Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 15:03:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089592.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_SRR089592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 15:03:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,328,769
Mapped reads	6,848,098 / 66.3%
Unmapped reads	3,480,671 / 33.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	257 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	360,115 / 3.49%
Duplication rate	4.2%
Clipped reads	715,906 / 6.93%

2.2. ACGT Content

Number/percentage of A's	93,793,547 / 29.13%
Number/percentage of C's	66,011,019 / 20.5%
Number/percentage of T's	92,363,202 / 28.69%
Number/percentage of G's	69,363,507 / 21.55%
Number/percentage of N's	407,701 / 0.13%
GC Percentage	42.05%

2.3. Coverage

Mean	0.104

Standard Deviation	0.5796

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

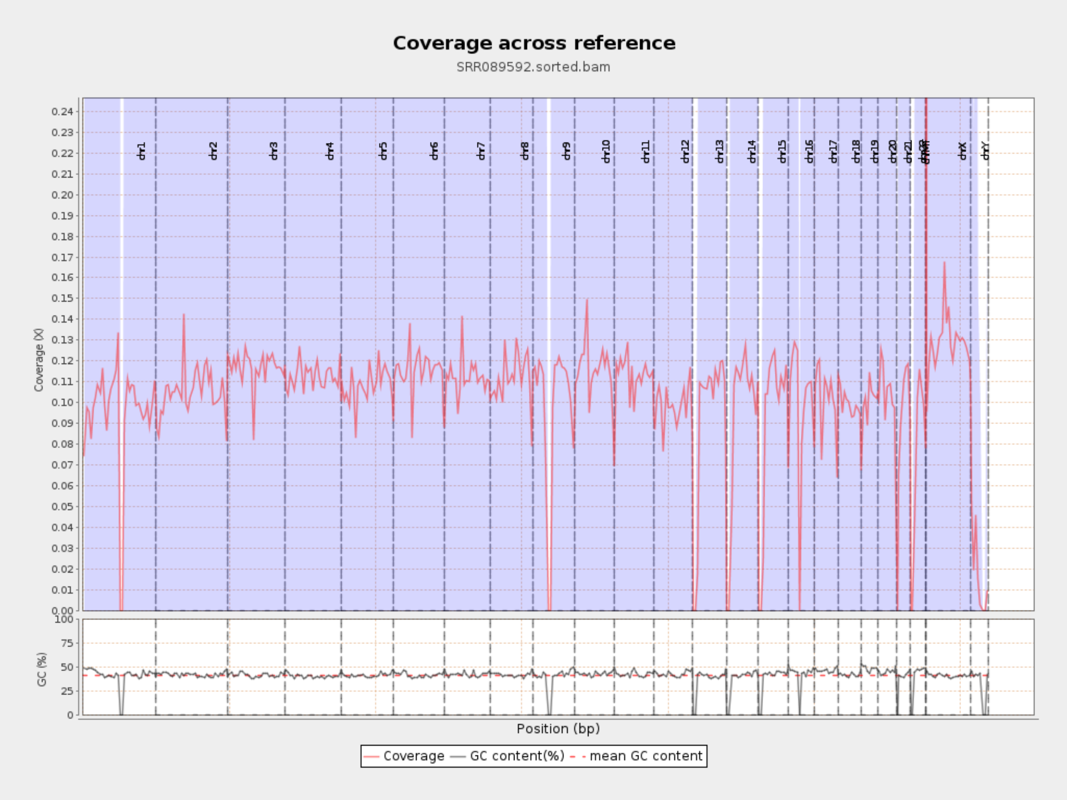
General error rate	0.97%
Mismatches	3,090,661
Insertions	15,039
Mapped reads with at least one insertion	0.22%
Deletions	42,252
Mapped reads with at least one deletion	0.62%
Homopolymer indels	43.62%

2.6. Chromosome stats

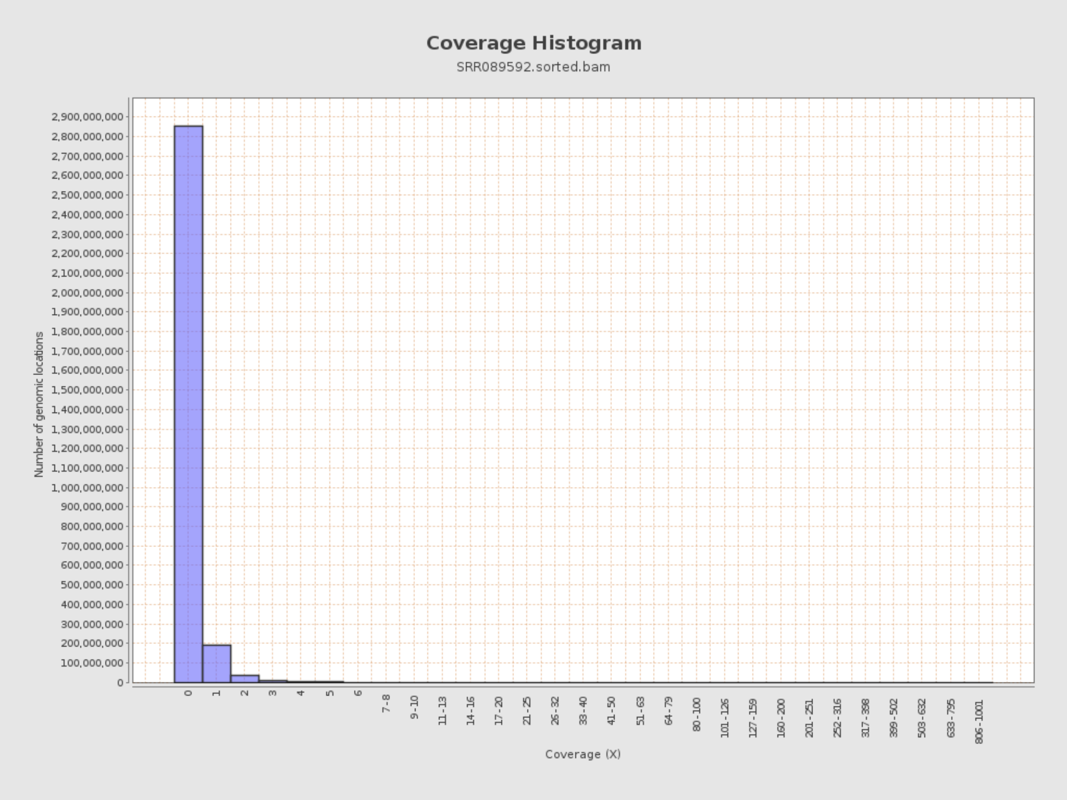
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23683292	0.095	0.8635
chr2	243199373	25662099	0.1055	0.6557
chr3	198022430	23162315	0.117	0.4365
chr4	191154276	21595850	0.113	0.4546
chr5	180915260	19585132	0.1083	0.4245
chr6	171115067	19812996	0.1158	0.512
chr7	159138663	17819202	0.112	0.7413

chr8	146364022	16352456	0.1117	0.7033
chr9	141213431	13734042	0.0973	0.5766
chr10	135534747	15807750	0.1166	0.6453
chr11	135006516	15246154	0.1129	0.5624
chr12	133851895	13216382	0.0987	0.4187
chr13	115169878	10607055	0.0921	0.3868
chr14	107349540	9986541	0.093	0.4468
chr15	102531392	9168724	0.0894	0.3822
chr16	90354753	8729576	0.0966	0.4382
chr17	81195210	8351267	0.1029	0.467
chr18	78077248	7784151	0.0997	0.9
chr19	59128983	5949428	0.1006	0.7476
chr20	63025520	6585300	0.1045	0.4495
chr21	48129895	4341141	0.0902	0.4445
chr22	51304566	3729491	0.0727	0.3466
chrMT	16571	82372	4.9709	4.192
chrX	155270560	20024425	0.129	0.5524
chrY	59373566	984714	0.0166	0.2276

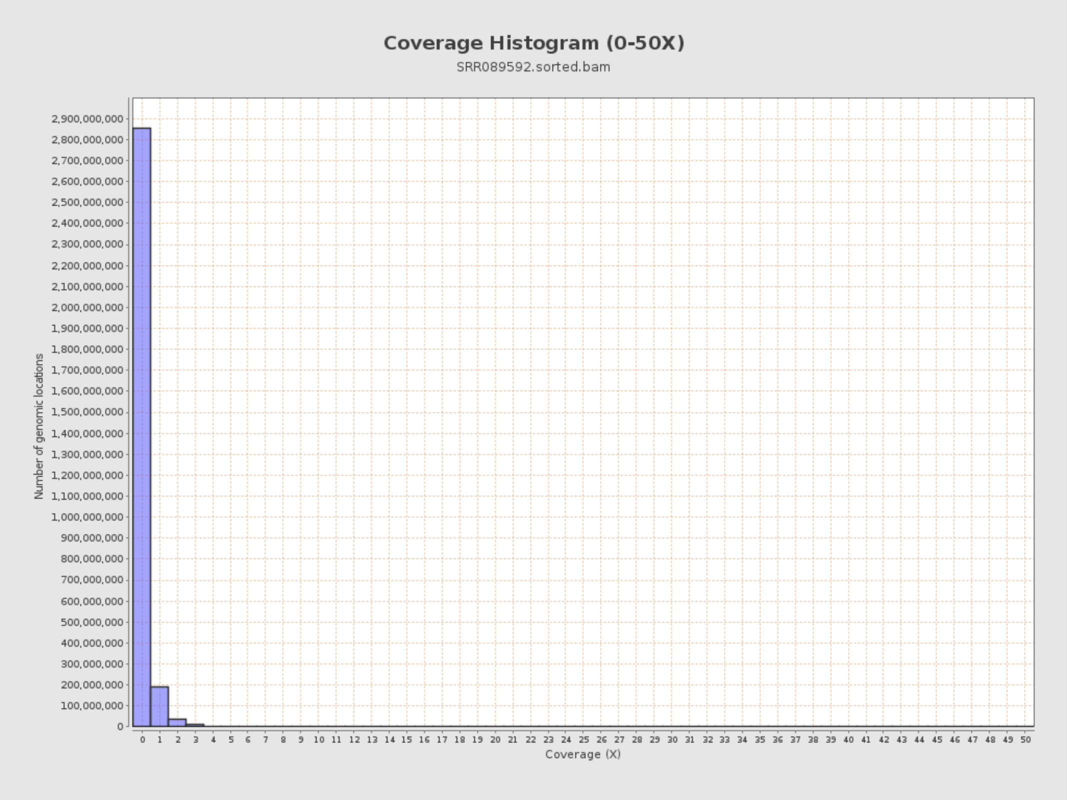
3. Results : Coverage across reference



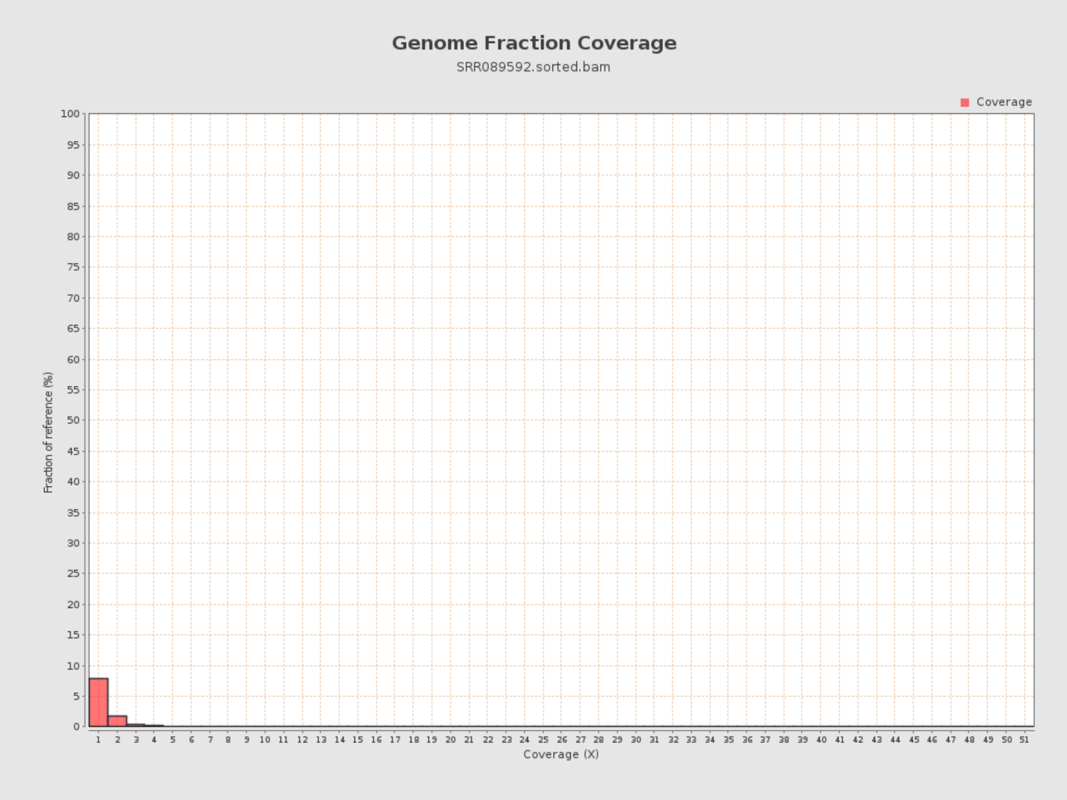
4. Results : Coverage Histogram



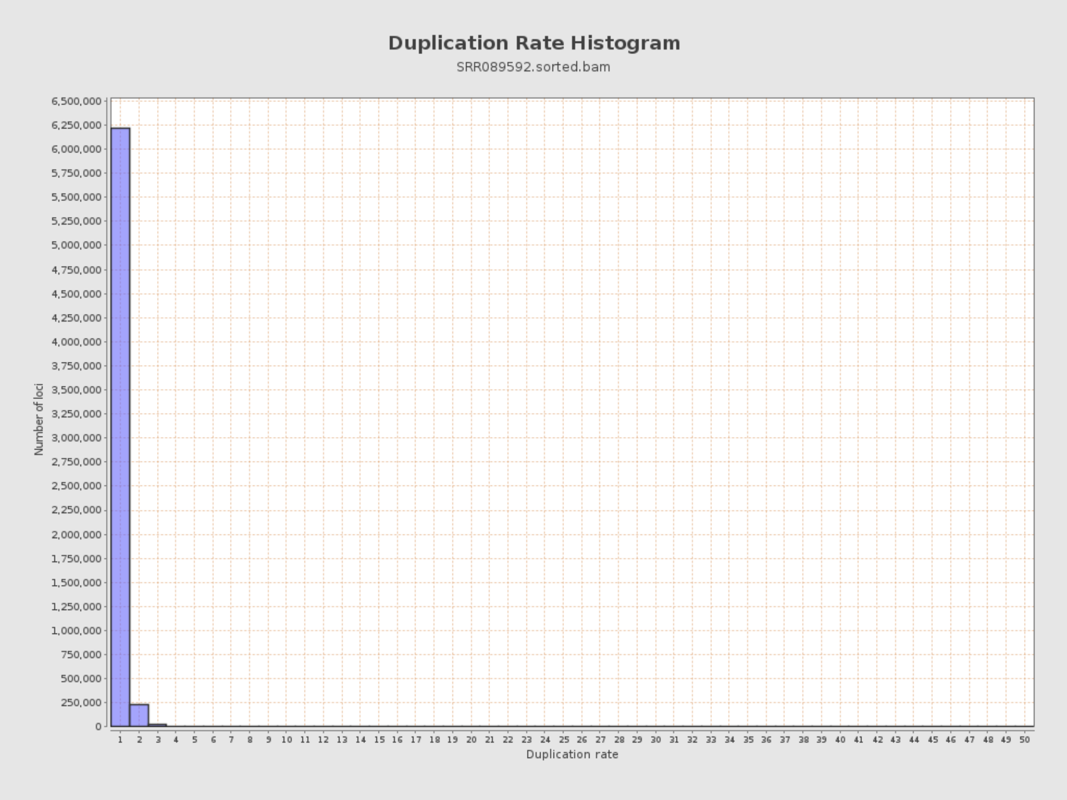
5. Results : Coverage Histogram (0-50X)



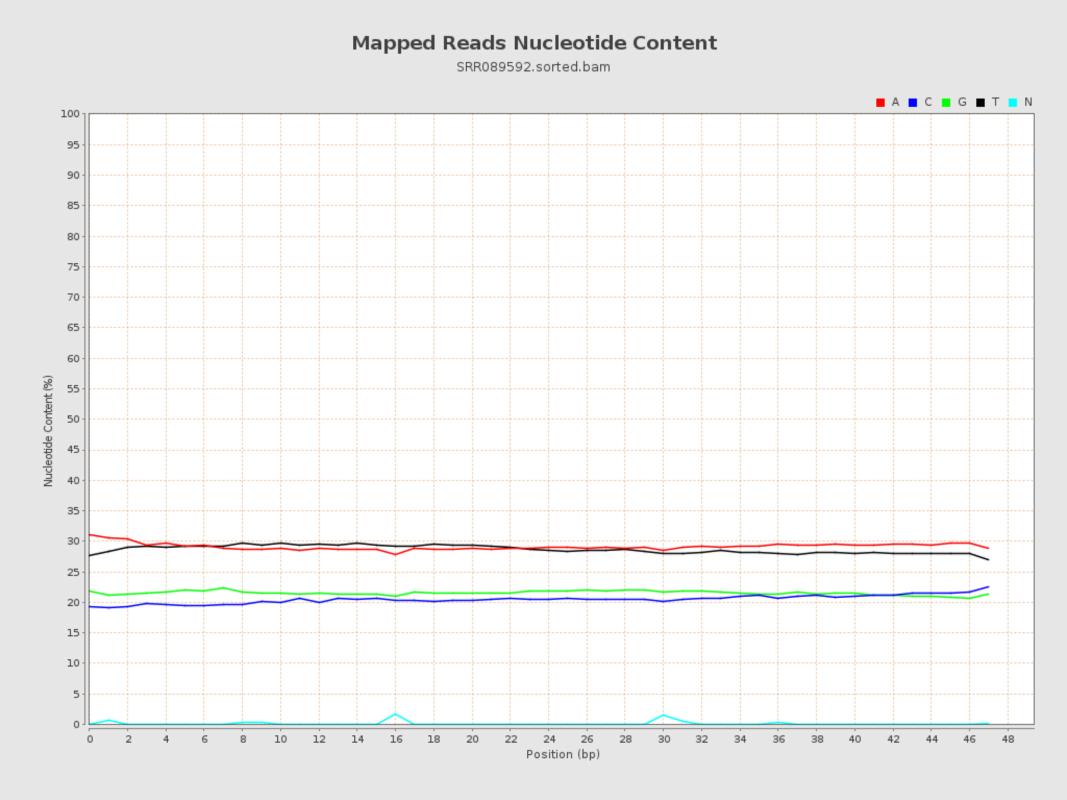
6. Results : Genome Fraction Coverage



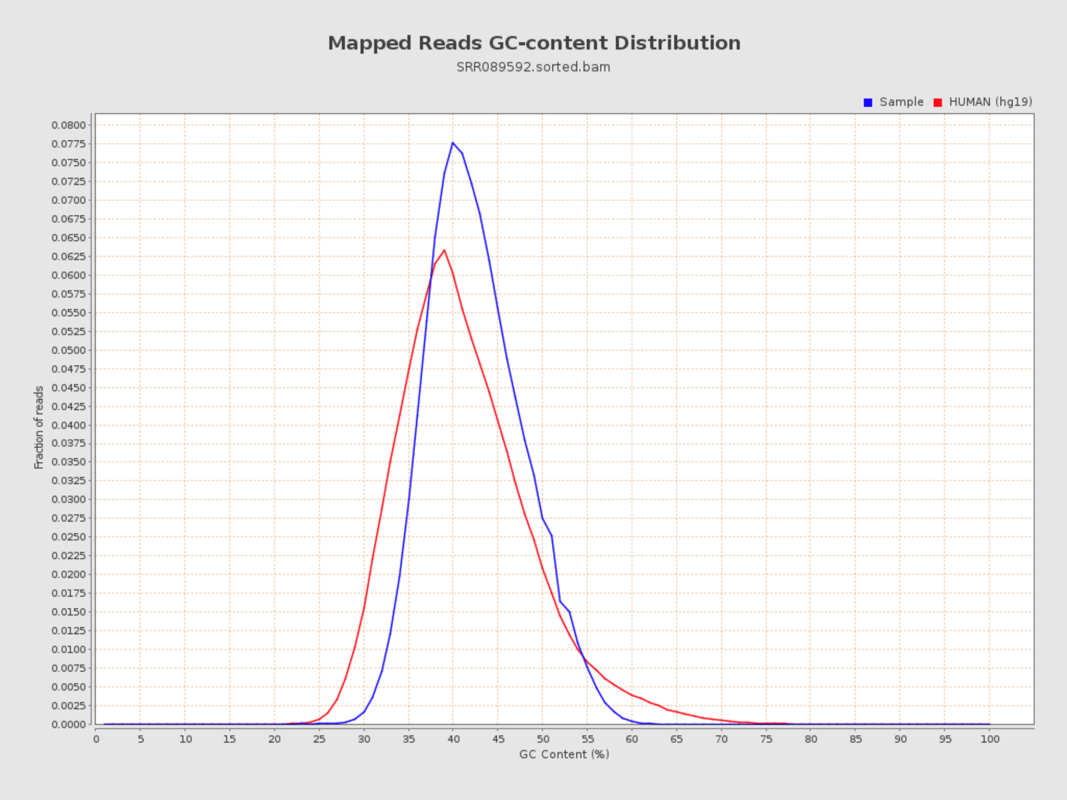
7. Results : Duplication Rate Histogram



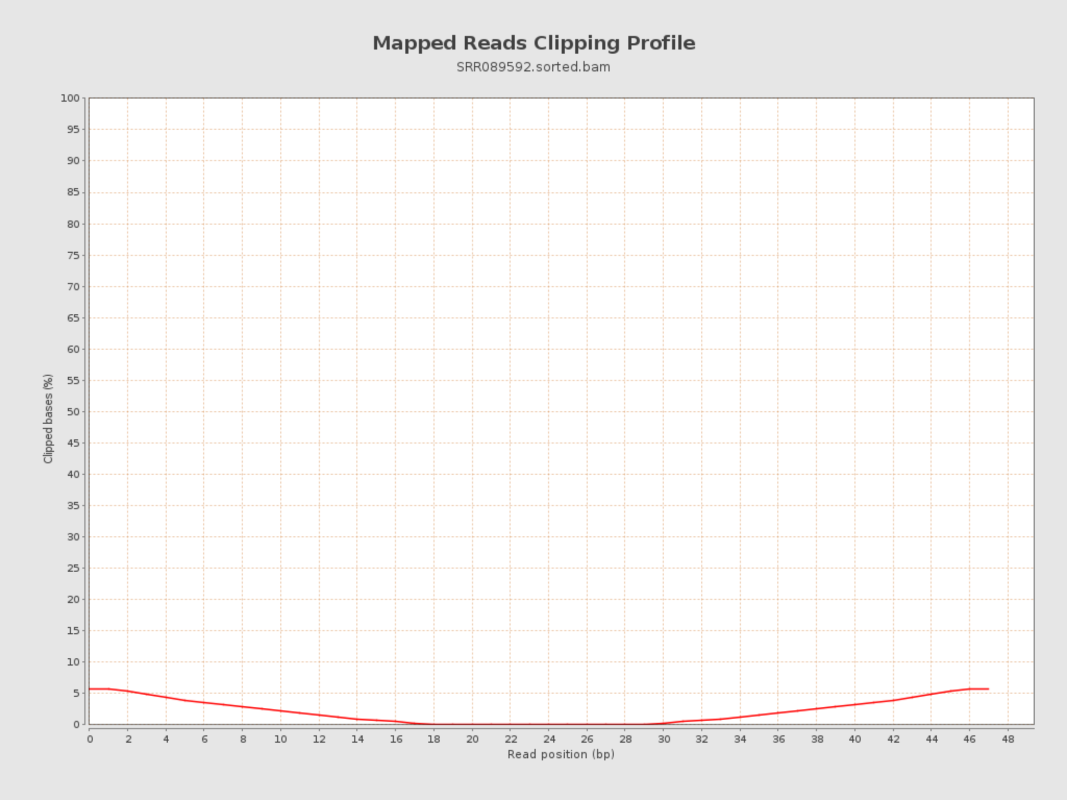
8. Results : Mapped Reads Nucleotide Content



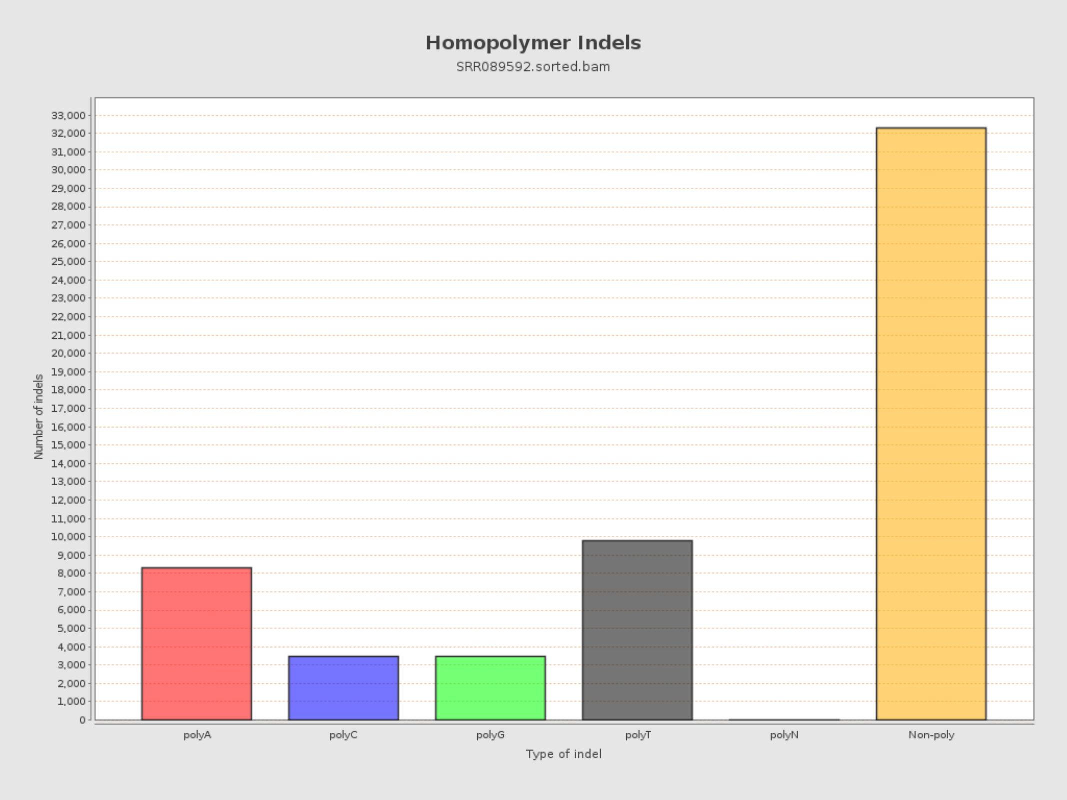
9. Results : Mapped Reads GC-content Distribution



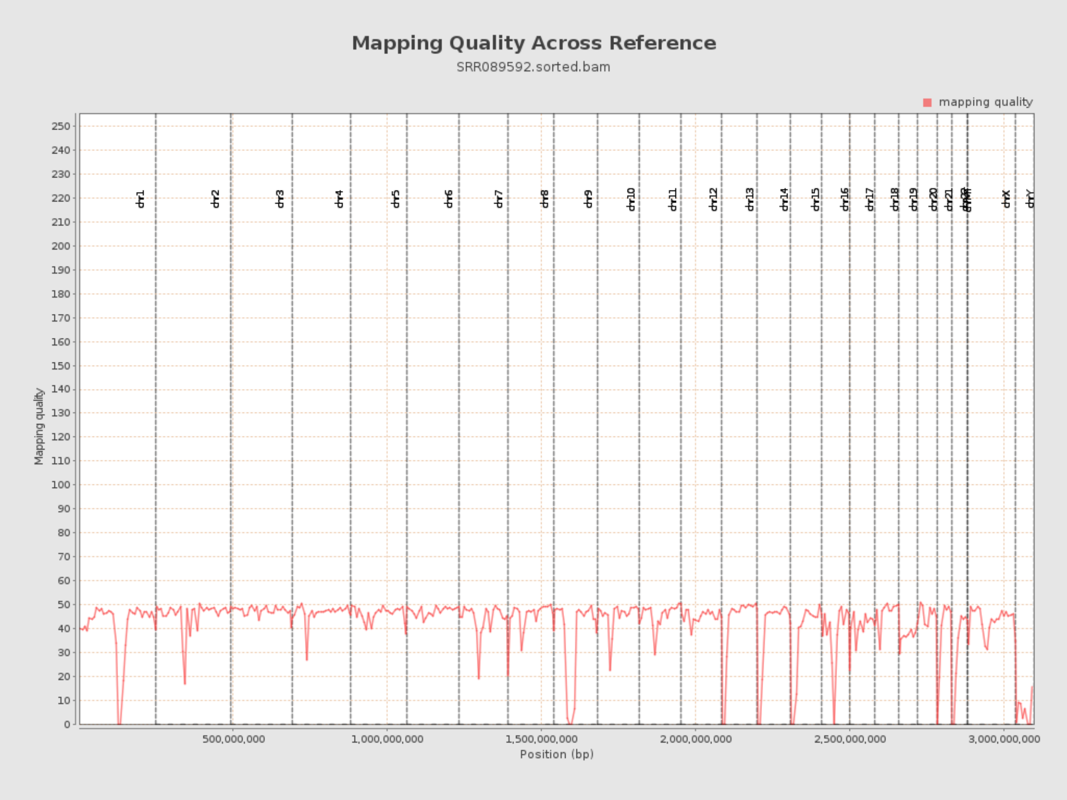
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram