

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 18:57:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089662.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_SRR089662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 18:57:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,576,523
Mapped reads	11,366,139 / 83.72%
Unmapped reads	2,210,384 / 16.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	383 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,346,780 / 24.65%
Duplication rate	19.75%
Clipped reads	796,905 / 5.87%

2.2. ACGT Content

Number/percentage of A's	161,704,639 / 30.03%
Number/percentage of C's	103,443,562 / 19.21%
Number/percentage of T's	156,265,992 / 29.02%
Number/percentage of G's	117,133,726 / 21.75%
Number/percentage of N's	320 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.174

Standard Deviation	1.3305
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2.4. Mapping Quality

Mean Mapping Quality	45.35
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2.5. Mismatches and indels

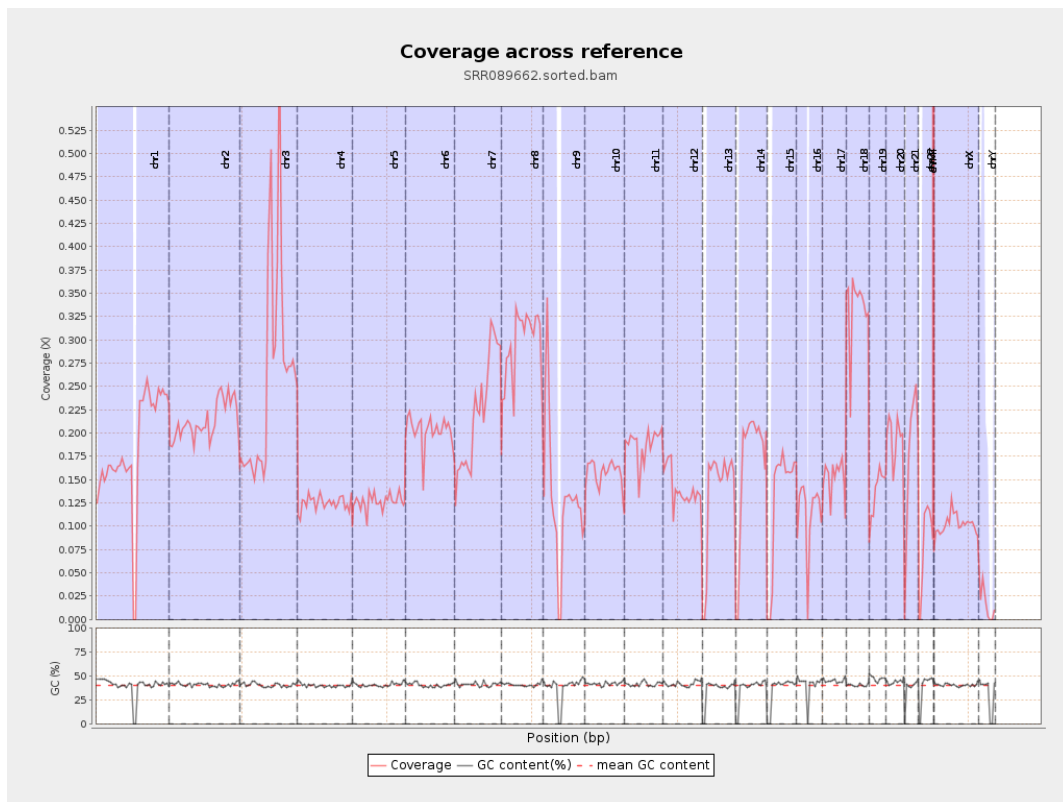
General error rate	0.48%
Mismatches	2,565,323
Insertions	20,989
Mapped reads with at least one insertion	0.18%
Deletions	73,832
Mapped reads with at least one deletion	0.65%
Homopolymer indels	48.19%

2.6. Chromosome stats

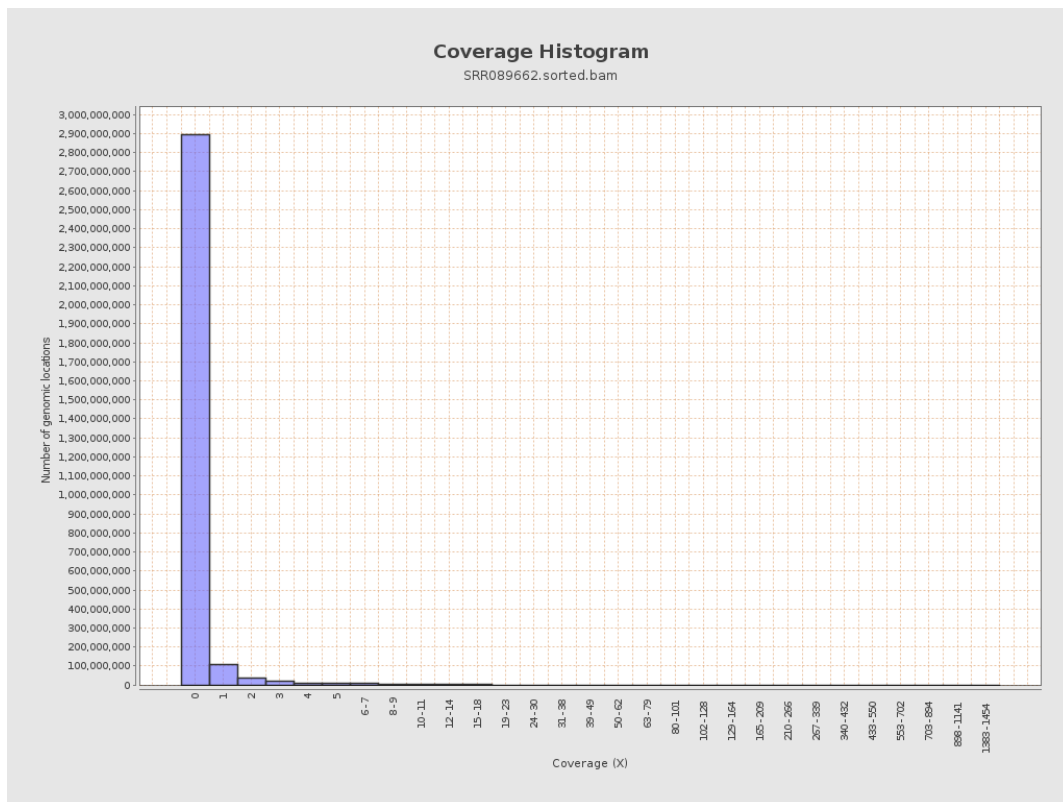
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	45462476	0.1824	1.3511
chr2	243199373	51913477	0.2135	1.6626
chr3	198022430	51071774	0.2579	1.6518
chr4	191154276	23860282	0.1248	0.9854
chr5	180915260	22859429	0.1264	0.996
chr6	171115067	34654960	0.2025	1.3845
chr7	159138663	35823813	0.2251	1.6171

chr8	146364022	43395480	0.2965	1.8958
chr9	141213431	18662448	0.1322	1.1226
chr10	135534747	21520775	0.1588	1.1962
chr11	135006516	25260244	0.1871	1.3123
chr12	133851895	18601960	0.139	1.0525
chr13	115169878	15460026	0.1342	1.0323
chr14	107349540	17839818	0.1662	1.2514
chr15	102531392	13348113	0.1302	1.0276
chr16	90354753	10309176	0.1141	0.9171
chr17	81195210	12328201	0.1518	1.1238
chr18	78077248	26103001	0.3343	1.9051
chr19	59128983	8190040	0.1385	1.5224
chr20	63025520	12104459	0.1921	1.2881
chr21	48129895	8490644	0.1764	1.287
chr22	51304566	4058692	0.0791	0.7434
chrMT	16571	579768	34.9869	51.7641
chrX	155270560	15788118	0.1017	0.9146
chrY	59373566	970515	0.0163	0.3612

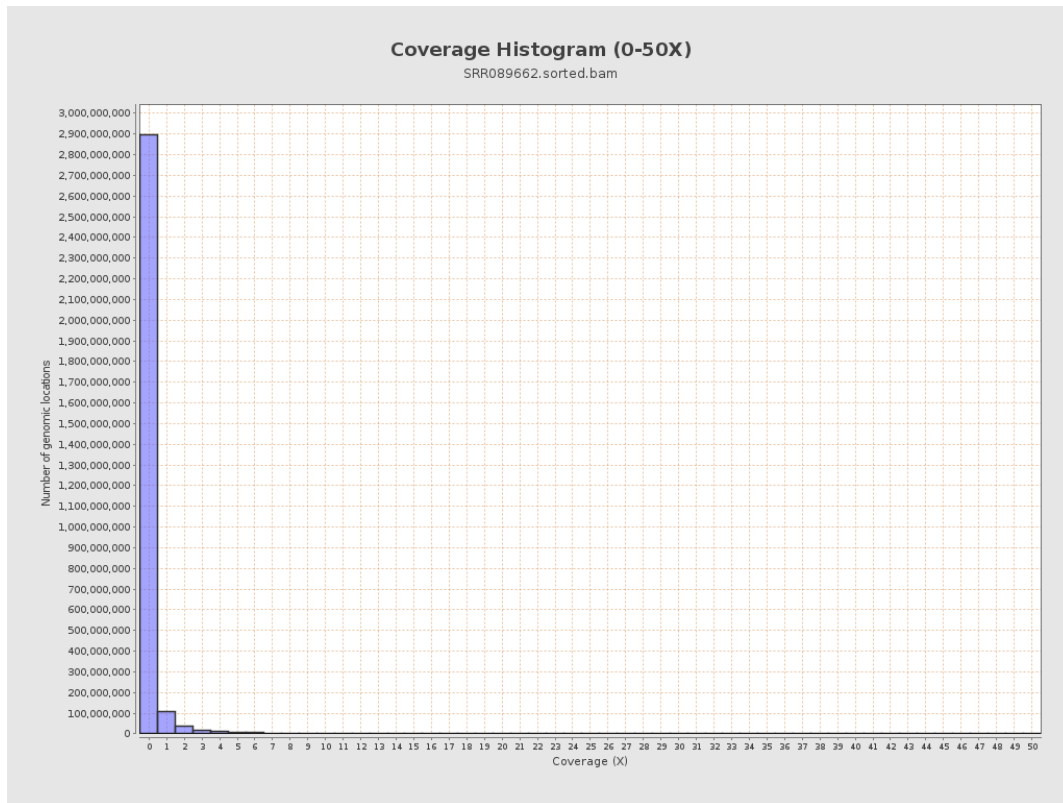
3. Results : Coverage across reference



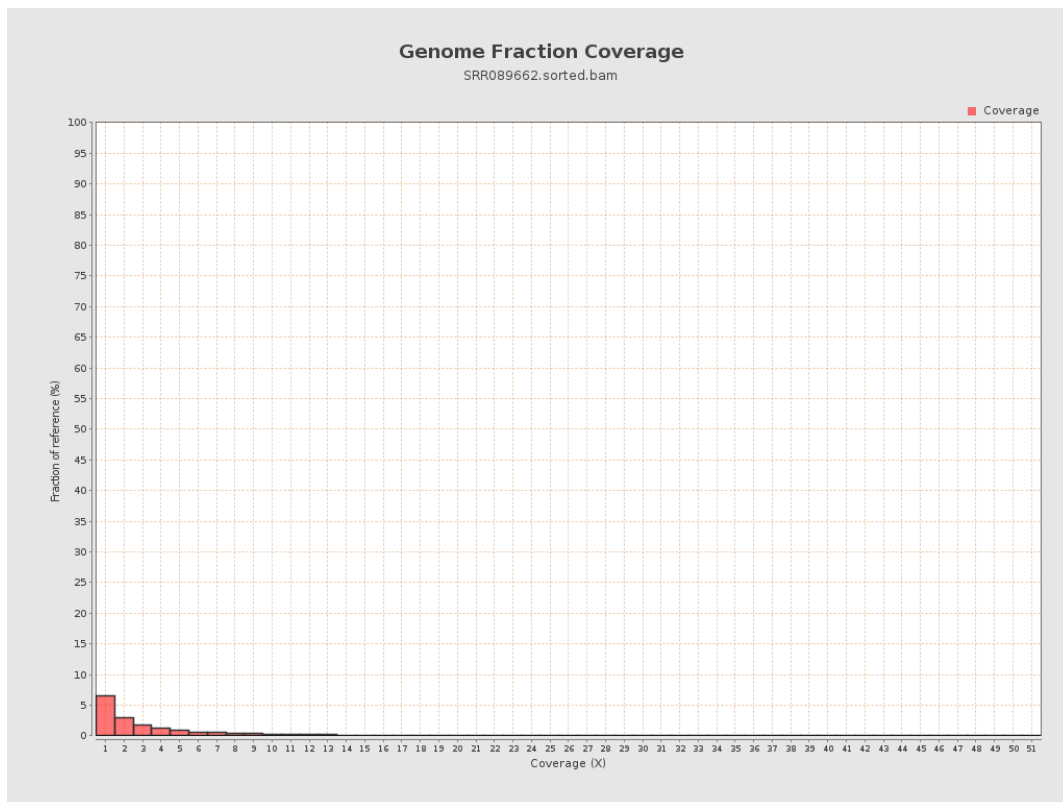
4. Results : Coverage Histogram



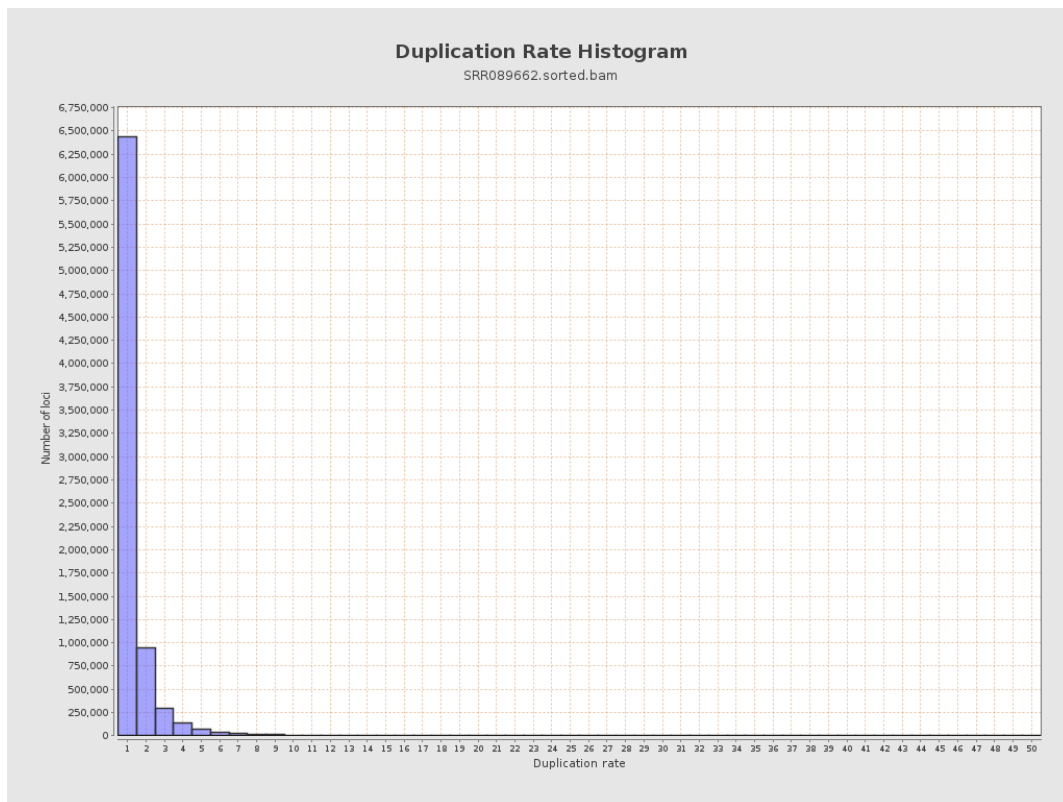
5. Results : Coverage Histogram (0-50X)



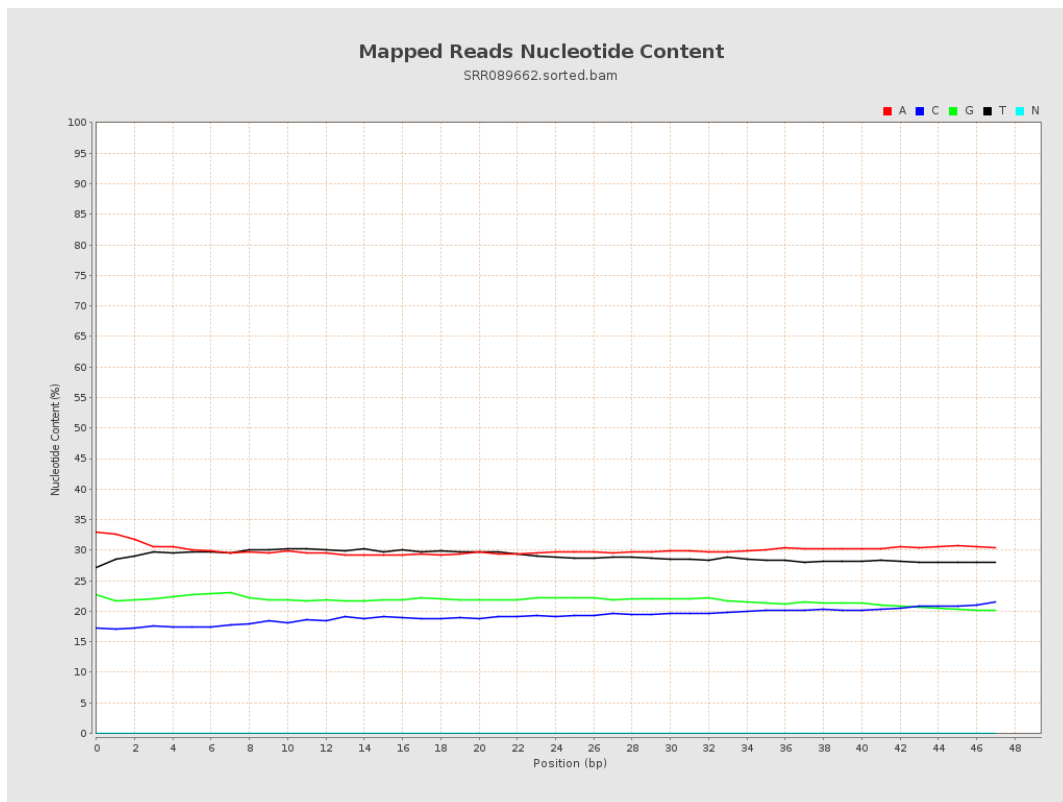
6. Results : Genome Fraction Coverage



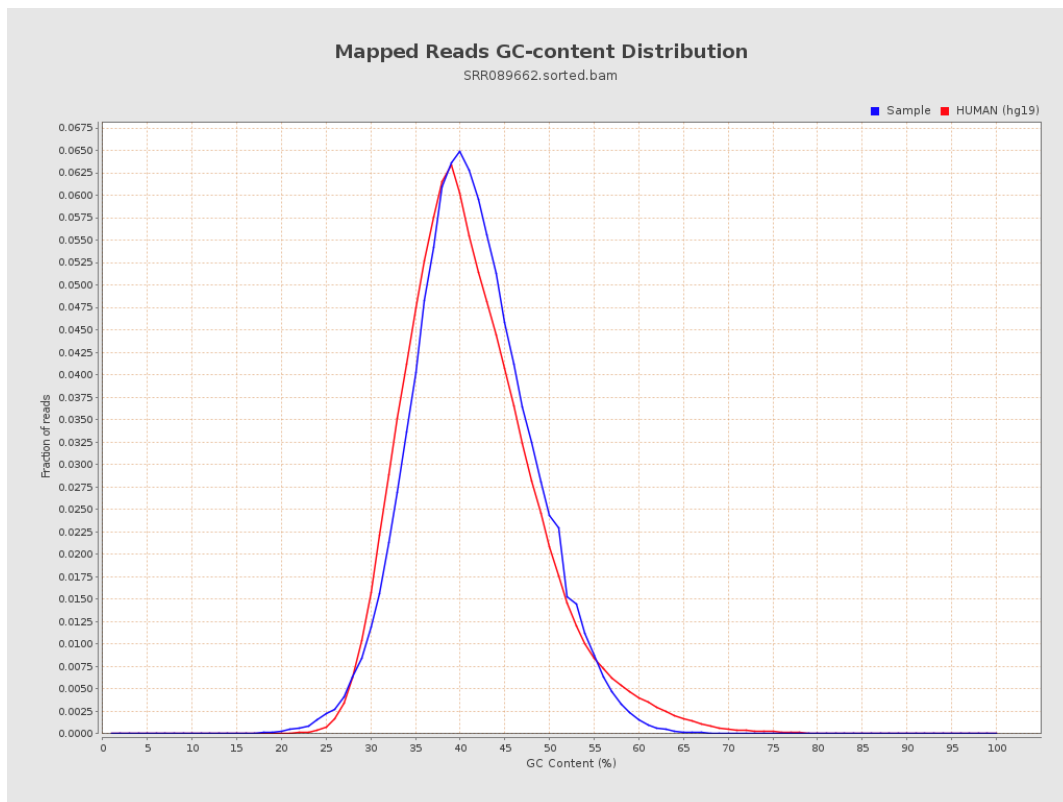
7. Results : Duplication Rate Histogram



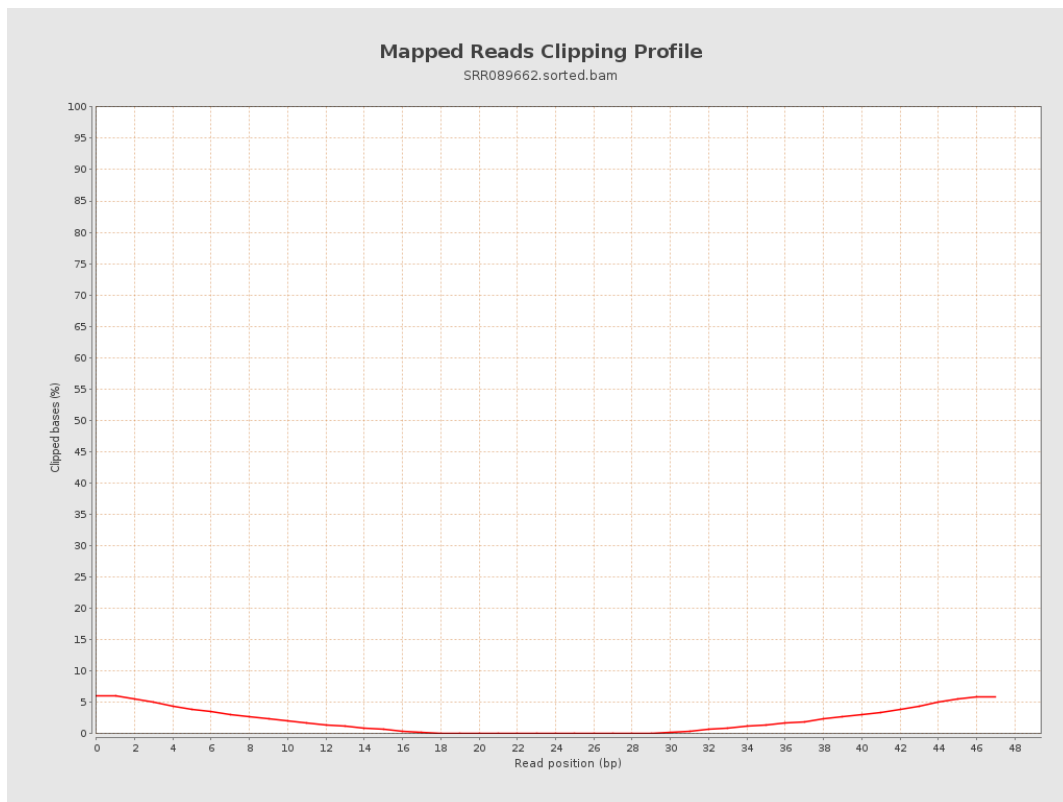
8. Results : Mapped Reads Nucleotide Content



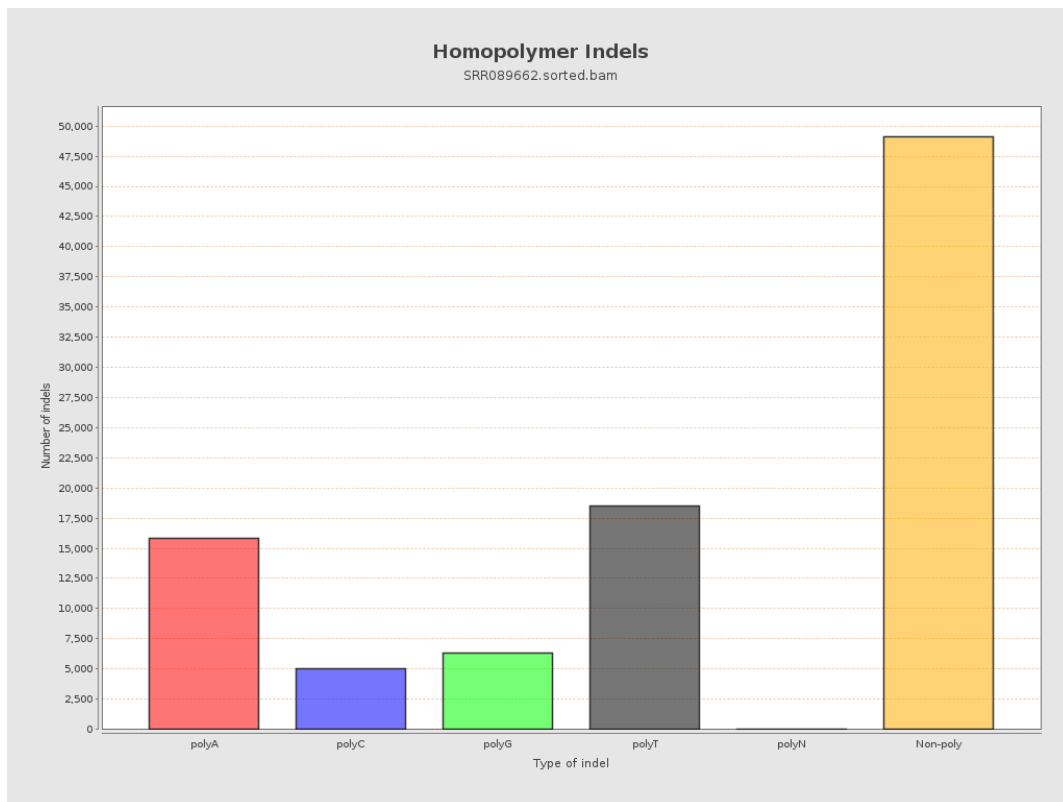
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

