Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:49:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053637.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_SRR053637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:49:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,964,738
Mapped reads	6,126,599 / 68.34%
Unmapped reads	2,838,139 / 31.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	155 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,515,178 / 16.9%
Duplication rate	20.38%
Clipped reads	632,869 / 7.06%

2.2. ACGT Content

Number/percentage of A's	85,309,640 / 29.59%
Number/percentage of C's	55,338,038 / 19.19%
Number/percentage of T's	85,479,968 / 29.65%
Number/percentage of G's	62,081,435 / 21.53%
Number/percentage of N's	130,256 / 0.05%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0932

Standard Deviation	0.7136

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

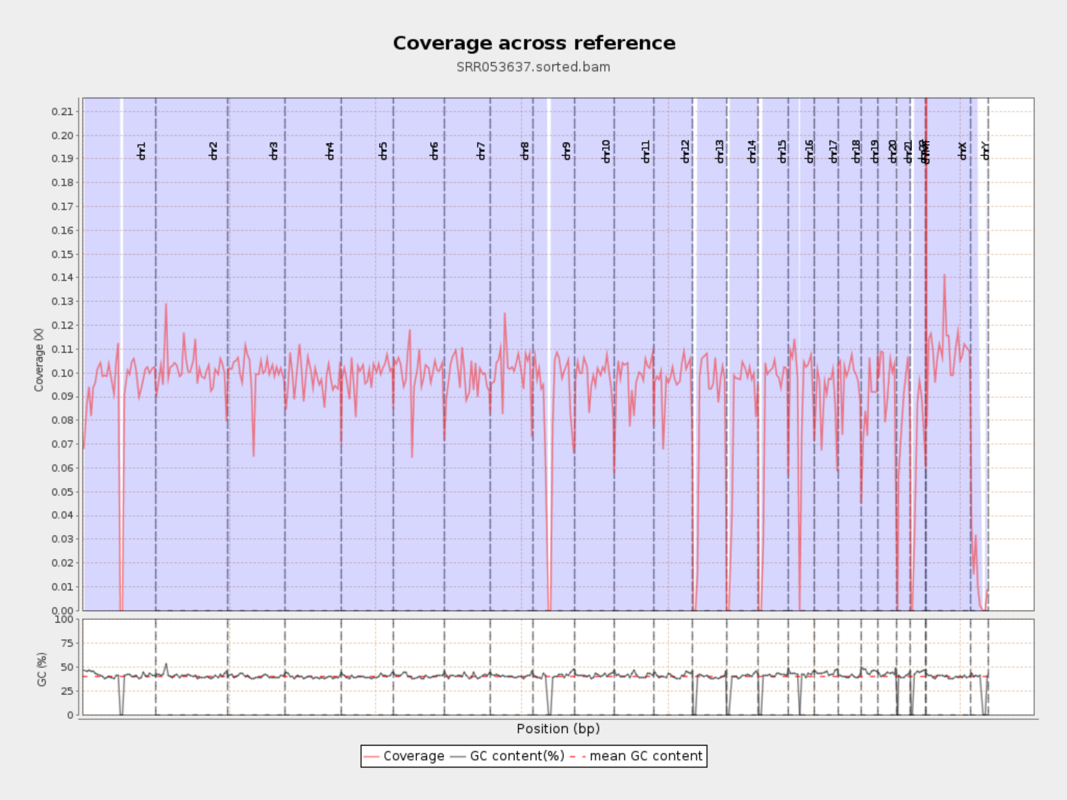
General error rate	0.83%
Mismatches	2,383,324
Insertions	13,755
Mapped reads with at least one insertion	0.22%
Deletions	36,989
Mapped reads with at least one deletion	0.6%
Homopolymer indels	46.95%

2.6. Chromosome stats

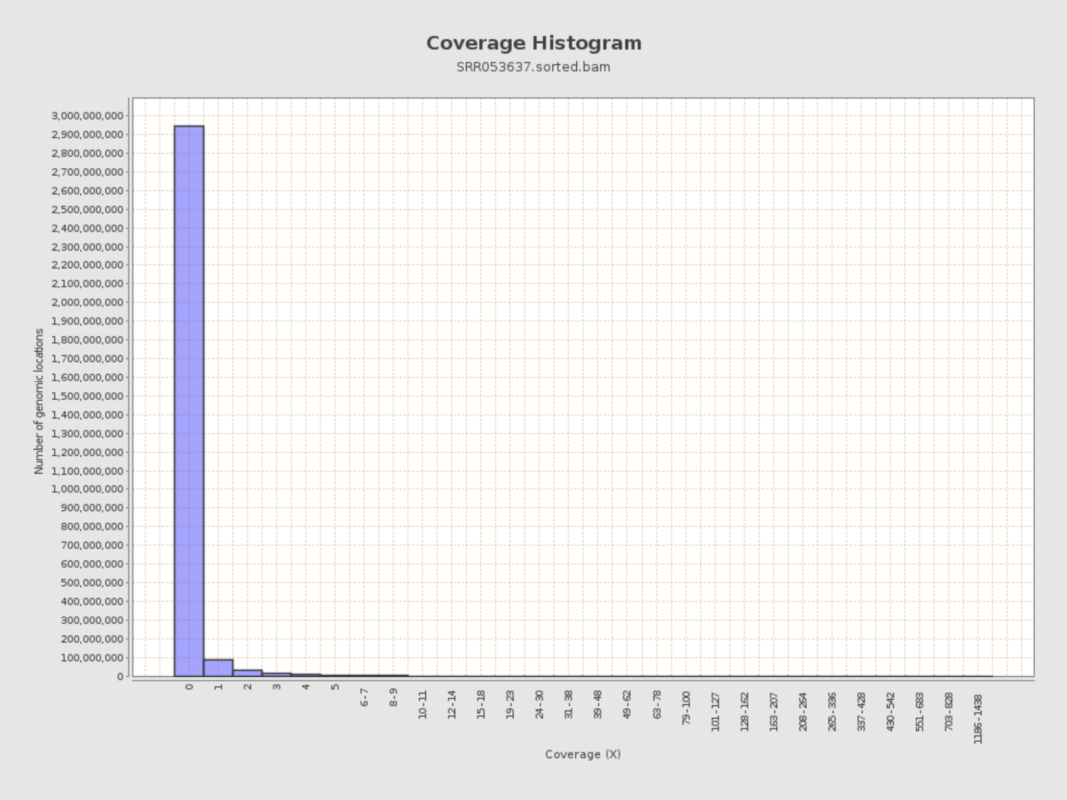
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22796584	0.0915	0.7668
chr2	243199373	24721396	0.1017	1.2791
chr3	198022430	19860374	0.1003	0.5881
chr4	191154276	18709425	0.0979	0.6038
chr5	180915260	17952797	0.0992	0.5826
chr6	171115067	17160644	0.1003	0.6859
chr7	159138663	15587089	0.0979	0.8551

chr8	146364022	14867663	0.1016	0.6482
chr9	141213431	11882251	0.0841	0.5858
chr10	135534747	13384822	0.0988	0.6834
chr11	135006516	13162253	0.0975	0.6805
chr12	133851895	13067631	0.0976	0.5838
chr13	115169878	9480880	0.0823	0.5353
chr14	107349540	8731768	0.0813	0.5686
chr15	102531392	8301701	0.081	0.5221
chr16	90354753	8103652	0.0897	0.5898
chr17	81195210	7320220	0.0902	0.5675
chr18	78077248	7663735	0.0982	0.7296
chr19	59128983	5092888	0.0861	0.7173
chr20	63025520	6115424	0.097	0.5904
chr21	48129895	3688073	0.0766	0.5632
chr22	51304566	3051460	0.0595	0.4344
chrMT	16571	37744	2.2777	3.7582
chrX	155270560	16943119	0.1091	0.7074
chrY	59373566	708920	0.0119	0.2297

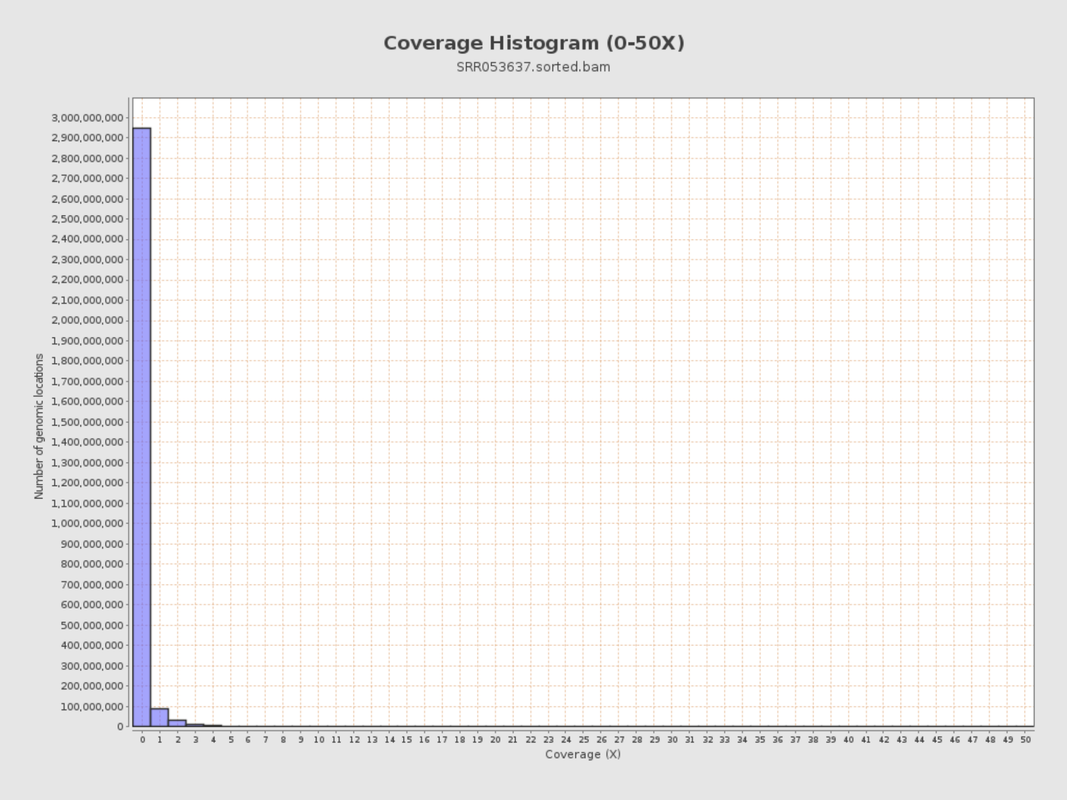
3. Results : Coverage across reference



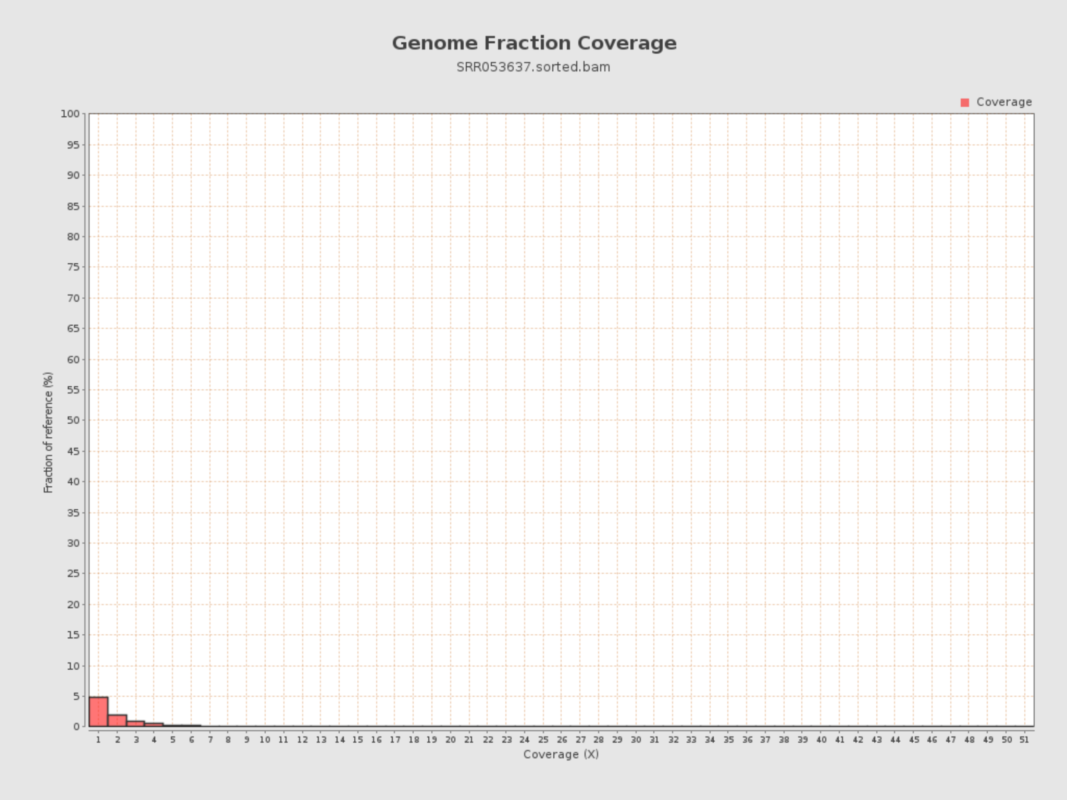
4. Results : Coverage Histogram



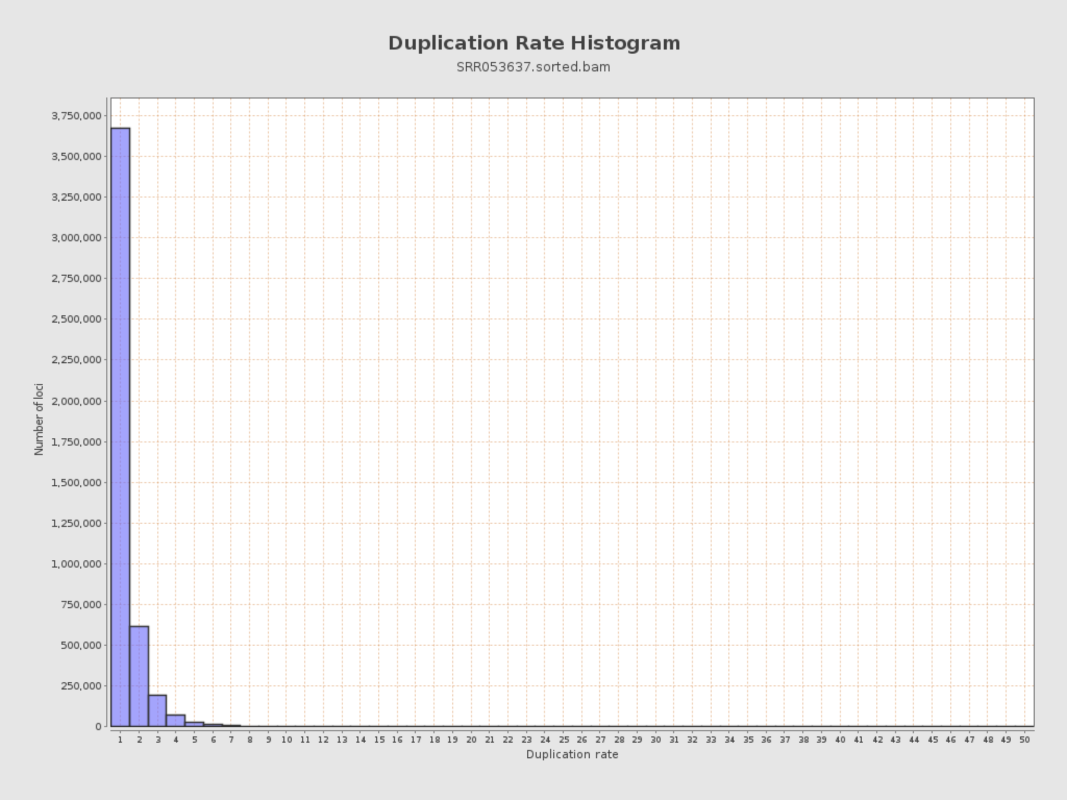
5. Results : Coverage Histogram (0-50X)



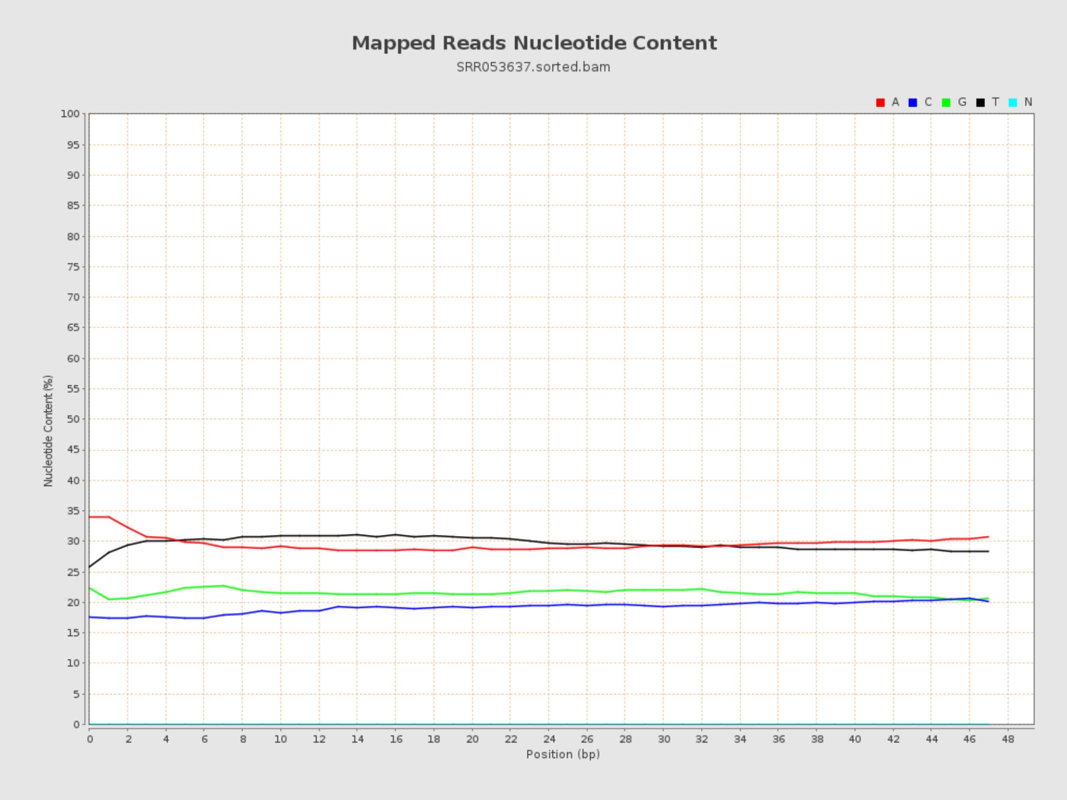
6. Results : Genome Fraction Coverage



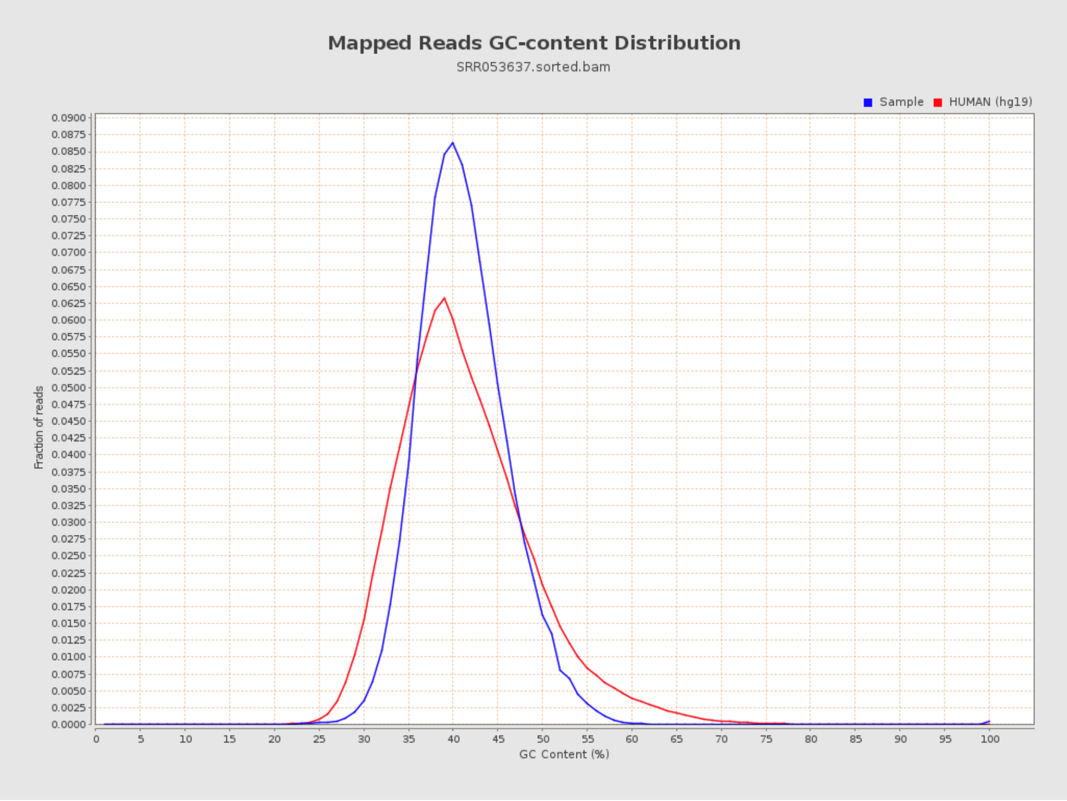
7. Results : Duplication Rate Histogram



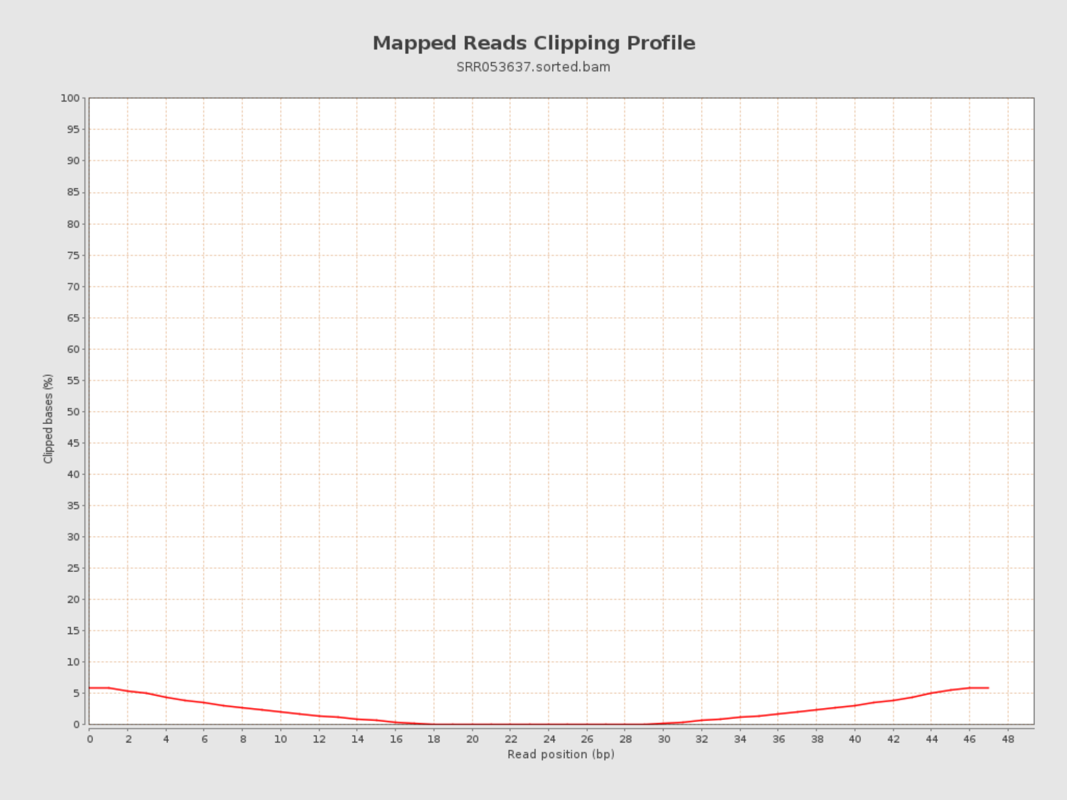
8. Results : Mapped Reads Nucleotide Content



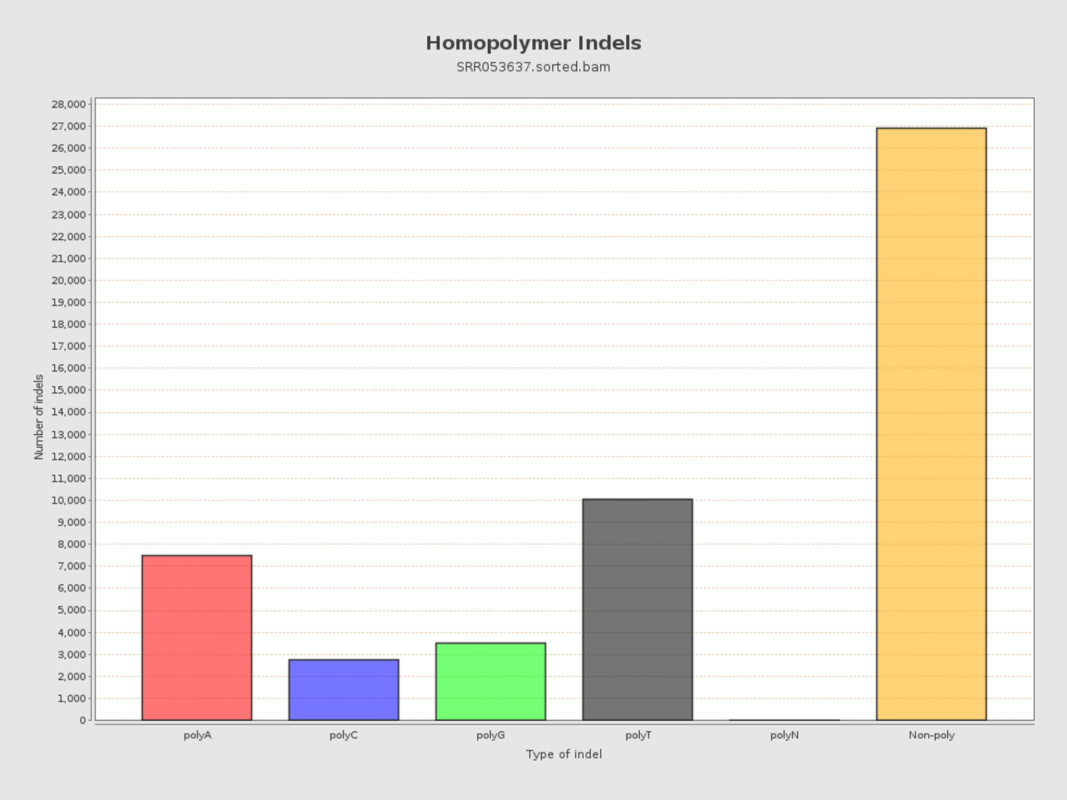
9. Results : Mapped Reads GC-content Distribution



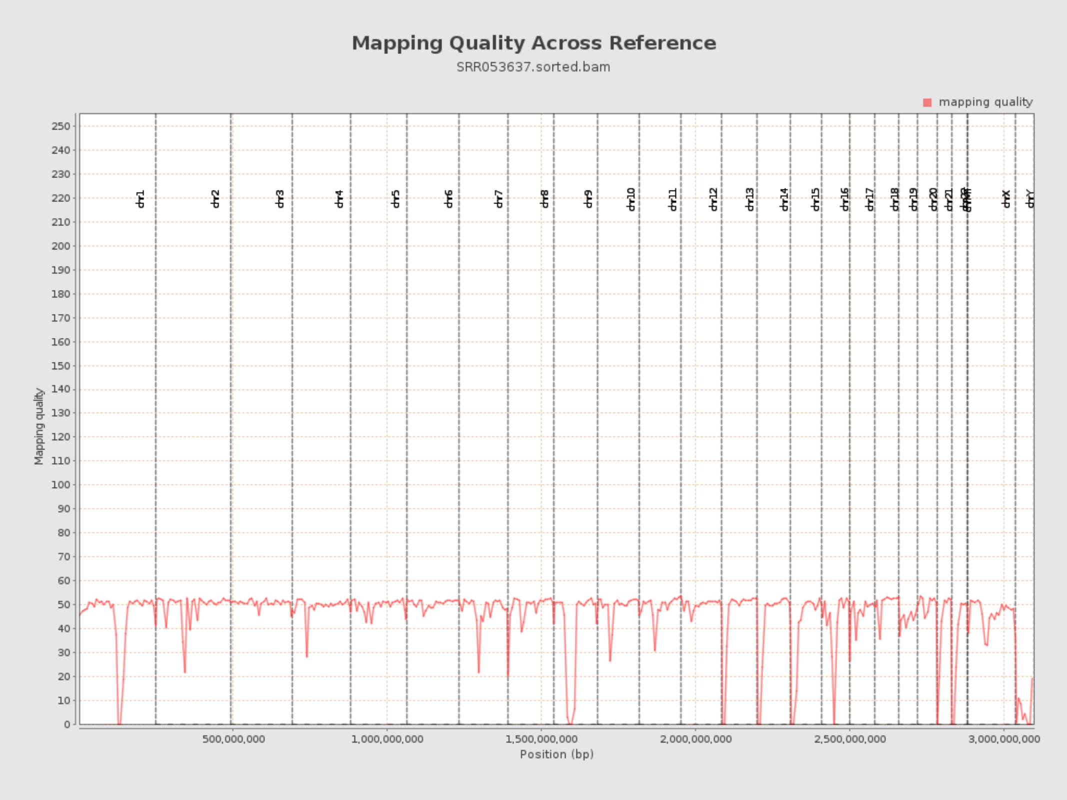
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram