

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006445.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_SRR1006445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006445.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:08:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,327,971
Mapped reads	1,271,932 / 95.78%
Unmapped reads	56,039 / 4.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,211 / 0.24%
Read min/max/mean length	30 / 59 / 57.69
Duplicated reads (estimated)	18,794 / 1.42%
Duplication rate	1.1%
Clipped reads	135,484 / 10.2%

2.2. ACGT Content

Number/percentage of A's	20,414,413 / 28.4%
Number/percentage of C's	15,118,473 / 21.03%
Number/percentage of T's	20,534,500 / 28.57%
Number/percentage of G's	15,814,541 / 22%
Number/percentage of N's	2,069 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.1956
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2.4. Mapping Quality

Mean Mapping Quality	45.89
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2.5. Mismatches and indels

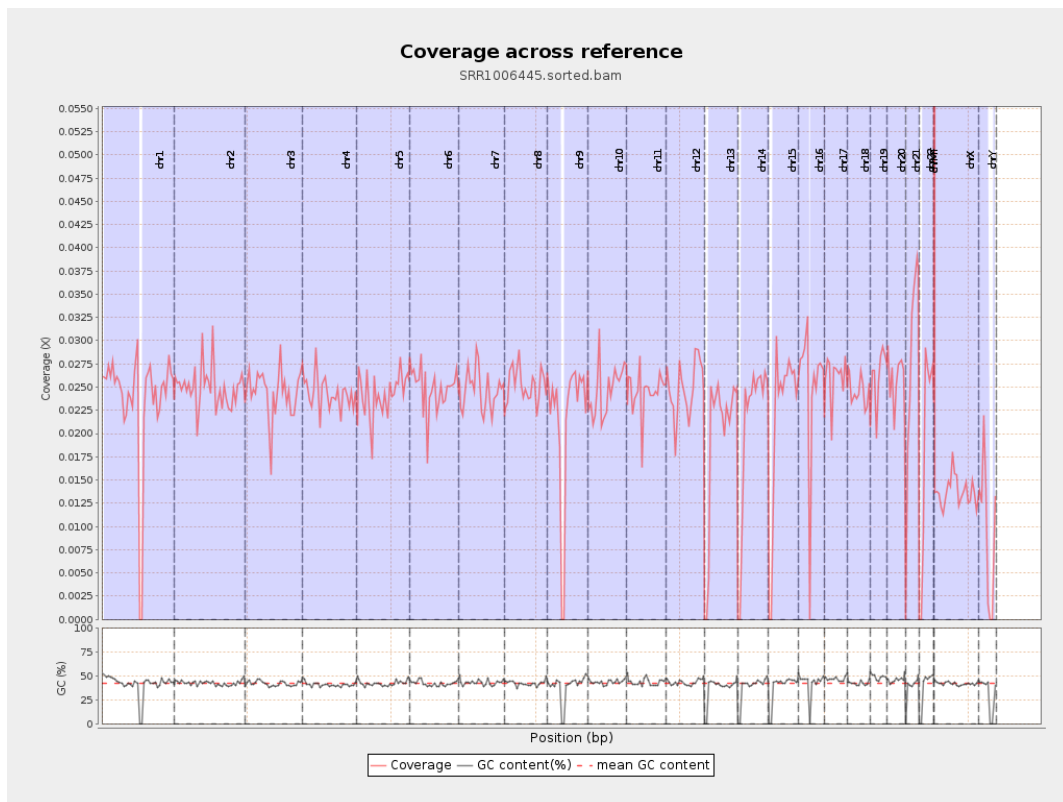
General error rate	0.43%
Mismatches	300,997
Insertions	4,422
Mapped reads with at least one insertion	0.35%
Deletions	13,692
Mapped reads with at least one deletion	1.07%
Homopolymer indels	46.78%

2.6. Chromosome stats

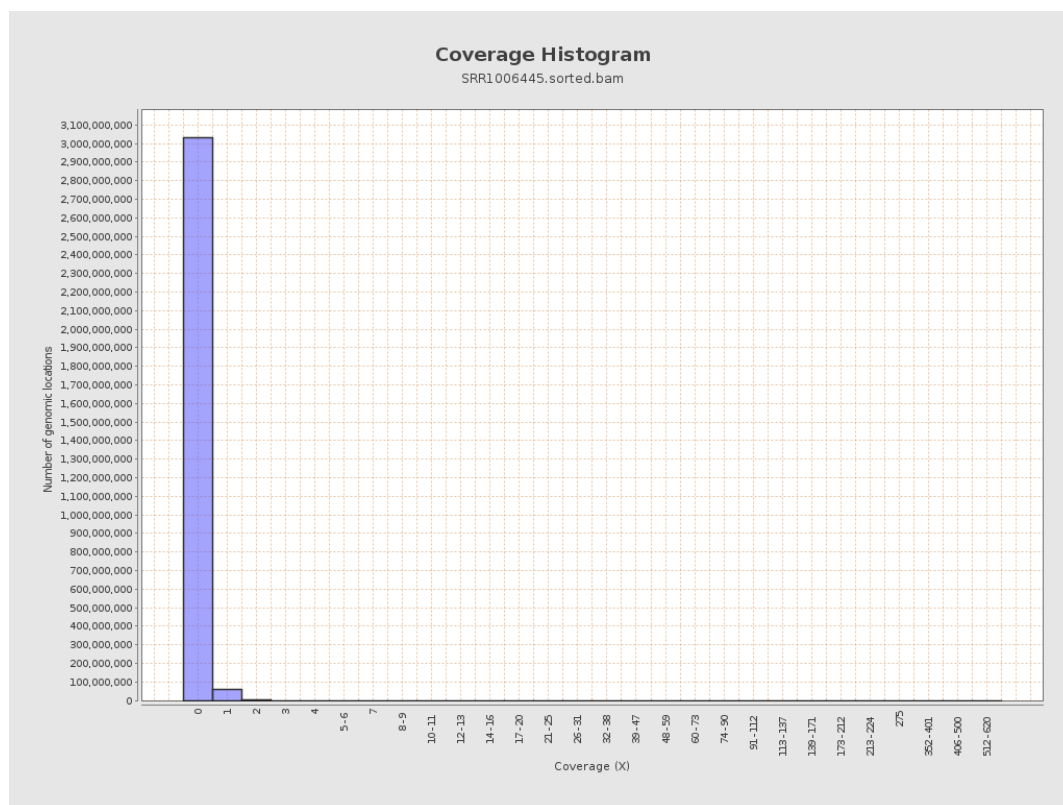
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5888207	0.0236	0.2378
chr2	243199373	6070939	0.025	0.1931
chr3	198022430	4838860	0.0244	0.1661
chr4	191154276	4653643	0.0243	0.1703
chr5	180915260	4403160	0.0243	0.1662
chr6	171115067	4243773	0.0248	0.1742
chr7	159138663	3927142	0.0247	0.1973

chr8	146364022	3680848	0.0251	0.3867
chr9	141213431	3044679	0.0216	0.1738
chr10	135534747	3352119	0.0247	0.1899
chr11	135006516	3308003	0.0245	0.1786
chr12	133851895	3308452	0.0247	0.1682
chr13	115169878	2244770	0.0195	0.1486
chr14	107349540	2232791	0.0208	0.1566
chr15	102531392	2203386	0.0215	0.1567
chr16	90354753	2261460	0.025	0.1821
chr17	81195210	2116356	0.0261	0.1782
chr18	78077248	1920961	0.0246	0.2313
chr19	59128983	1544928	0.0261	0.212
chr20	63025520	1619723	0.0257	0.1728
chr21	48129895	1344630	0.0279	0.1897
chr22	51304566	965909	0.0188	0.1544
chrMT	16571	32247	1.946	2.4484
chrX	155270560	2135801	0.0138	0.129
chrY	59373566	563711	0.0095	0.1275

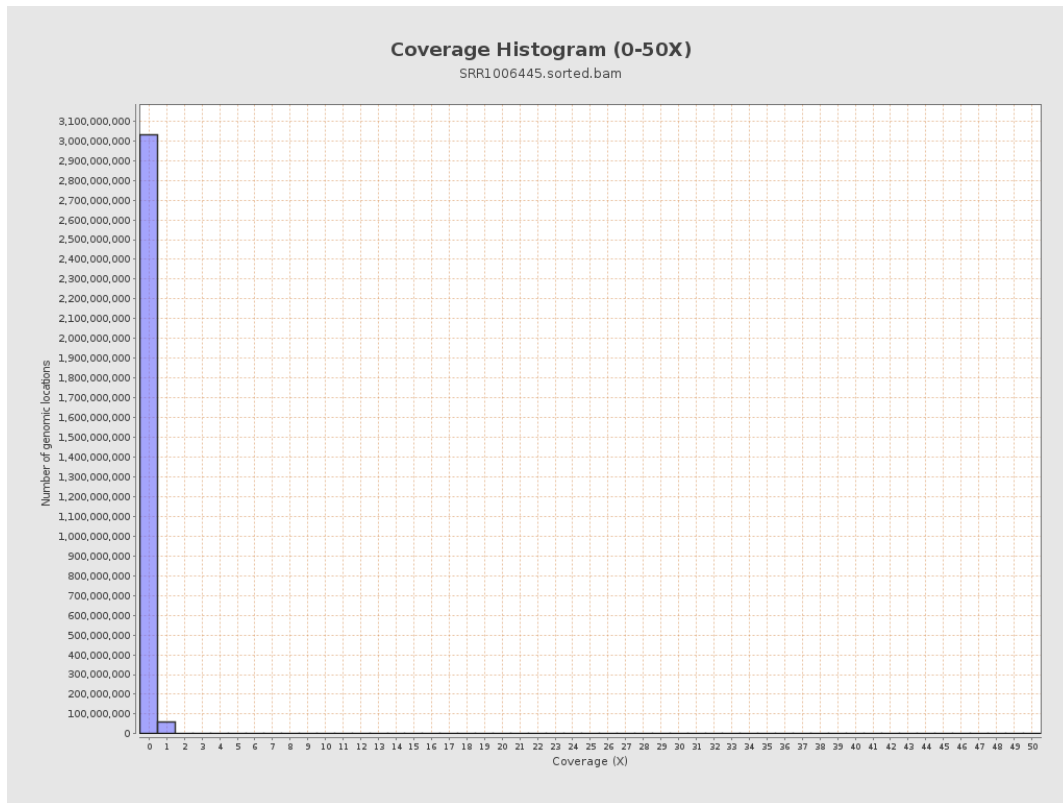
3. Results : Coverage across reference



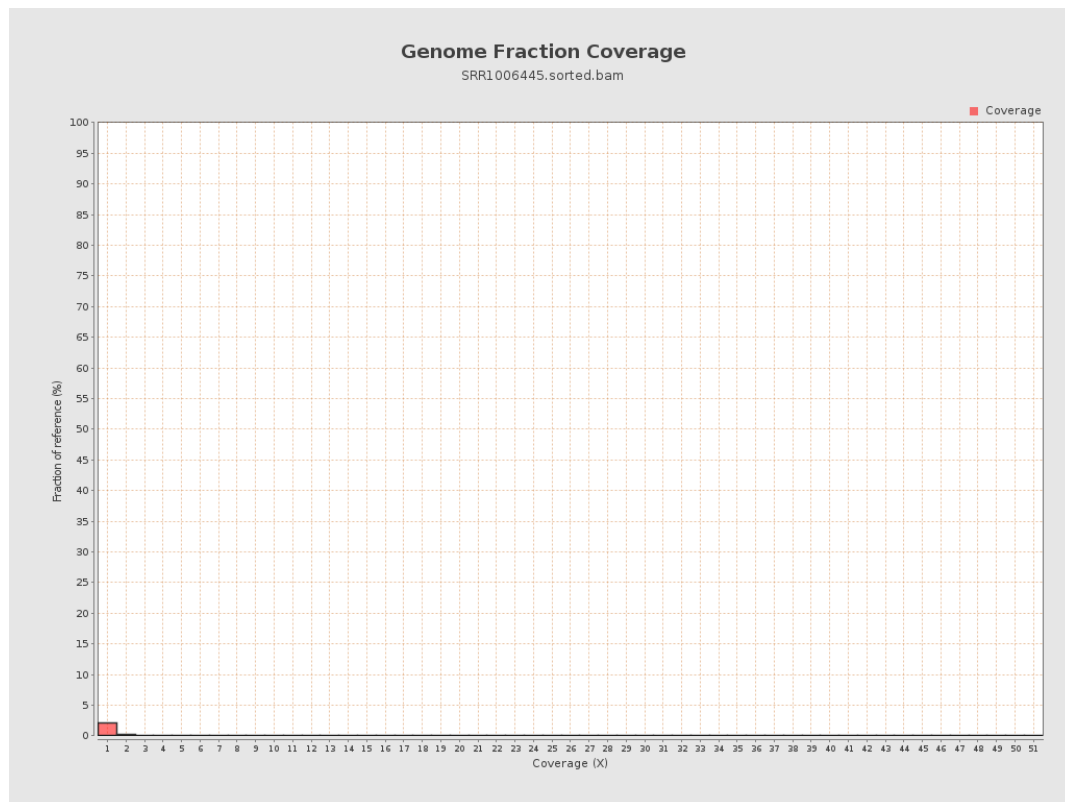
4. Results : Coverage Histogram



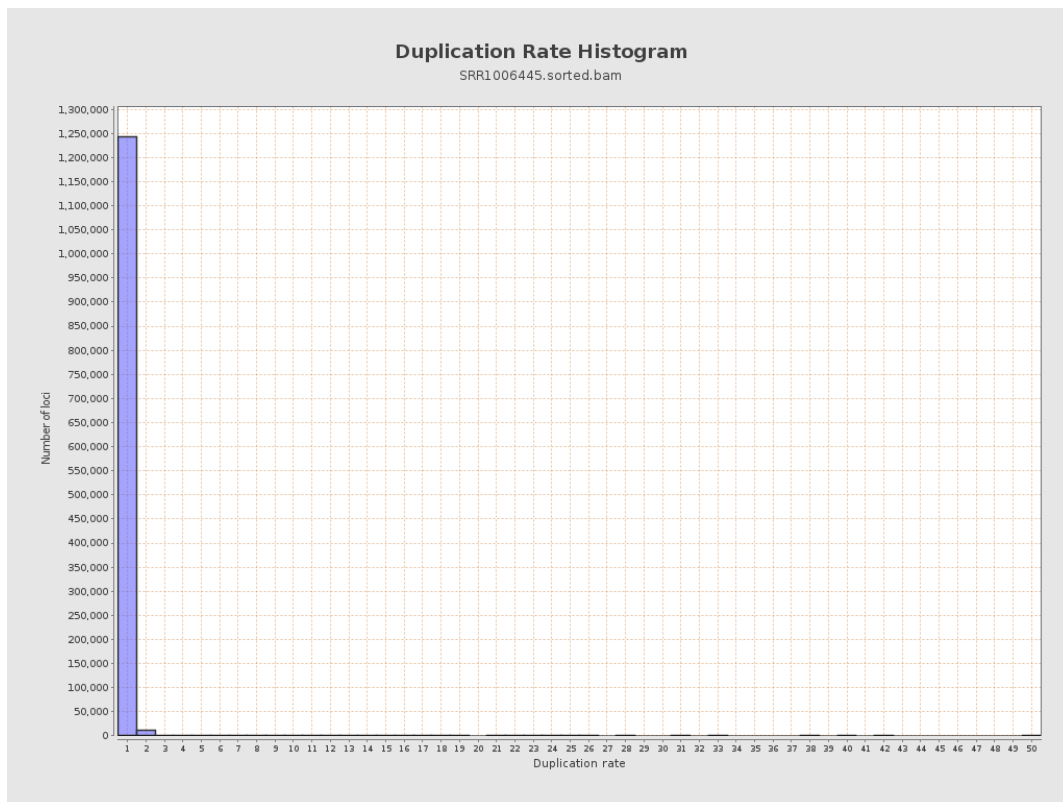
5. Results : Coverage Histogram (0-50X)



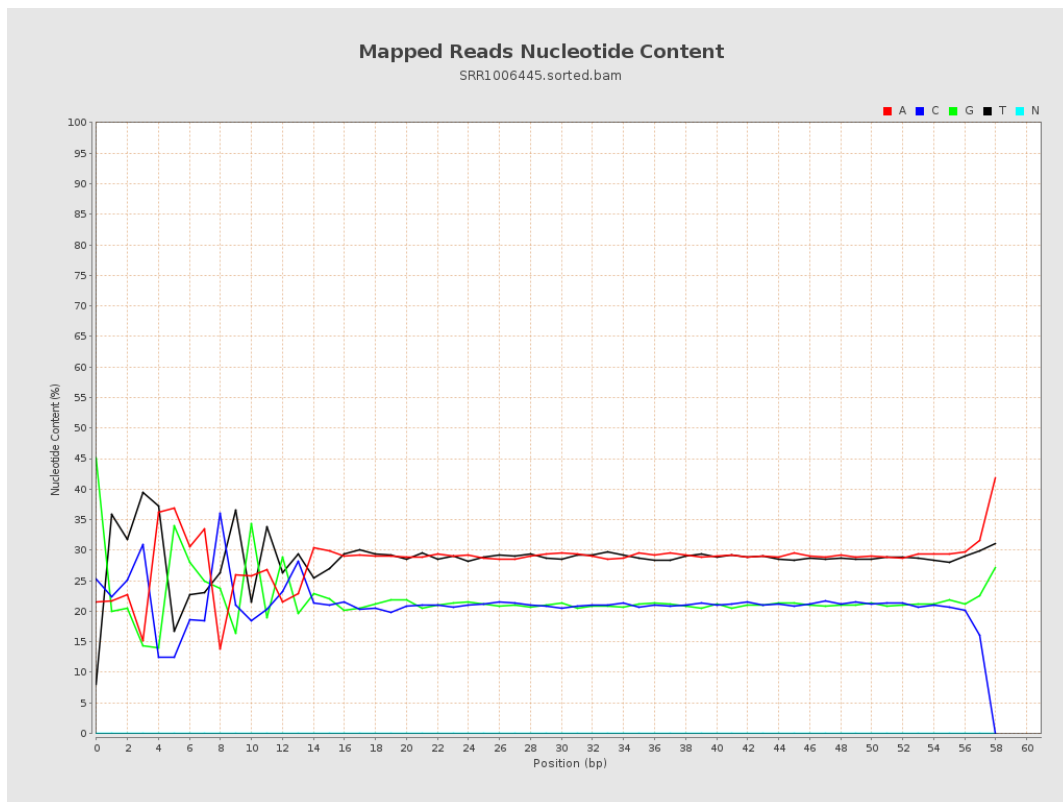
6. Results : Genome Fraction Coverage



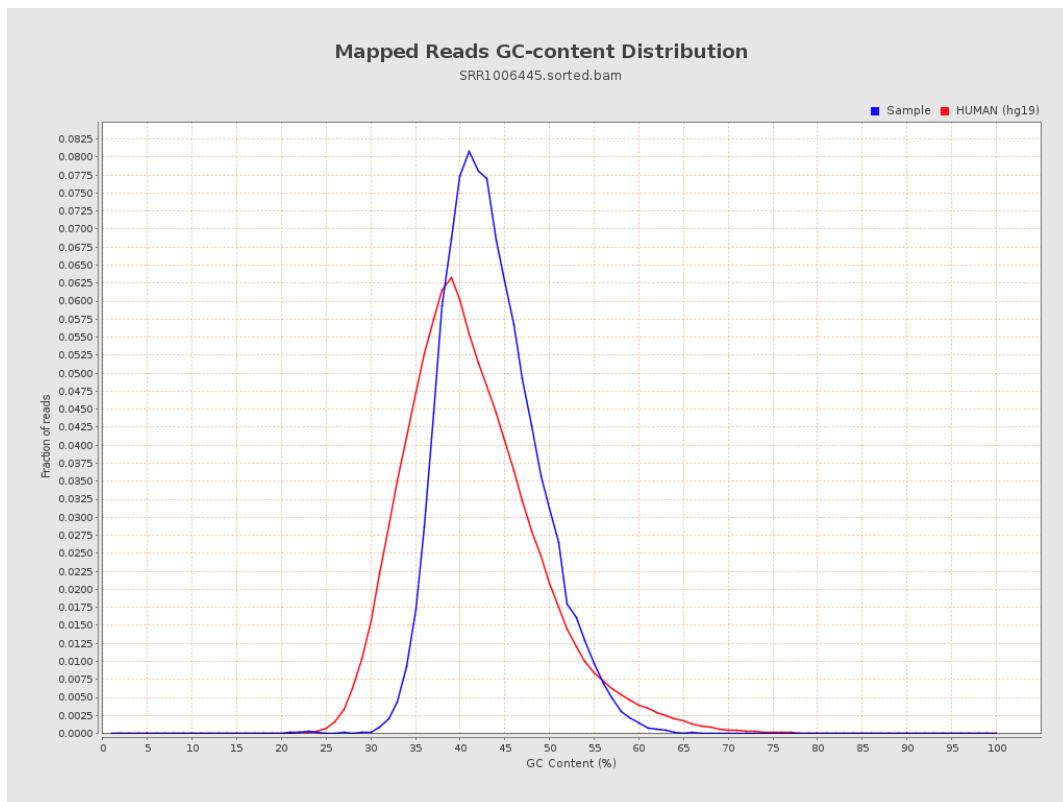
7. Results : Duplication Rate Histogram



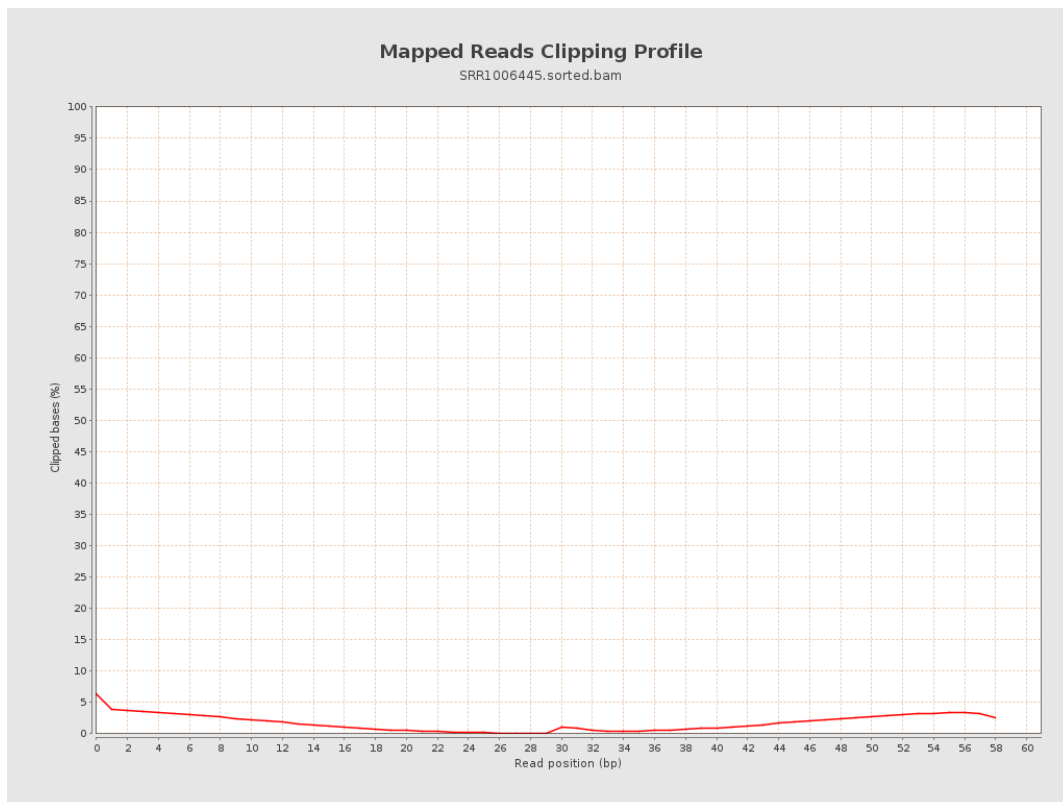
8. Results : Mapped Reads Nucleotide Content



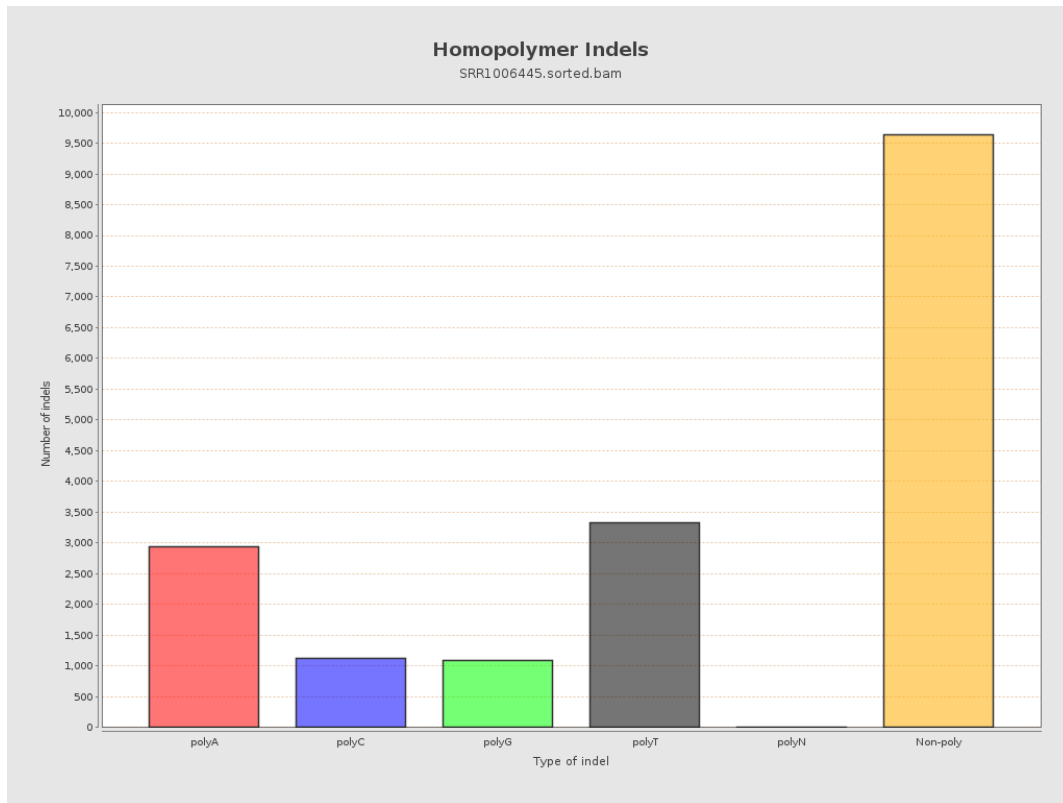
9. Results : Mapped Reads GC-content Distribution



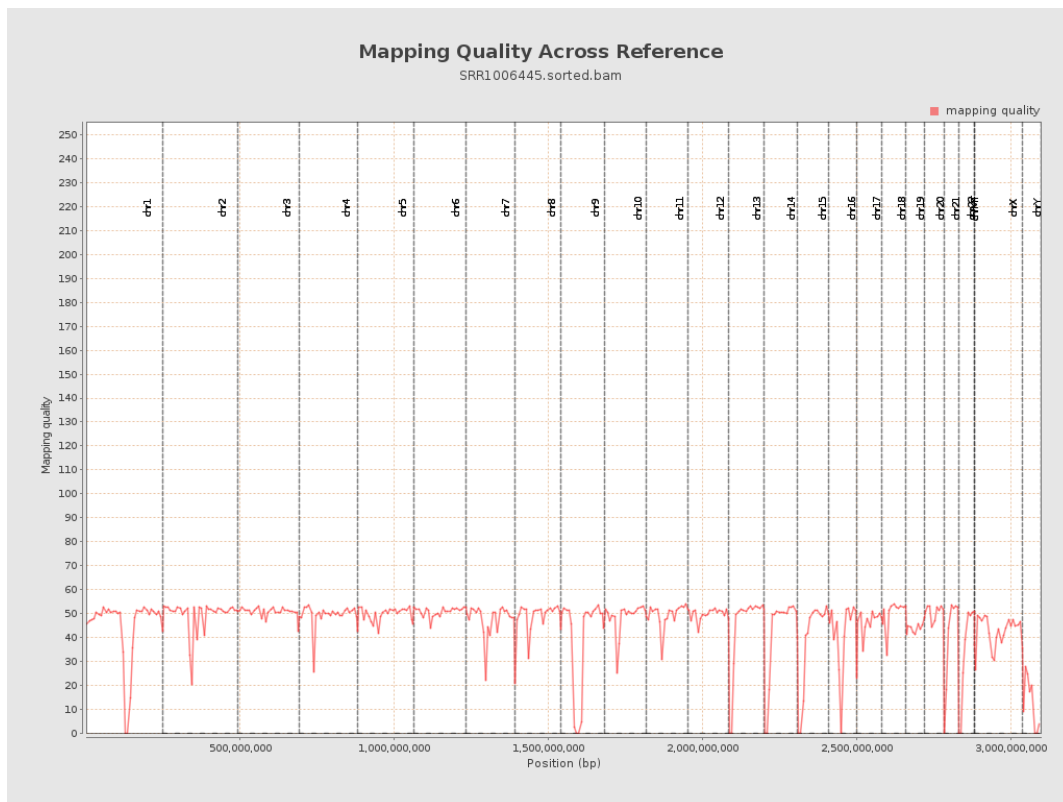
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

