Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:10:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080790.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_SRR3080790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:10:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,279,297
Mapped reads	2,049,891 / 89.94%
Unmapped reads	229,406 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,069 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	75,957 / 3.33%
Duplication rate	3.03%
Clipped reads	1,012,455 / 44.42%

2.2. ACGT Content

Number/percentage of A's	38,743,992 / 28.64%
Number/percentage of C's	25,889,233 / 19.14%
Number/percentage of T's	41,482,168 / 30.67%
Number/percentage of G's	29,148,104 / 21.55%
Number/percentage of N's	2,608 / 0%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0437

Standard Deviation	0.3245

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

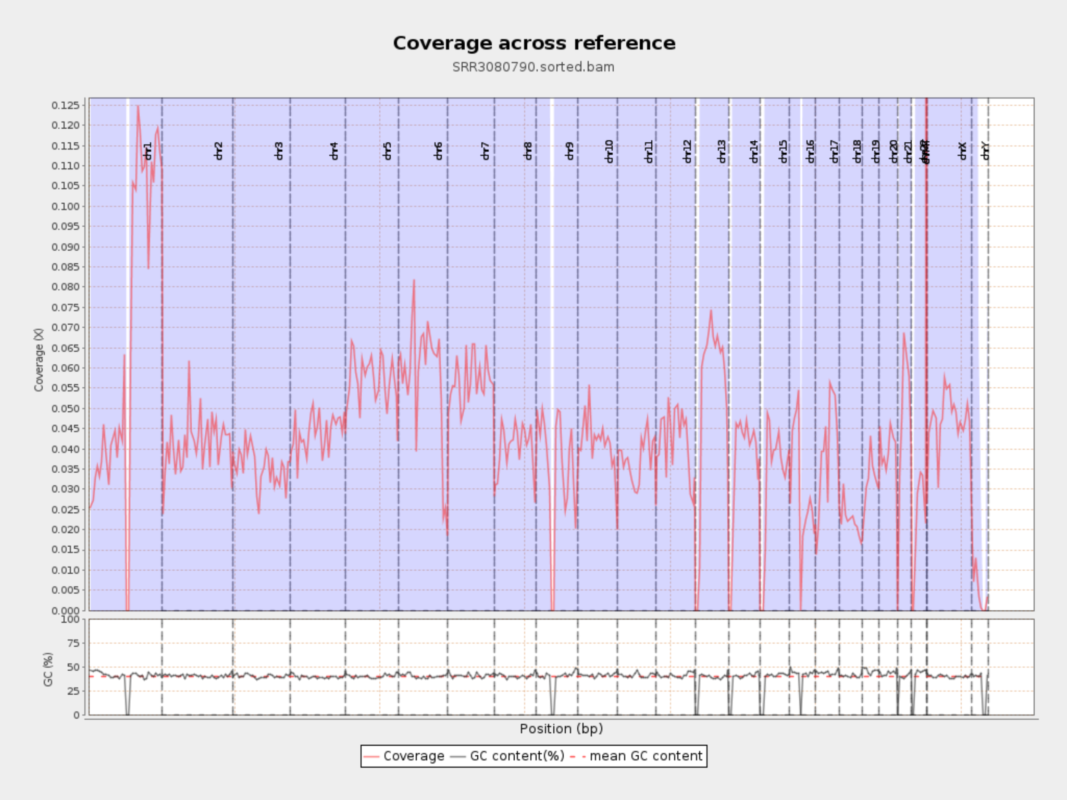
General error rate	0.77%
Mismatches	1,021,963
Insertions	10,309
Mapped reads with at least one insertion	0.5%
Deletions	29,725
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.73%

2.6. Chromosome stats

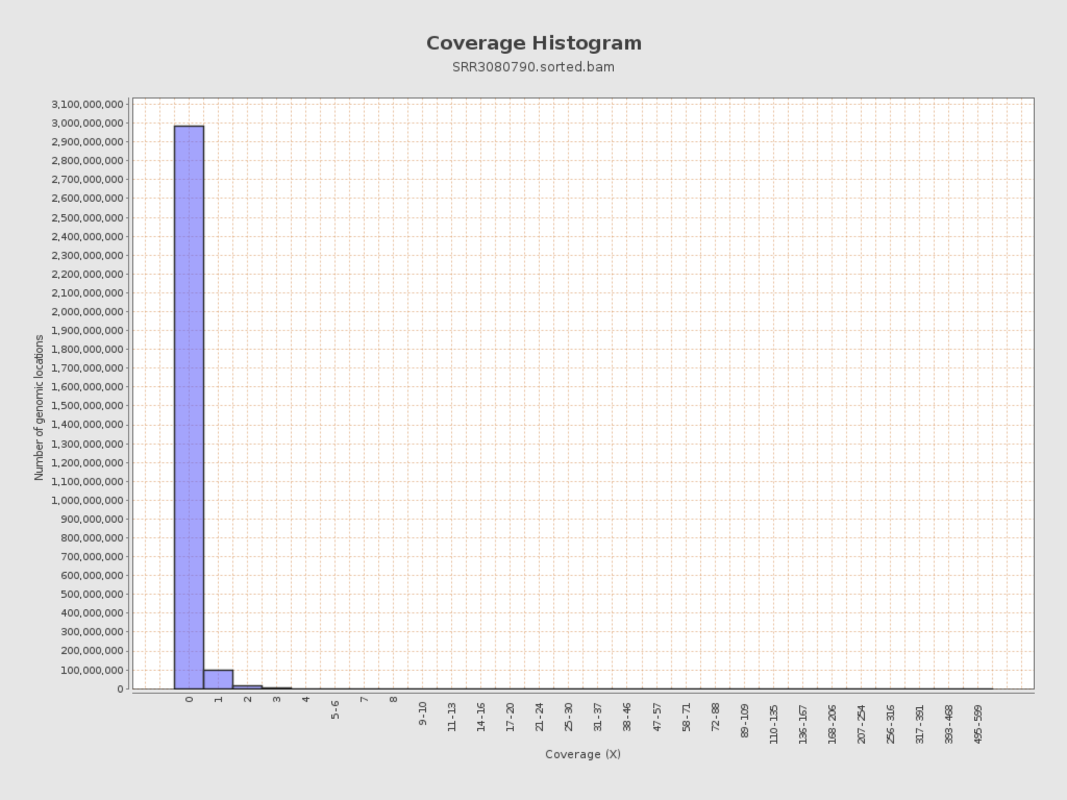
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16644971	0.0668	0.5002
chr2	243199373	10091179	0.0415	0.368
chr3	198022430	7049190	0.0356	0.2172
chr4	191154276	8432523	0.0441	0.2482
chr5	180915260	10402594	0.0575	0.2777
chr6	171115067	10001410	0.0584	0.3378
chr7	159138663	9091056	0.0571	0.4501

chr8	146364022	5917640	0.0404	0.3953
chr9	141213431	4947962	0.035	0.2869
chr10	135534747	5701456	0.0421	0.2966
chr11	135006516	5035370	0.0373	0.2678
chr12	133851895	5647793	0.0422	0.2377
chr13	115169878	6127750	0.0532	0.2685
chr14	107349540	3857361	0.0359	0.2308
chr15	102531392	3317372	0.0324	0.2179
chr16	90354753	2717660	0.0301	0.2175
chr17	81195210	3199362	0.0394	0.241
chr18	78077248	1761802	0.0226	0.5587
chr19	59128983	1895974	0.0321	0.3598
chr20	63025520	2502288	0.0397	0.2353
chr21	48129895	2284779	0.0475	0.2574
chr22	51304566	1093600	0.0213	0.1659
chrMT	16571	17335	1.0461	1.2615
chrX	155270560	7283231	0.0469	0.2661
chrY	59373566	291264	0.0049	0.1076

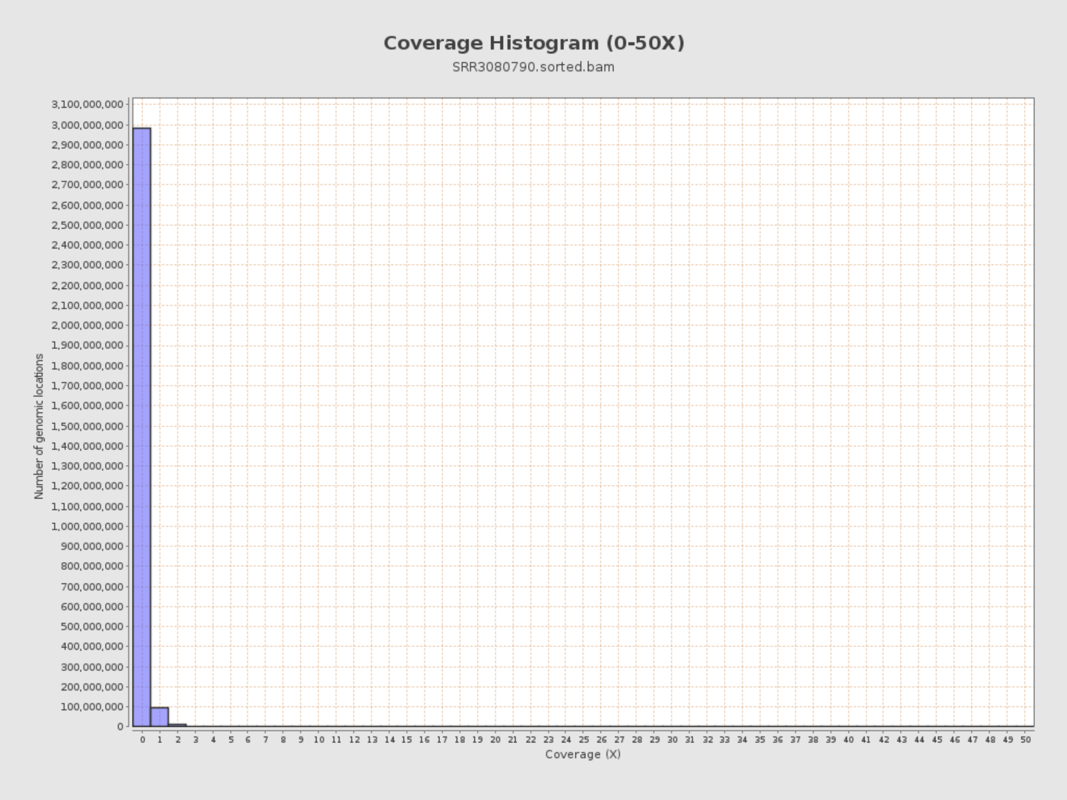
3. Results : Coverage across reference



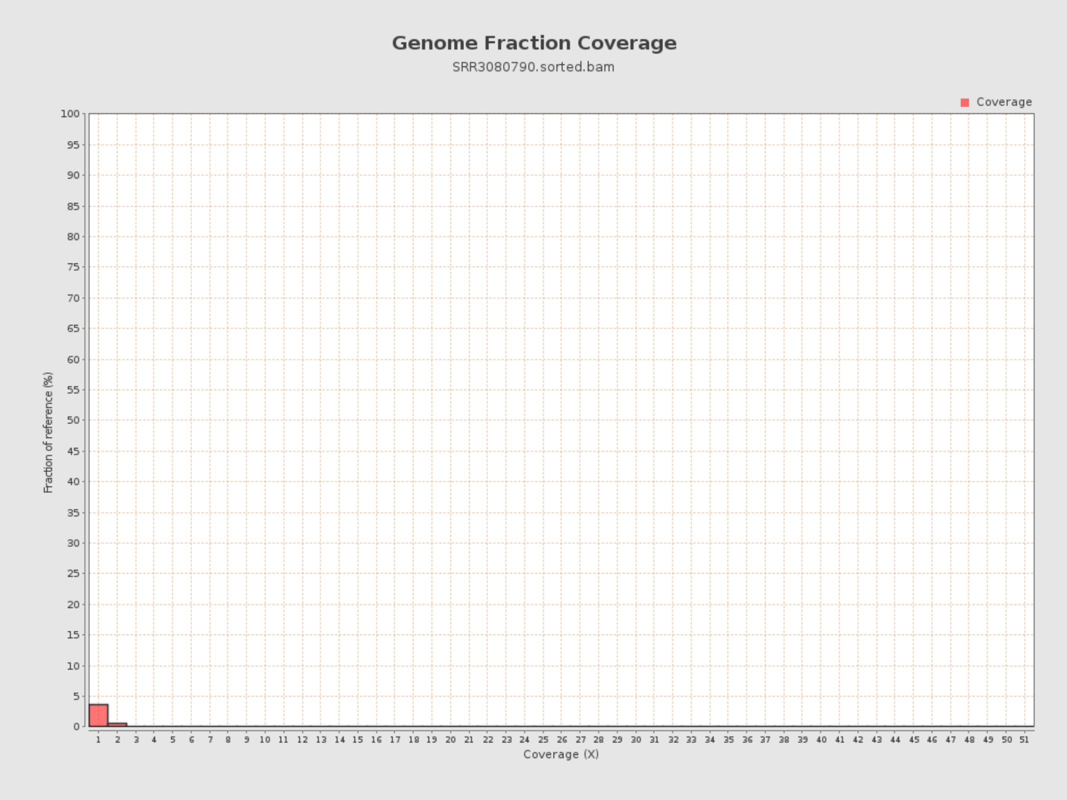
4. Results : Coverage Histogram



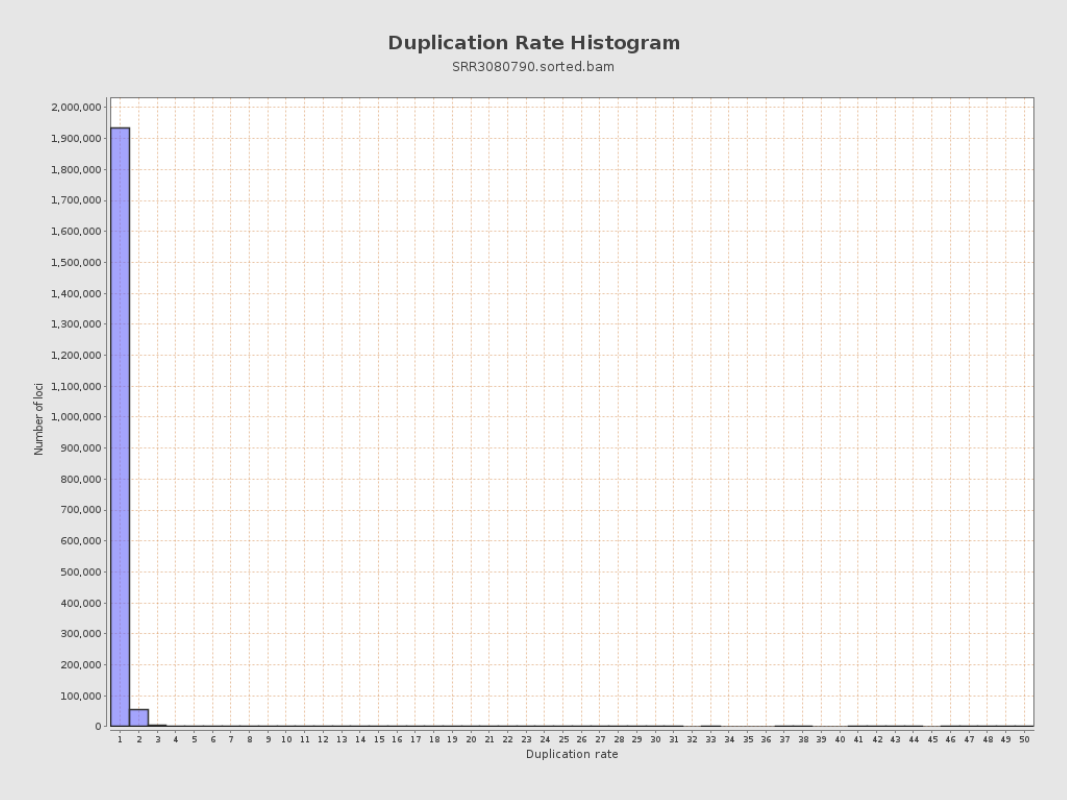
5. Results : Coverage Histogram (0-50X)



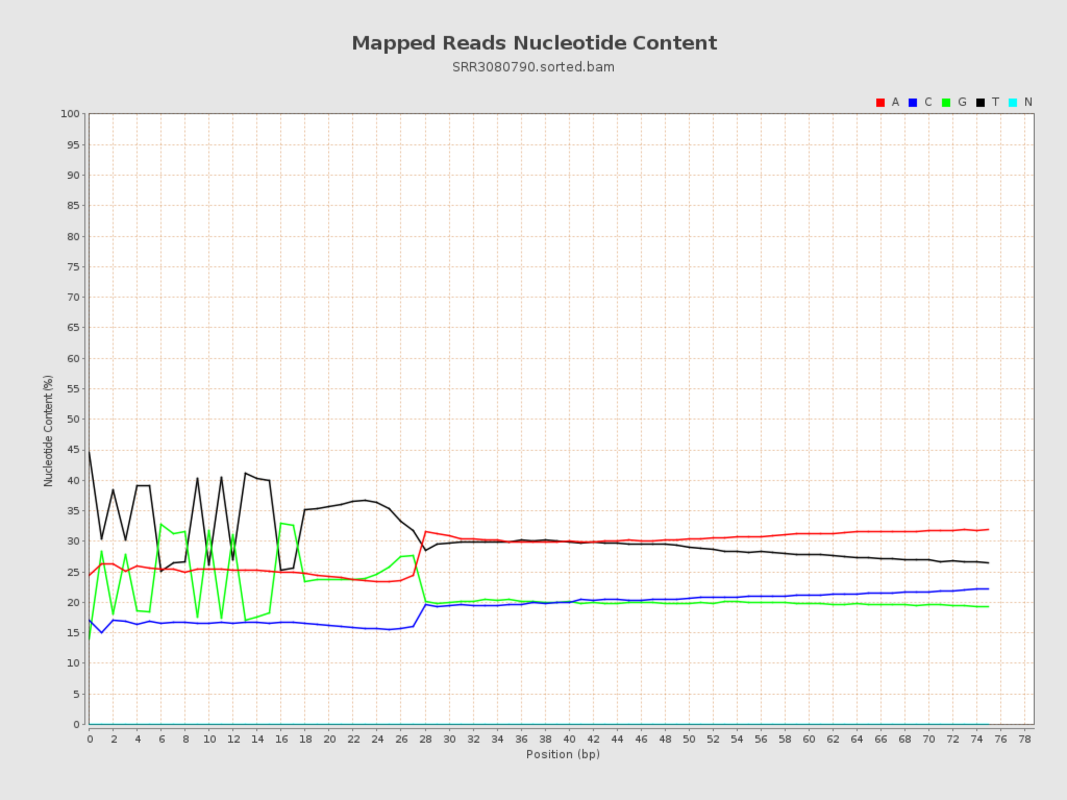
6. Results : Genome Fraction Coverage



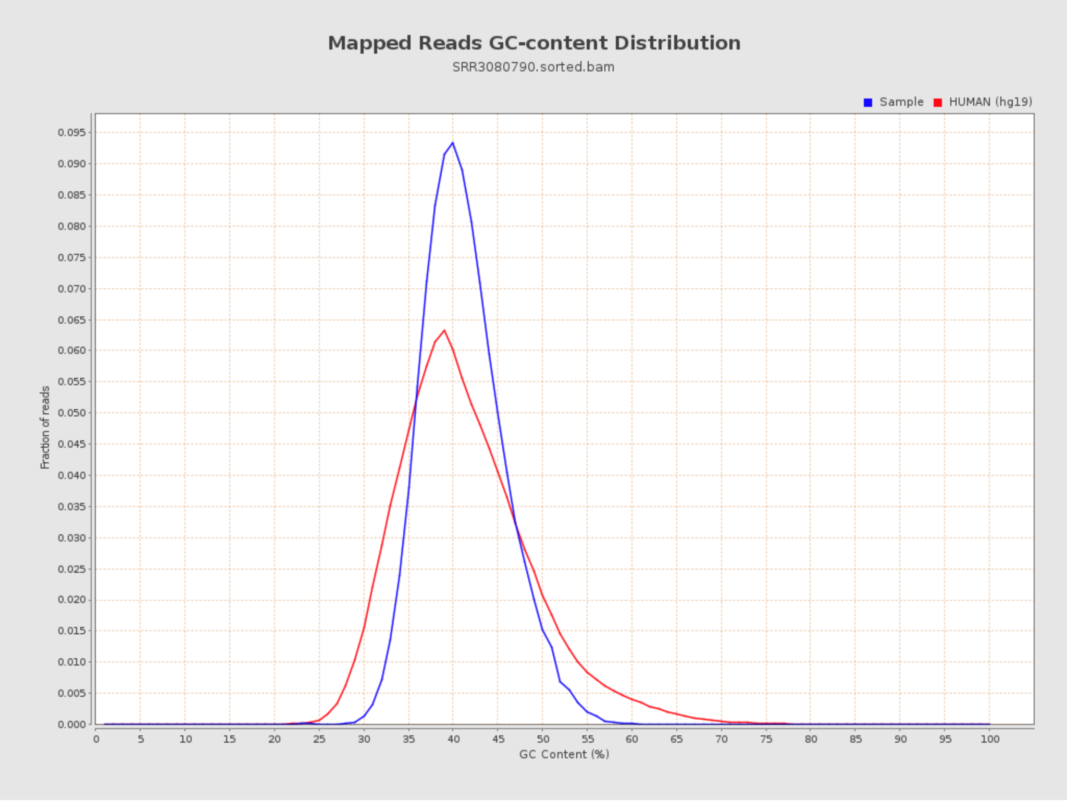
7. Results : Duplication Rate Histogram



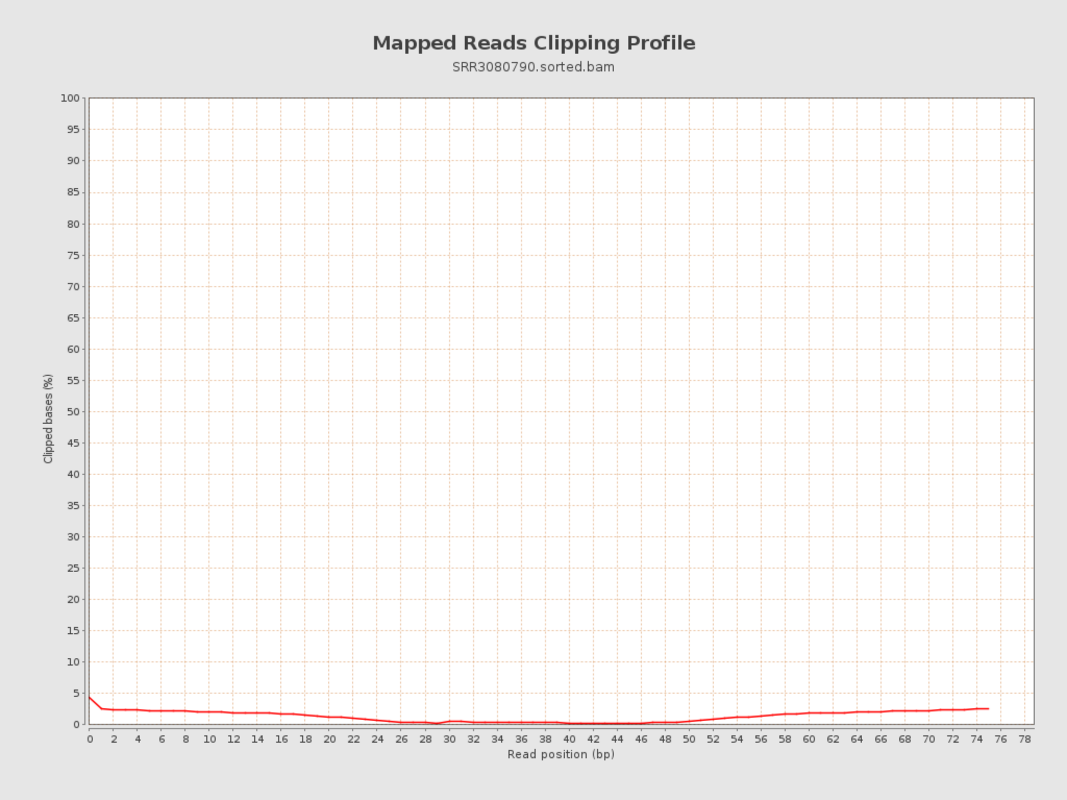
8. Results : Mapped Reads Nucleotide Content



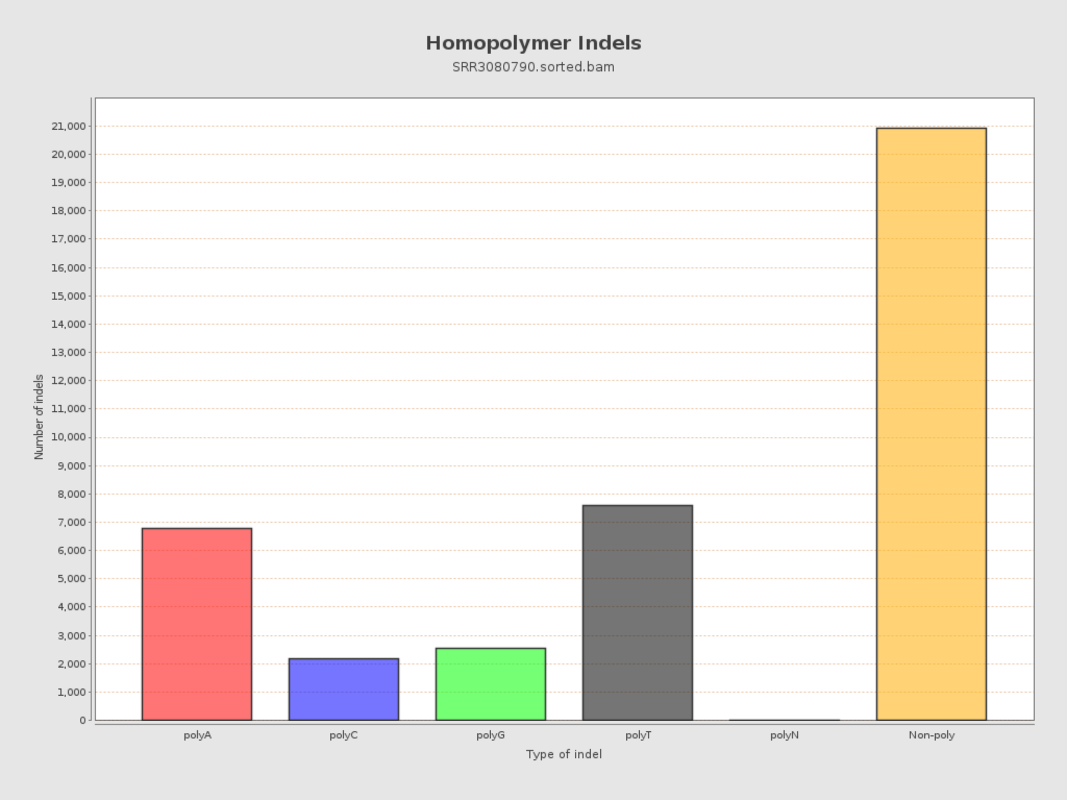
9. Results : Mapped Reads GC-content Distribution



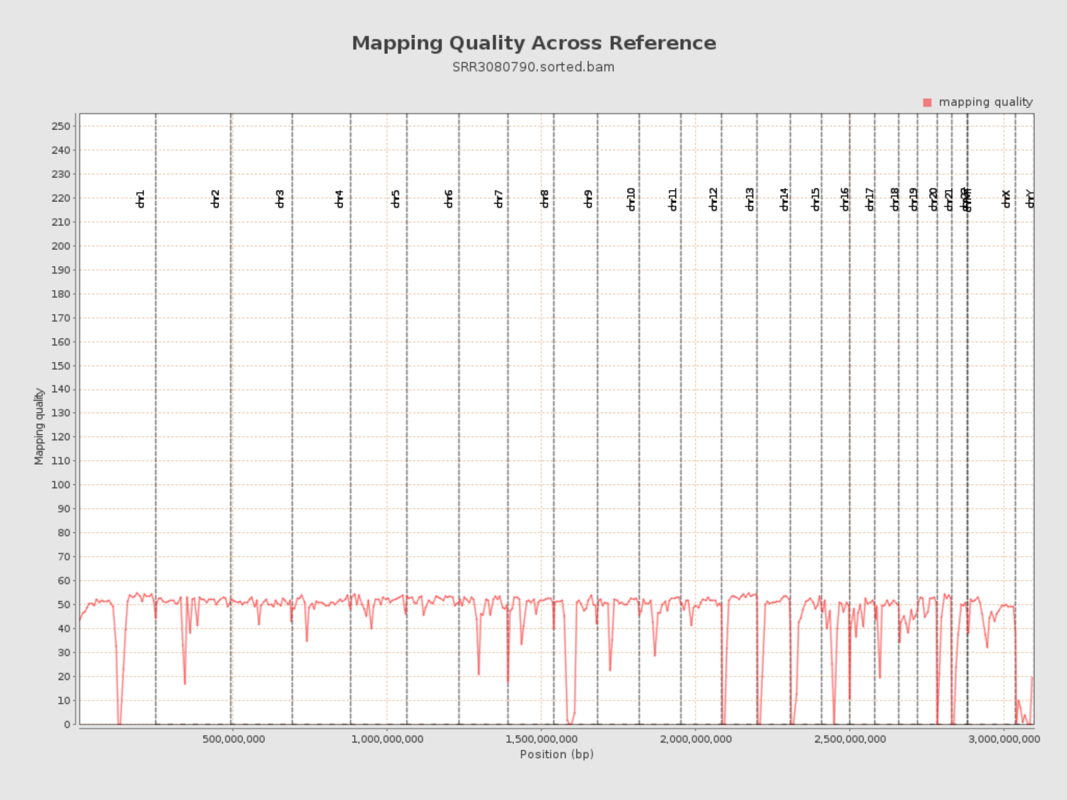
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram