Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:04:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089602.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_SRR089602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:04:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,562,002
Mapped reads	6,145,659 / 64.27%
Unmapped reads	3,416,343 / 35.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	186 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,811,289 / 18.94%
Duplication rate	22.69%
Clipped reads	958,330 / 10.02%

2.2. ACGT Content

Number/percentage of A's	92,480,738 / 32.3%
Number/percentage of C's	55,368,147 / 19.34%
Number/percentage of T's	73,858,388 / 25.8%
Number/percentage of G's	64,385,474 / 22.49%
Number/percentage of N's	209,891 / 0.07%
GC Percentage	41.83%

2.3. Coverage

Mean	0.0925

Standard Deviation	0.843

2.4. Mapping Quality

Mean Mapping Quality	42.11

2.5. Mismatches and indels

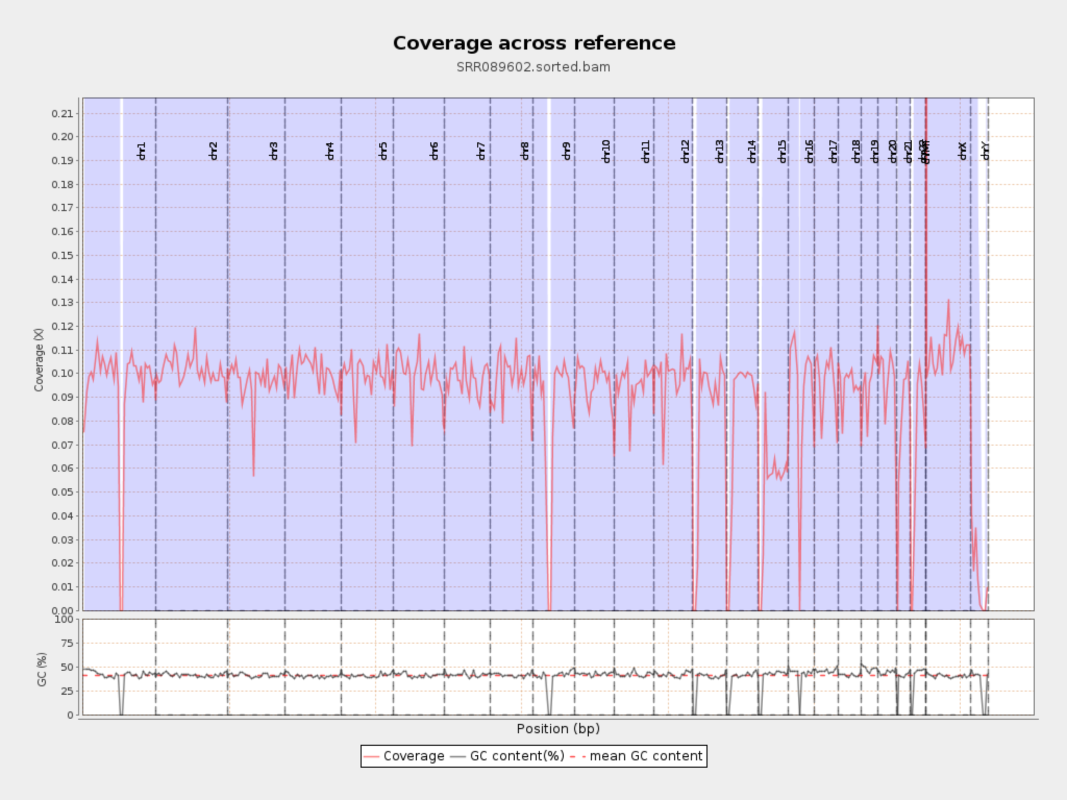
General error rate	1.05%
Mismatches	2,988,384
Insertions	15,808
Mapped reads with at least one insertion	0.26%
Deletions	38,320
Mapped reads with at least one deletion	0.62%
Homopolymer indels	40.61%

2.6. Chromosome stats

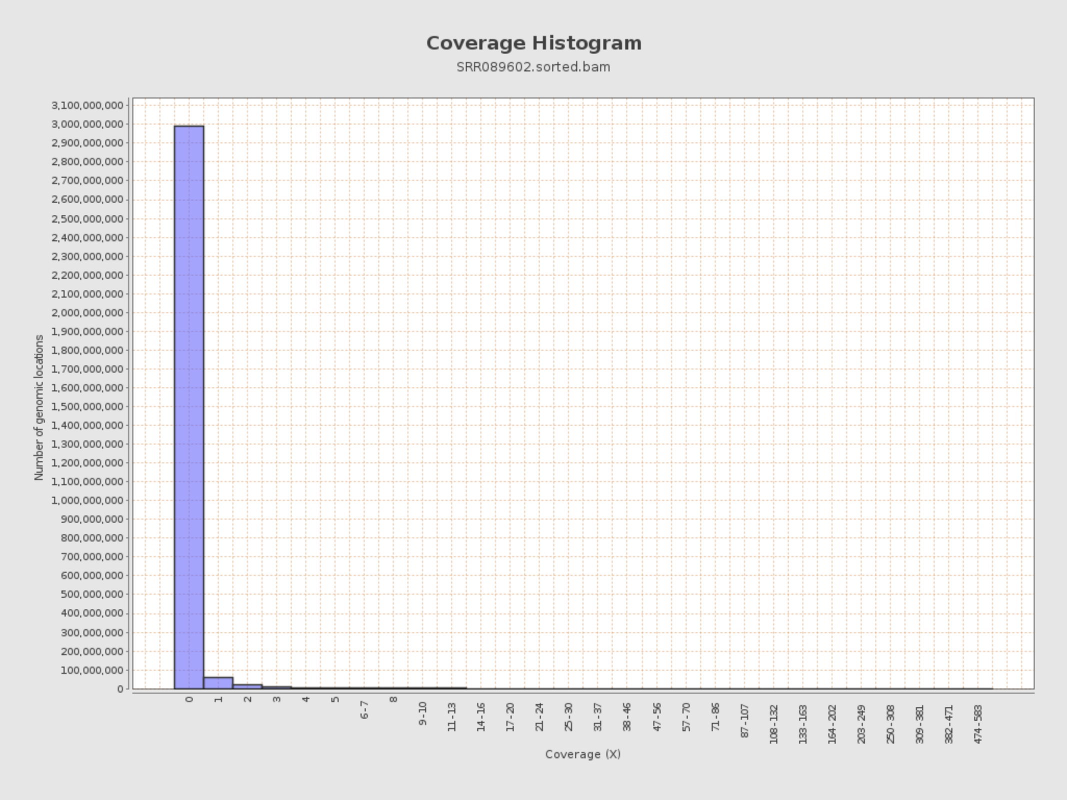
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23437098	0.094	0.891
chr2	243199373	24775770	0.1019	0.9544
chr3	198022430	19162248	0.0968	0.8315
chr4	191154276	19278161	0.1009	0.8741
chr5	180915260	17983838	0.0994	0.8378
chr6	171115067	17010255	0.0994	0.8825
chr7	159138663	15539262	0.0976	0.874

chr8	146364022	14453742	0.0988	0.9125
chr9	141213431	11832190	0.0838	0.773
chr10	135534747	13126187	0.0968	0.84
chr11	135006516	12867485	0.0953	0.8731
chr12	133851895	13280363	0.0992	0.8414
chr13	115169878	9286433	0.0806	0.76
chr14	107349540	8769316	0.0817	0.8067
chr15	102531392	5131016	0.05	0.5536
chr16	90354753	8146691	0.0902	0.797
chr17	81195210	7936212	0.0977	0.8089
chr18	78077248	7429252	0.0952	0.8758
chr19	59128983	5687662	0.0962	0.8256
chr20	63025520	6187670	0.0982	0.8574
chr21	48129895	3734621	0.0776	0.7622
chr22	51304566	3338480	0.0651	0.659
chrMT	16571	101888	6.1486	11.9127
chrX	155270560	17060391	0.1099	0.925
chrY	59373566	802468	0.0135	0.2837

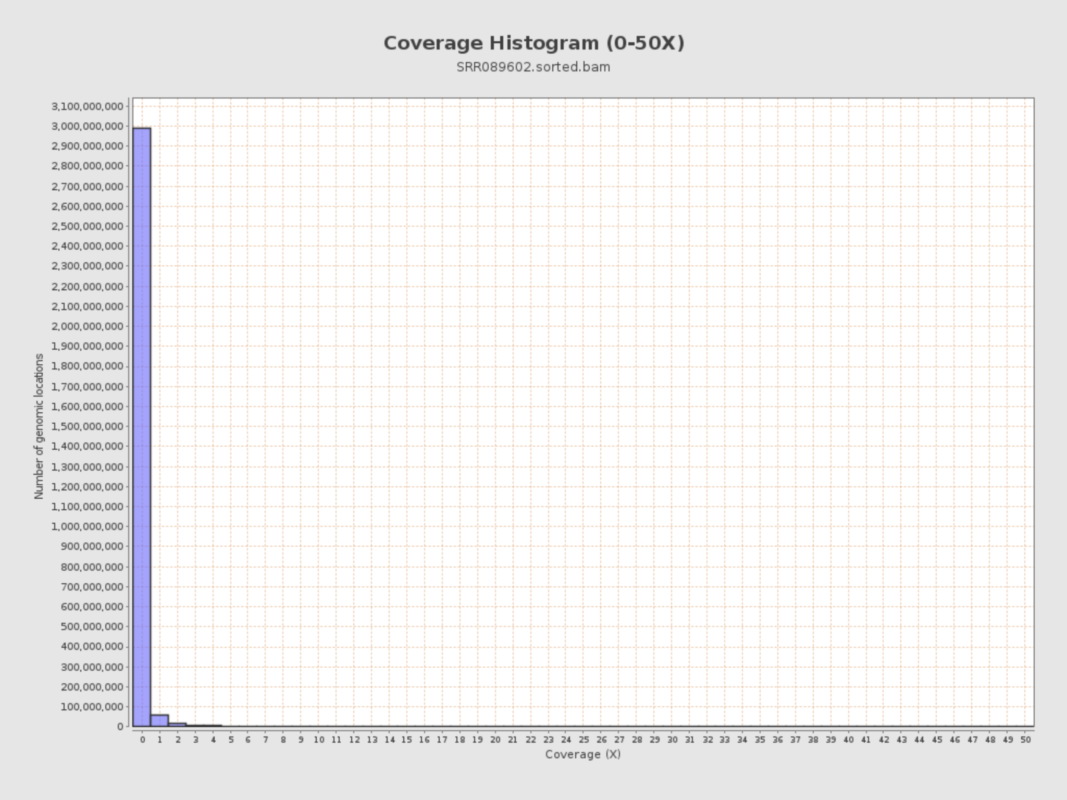
3. Results : Coverage across reference



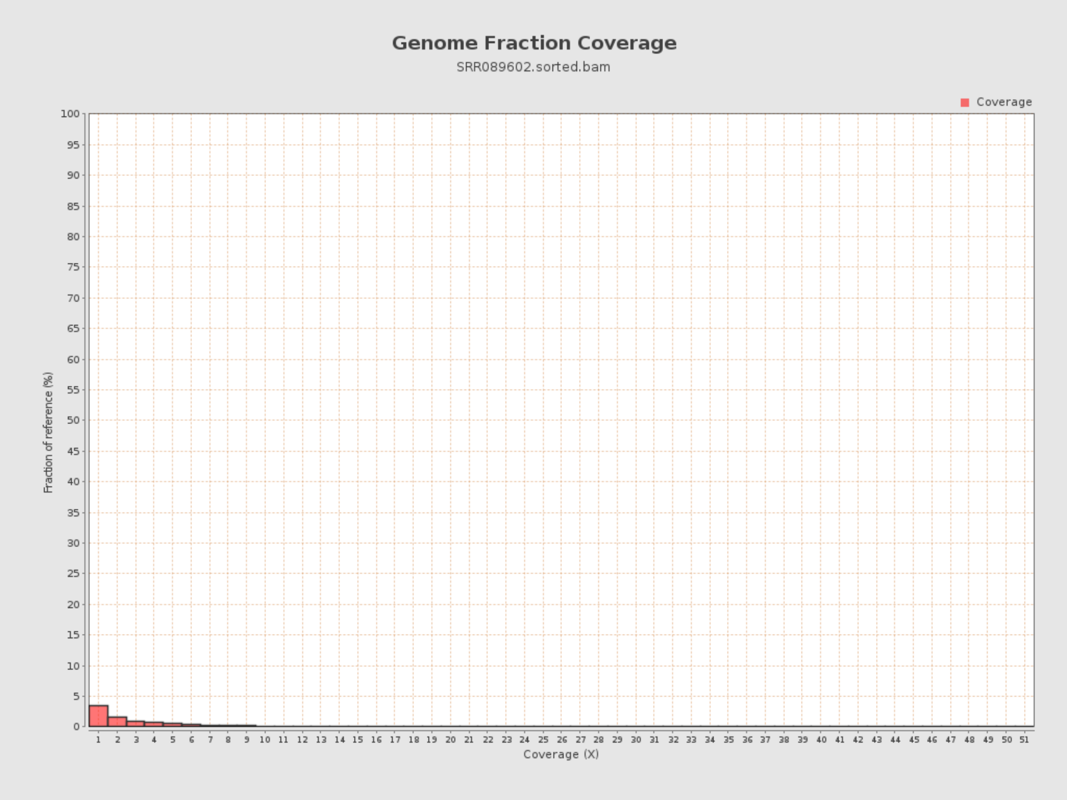
4. Results : Coverage Histogram



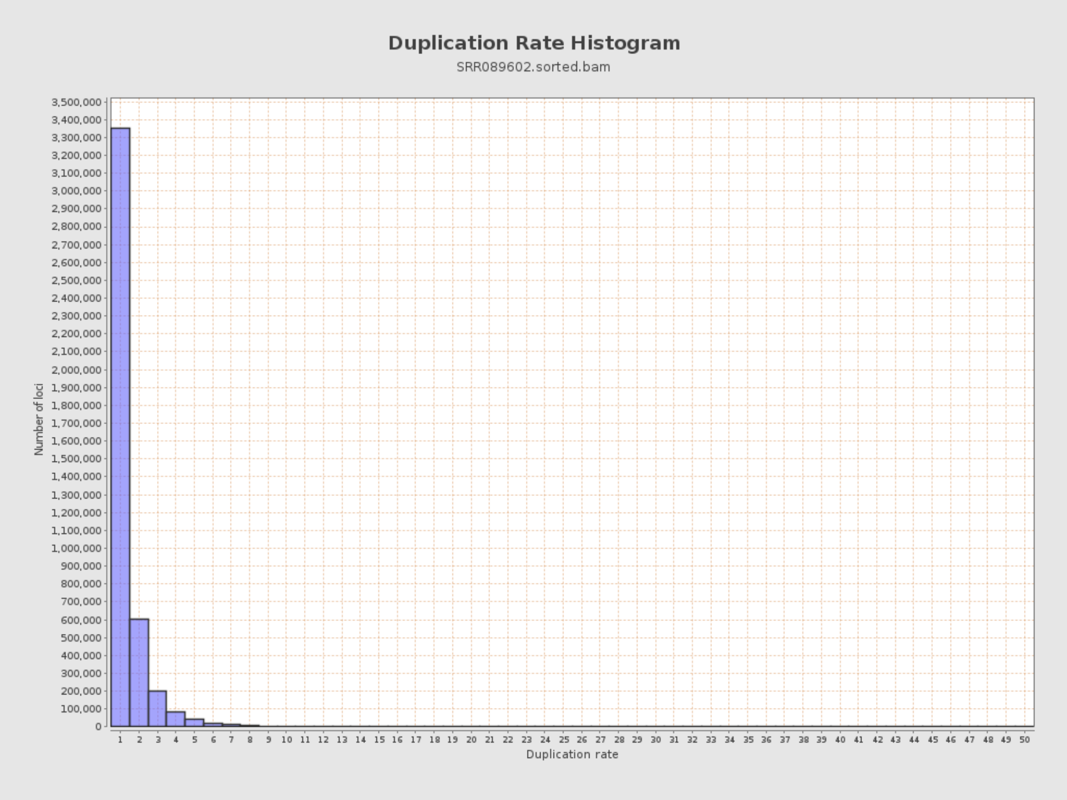
5. Results : Coverage Histogram (0-50X)



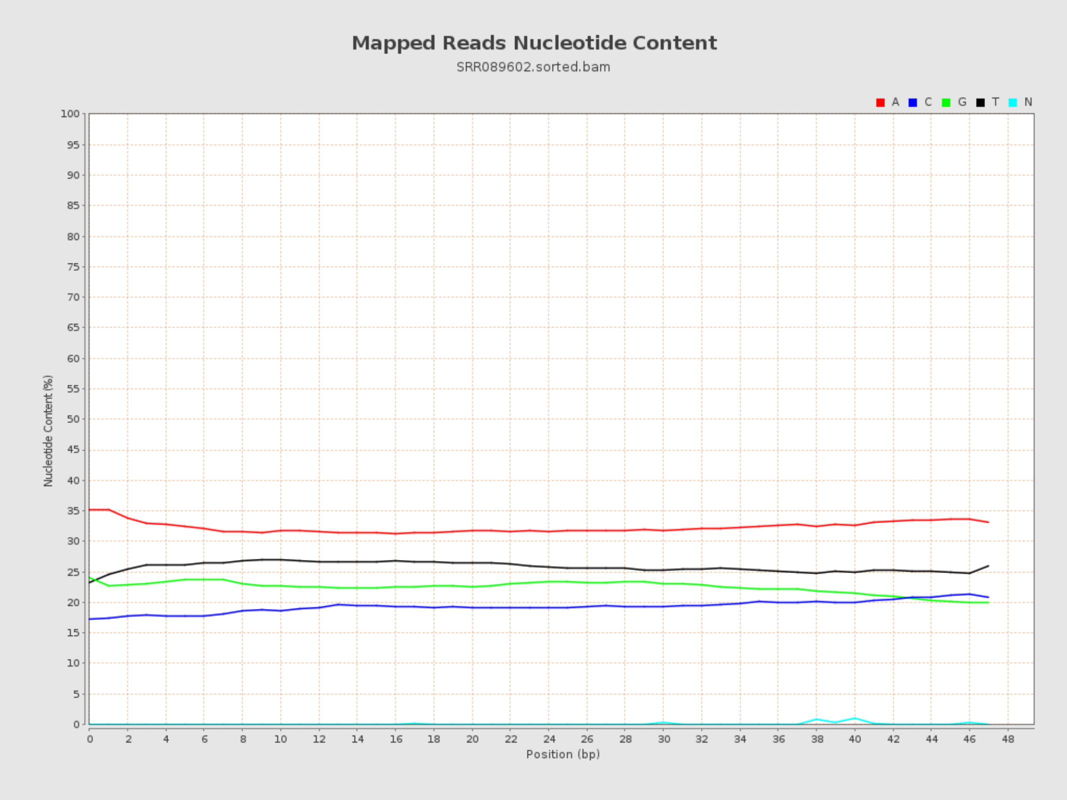
6. Results : Genome Fraction Coverage



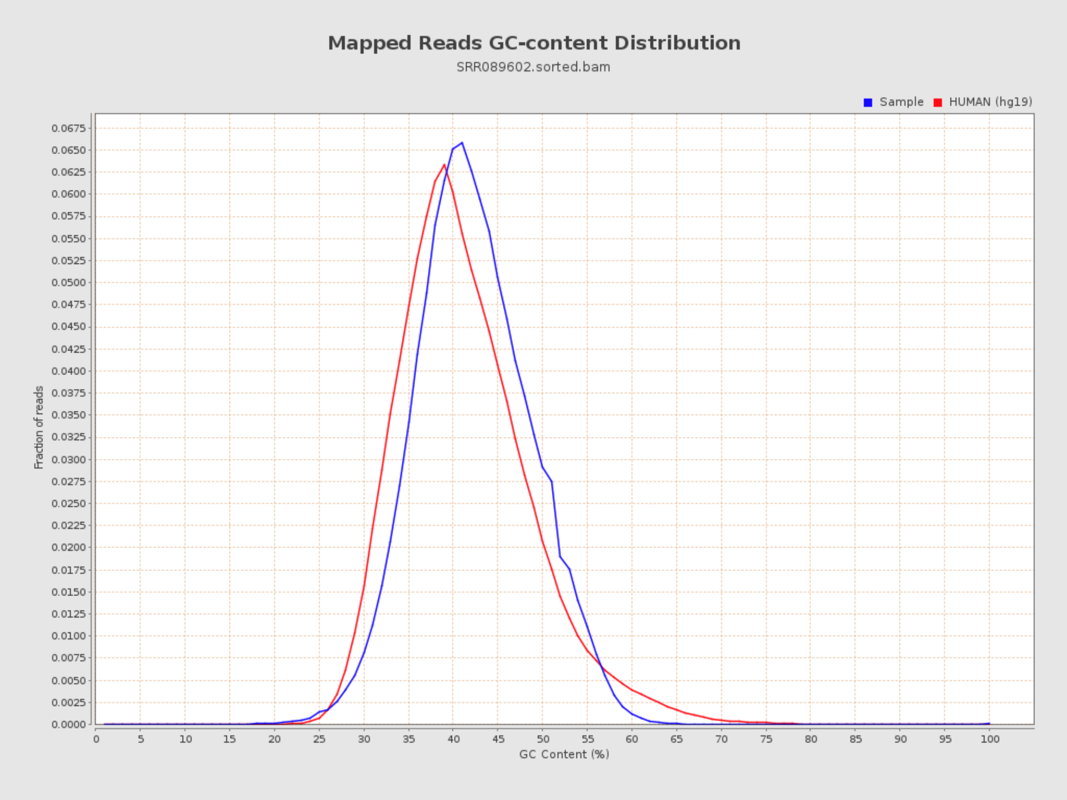
7. Results : Duplication Rate Histogram



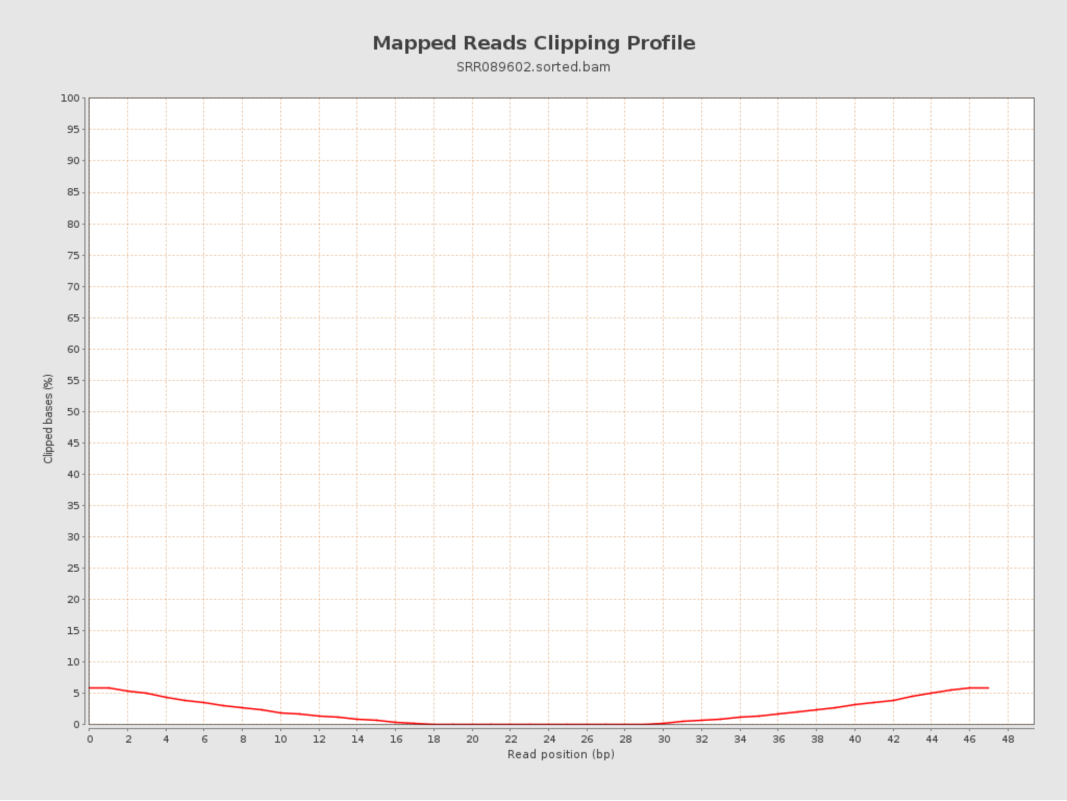
8. Results : Mapped Reads Nucleotide Content



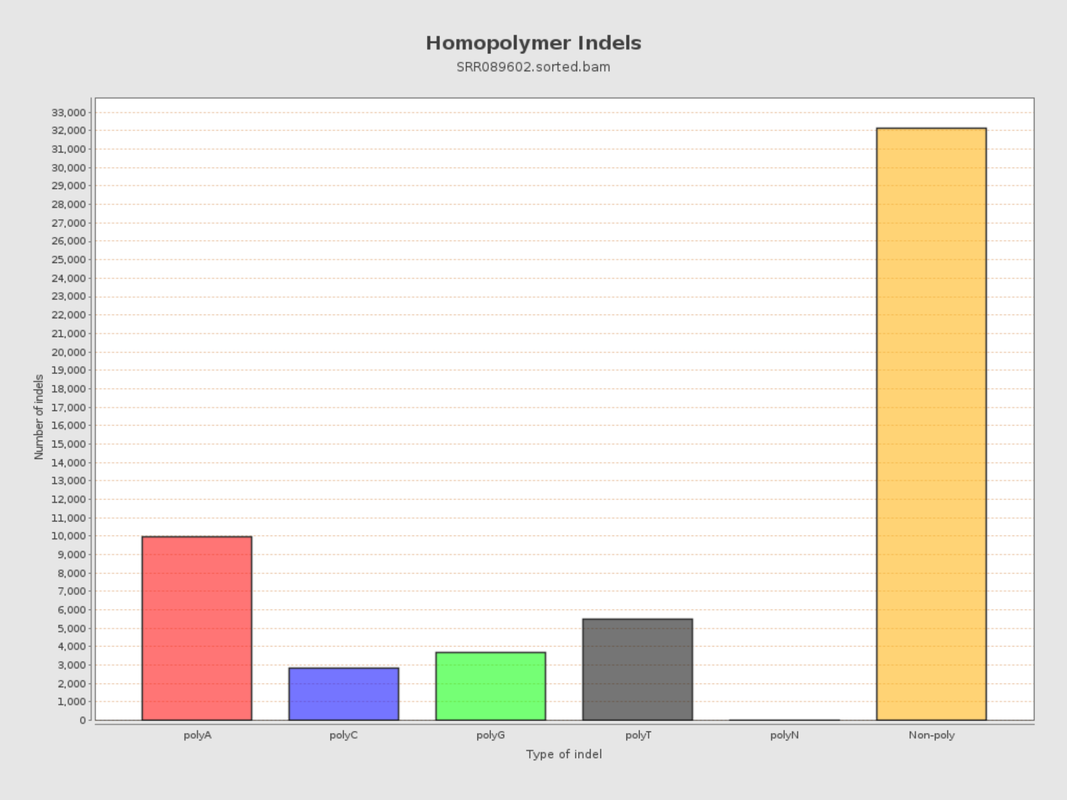
9. Results : Mapped Reads GC-content Distribution



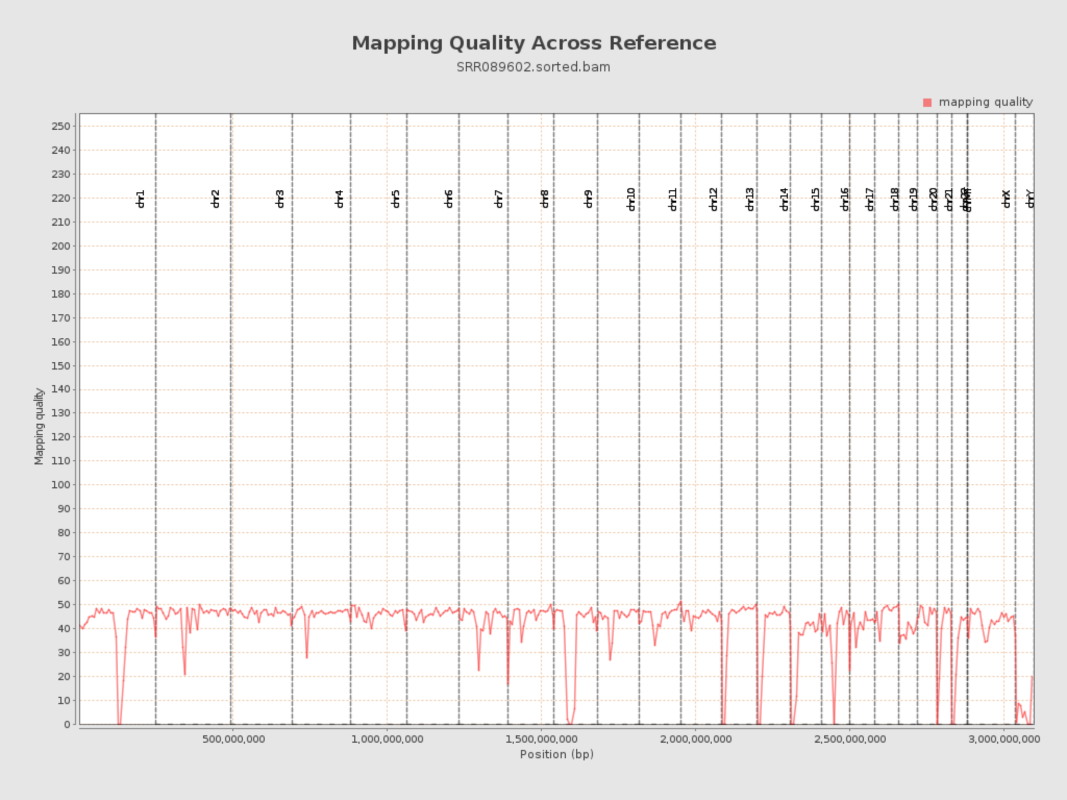
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram