Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 13:52:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089578.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_SRR089578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 13:52:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,515,399
Mapped reads	19,707,921 / 83.81%
Unmapped reads	3,807,478 / 16.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	772 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,090,368 / 8.89%
Duplication rate	7.92%
Clipped reads	2,865,122 / 12.18%

2.2. ACGT Content

Number/percentage of A's	285,830,472 / 31.1%
Number/percentage of C's	186,564,938 / 20.3%
Number/percentage of T's	252,551,205 / 27.48%
Number/percentage of G's	194,186,022 / 21.13%
Number/percentage of N's	1,155 / 0%
GC Percentage	41.42%

2.3. Coverage

Mean	0.297

Standard Deviation	1.6499

2.4. Mapping Quality

Mean Mapping Quality	43.95

2.5. Mismatches and indels

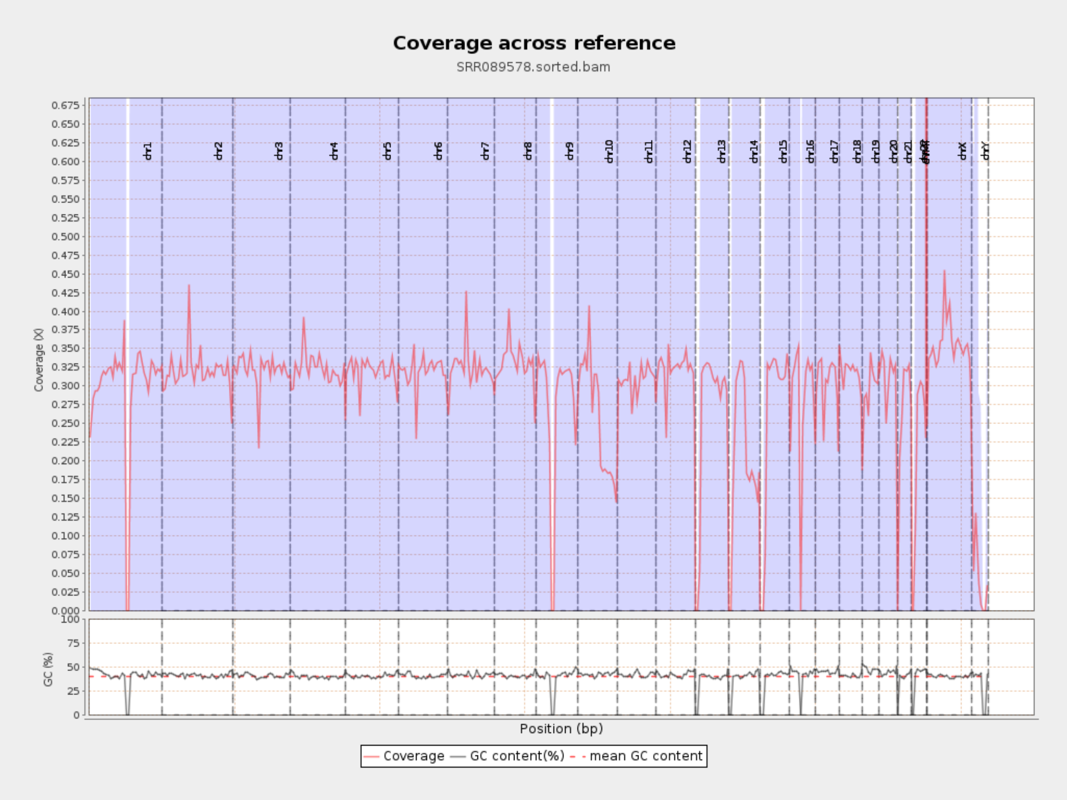
General error rate	0.46%
Mismatches	4,213,828
Insertions	40,283
Mapped reads with at least one insertion	0.2%
Deletions	127,283
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.36%

2.6. Chromosome stats

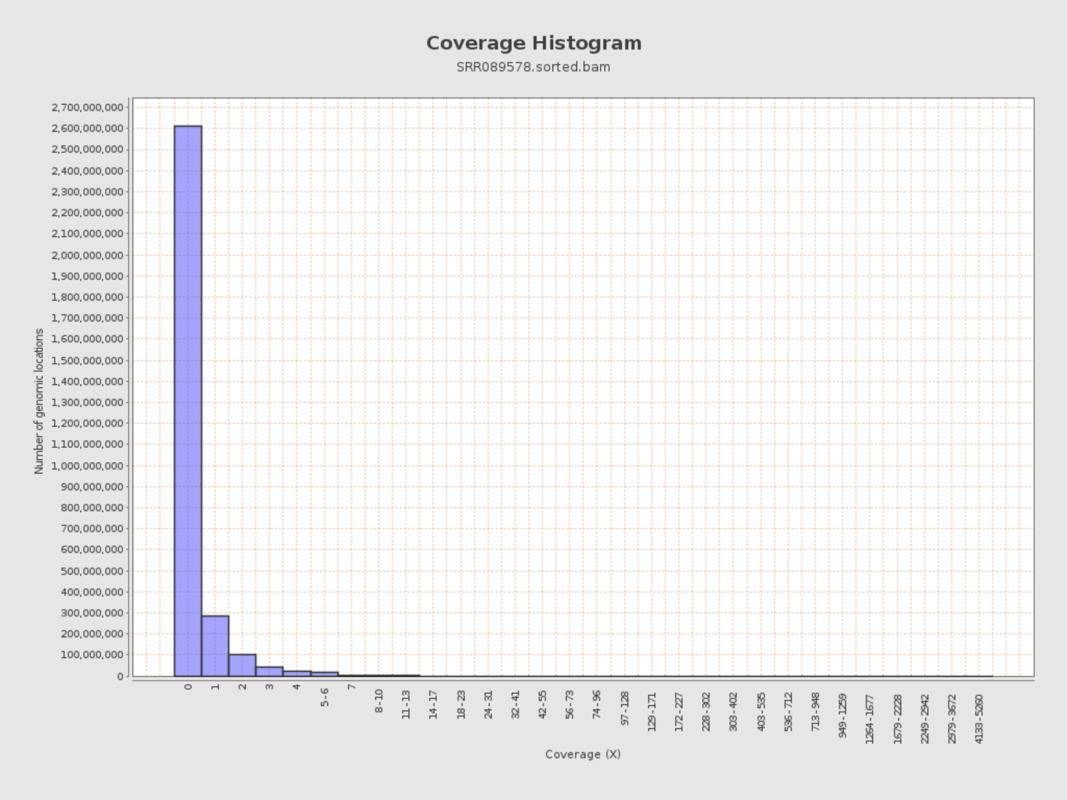
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	73924064	0.2966	2.444
chr2	243199373	78055394	0.321	2.0044
chr3	198022430	63689432	0.3216	0.9895
chr4	191154276	61652867	0.3225	1.0953
chr5	180915260	57878973	0.3199	1.0096
chr6	171115067	54732106	0.3199	1.2832
chr7	159138663	51915900	0.3262	2.3056

chr8	146364022	48468853	0.3312	3.0446
chr9	141213431	38405831	0.272	1.4843
chr10	135534747	35273672	0.2603	1.502
chr11	135006516	41440686	0.307	1.511
chr12	133851895	43058096	0.3217	1.0699
chr13	115169878	29783853	0.2586	0.8947
chr14	107349540	21794226	0.203	1.0695
chr15	102531392	26590199	0.2593	0.8905
chr16	90354753	25468248	0.2819	1.0756
chr17	81195210	24530376	0.3021	1.2017
chr18	78077248	24983023	0.32	2.4659
chr19	59128983	17558700	0.297	2.2341
chr20	63025520	19527172	0.3098	1.0765
chr21	48129895	12387608	0.2574	1.1239
chr22	51304566	10333471	0.2014	0.786
chrMT	16571	171091	10.3247	9.8697
chrX	155270560	55008799	0.3543	1.3859
chrY	59373566	2690322	0.0453	0.6856

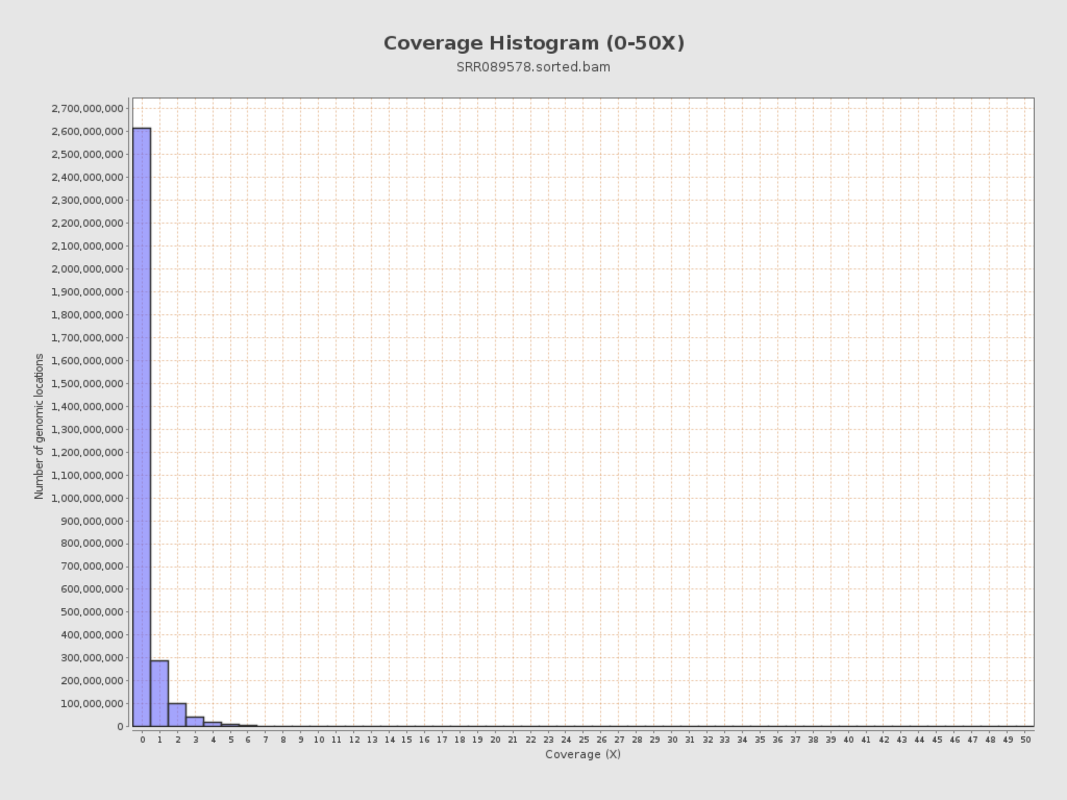
3. Results : Coverage across reference



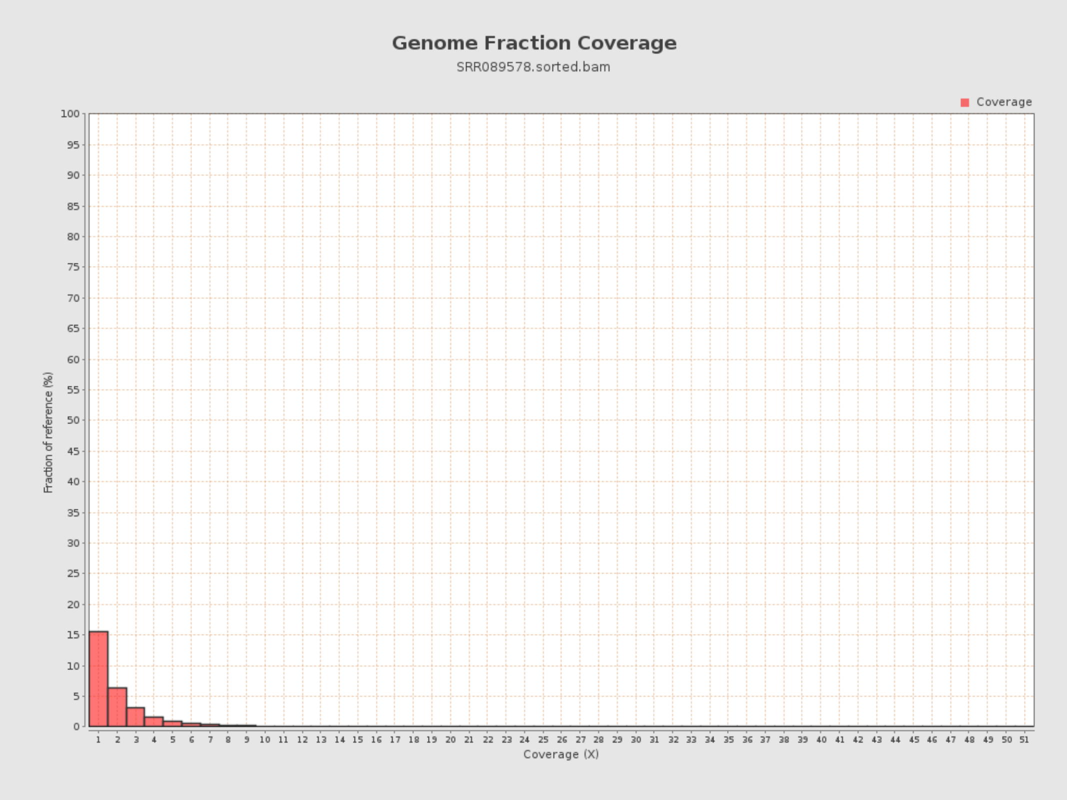
4. Results : Coverage Histogram



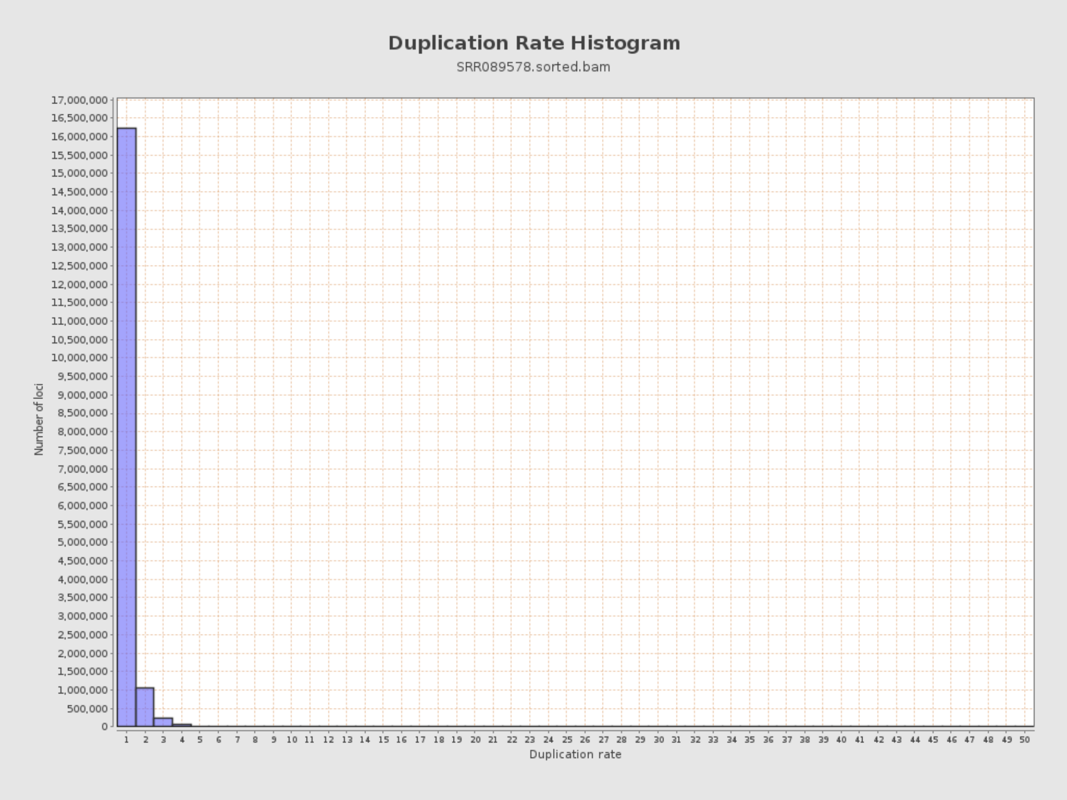
5. Results : Coverage Histogram (0-50X)



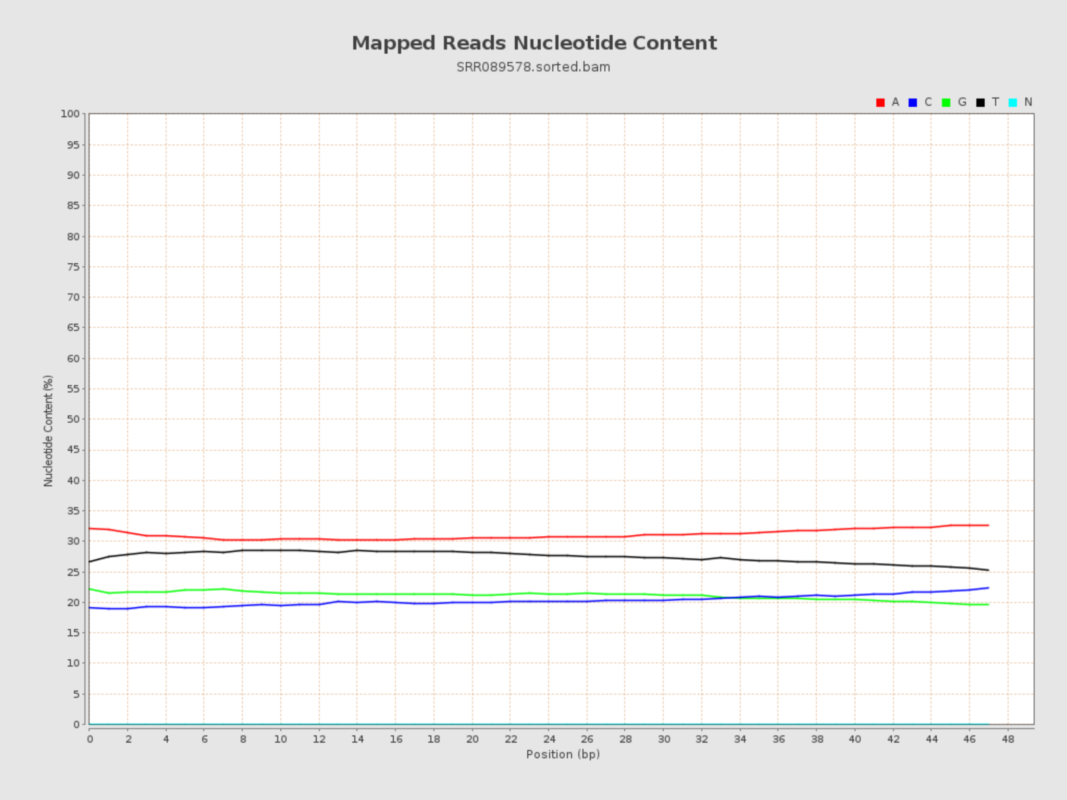
6. Results : Genome Fraction Coverage



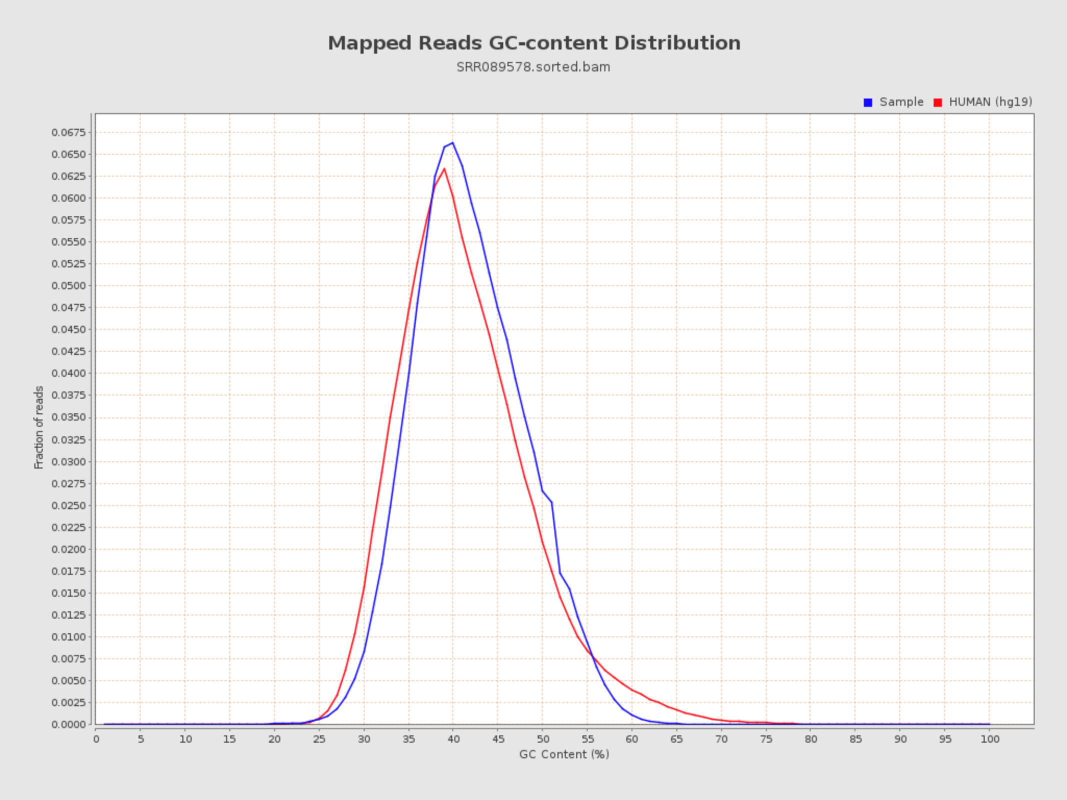
7. Results : Duplication Rate Histogram



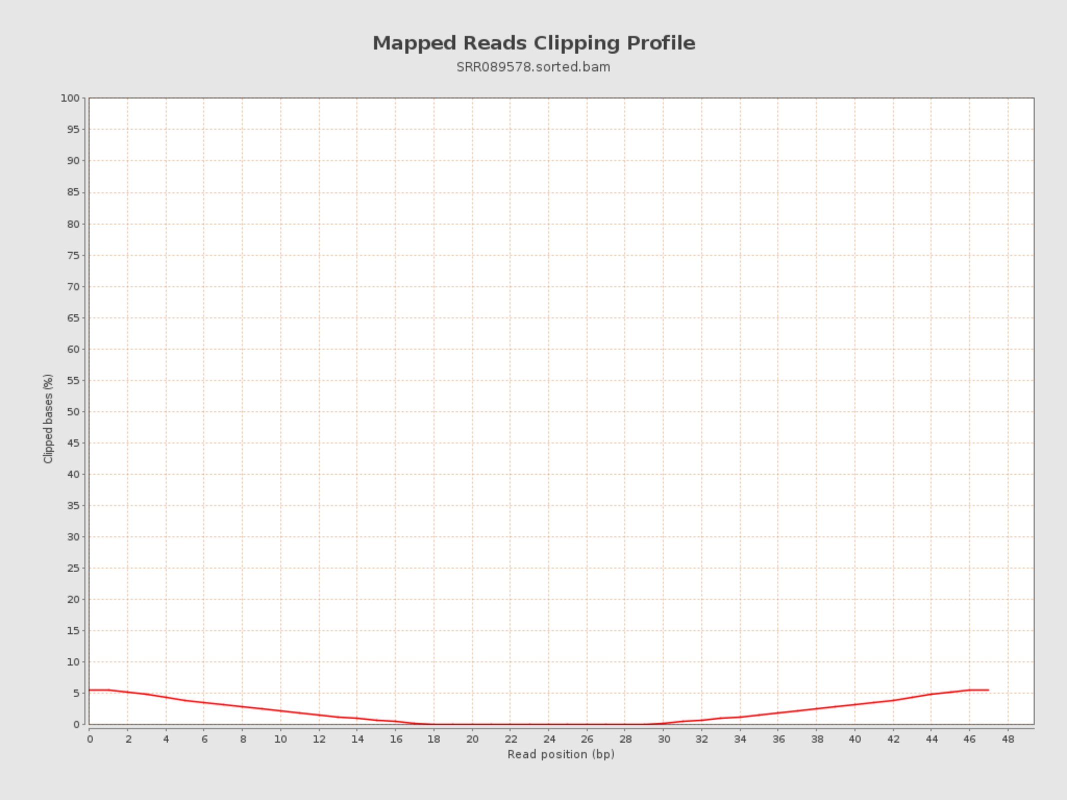
8. Results : Mapped Reads Nucleotide Content



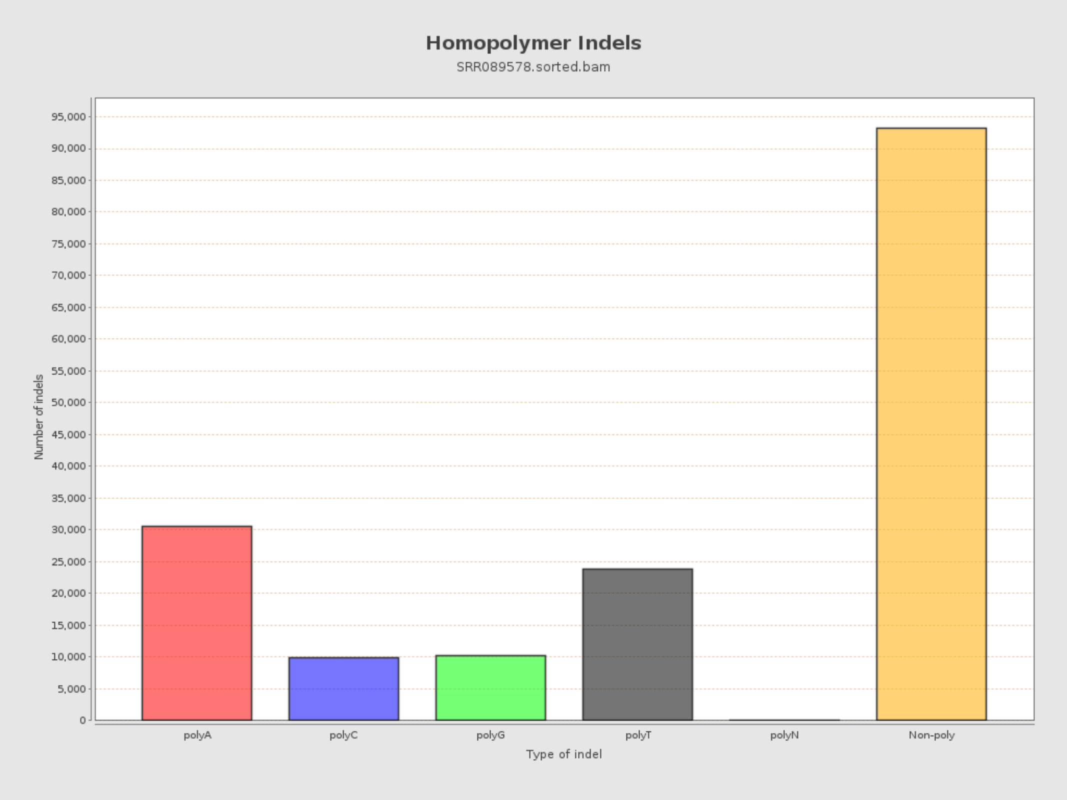
9. Results : Mapped Reads GC-content Distribution



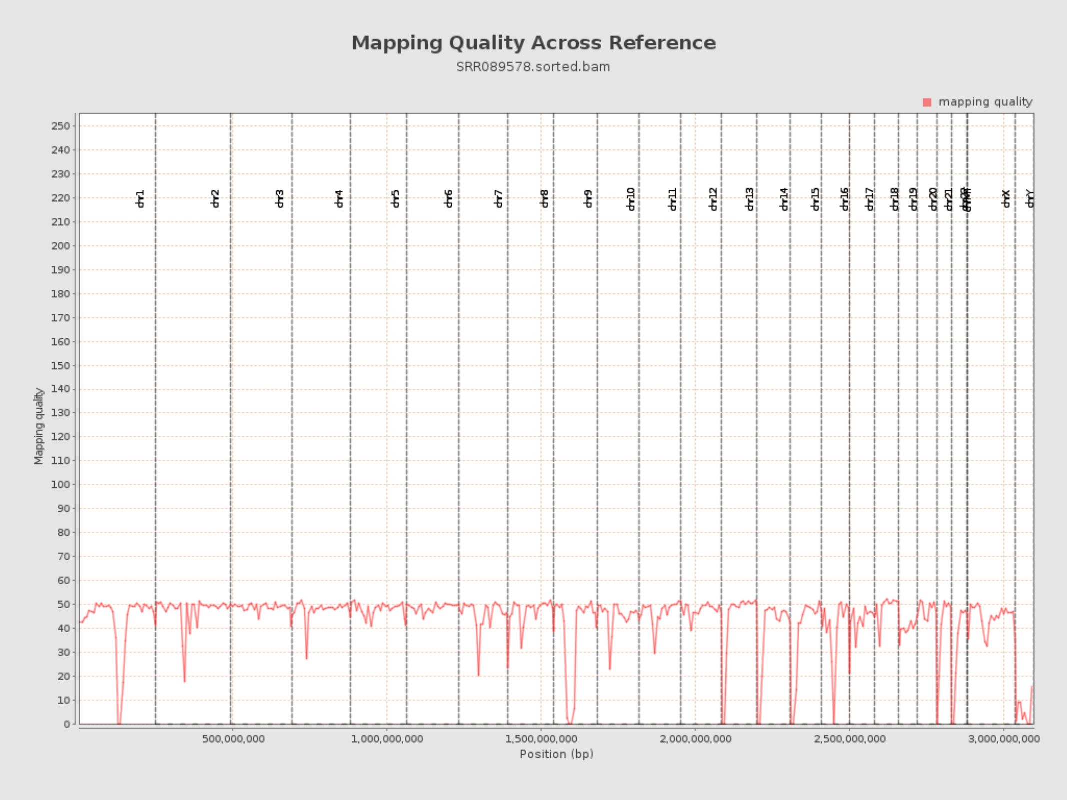
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram