Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 00:52:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089715.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_SRR089715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089715.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 00:52:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,254,261
Mapped reads	23,379,586 / 89.05%
Unmapped reads	2,874,675 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	180,730 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	6,373,372 / 24.28%
Duplication rate	14.47%
Clipped reads	8,804,470 / 33.54%

2.2. ACGT Content

Number/percentage of A's	438,834,478 / 27.63%
Number/percentage of C's	298,834,869 / 18.82%
Number/percentage of T's	493,335,562 / 31.06%
Number/percentage of G's	356,034,612 / 22.42%
Number/percentage of N's	1,097,503 / 0.07%
GC Percentage	41.24%

2.3. Coverage

Mean	0.5132

Standard Deviation	3.5158

2.4. Mapping Quality

Mean Mapping Quality	47.55

2.5. Mismatches and indels

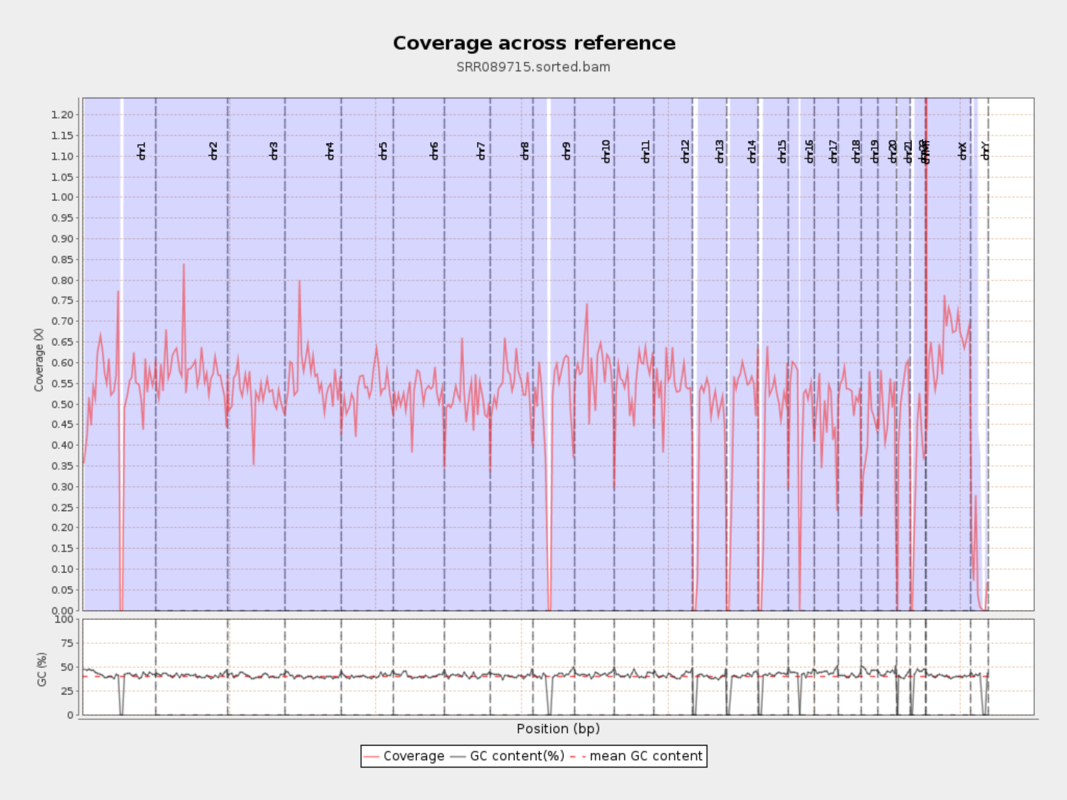
General error rate	0.74%
Mismatches	11,509,325
Insertions	104,476
Mapped reads with at least one insertion	0.44%
Deletions	311,509
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.58%

2.6. Chromosome stats

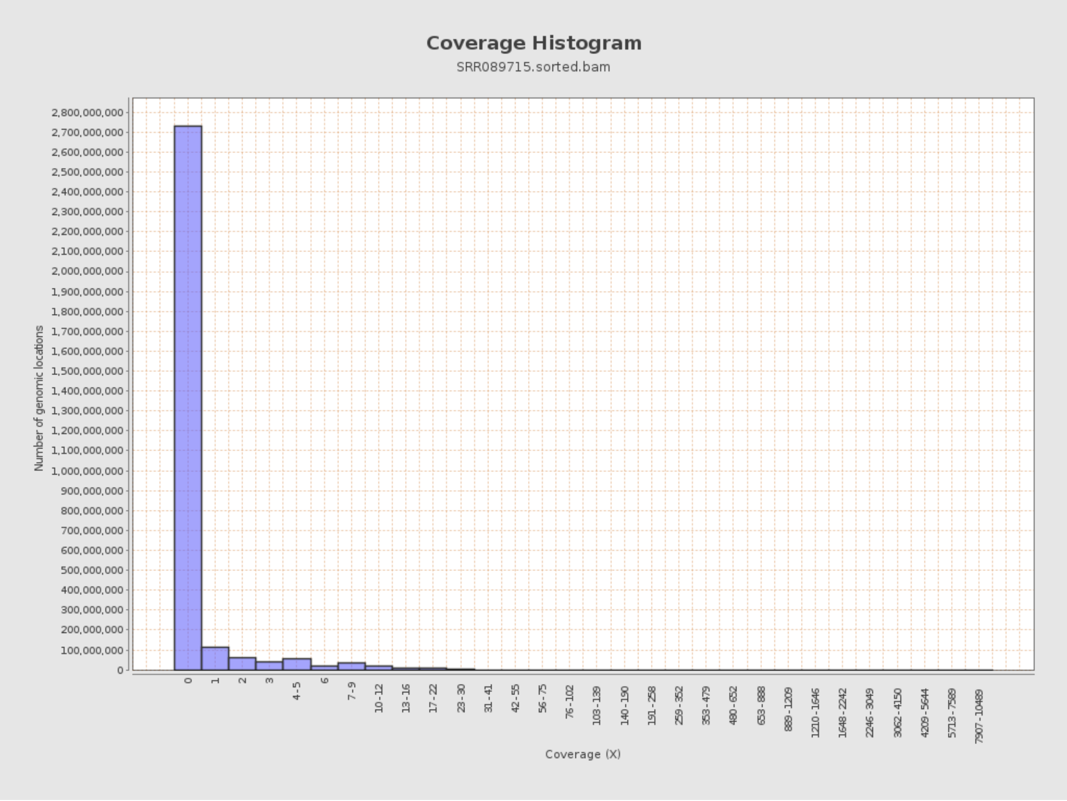
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	128666434	0.5162	6.1577
chr2	243199373	141468204	0.5817	3.9878
chr3	198022430	103671575	0.5235	2.2037
chr4	191154276	108665264	0.5685	2.5359
chr5	180915260	95936610	0.5303	2.2027
chr6	171115067	89748043	0.5245	2.4462
chr7	159138663	80988171	0.5089	3.8656

chr8	146364022	79590819	0.5438	6.5213
chr9	141213431	67176234	0.4757	3.0145
chr10	135534747	79672663	0.5878	3.1328
chr11	135006516	75505117	0.5593	2.8251
chr12	133851895	73267989	0.5474	2.318
chr13	115169878	48802996	0.4237	1.9411
chr14	107349540	50152793	0.4672	2.229
chr15	102531392	43977601	0.4289	2.0287
chr16	90354753	42422060	0.4695	2.2429
chr17	81195210	37649877	0.4637	2.5803
chr18	78077248	41587293	0.5326	5.6032
chr19	59128983	25312739	0.4281	3.8373
chr20	63025520	30530611	0.4844	2.2594
chr21	48129895	22757721	0.4728	2.3824
chr22	51304566	16092631	0.3137	1.7313
chrMT	16571	576449	34.7866	25.5029
chrX	155270560	99964174	0.6438	2.5858
chrY	59373566	4504242	0.0759	2.2356

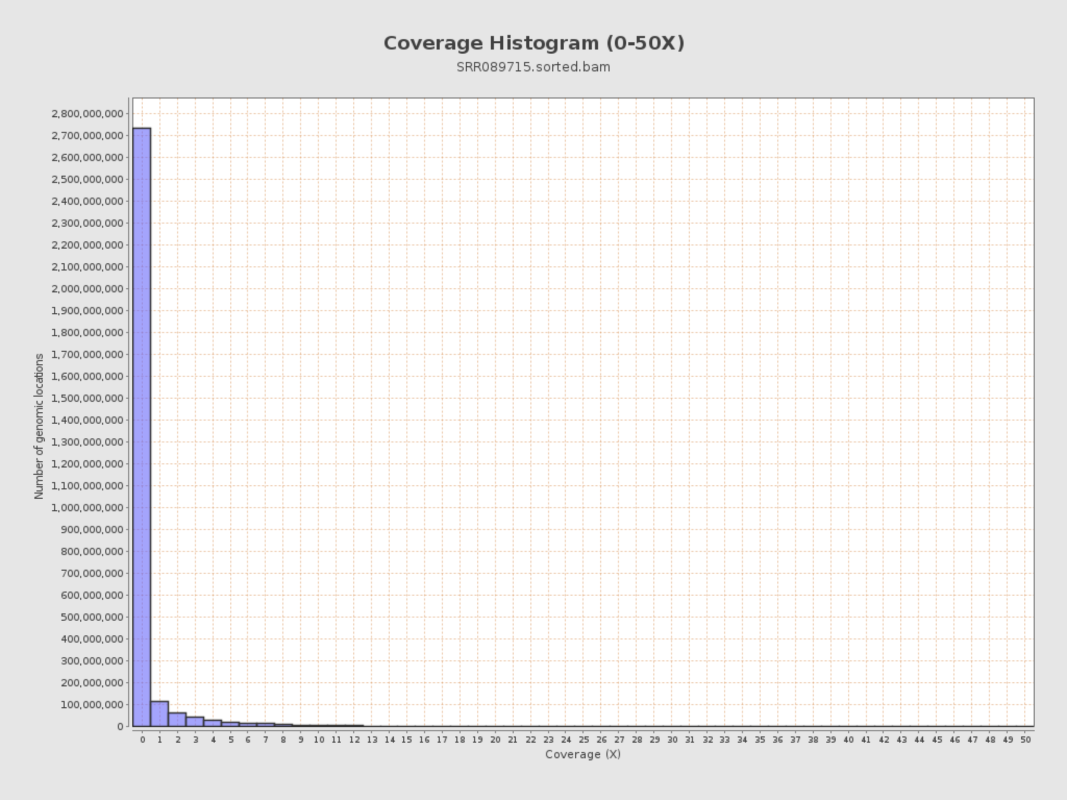
3. Results : Coverage across reference



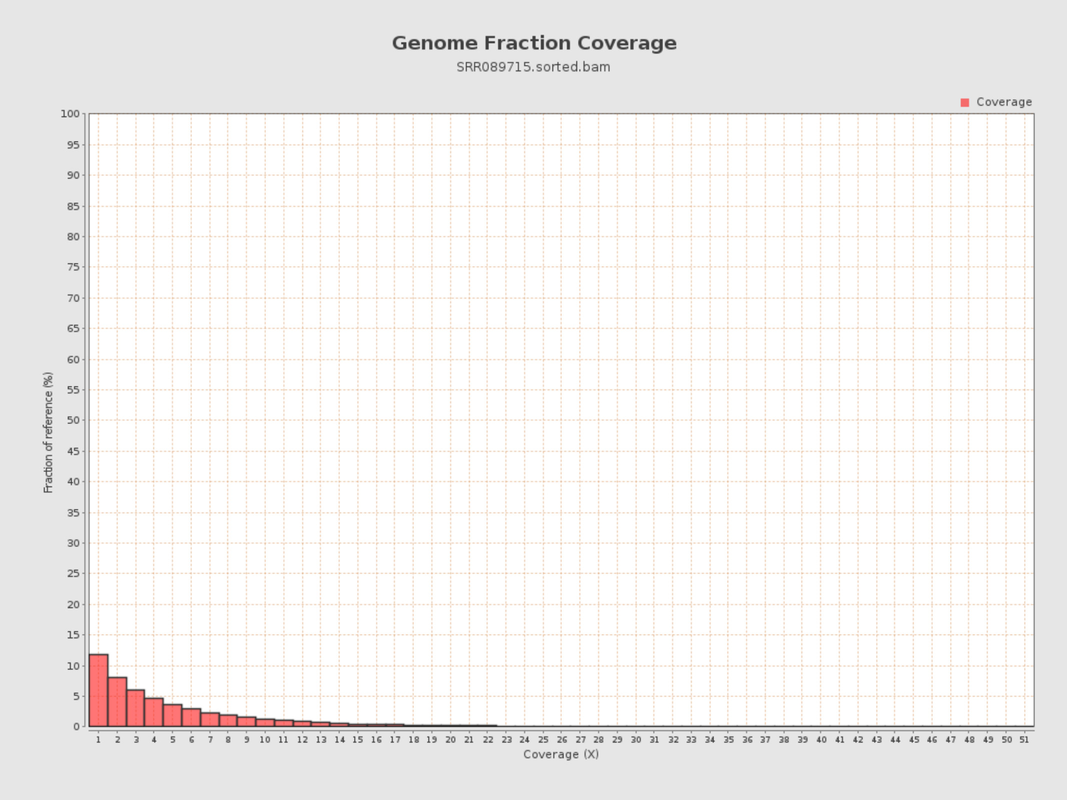
4. Results : Coverage Histogram



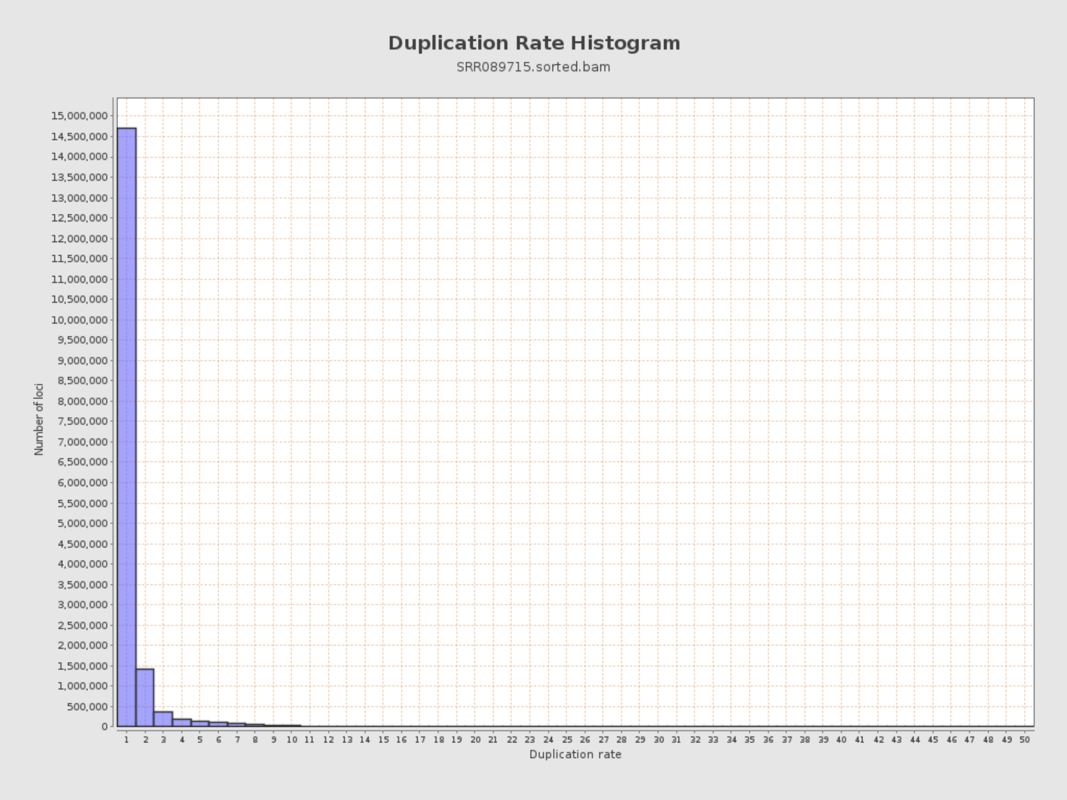
5. Results : Coverage Histogram (0-50X)



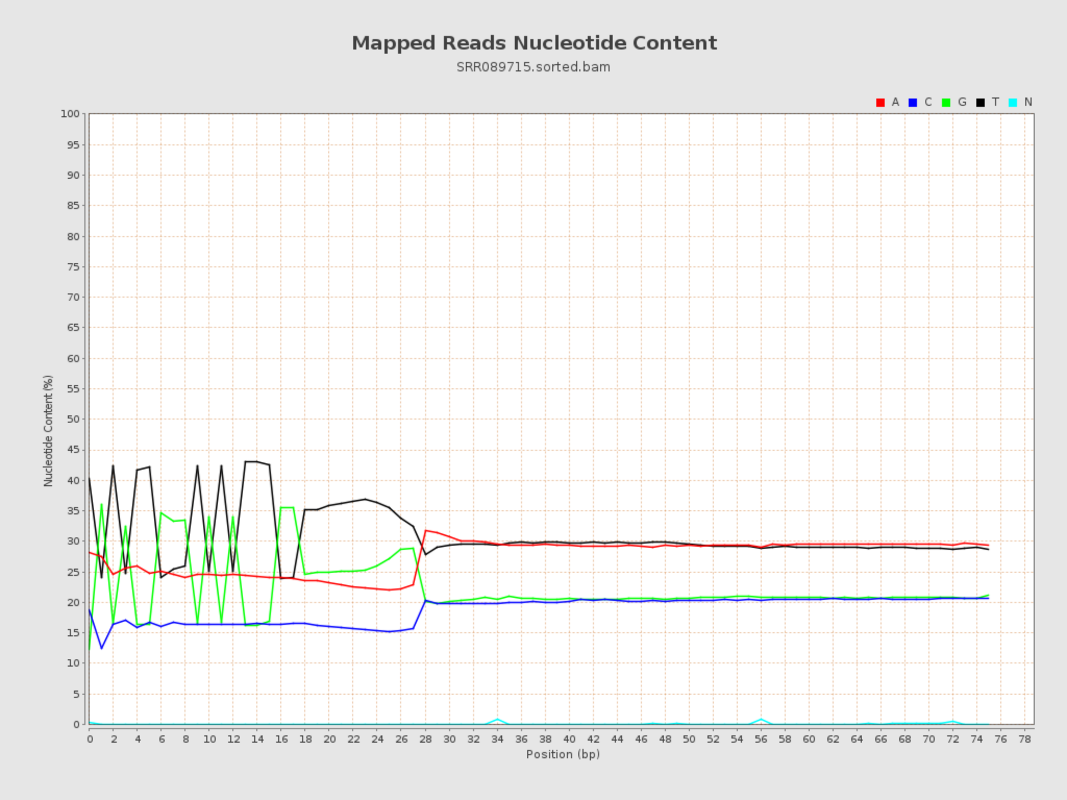
6. Results : Genome Fraction Coverage



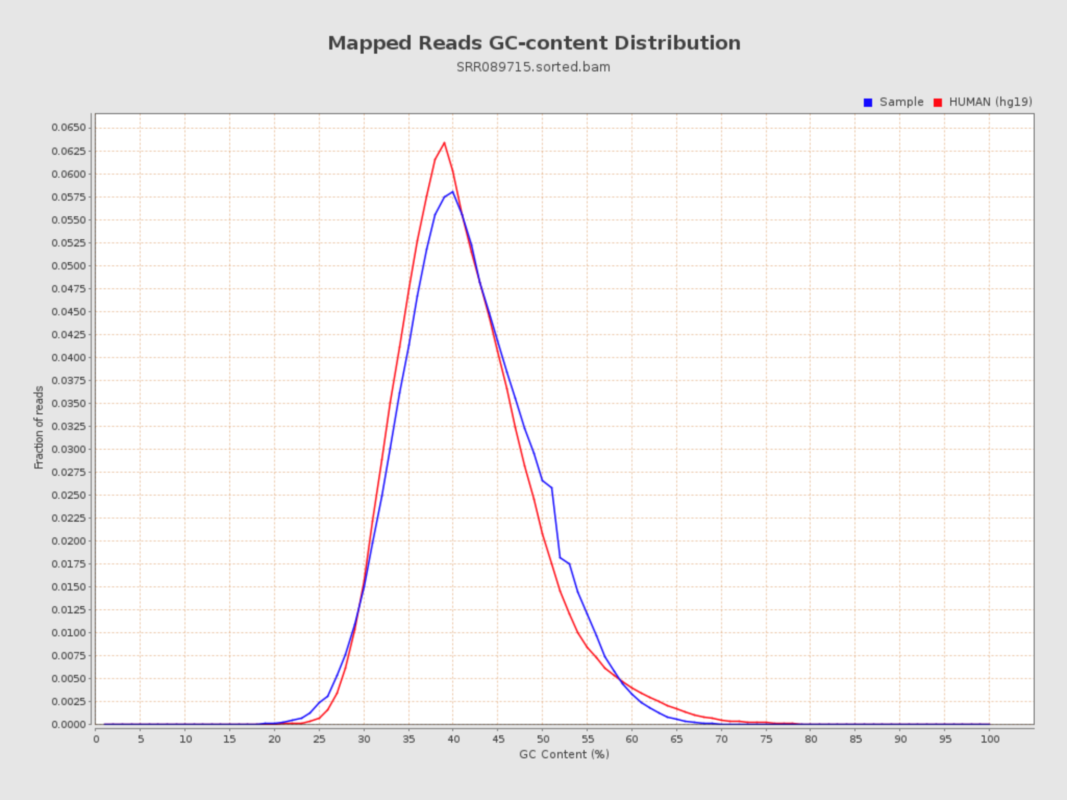
7. Results : Duplication Rate Histogram



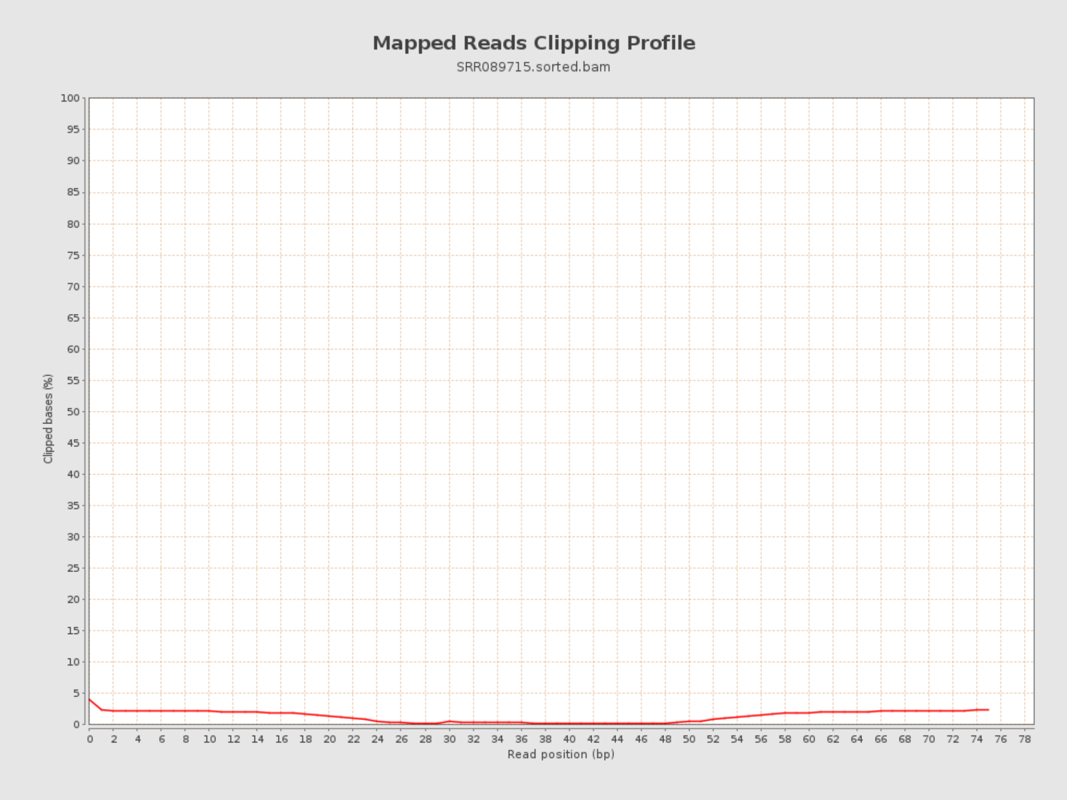
8. Results : Mapped Reads Nucleotide Content



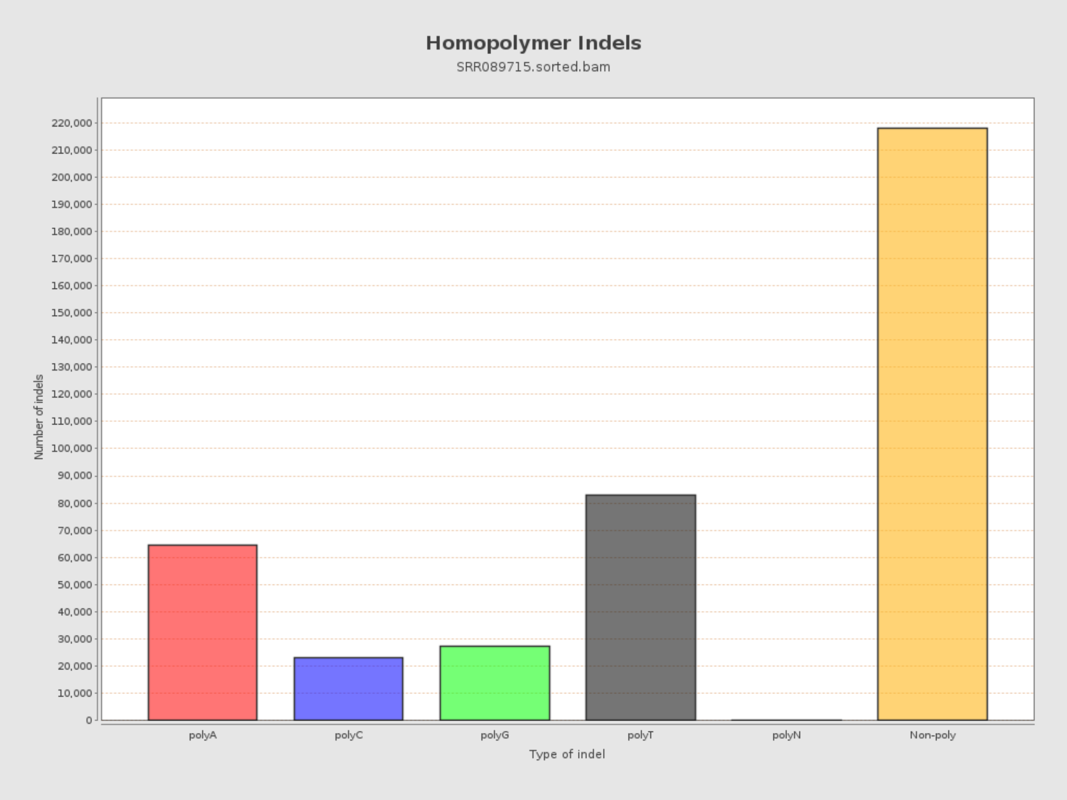
9. Results : Mapped Reads GC-content Distribution



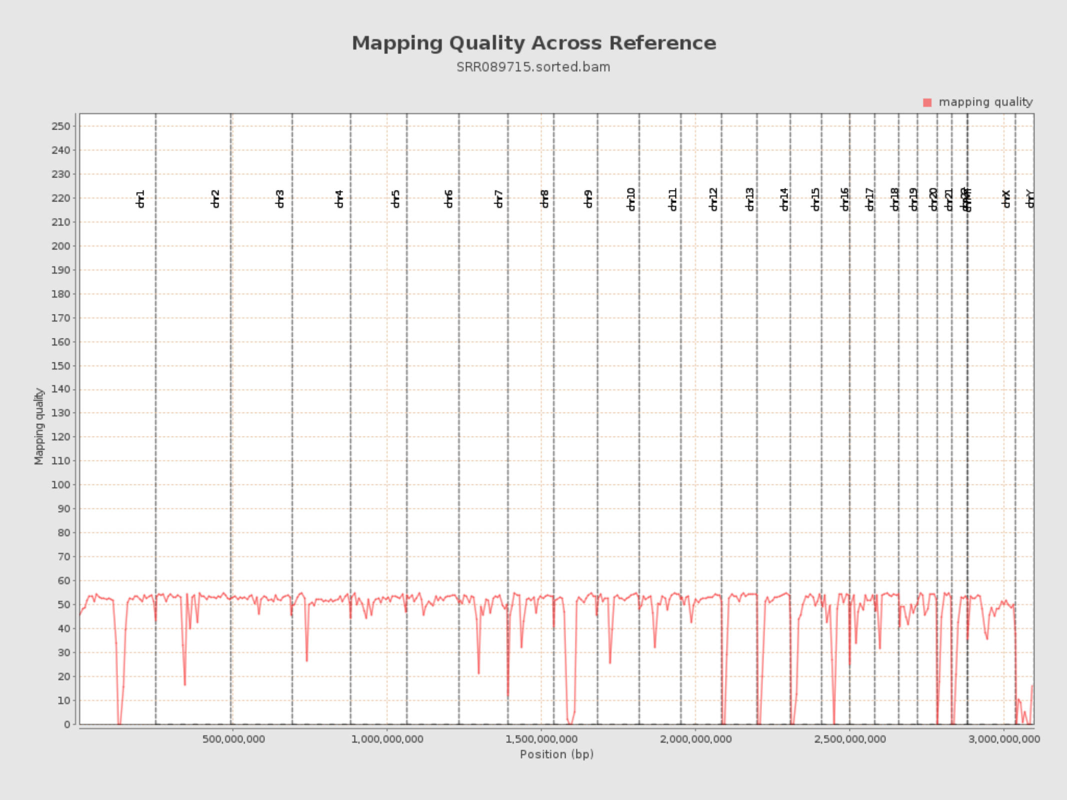
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram