Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 20:37:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089697.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_SRR089697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089697.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 20:37:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,237,049
Mapped reads	8,623,313 / 76.74%
Unmapped reads	2,613,736 / 23.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	61,217 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	733,518 / 6.53%
Duplication rate	5.89%
Clipped reads	5,977,886 / 53.2%

2.2. ACGT Content

Number/percentage of A's	153,624,920 / 29.65%
Number/percentage of C's	101,129,538 / 19.52%
Number/percentage of T's	146,628,235 / 28.3%
Number/percentage of G's	116,223,246 / 22.43%
Number/percentage of N's	587,188 / 0.11%
GC Percentage	41.94%

2.3. Coverage

Mean	0.1674

Standard Deviation	5.5159

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Mismatches and indels

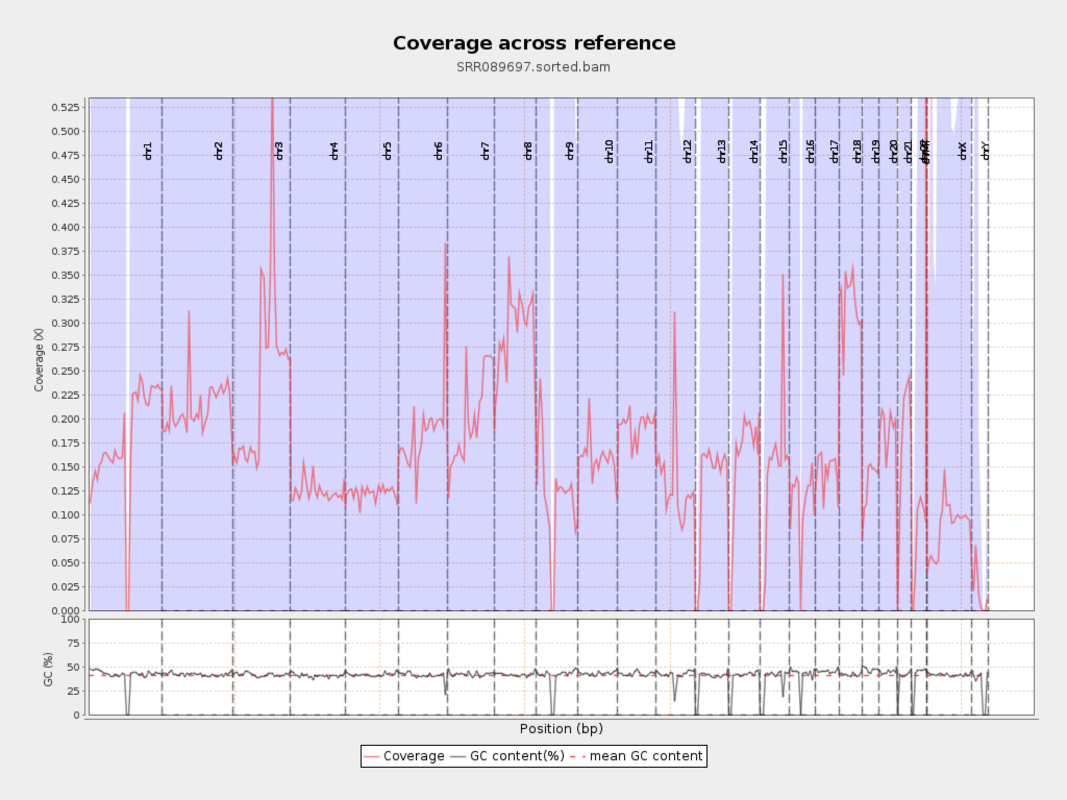
General error rate	0.91%
Mismatches	4,633,294
Insertions	38,825
Mapped reads with at least one insertion	0.45%
Deletions	104,137
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.54%

2.6. Chromosome stats

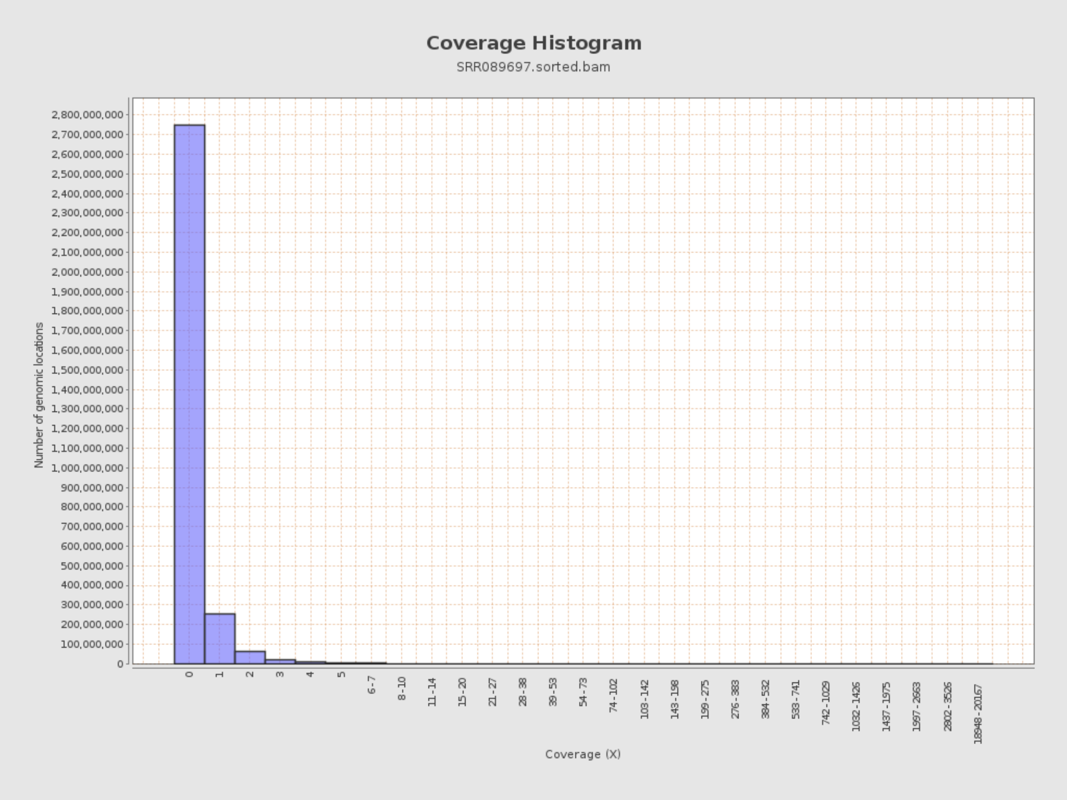
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43892424	0.1761	1.2561
chr2	243199373	51703580	0.2126	1.8858
chr3	198022430	48022404	0.2425	0.7315
chr4	191154276	23725469	0.1241	1.524
chr5	180915260	22215212	0.1228	0.4971
chr6	171115067	32153543	0.1879	13.0032
chr7	159138663	32251407	0.2027	1.9011

chr8	146364022	42971440	0.2936	1.4015
chr9	141213431	16908293	0.1197	0.9357
chr10	135534747	21696775	0.1601	1.0302
chr11	135006516	25884963	0.1917	0.8923
chr12	133851895	17562265	0.1312	15.1108
chr13	115169878	15066788	0.1308	0.5011
chr14	107349540	16152940	0.1505	0.6025
chr15	102531392	14361976	0.1401	17.1758
chr16	90354753	10228469	0.1132	2.9075
chr17	81195210	11764166	0.1449	0.6583
chr18	78077248	25048424	0.3208	1.5648
chr19	59128983	7966264	0.1347	1.1341
chr20	63025520	11760874	0.1866	0.6677
chr21	48129895	8386654	0.1743	0.7566
chr22	51304566	3863060	0.0753	0.3878
chrMT	16571	201818	12.179	9.4929
chrX	155270560	13507594	0.087	0.6811
chrY	59373566	1060206	0.0179	1.0778

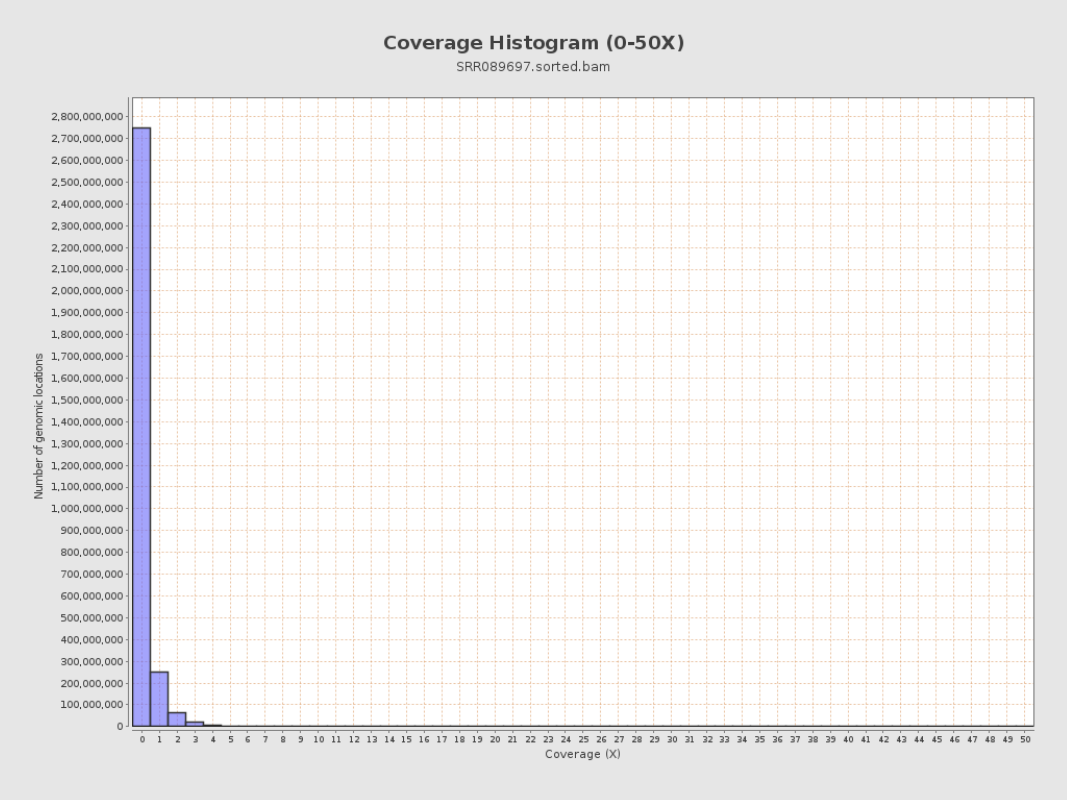
3. Results : Coverage across reference



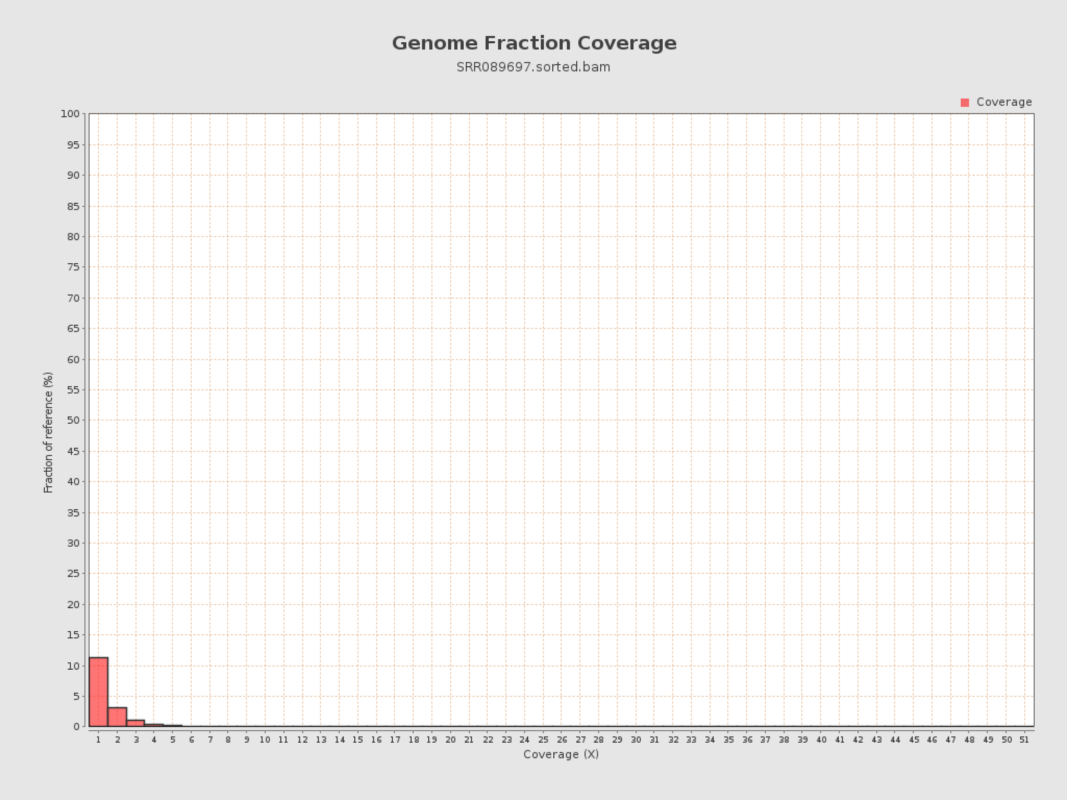
4. Results : Coverage Histogram



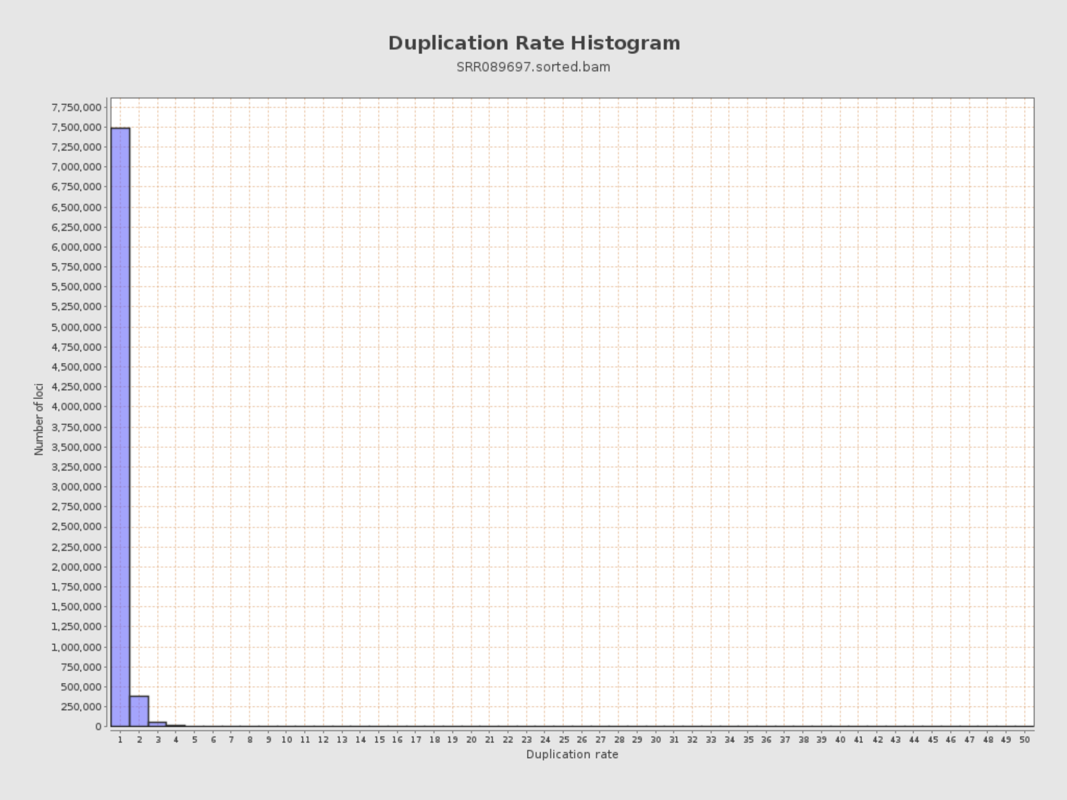
5. Results : Coverage Histogram (0-50X)



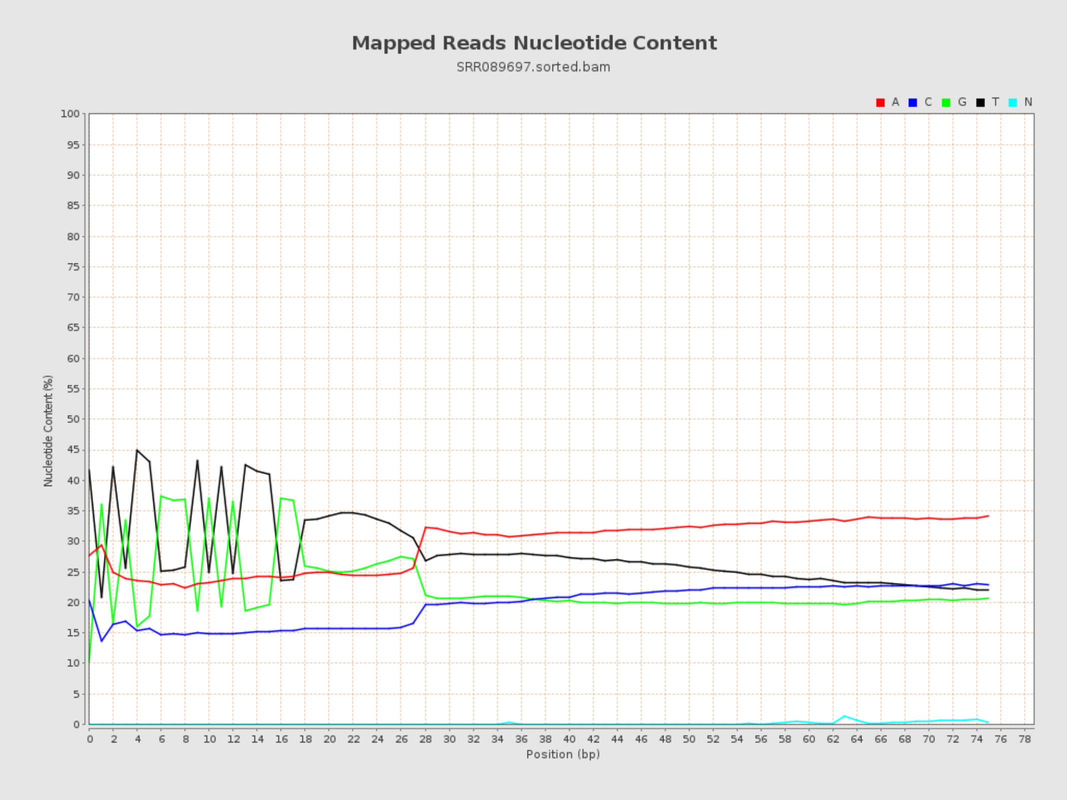
6. Results : Genome Fraction Coverage



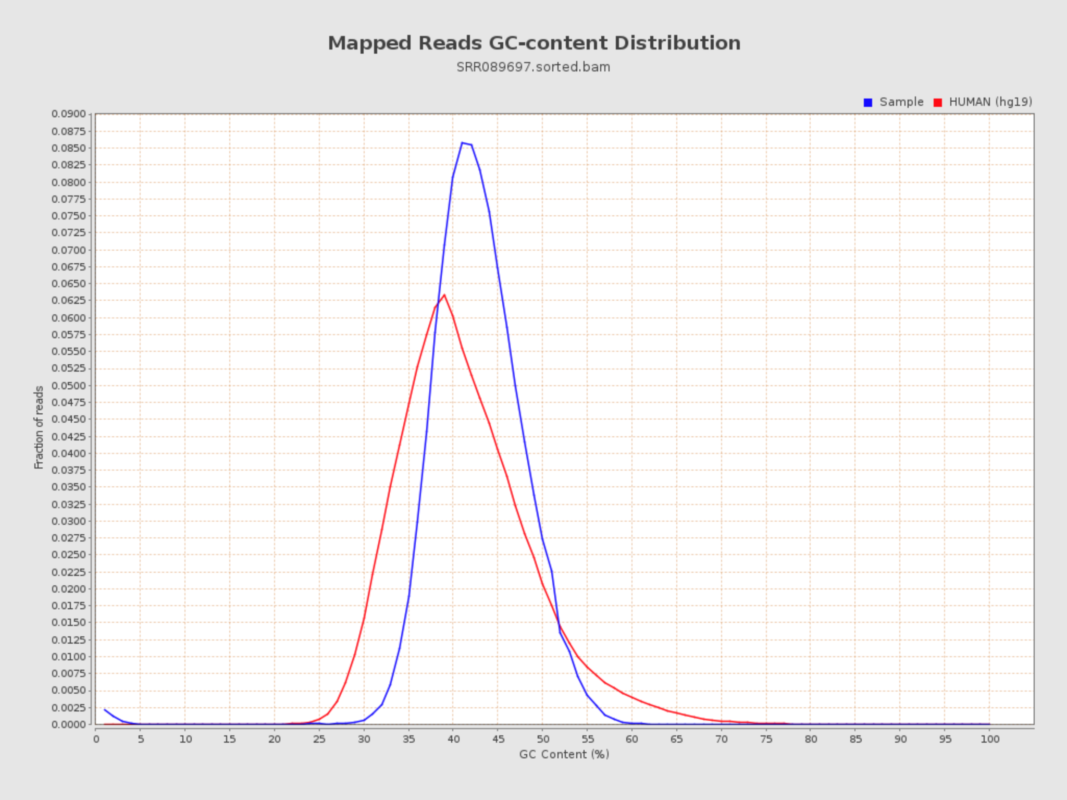
7. Results : Duplication Rate Histogram



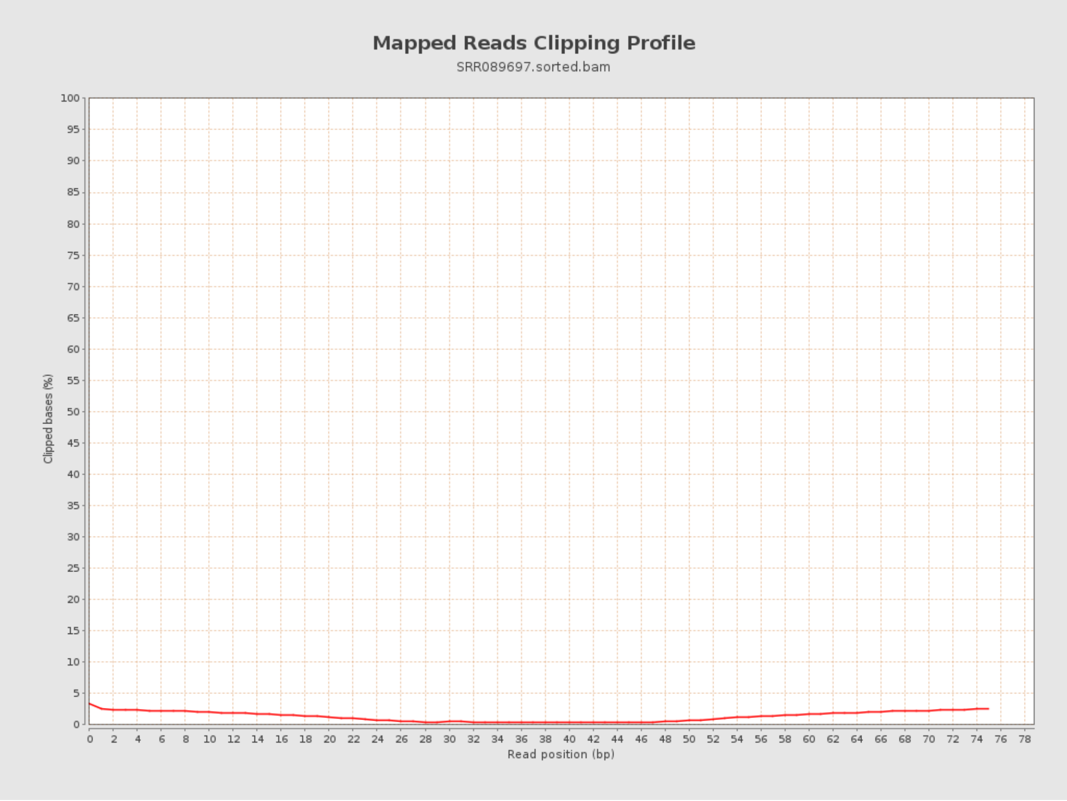
8. Results : Mapped Reads Nucleotide Content



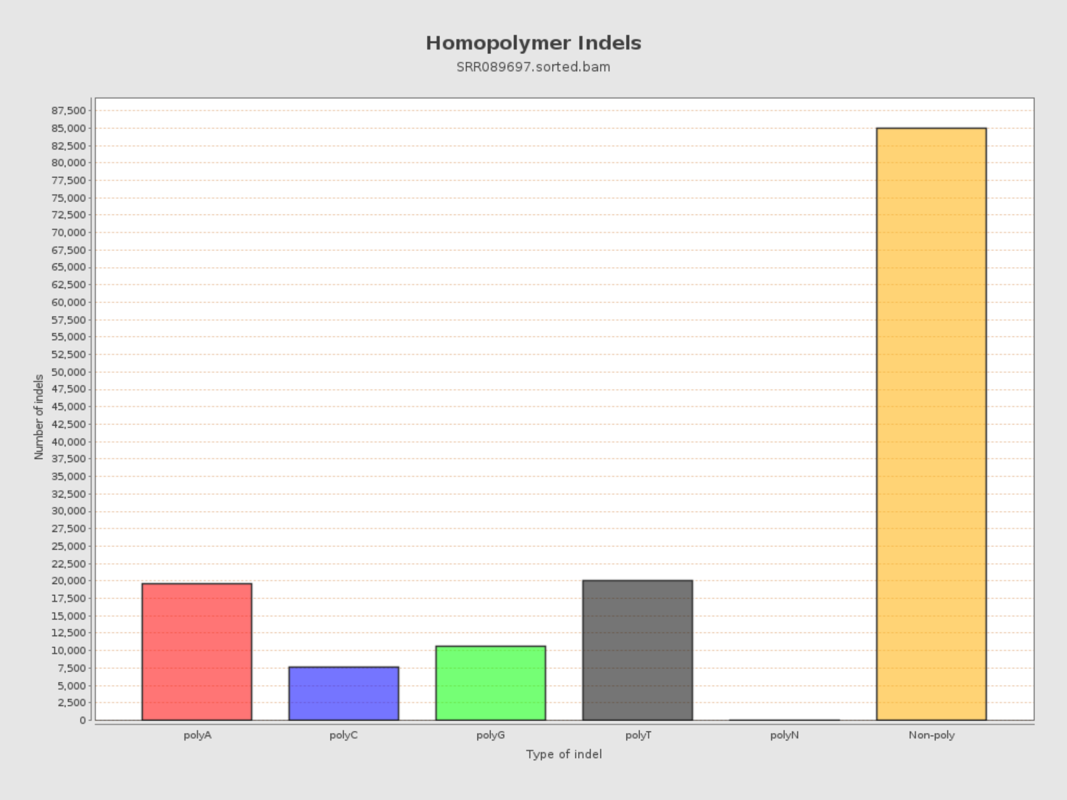
9. Results : Mapped Reads GC-content Distribution



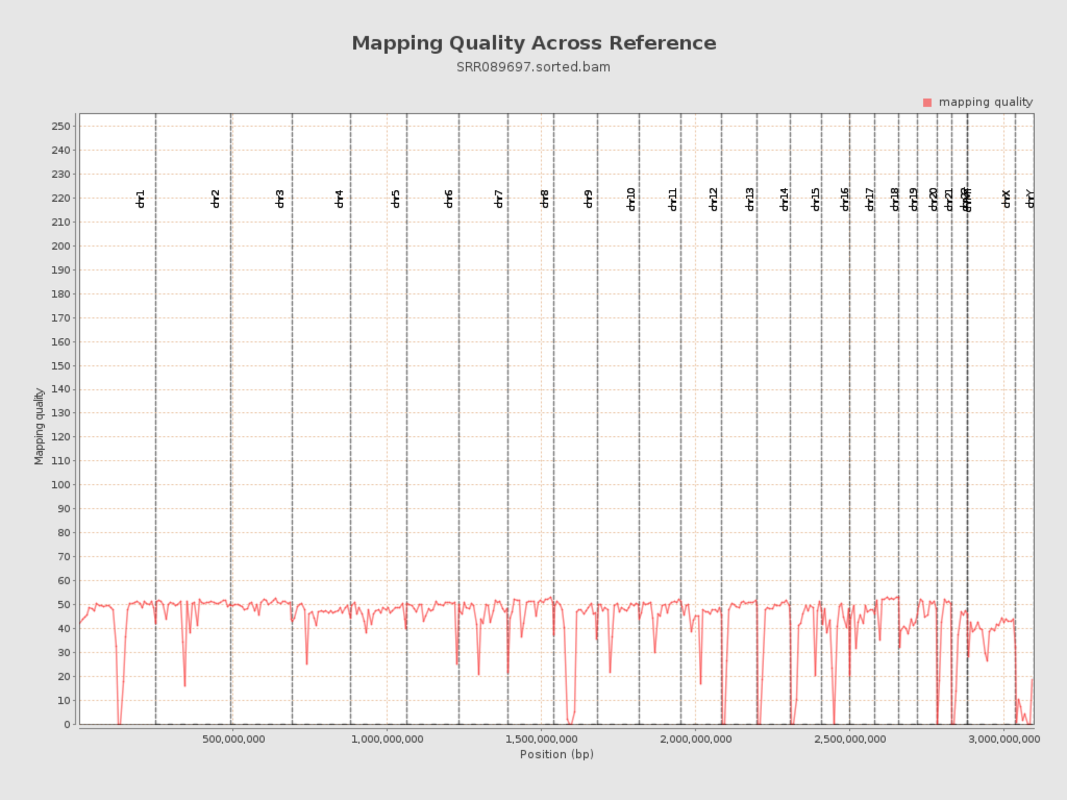
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram