Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:10:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089603.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_SRR089603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:10:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,821,636
Mapped reads	7,462,830 / 75.98%
Unmapped reads	2,358,806 / 24.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	274 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,948,659 / 30.02%
Duplication rate	29.39%
Clipped reads	985,957 / 10.04%

2.2. ACGT Content

Number/percentage of A's	112,636,515 / 32.25%
Number/percentage of C's	67,020,795 / 19.19%
Number/percentage of T's	94,038,560 / 26.93%
Number/percentage of G's	75,509,757 / 21.62%
Number/percentage of N's	3,836 / 0%
GC Percentage	40.82%

2.3. Coverage

Mean	0.1128

Standard Deviation	1.0824

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

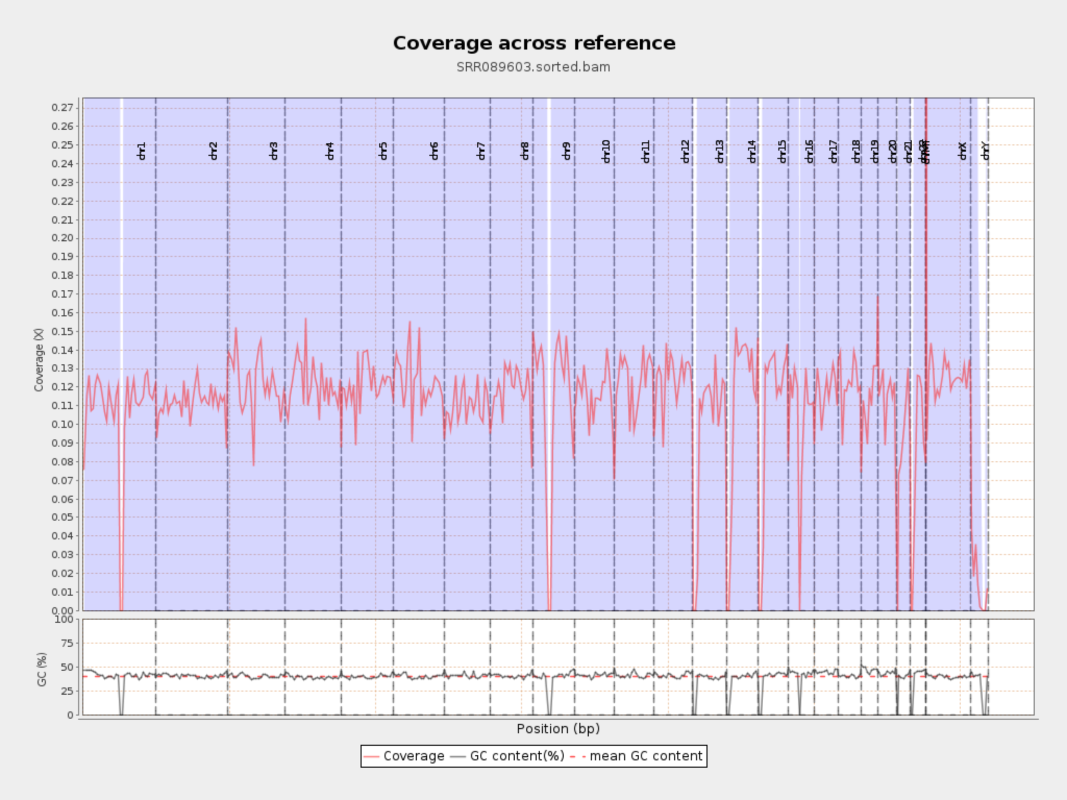
General error rate	0.58%
Mismatches	1,990,385
Insertions	16,167
Mapped reads with at least one insertion	0.22%
Deletions	48,243
Mapped reads with at least one deletion	0.64%
Homopolymer indels	45.1%

2.6. Chromosome stats

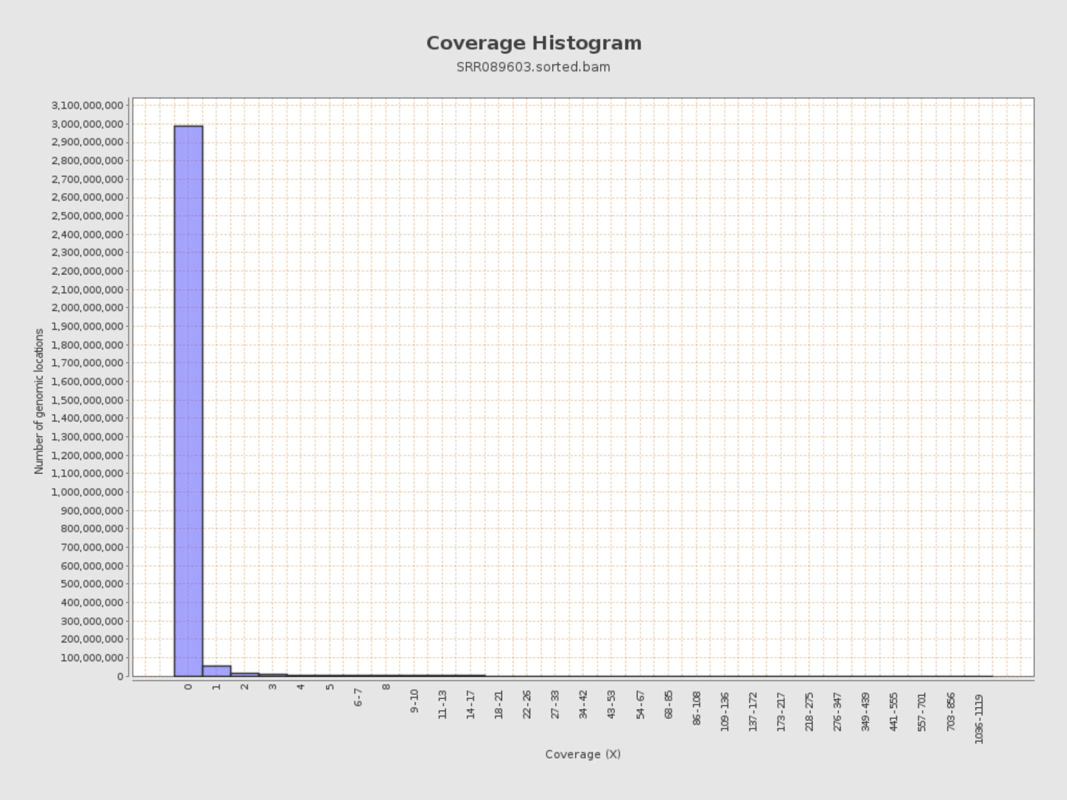
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26657582	0.107	1.1347
chr2	243199373	27281982	0.1122	1.1599
chr3	198022430	24238249	0.1224	1.0687
chr4	191154276	23279806	0.1218	1.0939
chr5	180915260	22019451	0.1217	1.0575
chr6	171115067	21107266	0.1234	1.1438
chr7	159138663	17579431	0.1105	1.114

chr8	146364022	17277152	0.118	1.2439
chr9	141213431	15814119	0.112	1.0355
chr10	135534747	15861216	0.117	1.0622
chr11	135006516	16547597	0.1226	1.1937
chr12	133851895	16750555	0.1251	1.0814
chr13	115169878	11078921	0.0962	0.97
chr14	107349540	12059311	0.1123	1.0905
chr15	102531392	10647518	0.1038	0.955
chr16	90354753	9196408	0.1018	0.983
chr17	81195210	9644657	0.1188	1.0366
chr18	78077248	9571832	0.1226	1.1307
chr19	59128983	6735199	0.1139	1.0898
chr20	63025520	7218404	0.1145	1.0343
chr21	48129895	4247911	0.0883	0.9444
chr22	51304566	4083164	0.0796	0.7983
chrMT	16571	92358	5.5735	13.9399
chrX	155270560	19437821	0.1252	1.1137
chrY	59373566	853699	0.0144	0.3142

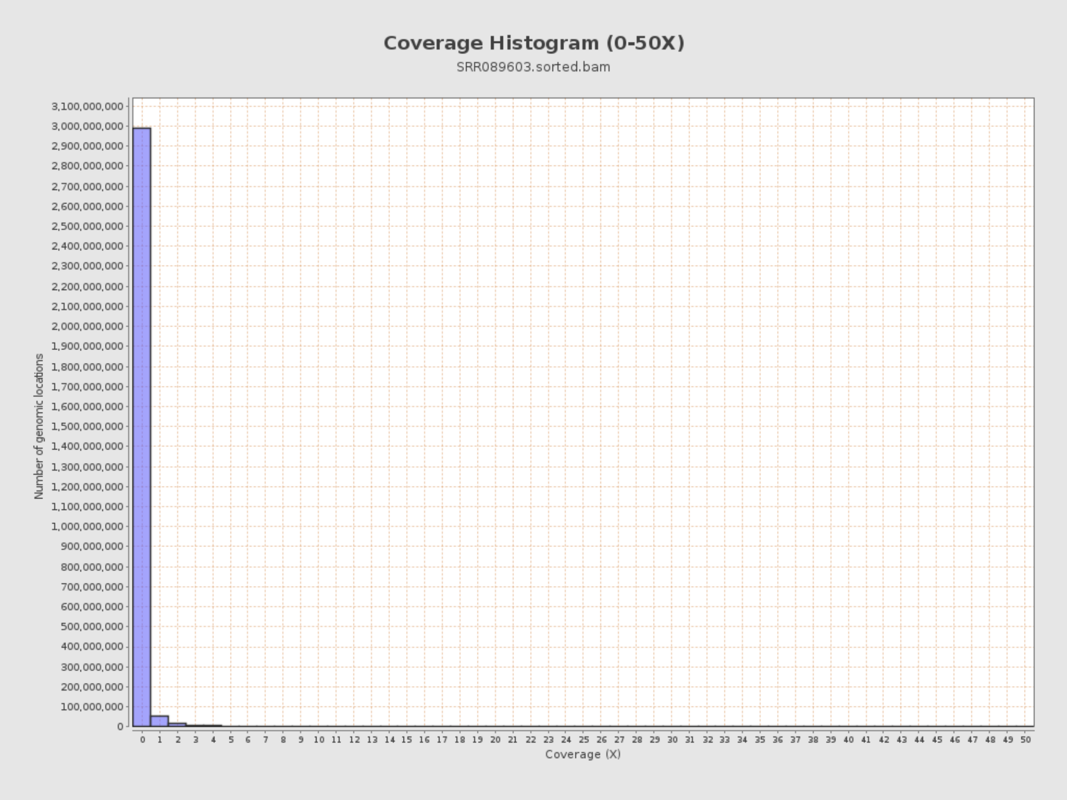
3. Results : Coverage across reference



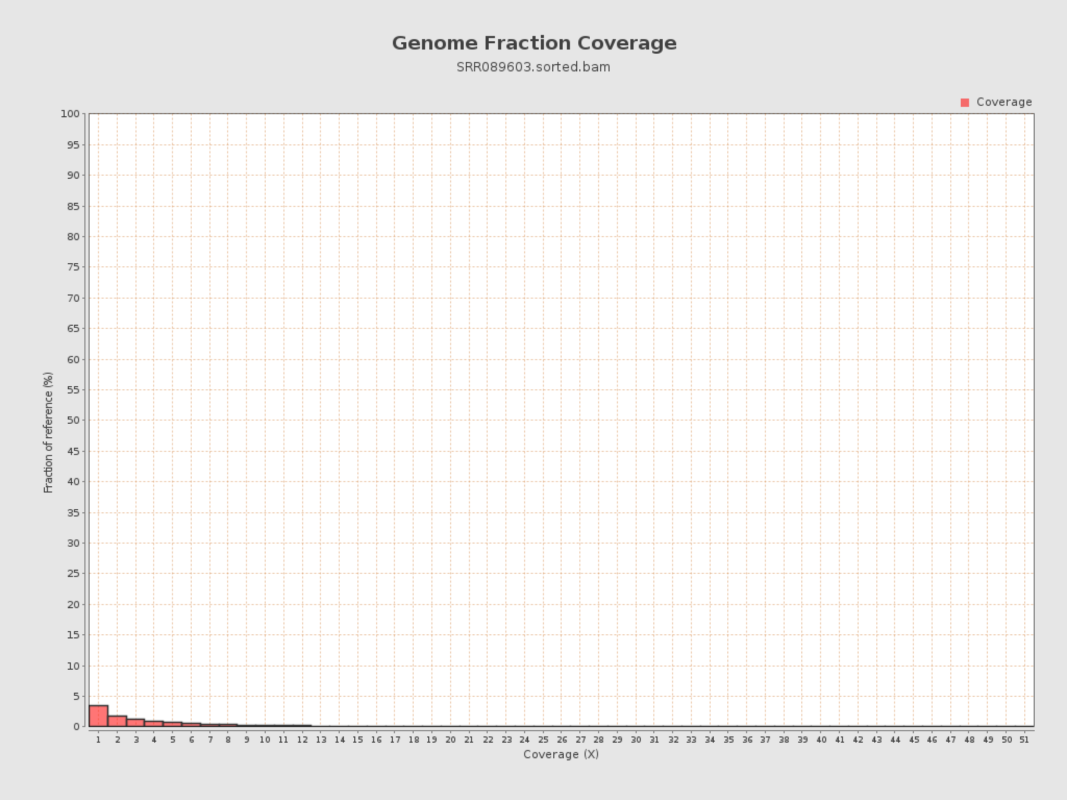
4. Results : Coverage Histogram



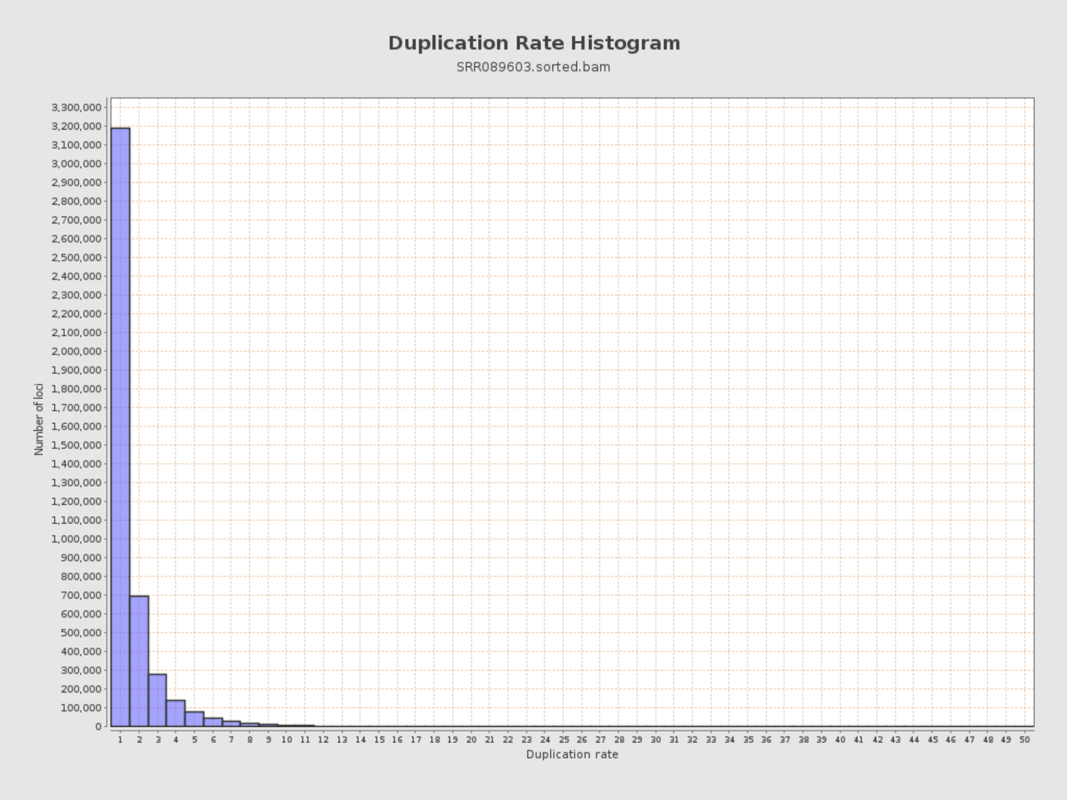
5. Results : Coverage Histogram (0-50X)



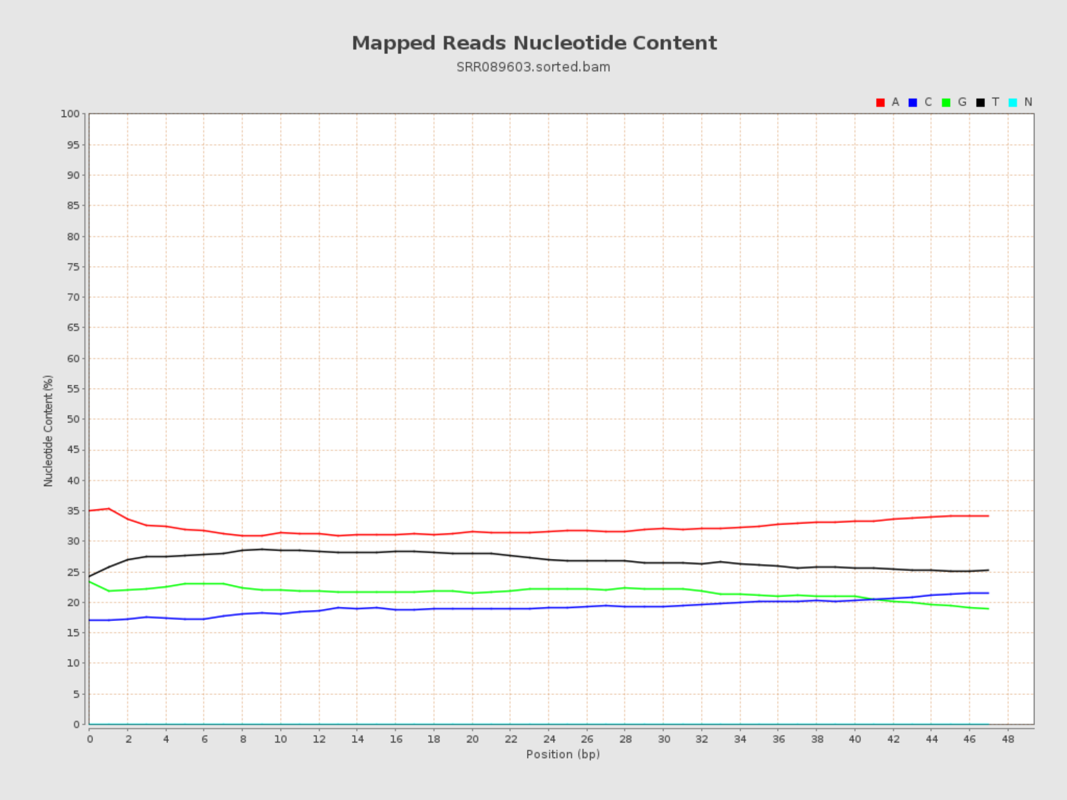
6. Results : Genome Fraction Coverage



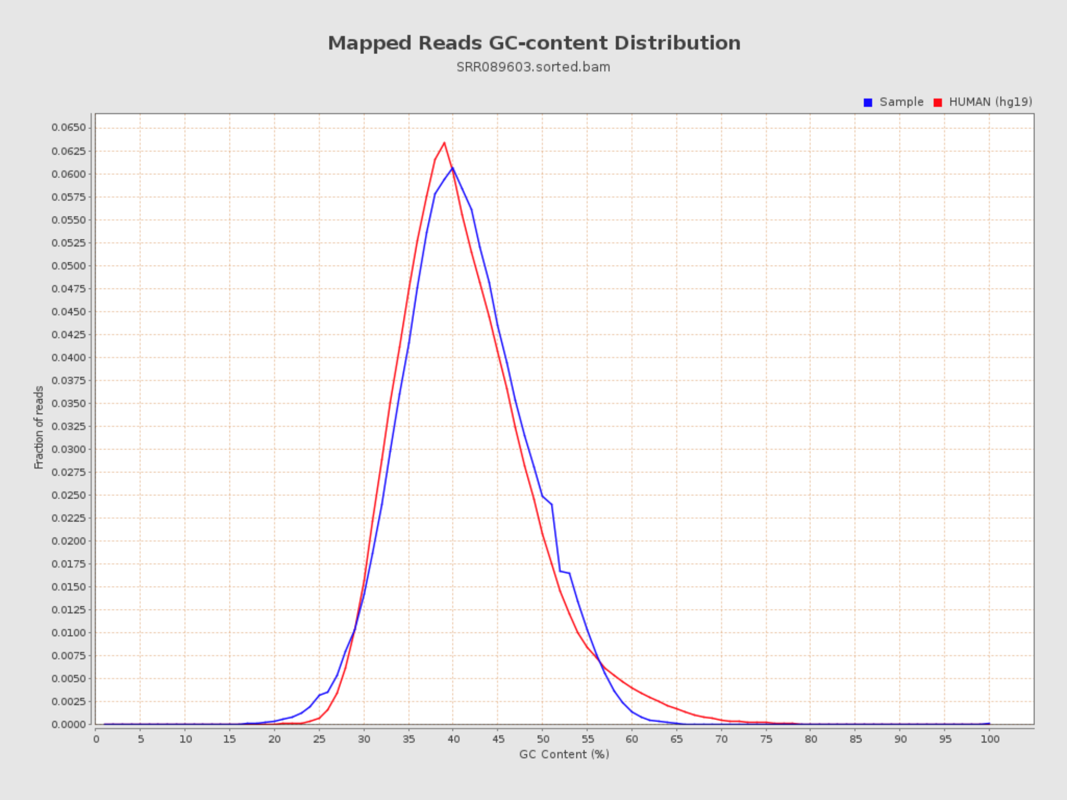
7. Results : Duplication Rate Histogram



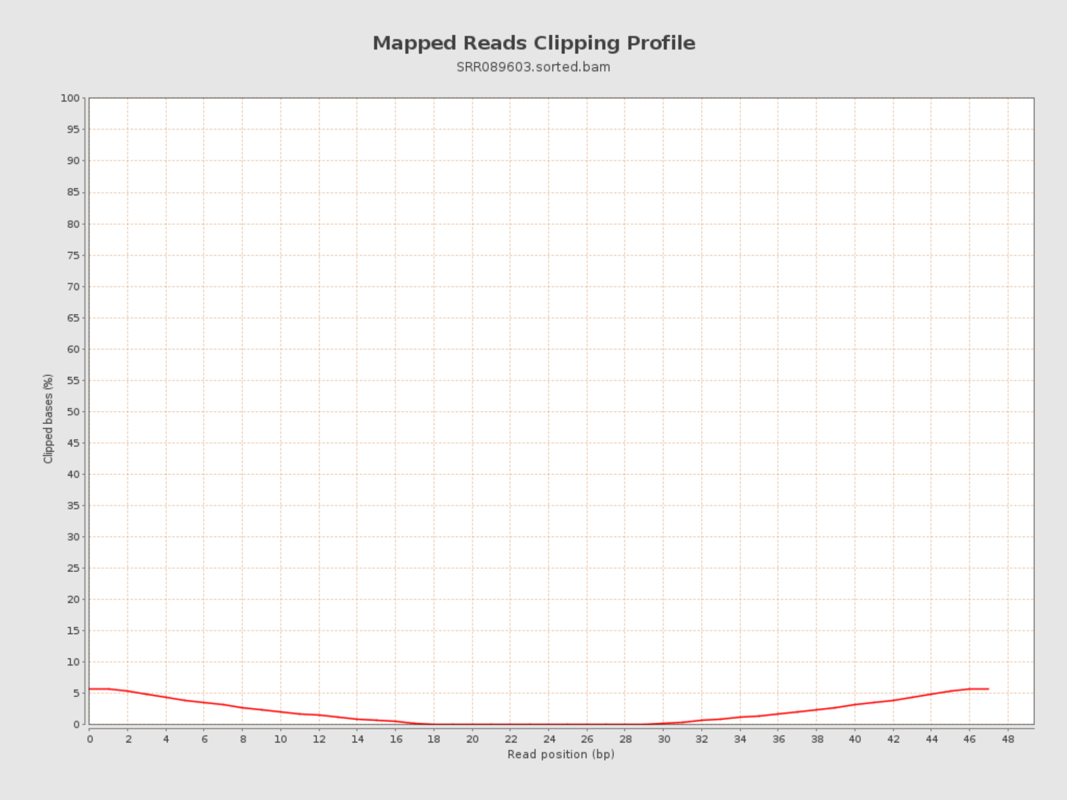
8. Results : Mapped Reads Nucleotide Content



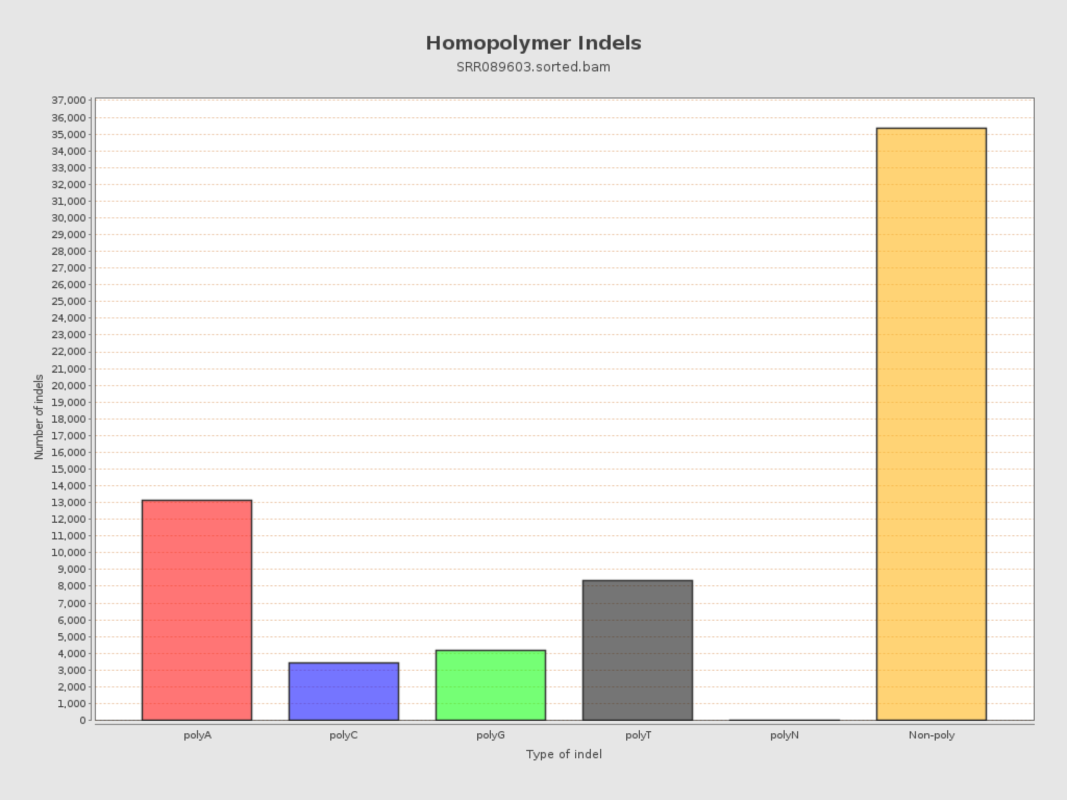
9. Results : Mapped Reads GC-content Distribution



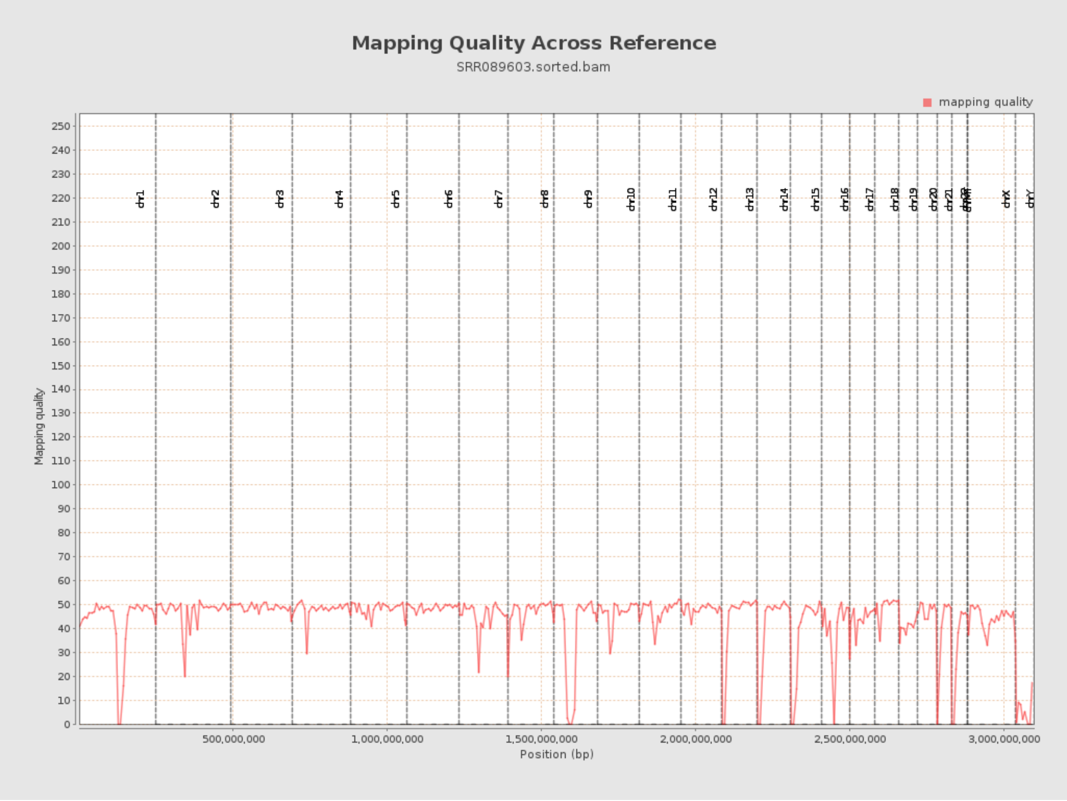
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram