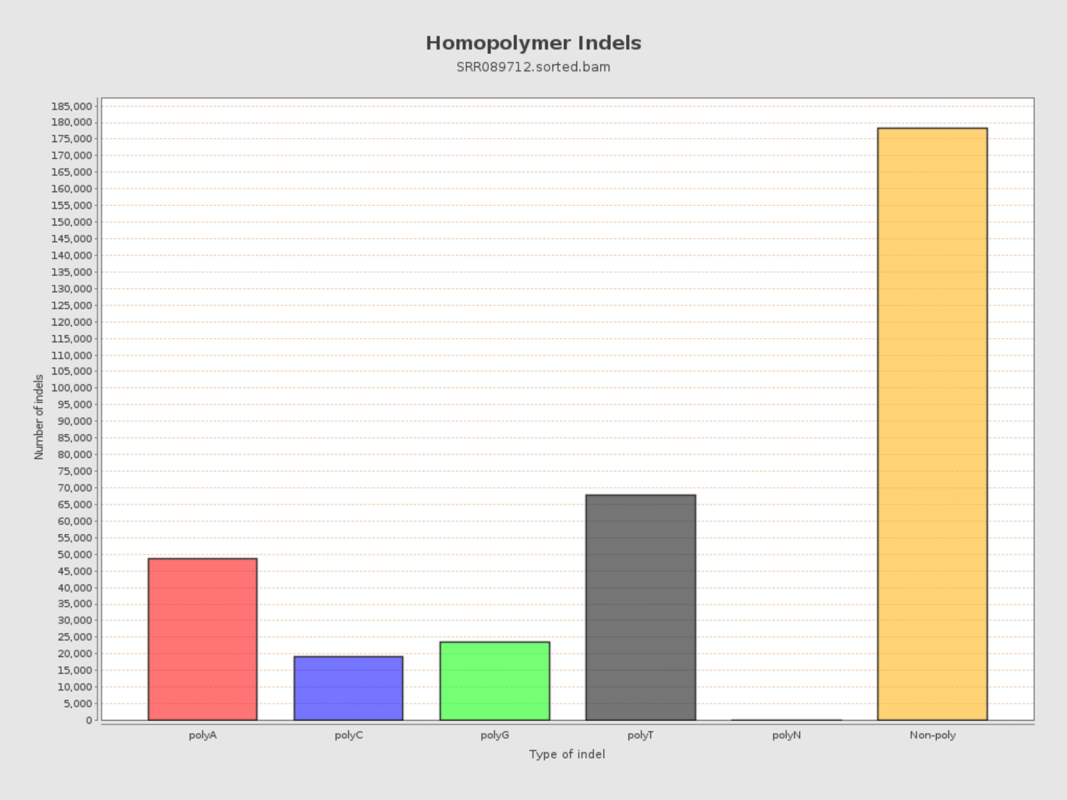
9. Results : Mapped Reads GC-content Distribution



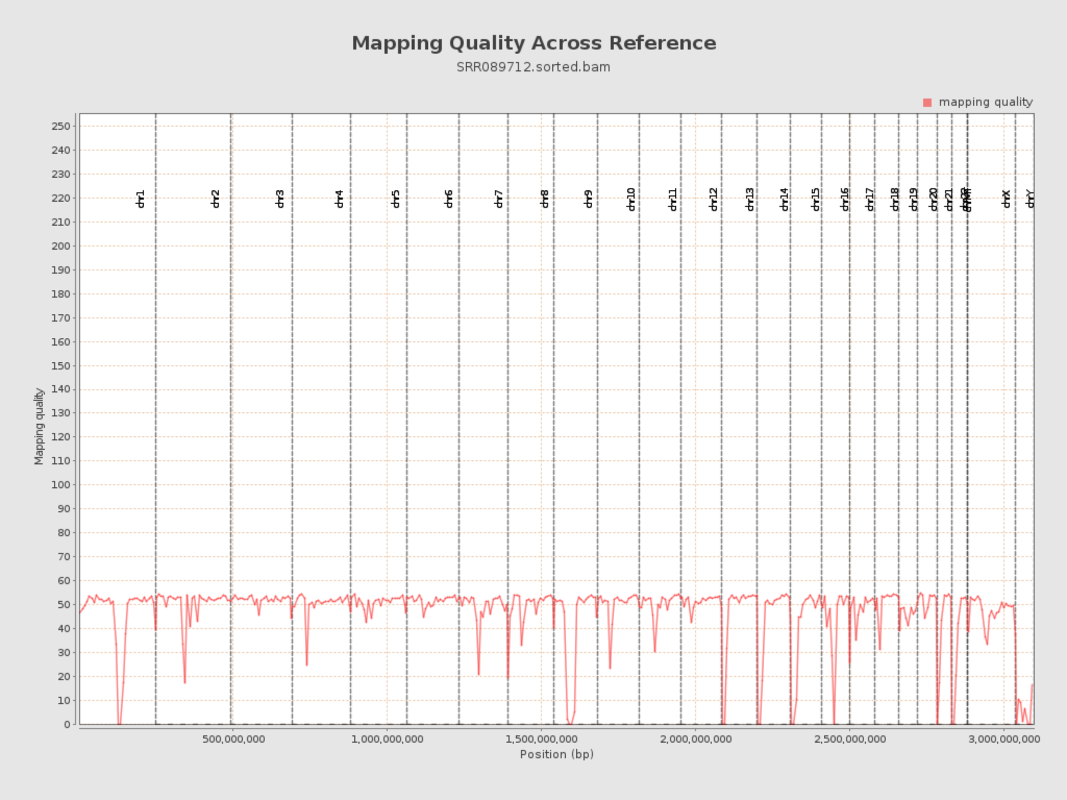
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram