Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:43:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054607.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_SRR054607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:43:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,647,369
Mapped reads	10,598,118 / 77.66%
Unmapped reads	3,049,251 / 22.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	309 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,693,754 / 12.41%
Duplication rate	11.05%
Clipped reads	942,420 / 6.91%

2.2. ACGT Content

Number/percentage of A's	148,720,451 / 29.74%
Number/percentage of C's	96,922,783 / 19.38%
Number/percentage of T's	149,472,182 / 29.89%
Number/percentage of G's	104,949,385 / 20.99%
Number/percentage of N's	3,819 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.1616

Standard Deviation	1.0217

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

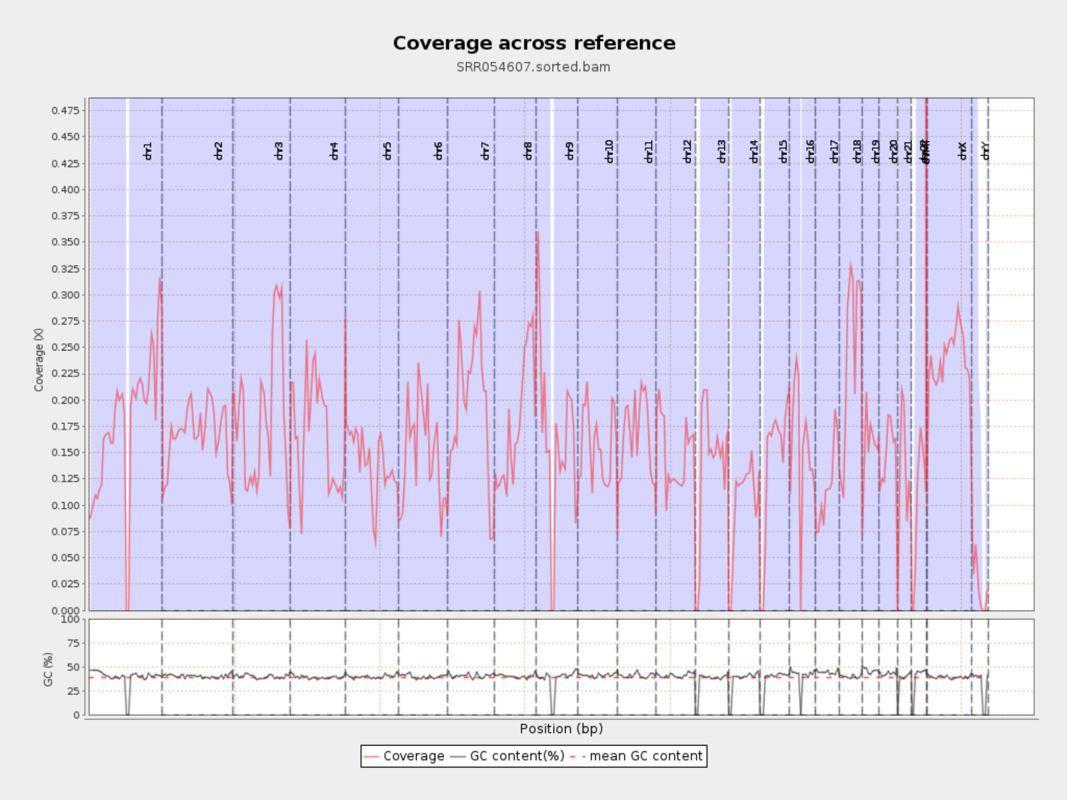
General error rate	0.51%
Mismatches	2,530,798
Insertions	19,940
Mapped reads with at least one insertion	0.19%
Deletions	65,442
Mapped reads with at least one deletion	0.62%
Homopolymer indels	46.81%

2.6. Chromosome stats

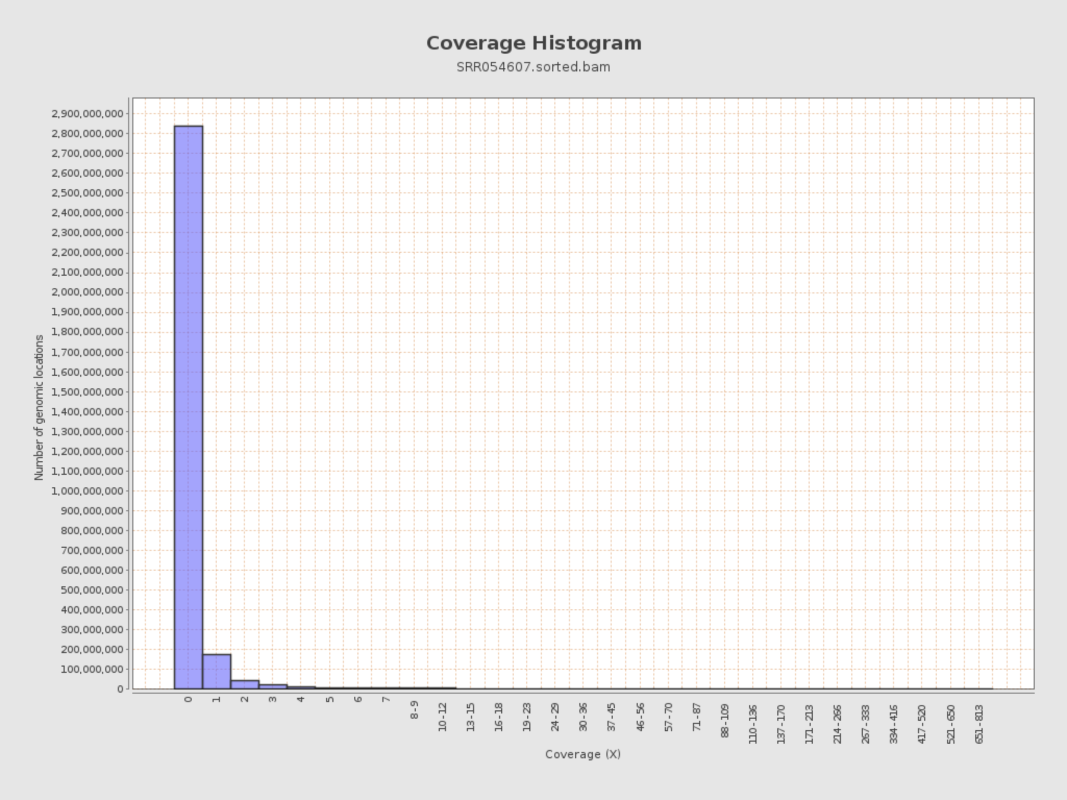
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43854138	0.1759	1.151
chr2	243199373	40705267	0.1674	1.1517
chr3	198022430	36652688	0.1851	1.0049
chr4	191154276	31864539	0.1667	1.0201
chr5	180915260	25533544	0.1411	0.799
chr6	171115067	25197106	0.1473	0.9403
chr7	159138663	31417773	0.1974	1.2109

chr8	146364022	26222159	0.1792	1.0732
chr9	141213431	23213387	0.1644	1.0699
chr10	135534747	21454886	0.1583	1.018
chr11	135006516	22418880	0.1661	1.0262
chr12	133851895	19786193	0.1478	0.8411
chr13	115169878	15730533	0.1366	0.8228
chr14	107349540	10826772	0.1009	0.8228
chr15	102531392	14365944	0.1401	0.813
chr16	90354753	14091389	0.156	1.0383
chr17	81195210	9675085	0.1192	0.717
chr18	78077248	18810704	0.2409	1.3944
chr19	59128983	9488730	0.1605	1.0628
chr20	63025520	9402525	0.1492	0.9093
chr21	48129895	6173308	0.1283	1.0199
chr22	51304566	5093718	0.0993	0.636
chrMT	16571	78669	4.7474	8.1093
chrX	155270560	36702725	0.2364	1.2745
chrY	59373566	1405784	0.0237	0.513

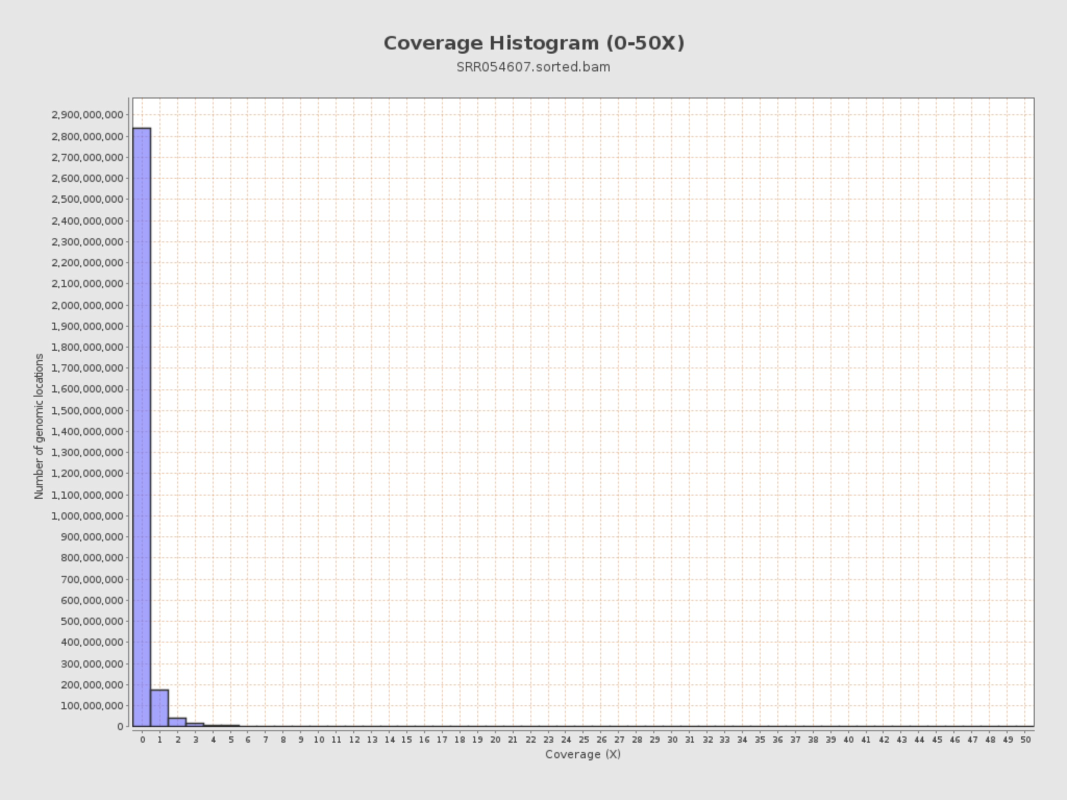
3. Results : Coverage across reference



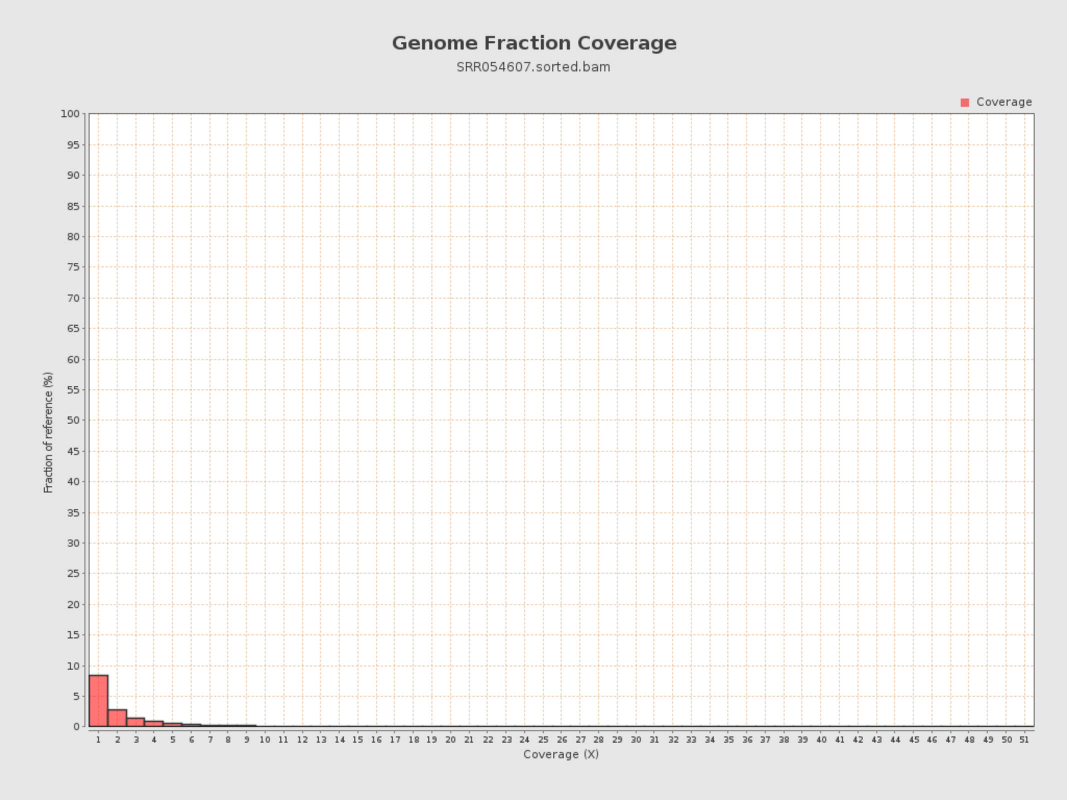
4. Results : Coverage Histogram



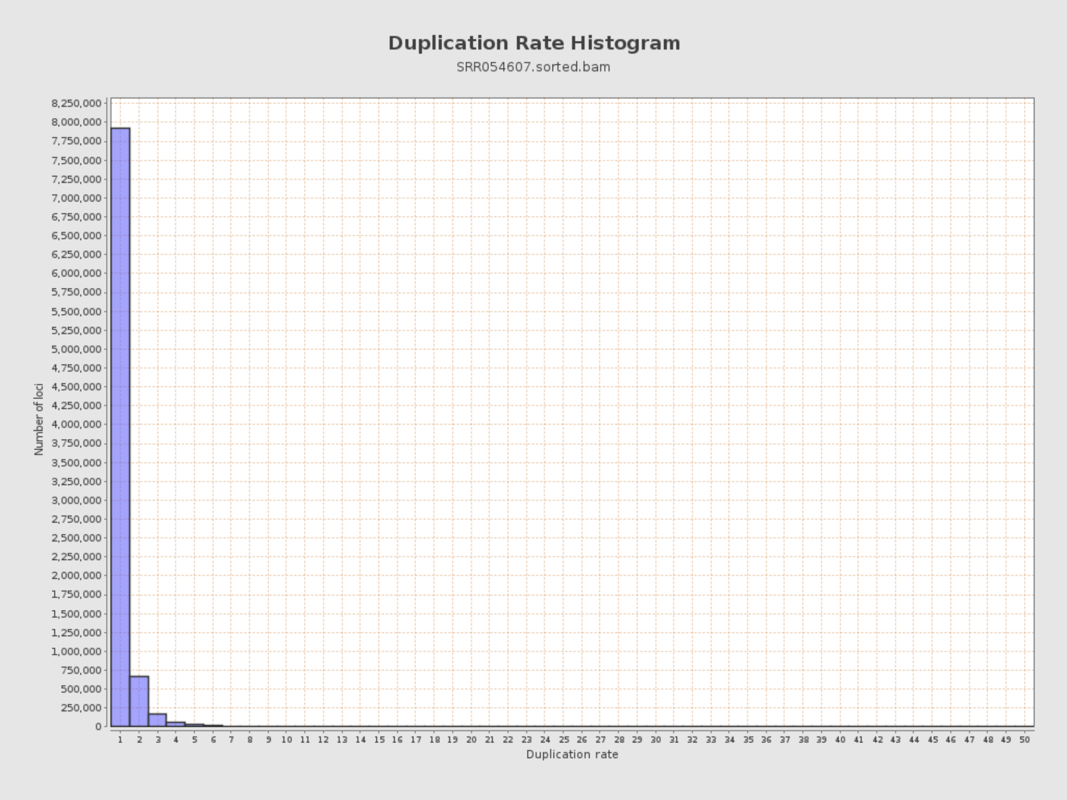
5. Results : Coverage Histogram (0-50X)



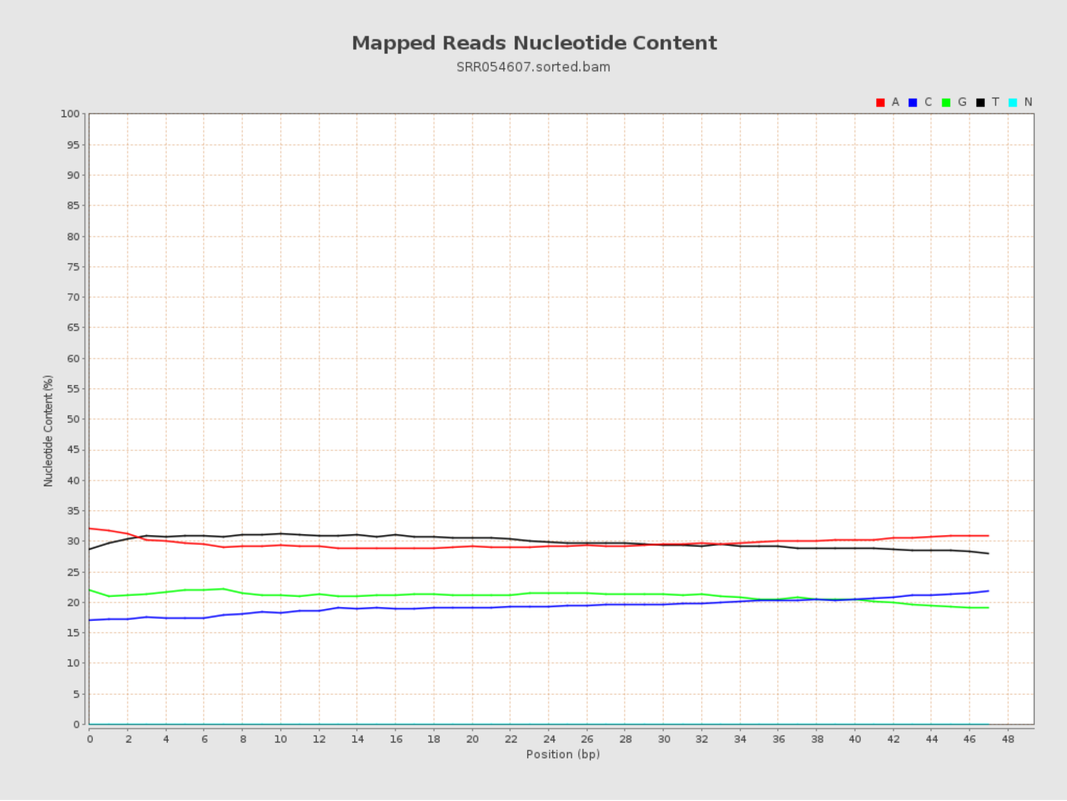
6. Results : Genome Fraction Coverage



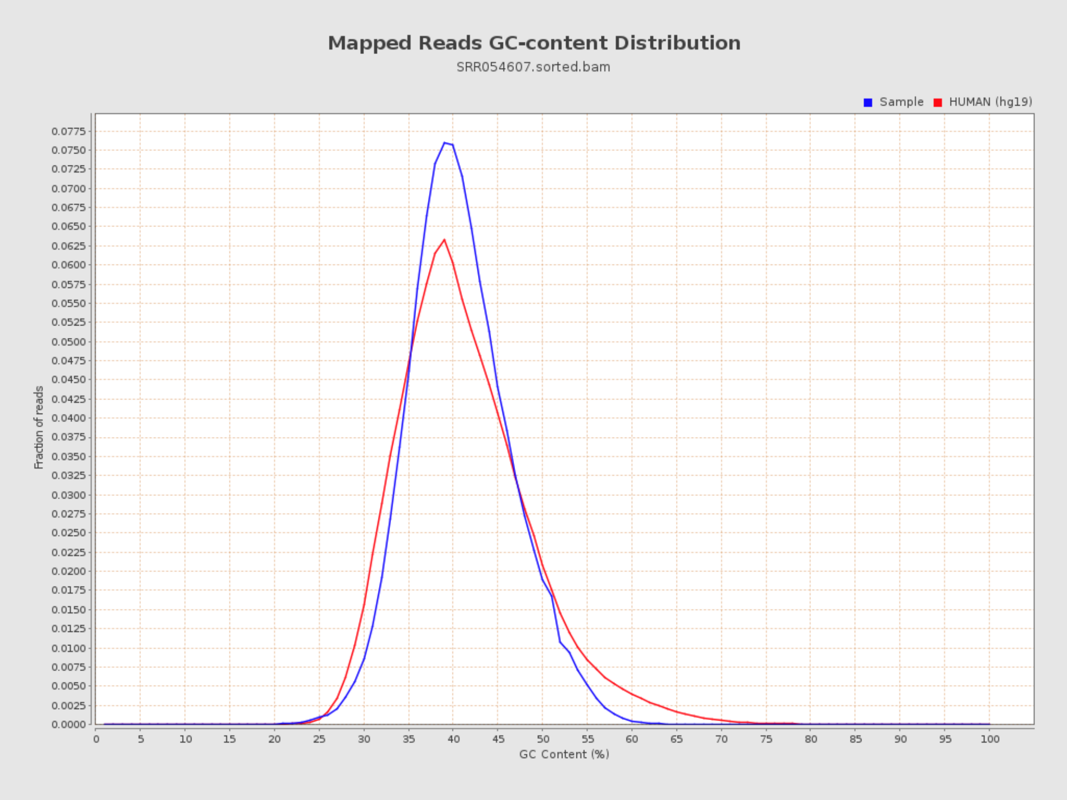
7. Results : Duplication Rate Histogram



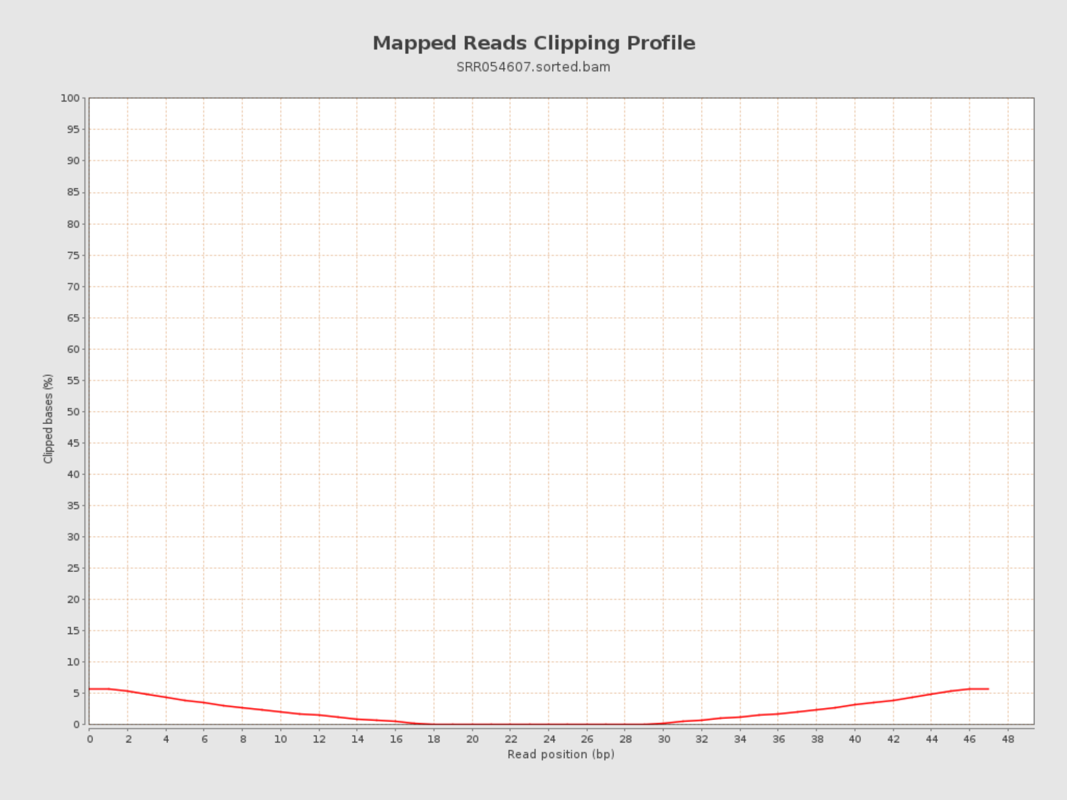
8. Results : Mapped Reads Nucleotide Content



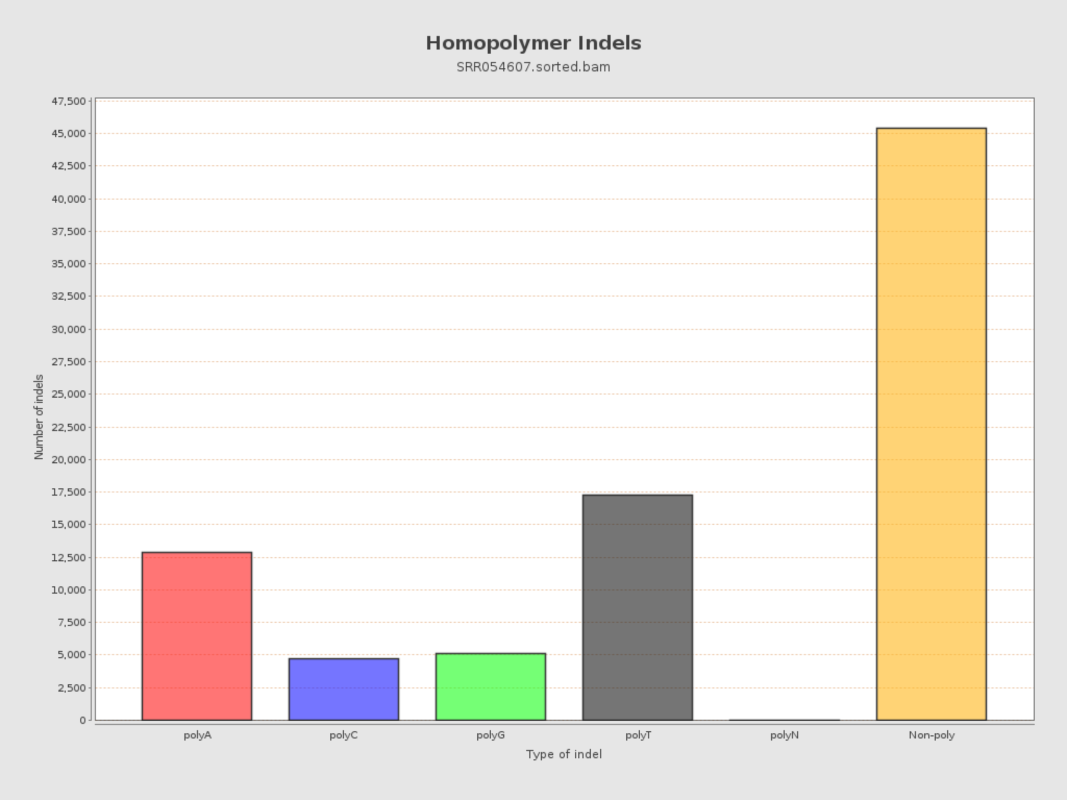
9. Results : Mapped Reads GC-content Distribution



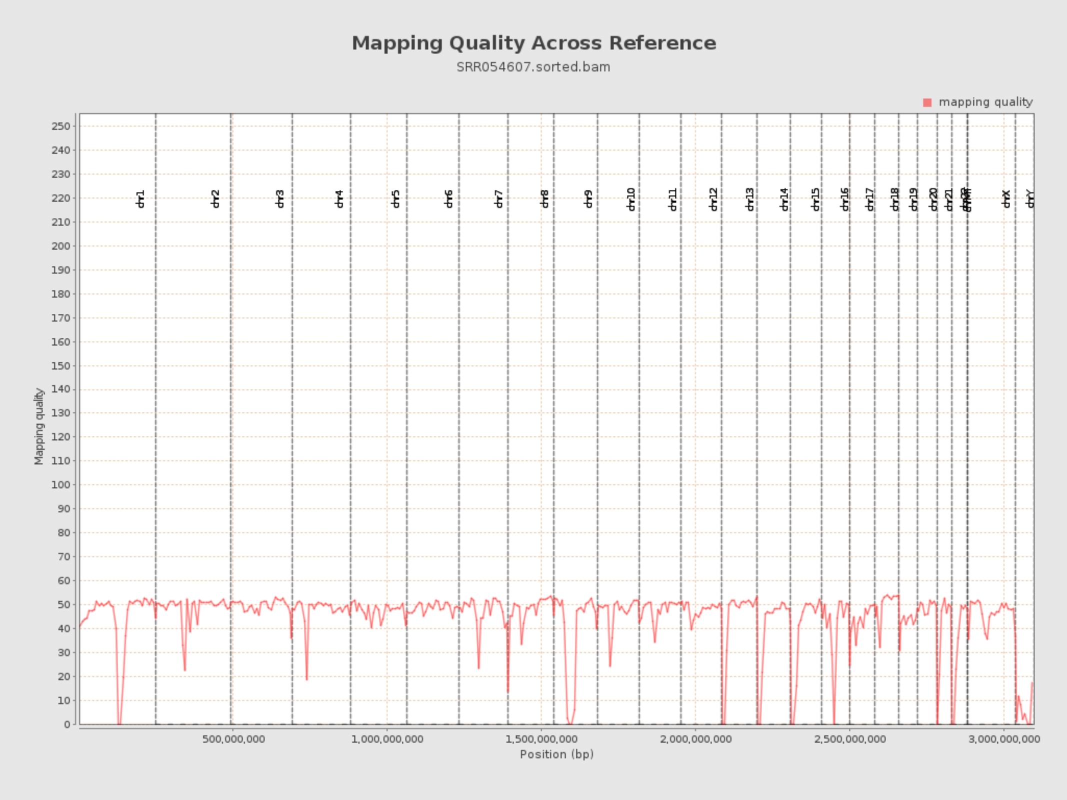
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram