Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 21:05:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089699.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_SRR089699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 21:05:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,819,058
Mapped reads	19,049,141 / 83.48%
Unmapped reads	3,769,917 / 16.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	807 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,681,055 / 7.37%
Duplication rate	6.25%
Clipped reads	2,569,091 / 11.26%

2.2. ACGT Content

Number/percentage of A's	259,356,199 / 29.14%
Number/percentage of C's	189,528,406 / 21.29%
Number/percentage of T's	249,503,405 / 28.03%
Number/percentage of G's	191,608,512 / 21.53%
Number/percentage of N's	168,709 / 0.02%
GC Percentage	42.82%

2.3. Coverage

Mean	0.2876

Standard Deviation	1.6486

2.4. Mapping Quality

Mean Mapping Quality	41.64

2.5. Mismatches and indels

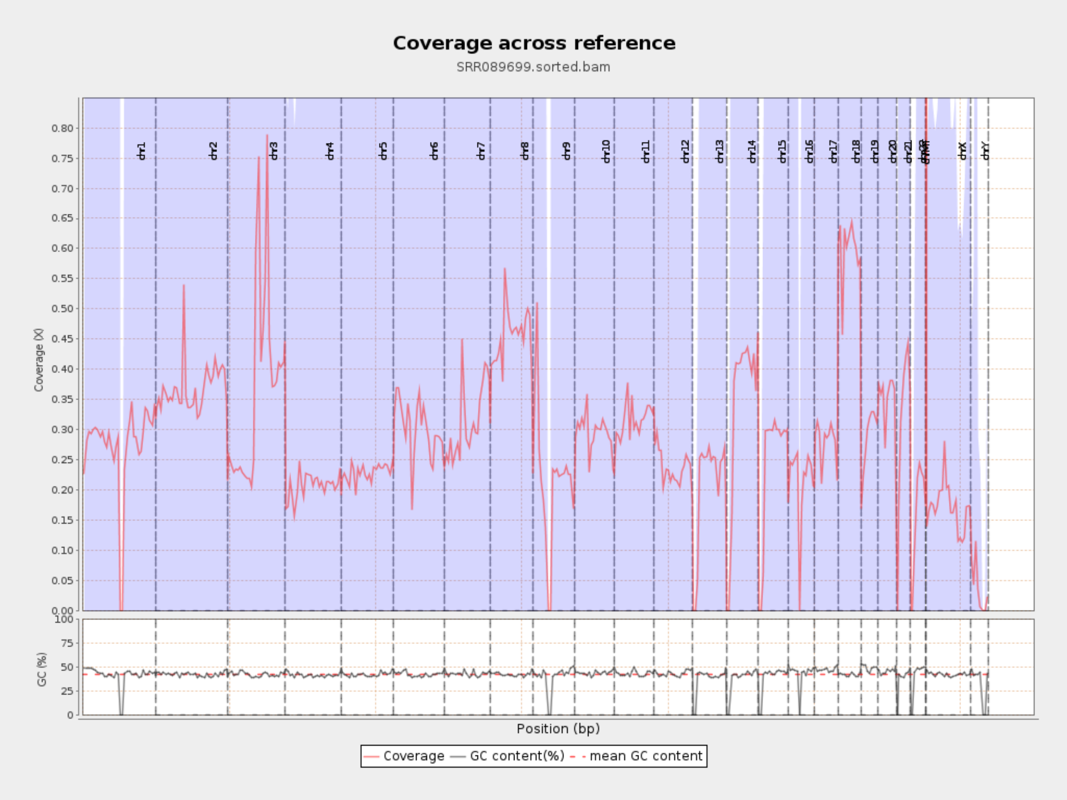
General error rate	0.55%
Mismatches	4,815,234
Insertions	38,783
Mapped reads with at least one insertion	0.2%
Deletions	116,453
Mapped reads with at least one deletion	0.61%
Homopolymer indels	44.06%

2.6. Chromosome stats

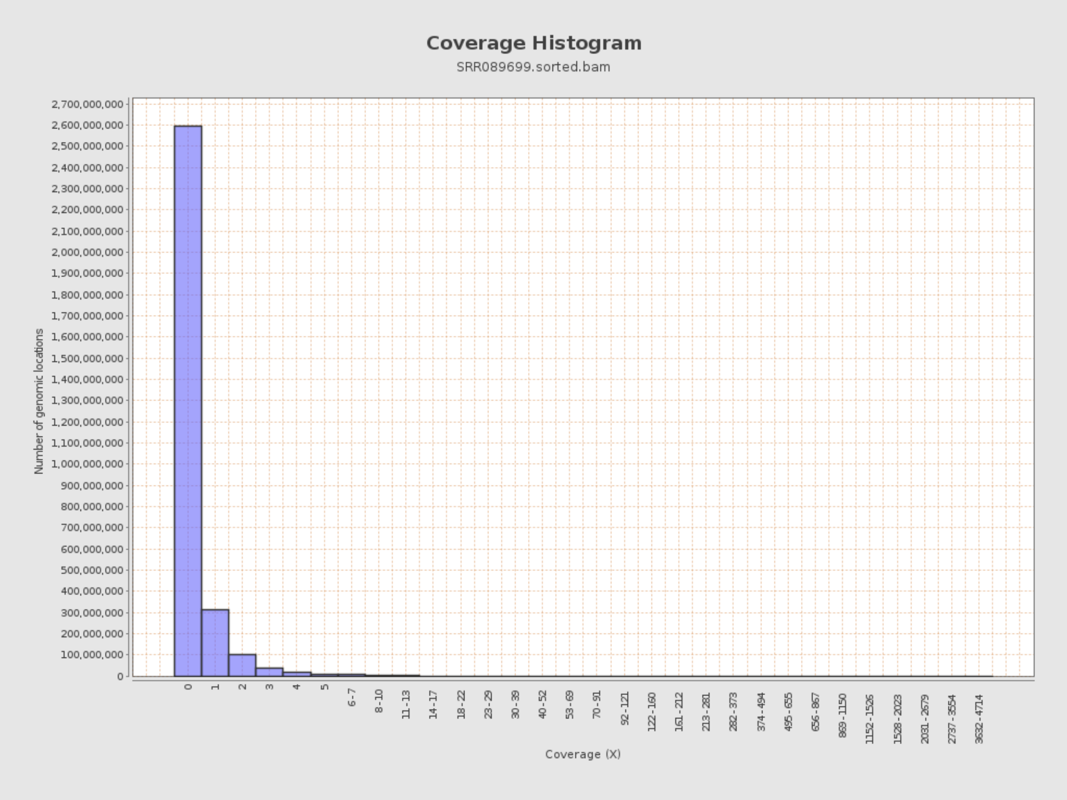
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68025425	0.2729	1.82
chr2	243199373	89782243	0.3692	2.9799
chr3	198022430	72016004	0.3637	1.0925
chr4	191154276	39660798	0.2075	0.8003
chr5	180915260	41394727	0.2288	0.8127
chr6	171115067	51653118	0.3019	1.099
chr7	159138663	49830514	0.3131	2.6008

chr8	146364022	66694364	0.4557	2.3437
chr9	141213431	30870010	0.2186	1.6762
chr10	135534747	40101358	0.2959	1.3086
chr11	135006516	42436466	0.3143	1.6574
chr12	133851895	31862435	0.238	0.8815
chr13	115169878	24076307	0.2091	0.7517
chr14	107349540	36514198	0.3401	1.1194
chr15	102531392	24524311	0.2392	0.8269
chr16	90354753	19015759	0.2105	0.8717
chr17	81195210	23004805	0.2833	1.0841
chr18	78077248	46665700	0.5977	2.5471
chr19	59128983	17198265	0.2909	2.1651
chr20	63025520	22116710	0.3509	1.1087
chr21	48129895	15248408	0.3168	1.1534
chr22	51304566	8152269	0.1589	0.655
chrMT	16571	886139	53.4753	43.9225
chrX	155270560	26446585	0.1703	1.2608
chrY	59373566	2161222	0.0364	0.6702

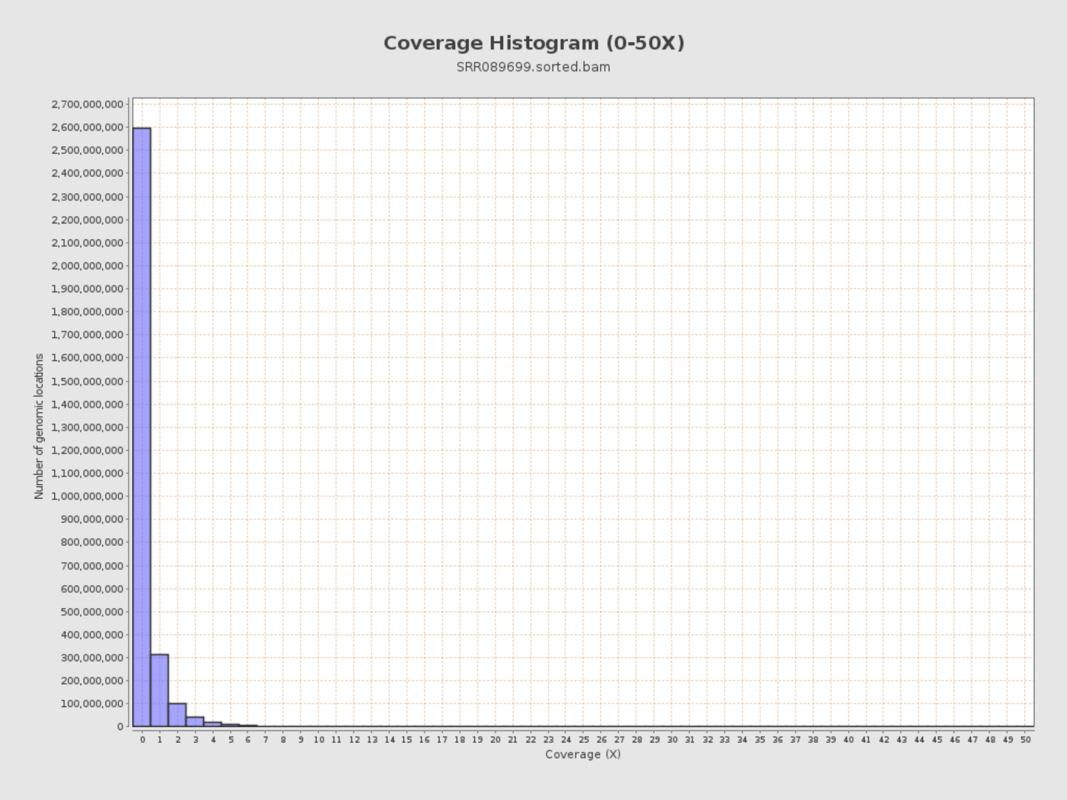
3. Results : Coverage across reference



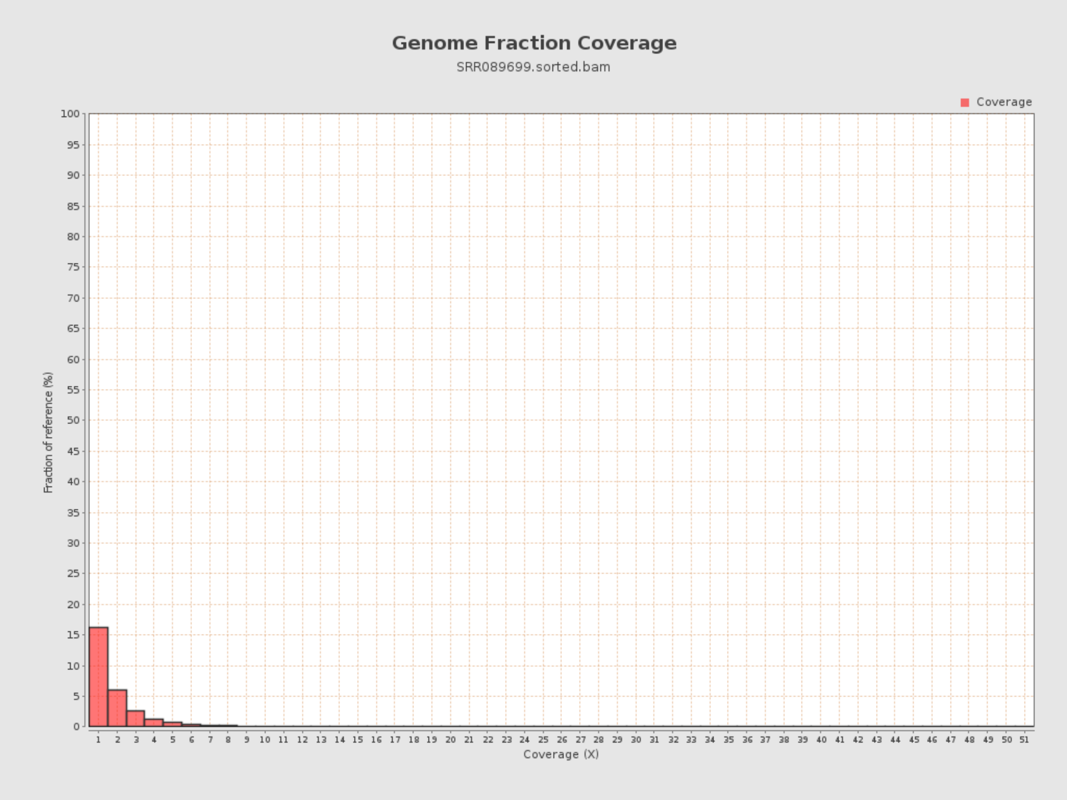
4. Results : Coverage Histogram



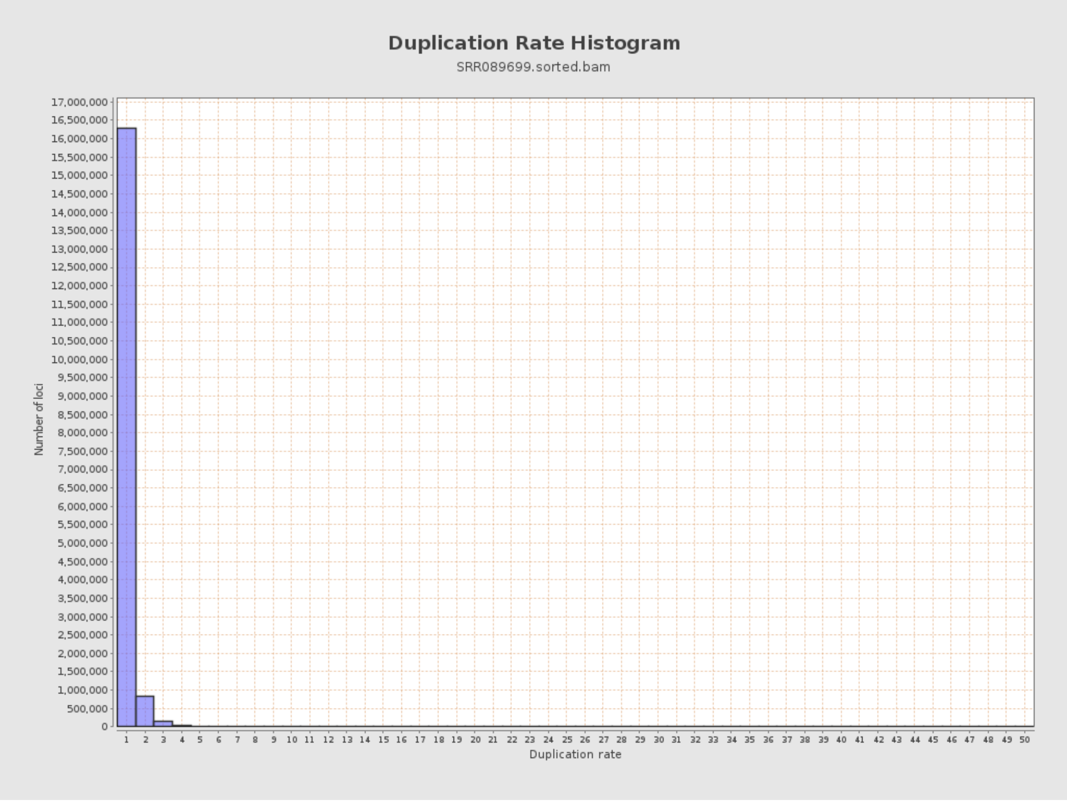
5. Results : Coverage Histogram (0-50X)



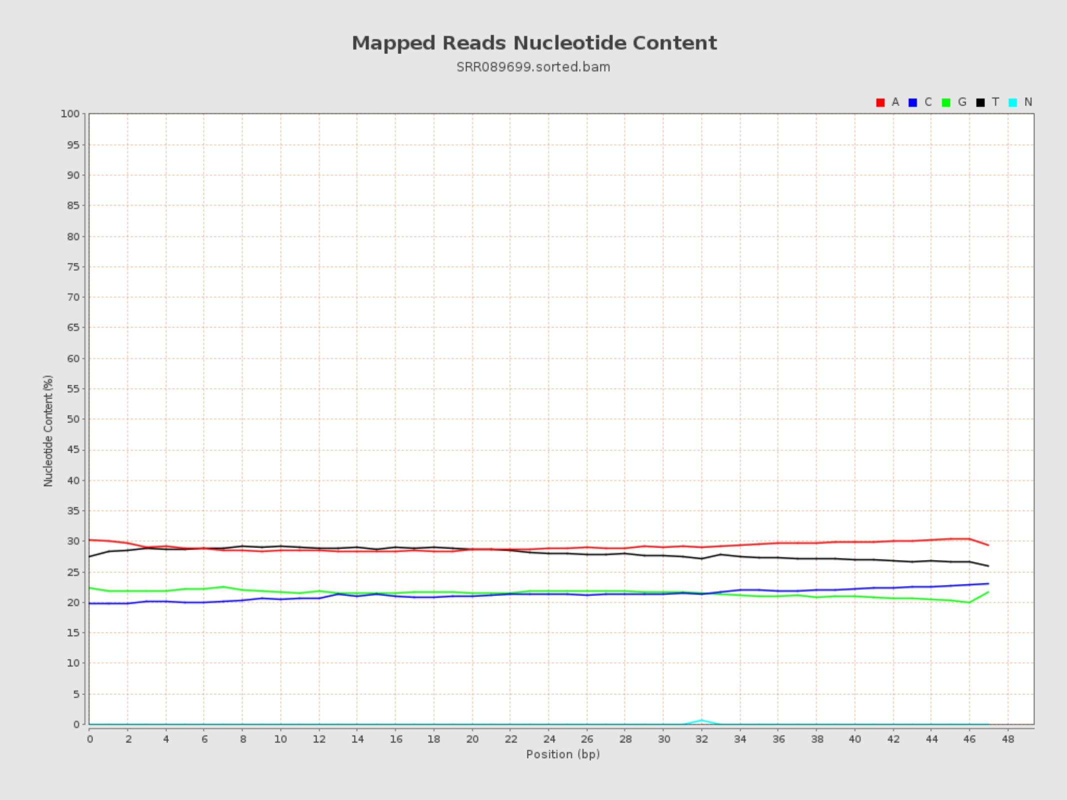
6. Results : Genome Fraction Coverage



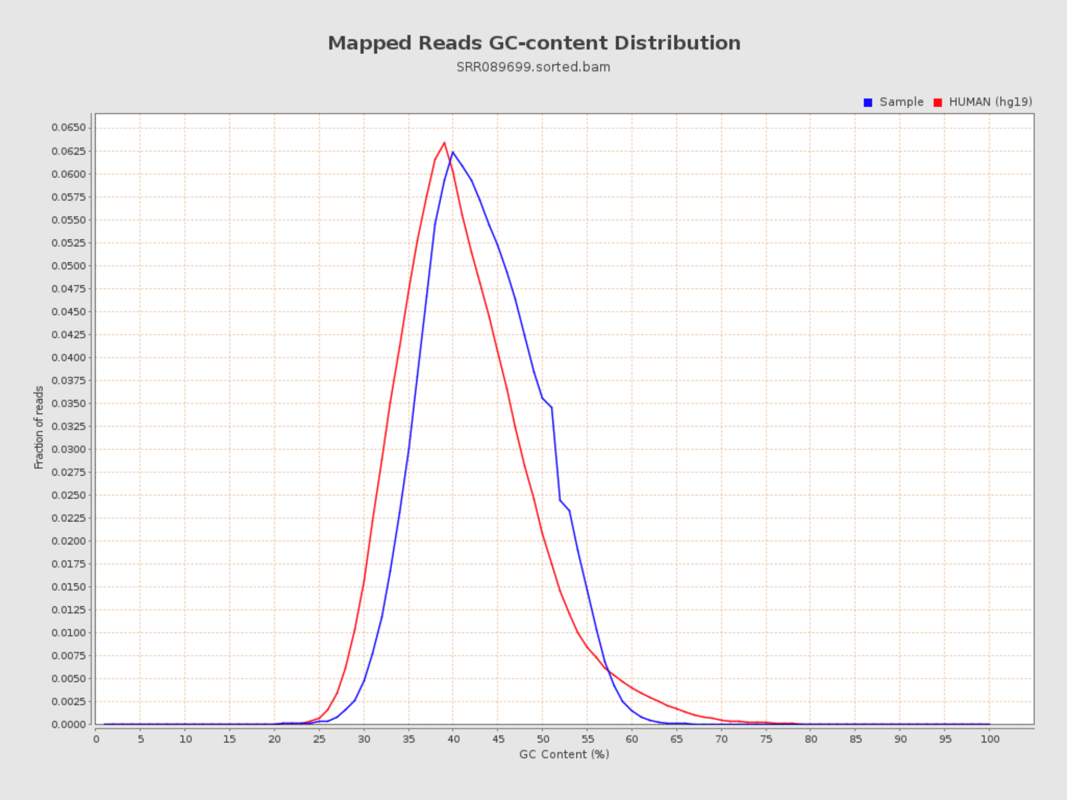
7. Results : Duplication Rate Histogram



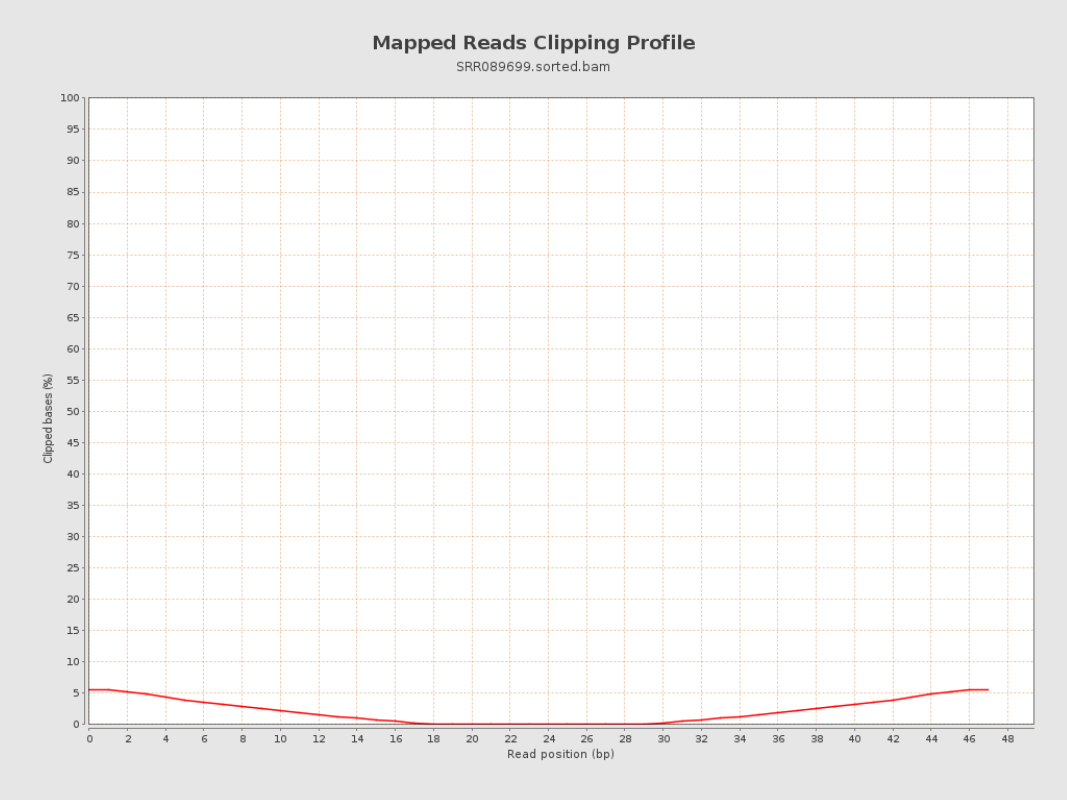
8. Results : Mapped Reads Nucleotide Content



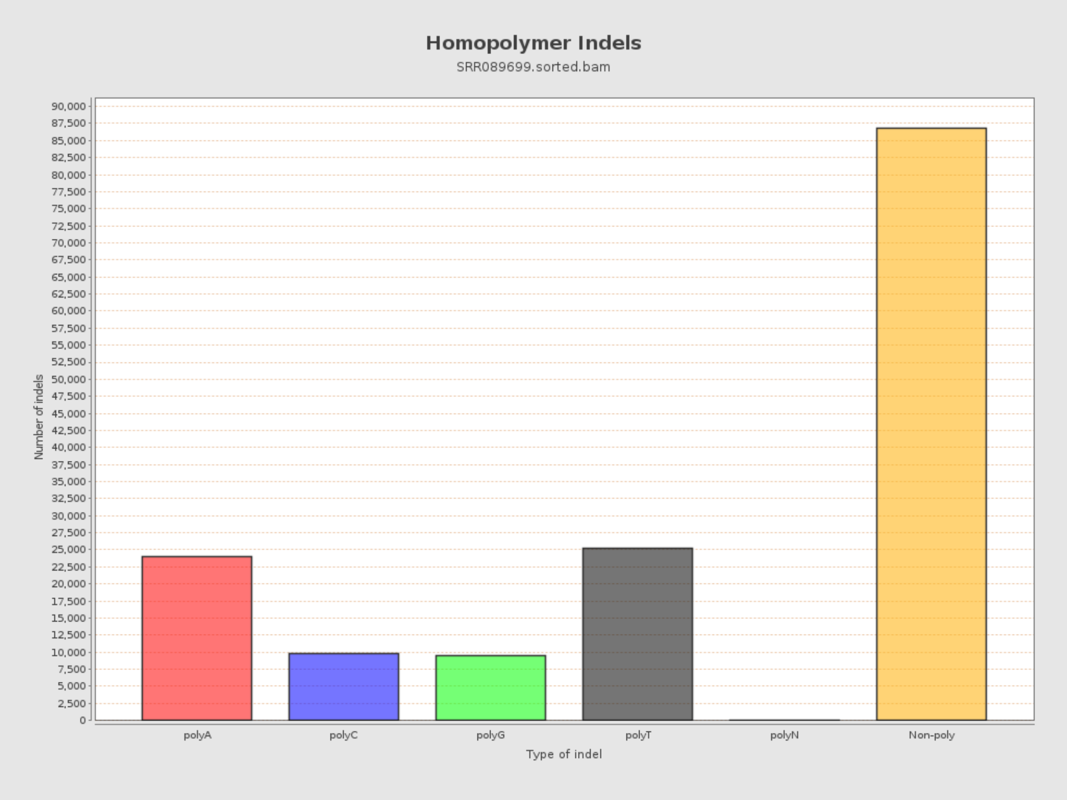
9. Results : Mapped Reads GC-content Distribution



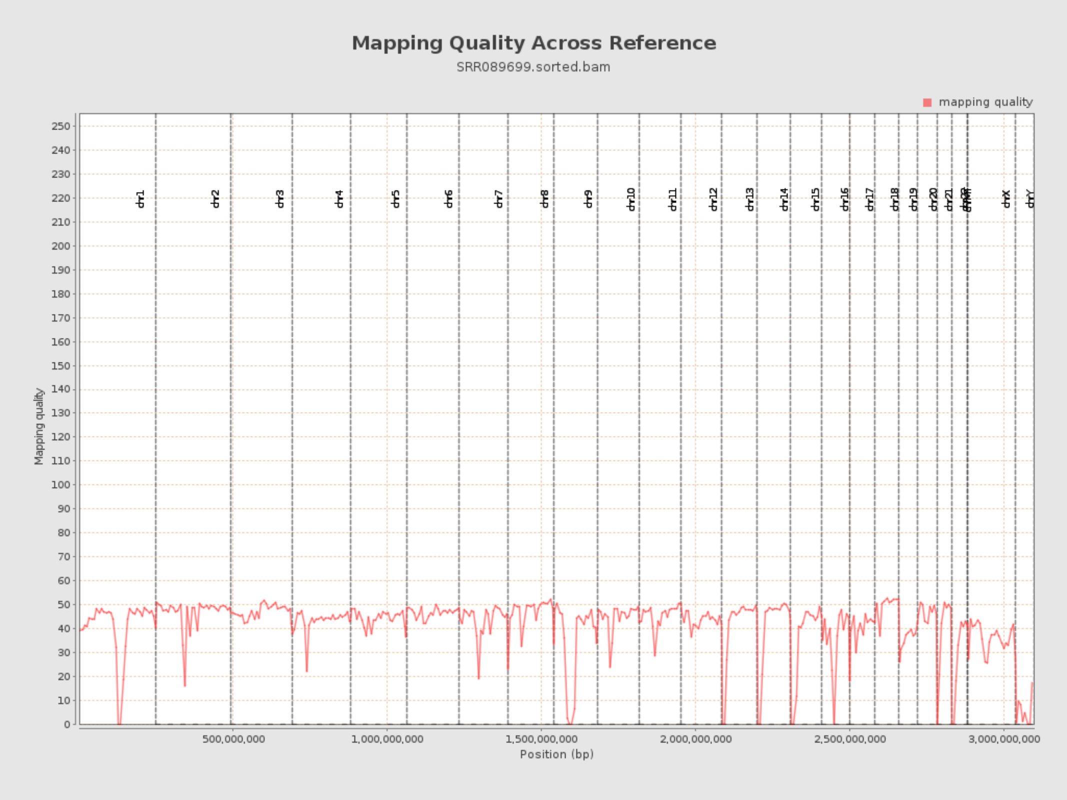
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram