Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:16:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053607.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_SRR053607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:16:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,268,603
Mapped reads	3,889,516 / 62.05%
Unmapped reads	2,379,087 / 37.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	95 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	712,601 / 11.37%
Duplication rate	13.97%
Clipped reads	514,818 / 8.21%

2.2. ACGT Content

Number/percentage of A's	54,579,134 / 30.01%
Number/percentage of C's	35,491,110 / 19.51%
Number/percentage of T's	53,729,604 / 29.54%
Number/percentage of G's	37,988,249 / 20.89%
Number/percentage of N's	93,585 / 0.05%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0588

Standard Deviation	0.78

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

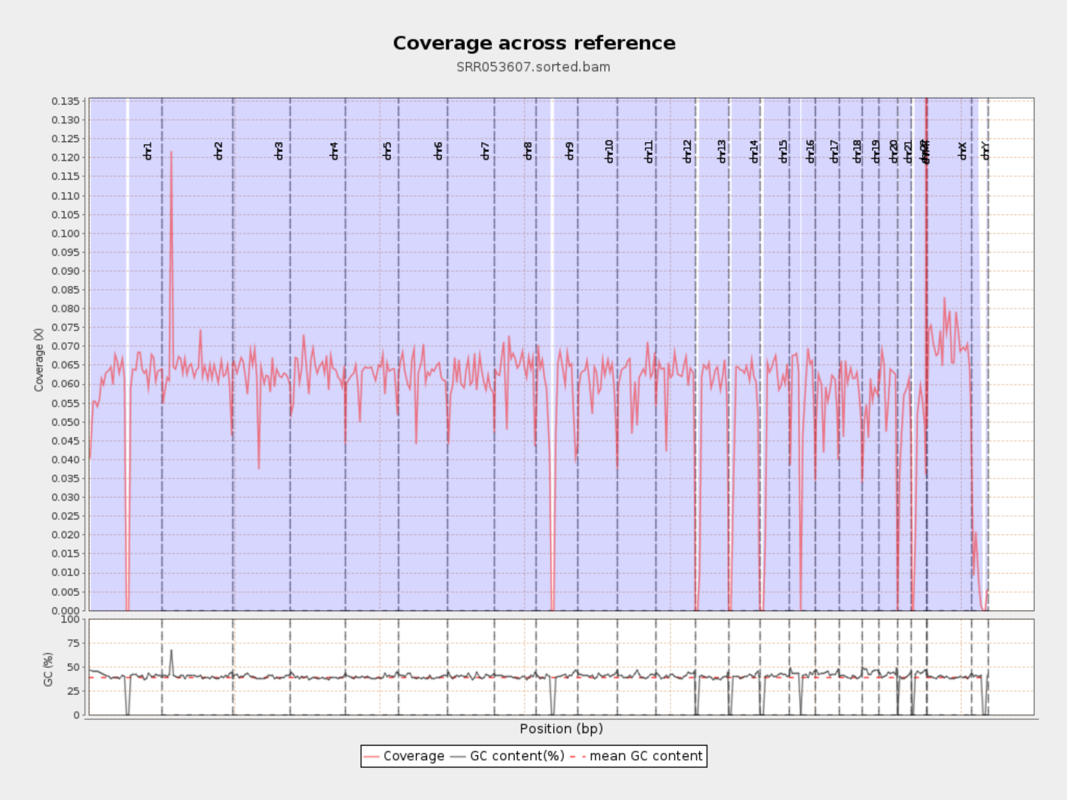
General error rate	0.83%
Mismatches	1,503,596
Insertions	9,727
Mapped reads with at least one insertion	0.25%
Deletions	25,597
Mapped reads with at least one deletion	0.66%
Homopolymer indels	45.08%

2.6. Chromosome stats

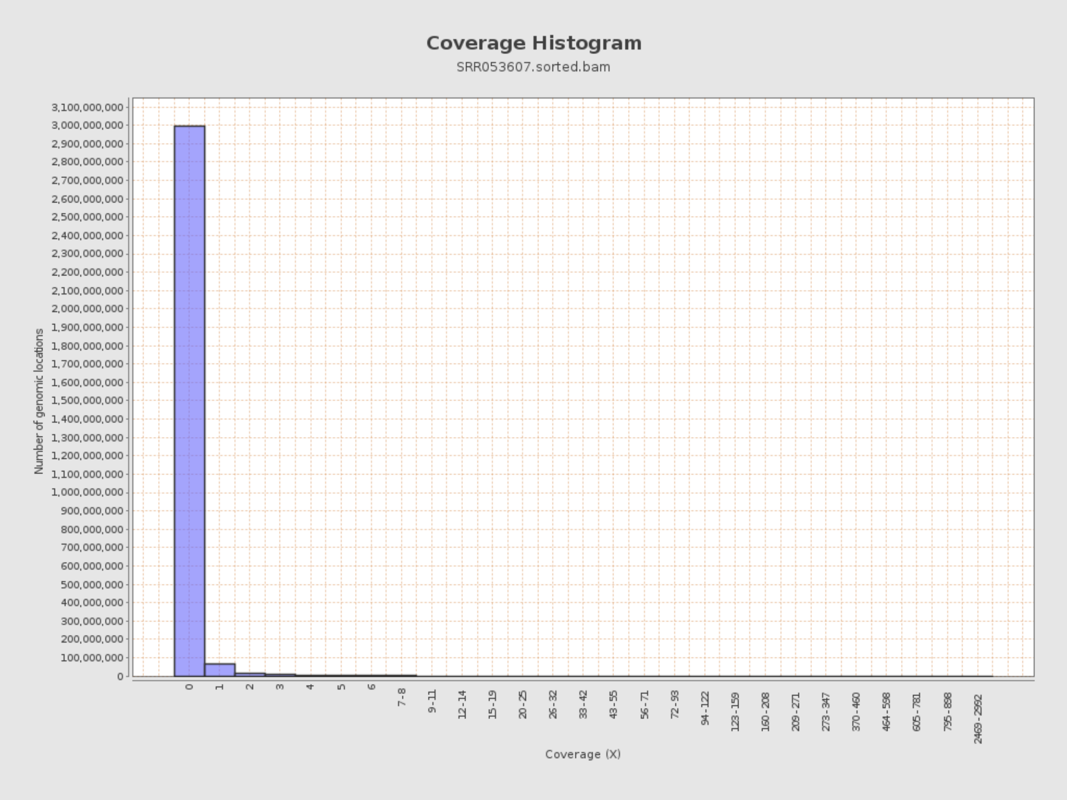
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14460203	0.058	0.515
chr2	243199373	15824307	0.0651	2.2118
chr3	198022430	12344142	0.0623	0.4719
chr4	191154276	12136710	0.0635	0.4953
chr5	180915260	11252293	0.0622	0.4704
chr6	171115067	10752083	0.0628	0.5064
chr7	159138663	9764116	0.0614	0.549

chr8	146364022	9378307	0.0641	0.5167
chr9	141213431	7548868	0.0535	0.4507
chr10	135534747	8346102	0.0616	0.5006
chr11	135006516	8325473	0.0617	0.5131
chr12	133851895	8293417	0.062	0.4668
chr13	115169878	5955552	0.0517	0.4324
chr14	107349540	5543196	0.0516	0.4813
chr15	102531392	5200171	0.0507	0.4207
chr16	90354753	5050071	0.0559	0.4562
chr17	81195210	4511831	0.0556	0.438
chr18	78077248	4699119	0.0602	0.5118
chr19	59128983	3205160	0.0542	0.4777
chr20	63025520	3757860	0.0596	0.4592
chr21	48129895	2249575	0.0467	0.4232
chr22	51304566	1888500	0.0368	0.3494
chrMT	16571	19098	1.1525	3.0119
chrX	155270560	10949451	0.0705	0.6963
chrY	59373566	462939	0.0078	0.1666

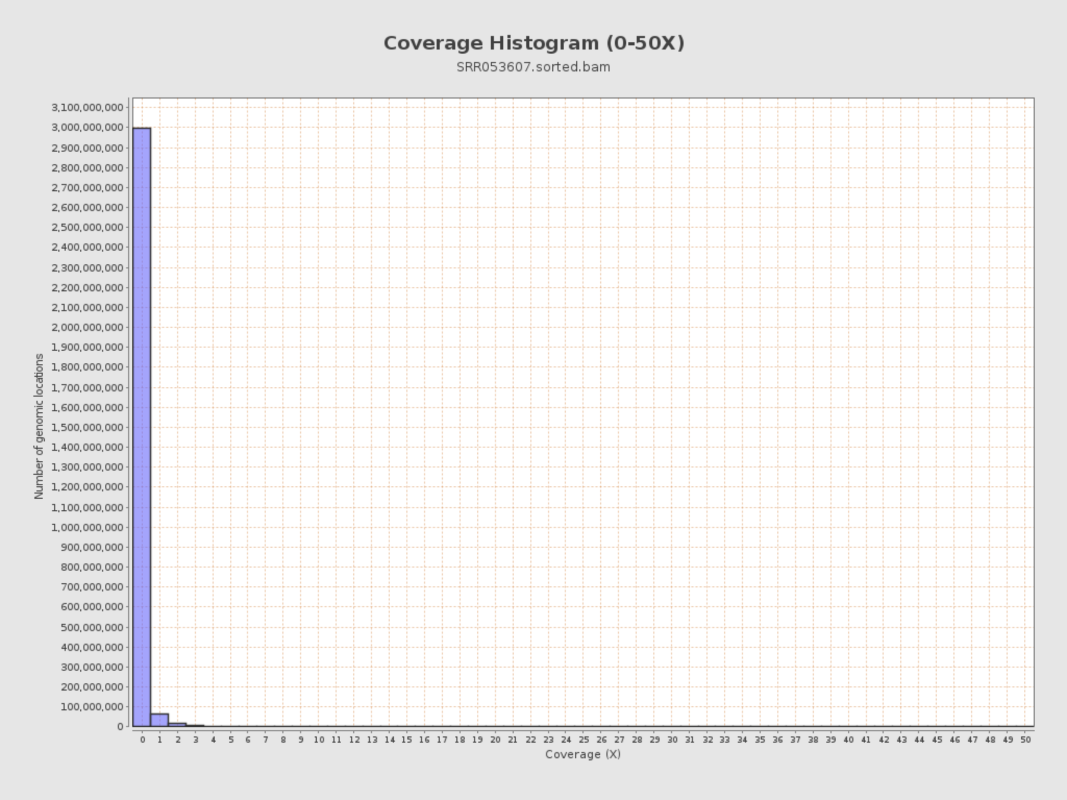
3. Results : Coverage across reference



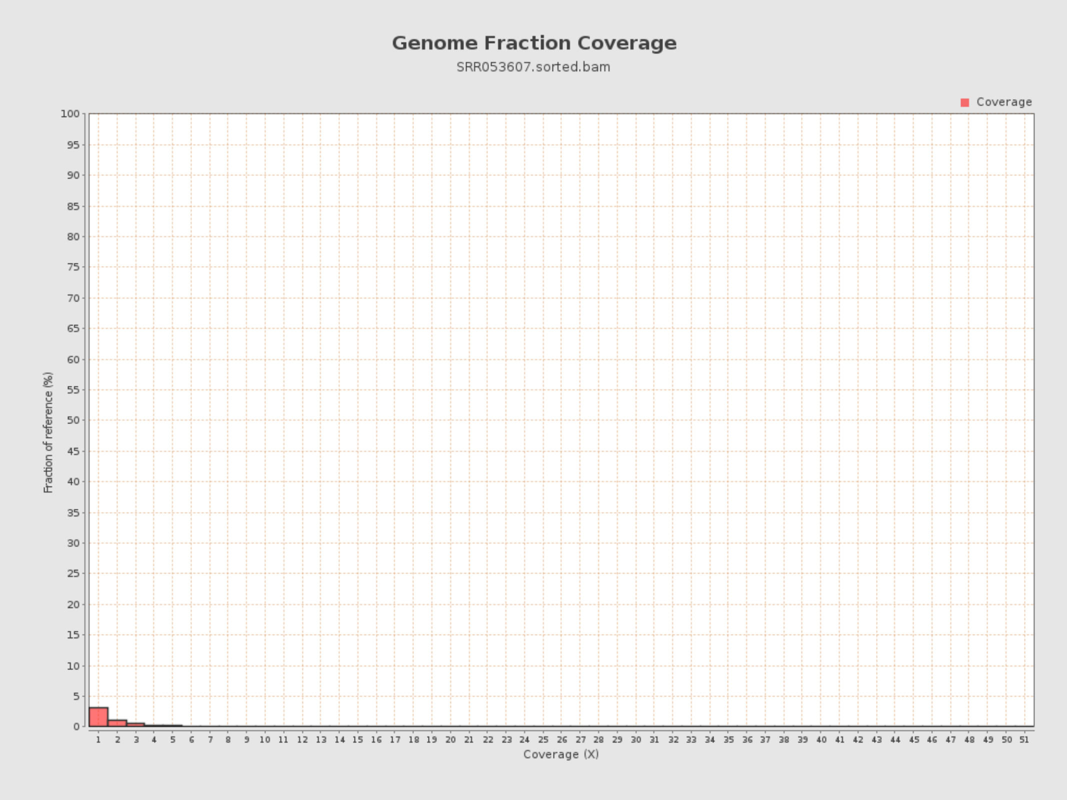
4. Results : Coverage Histogram



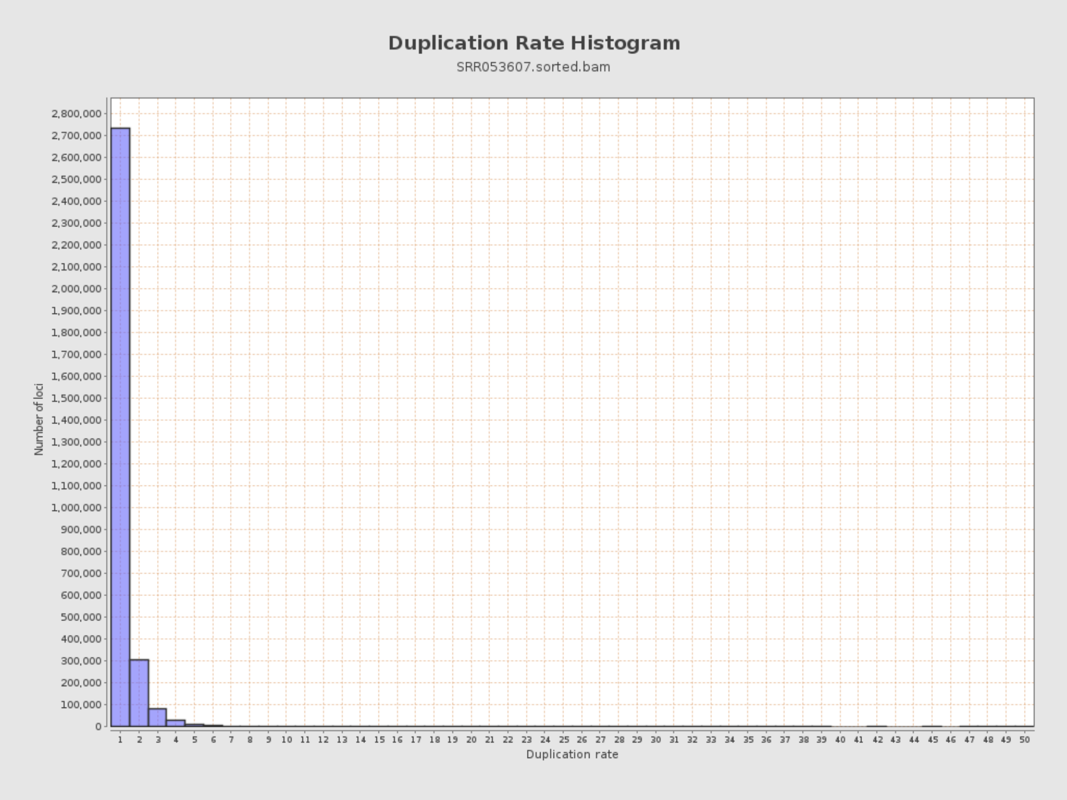
5. Results : Coverage Histogram (0-50X)



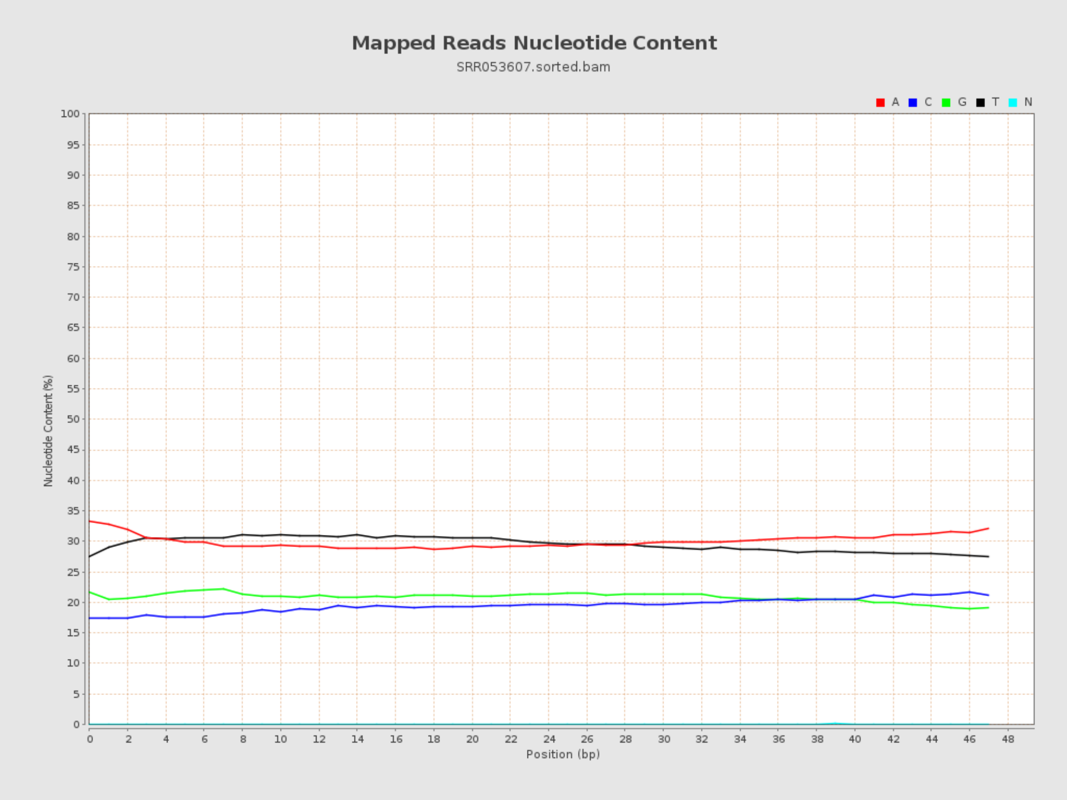
6. Results : Genome Fraction Coverage



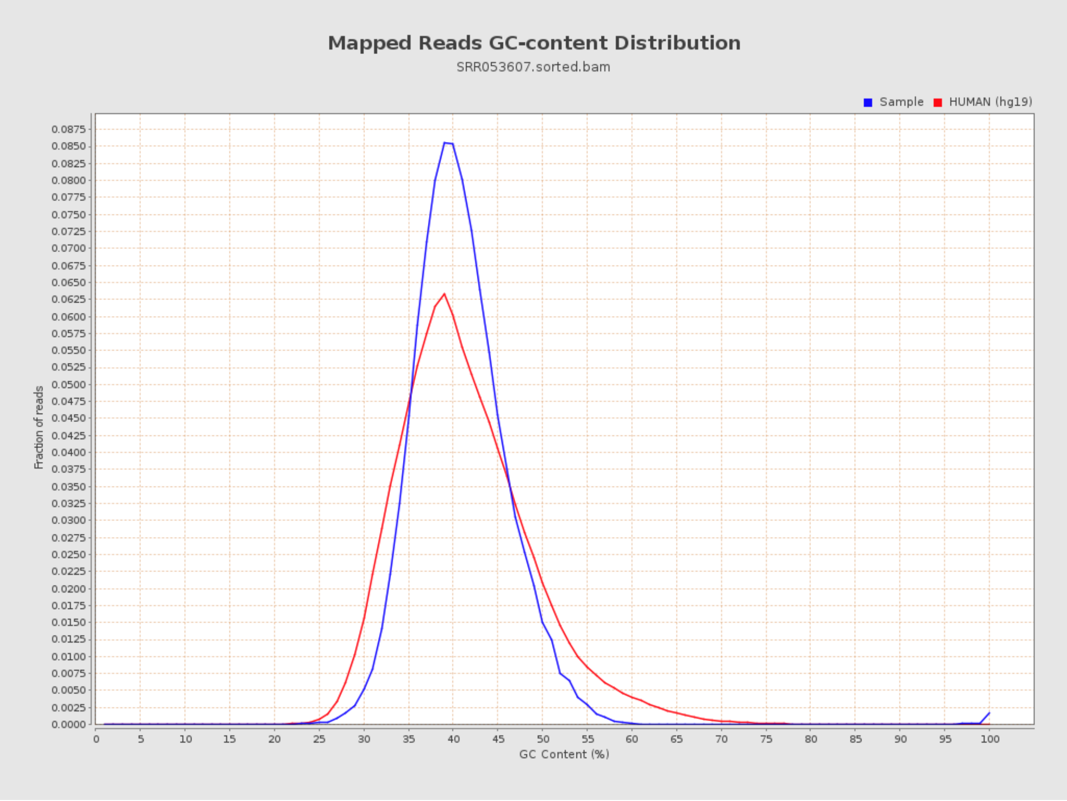
7. Results : Duplication Rate Histogram



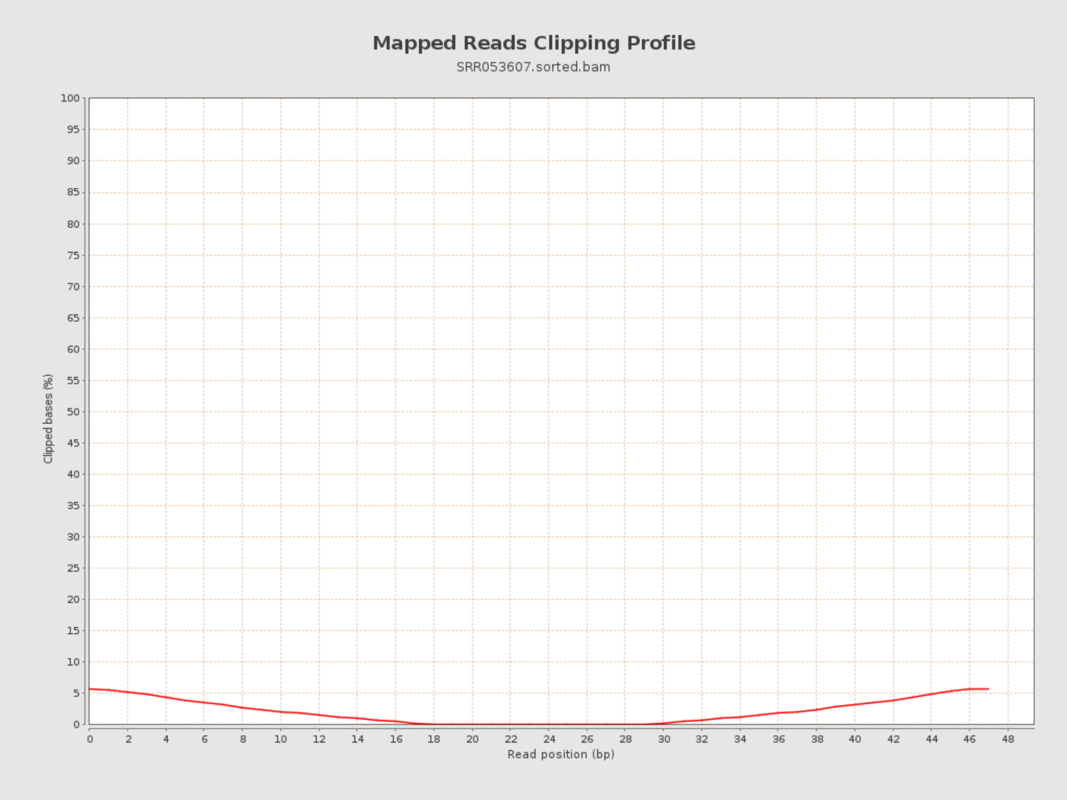
8. Results : Mapped Reads Nucleotide Content



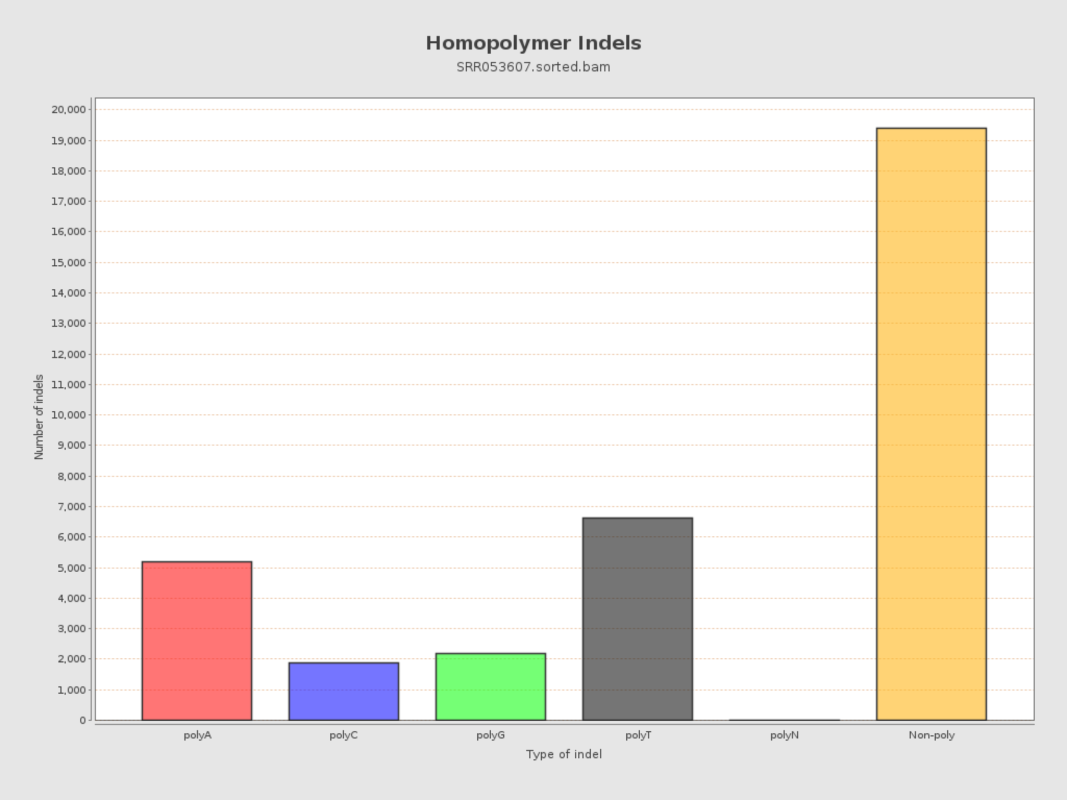
9. Results : Mapped Reads GC-content Distribution



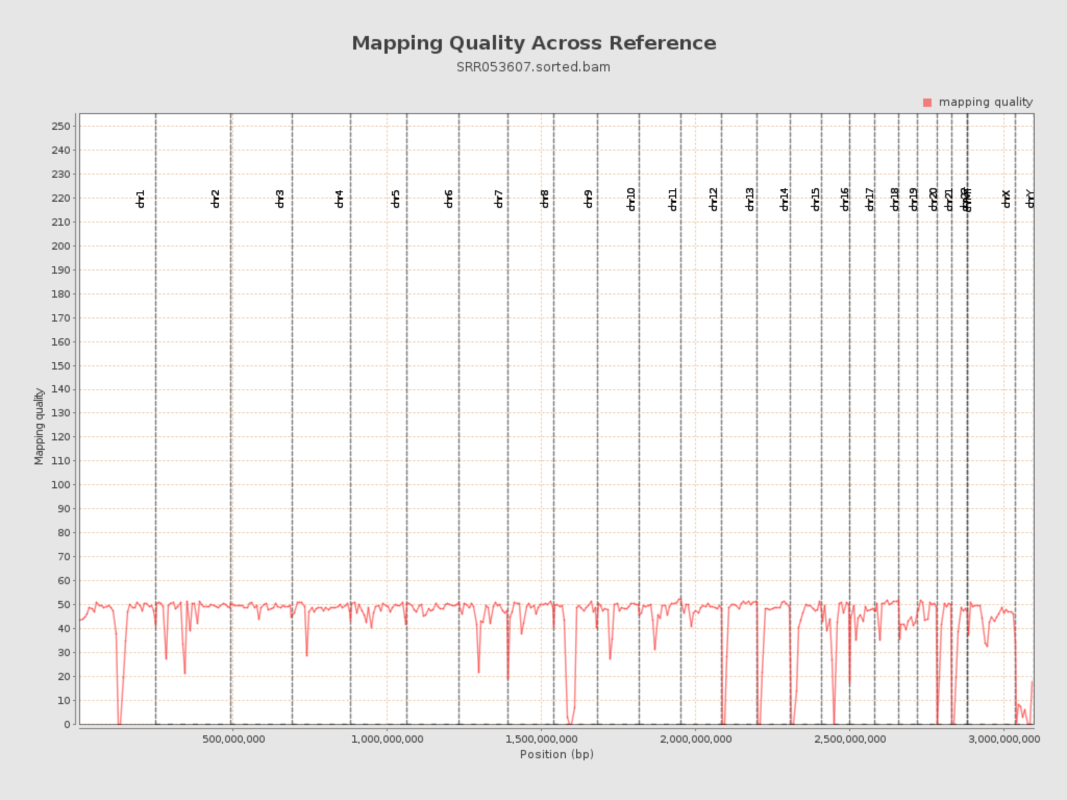
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram