Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 03:10:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089749.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_SRR089749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 03:10:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,549,449
Mapped reads	19,834,347 / 92.04%
Unmapped reads	1,715,102 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	117,934 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	4,389,588 / 20.37%
Duplication rate	14.42%
Clipped reads	9,767,797 / 45.33%

2.2. ACGT Content

Number/percentage of A's	331,147,633 / 25.64%
Number/percentage of C's	244,585,499 / 18.94%
Number/percentage of T's	399,731,309 / 30.95%
Number/percentage of G's	314,821,090 / 24.38%
Number/percentage of N's	1,197,755 / 0.09%
GC Percentage	43.32%

2.3. Coverage

Mean	0.4173

Standard Deviation	2.2993

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

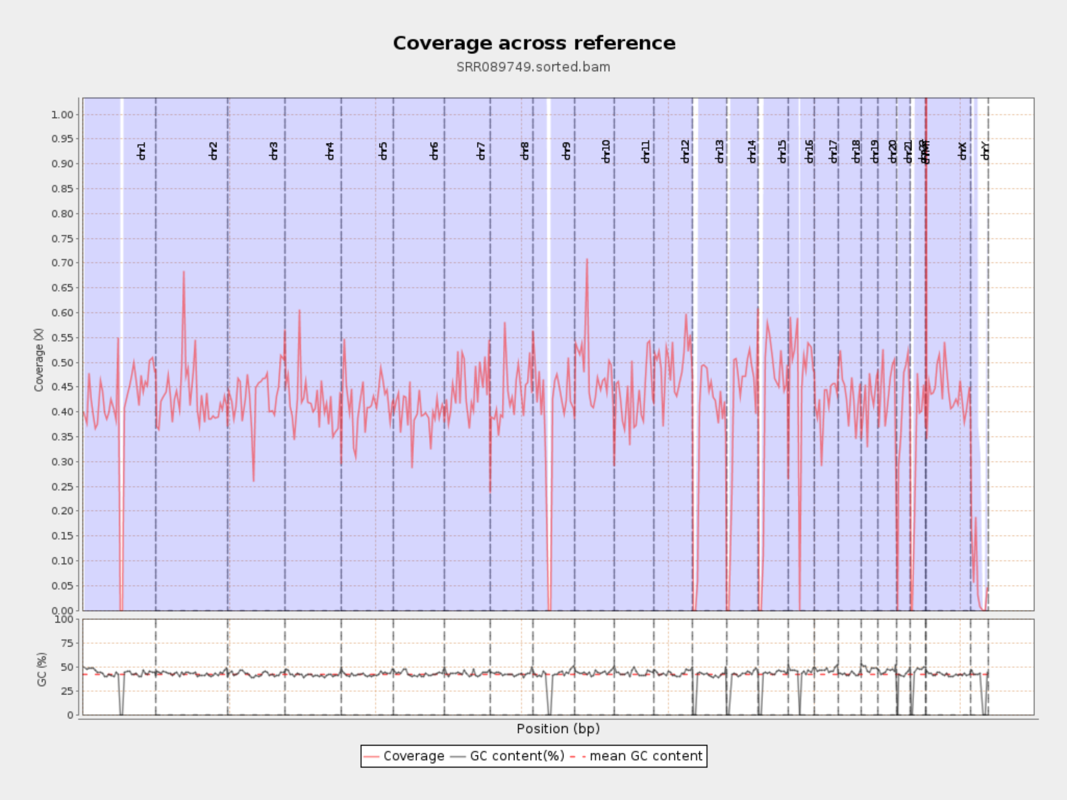
General error rate	0.96%
Mismatches	12,199,437
Insertions	83,386
Mapped reads with at least one insertion	0.42%
Deletions	255,247
Mapped reads with at least one deletion	1.27%
Homopolymer indels	45.98%

2.6. Chromosome stats

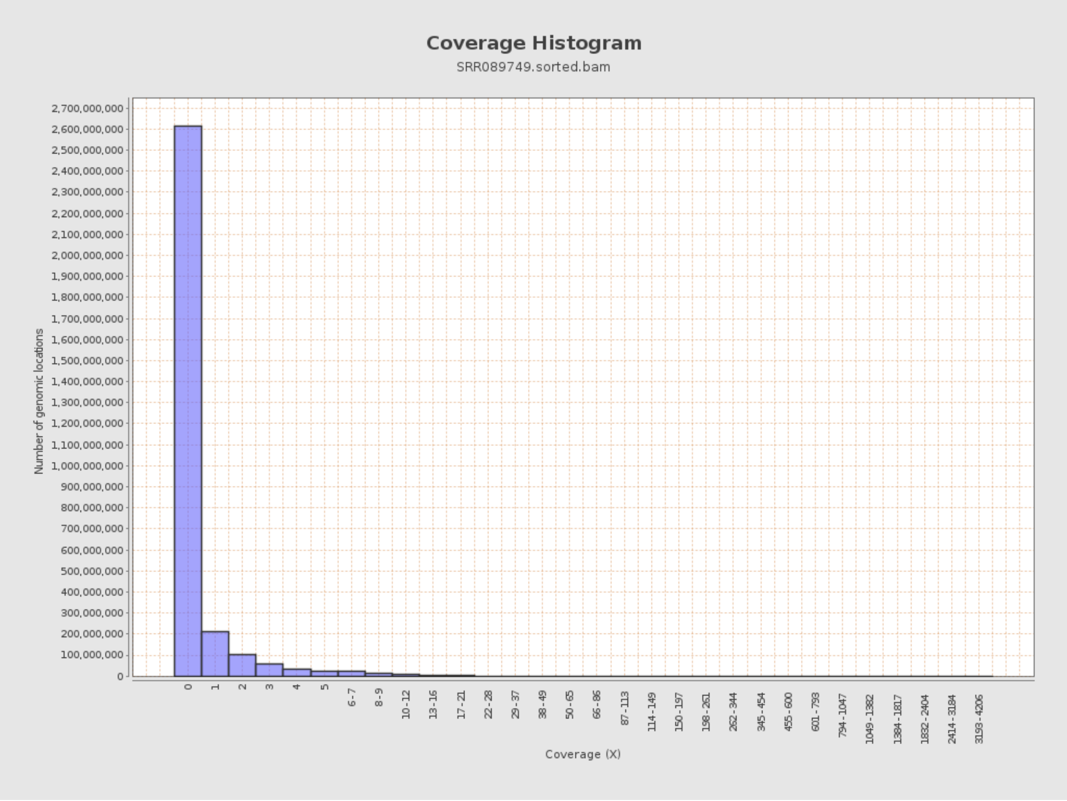
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	102481063	0.4112	3.8205
chr2	243199373	105008527	0.4318	2.6891
chr3	198022430	85739639	0.433	1.4751
chr4	191154276	80072629	0.4189	1.7211
chr5	180915260	76110798	0.4207	1.4324
chr6	171115067	68060604	0.3977	1.7461
chr7	159138663	71323431	0.4482	2.6802

chr8	146364022	63389403	0.4331	2.2055
chr9	141213431	54962880	0.3892	2.4593
chr10	135534747	65656771	0.4844	2.9121
chr11	135006516	57731338	0.4276	2.0524
chr12	133851895	66510819	0.4969	1.7458
chr13	115169878	41998347	0.3647	1.3417
chr14	107349540	43172849	0.4022	1.4864
chr15	102531392	40622204	0.3962	1.5314
chr16	90354753	41793552	0.4625	1.8527
chr17	81195210	34061432	0.4195	1.7628
chr18	78077248	34094902	0.4367	4.5758
chr19	59128983	25089379	0.4243	2.6292
chr20	63025520	28072992	0.4454	1.6987
chr21	48129895	18529108	0.385	1.8103
chr22	51304566	15441566	0.301	1.2876
chrMT	16571	62475	3.7701	4.0999
chrX	155270560	68555257	0.4415	1.6732
chrY	59373566	3392698	0.0571	1.1768

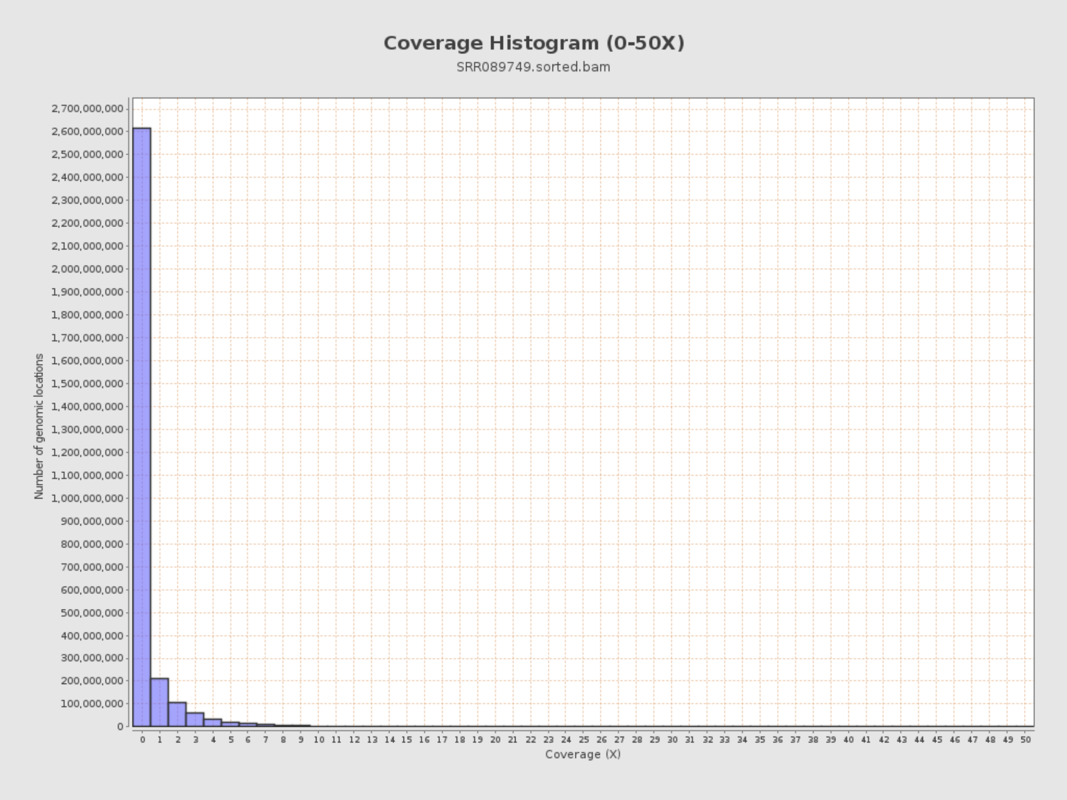
3. Results : Coverage across reference



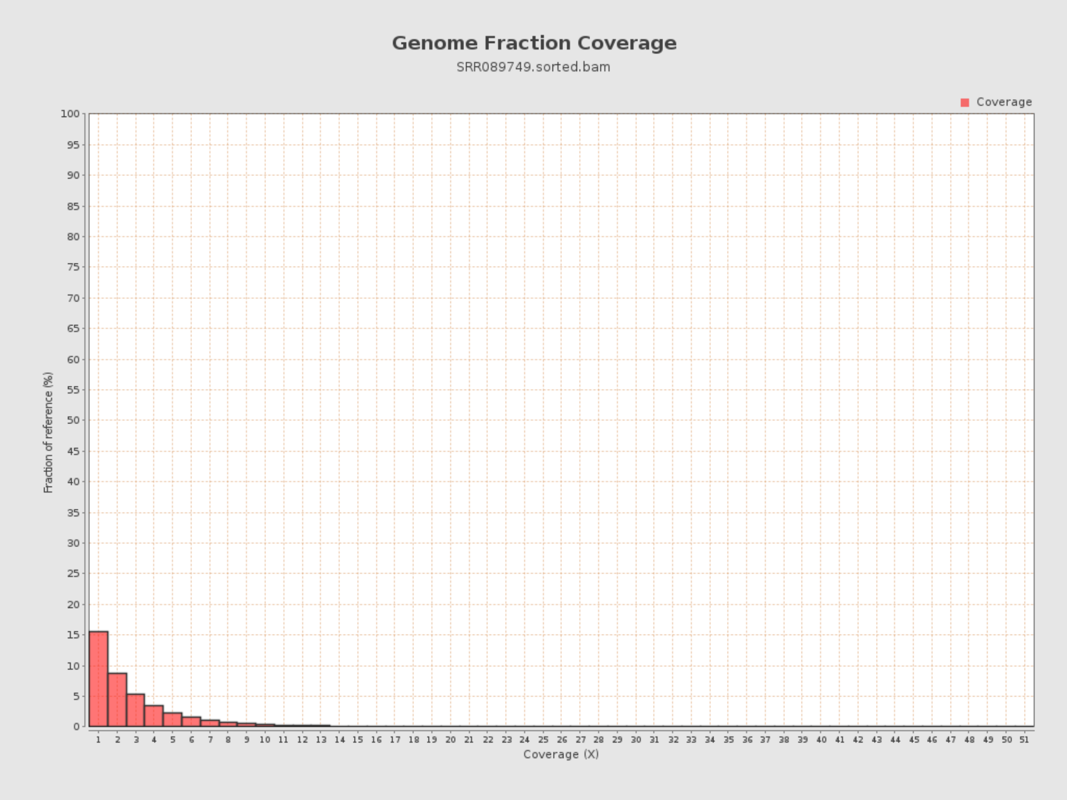
4. Results : Coverage Histogram



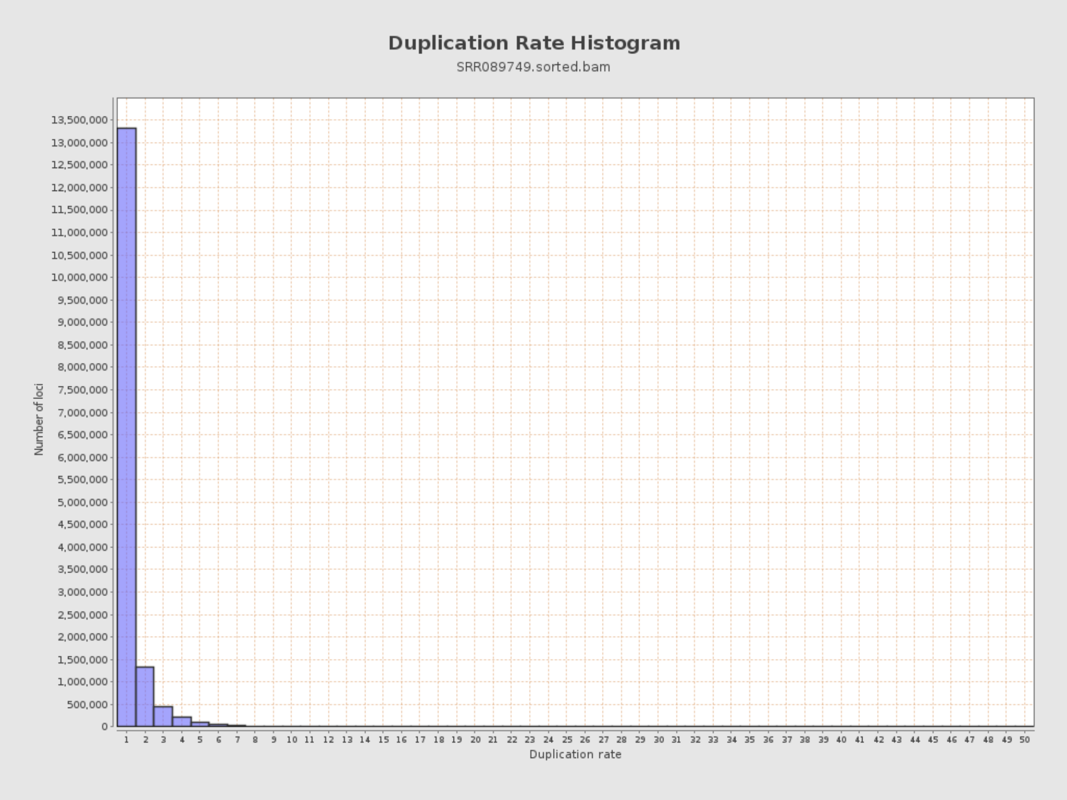
5. Results : Coverage Histogram (0-50X)



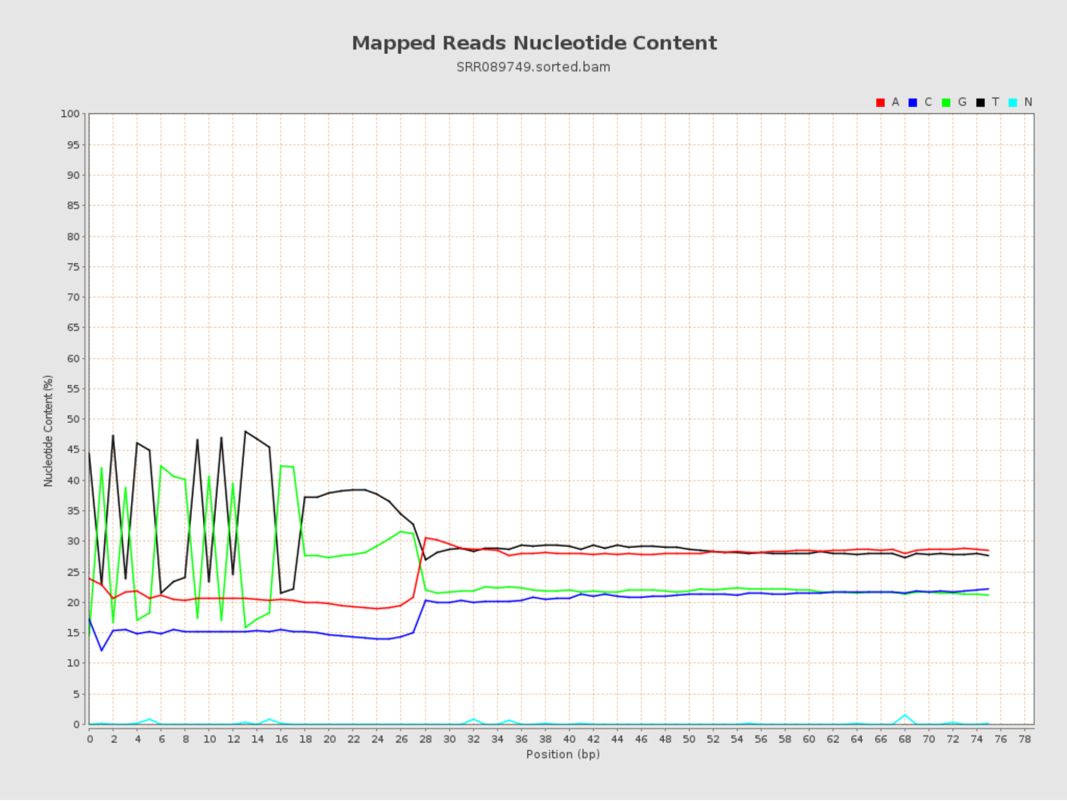
6. Results : Genome Fraction Coverage



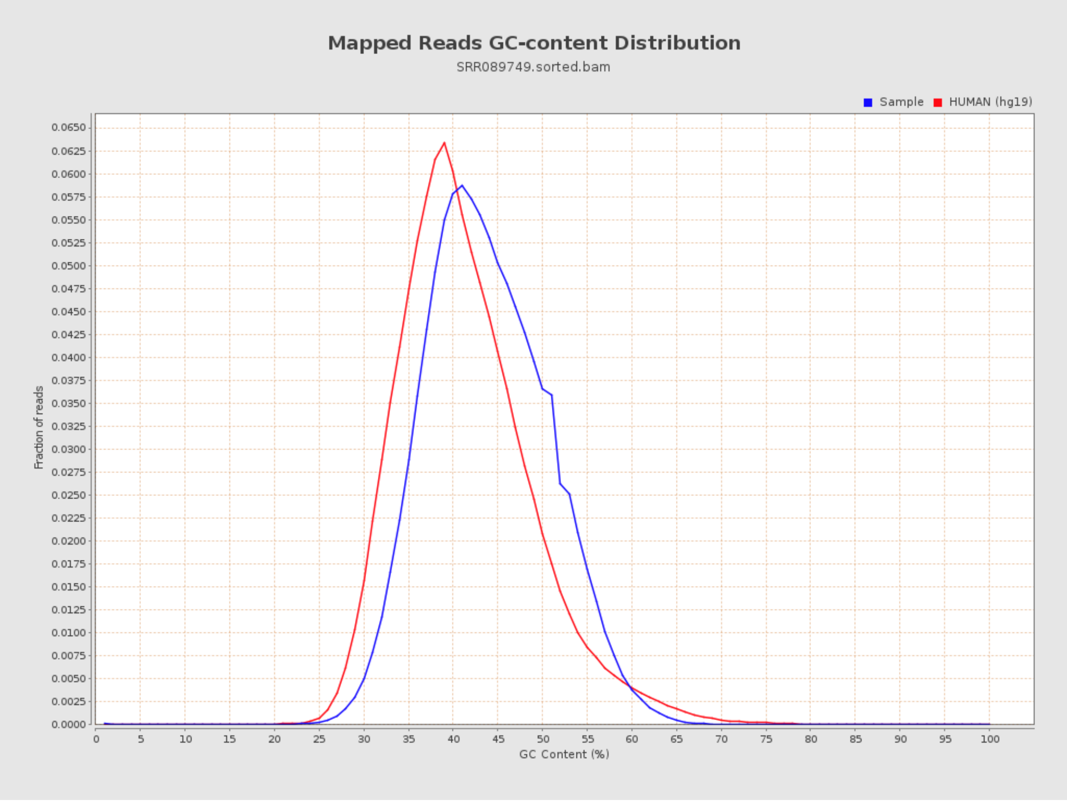
7. Results : Duplication Rate Histogram



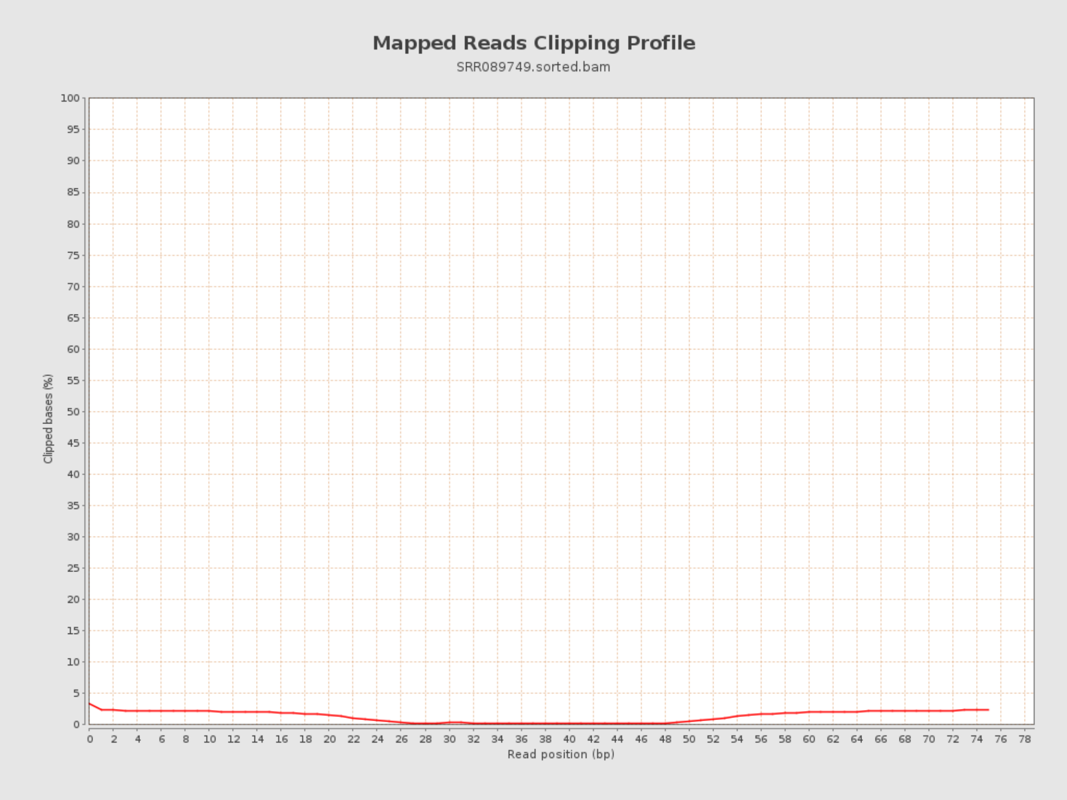
8. Results : Mapped Reads Nucleotide Content



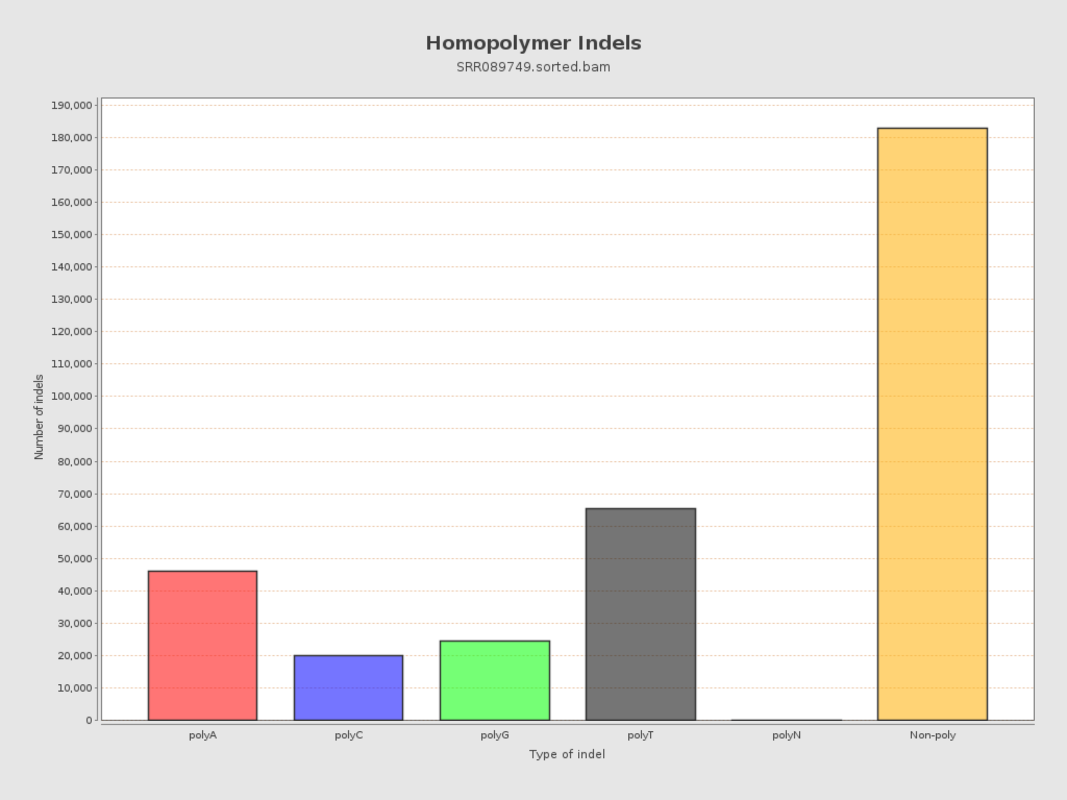
9. Results : Mapped Reads GC-content Distribution



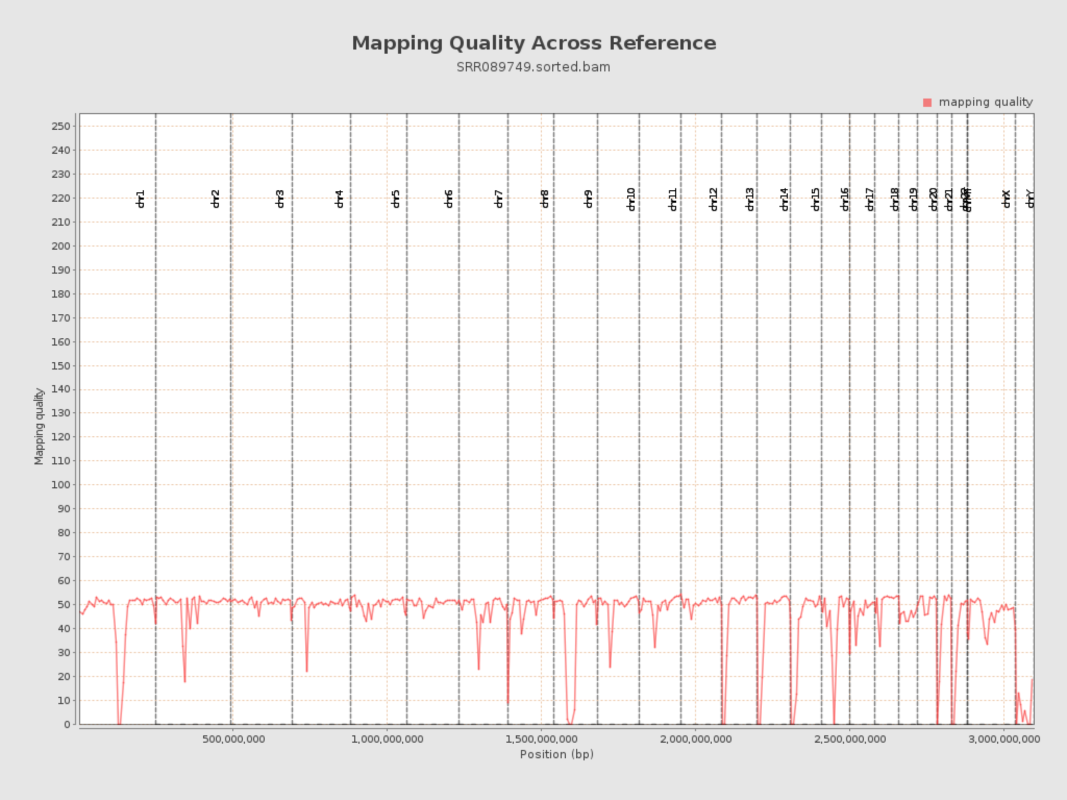
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram