Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 02:14:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514709.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_SRR5514709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 02:14:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	73,804,806
Mapped reads	72,816,936 / 98.66%
Unmapped reads	987,870 / 1.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,226,995 / 4.37%
Read min/max/mean length	30 / 100 / 99.58
Duplicated reads (estimated)	39,551,116 / 53.59%
Duplication rate	37.01%
Clipped reads	14,225,127 / 19.27%

2.2. ACGT Content

Number/percentage of A's	2,007,526,866 / 28.88%
Number/percentage of C's	1,467,718,657 / 21.11%
Number/percentage of T's	1,987,338,359 / 28.59%
Number/percentage of G's	1,486,502,862 / 21.38%
Number/percentage of N's	3,137,786 / 0.05%
GC Percentage	42.49%

2.3. Coverage

Mean	2.2476

Standard Deviation	155.9774

2.4. Mapping Quality

Mean Mapping Quality	48.85

2.5. Mismatches and indels

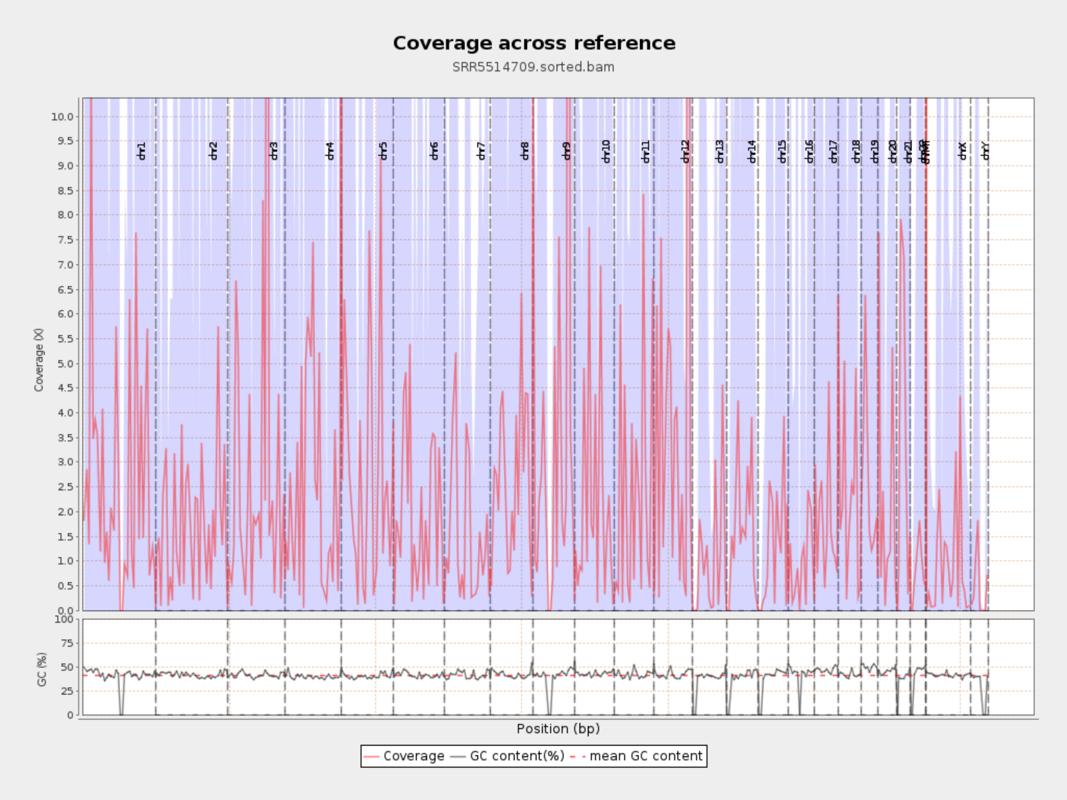
General error rate	0.65%
Mismatches	41,485,874
Insertions	2,233,717
Mapped reads with at least one insertion	2.96%
Deletions	2,330,004
Mapped reads with at least one deletion	3.06%
Homopolymer indels	43.02%

2.6. Chromosome stats

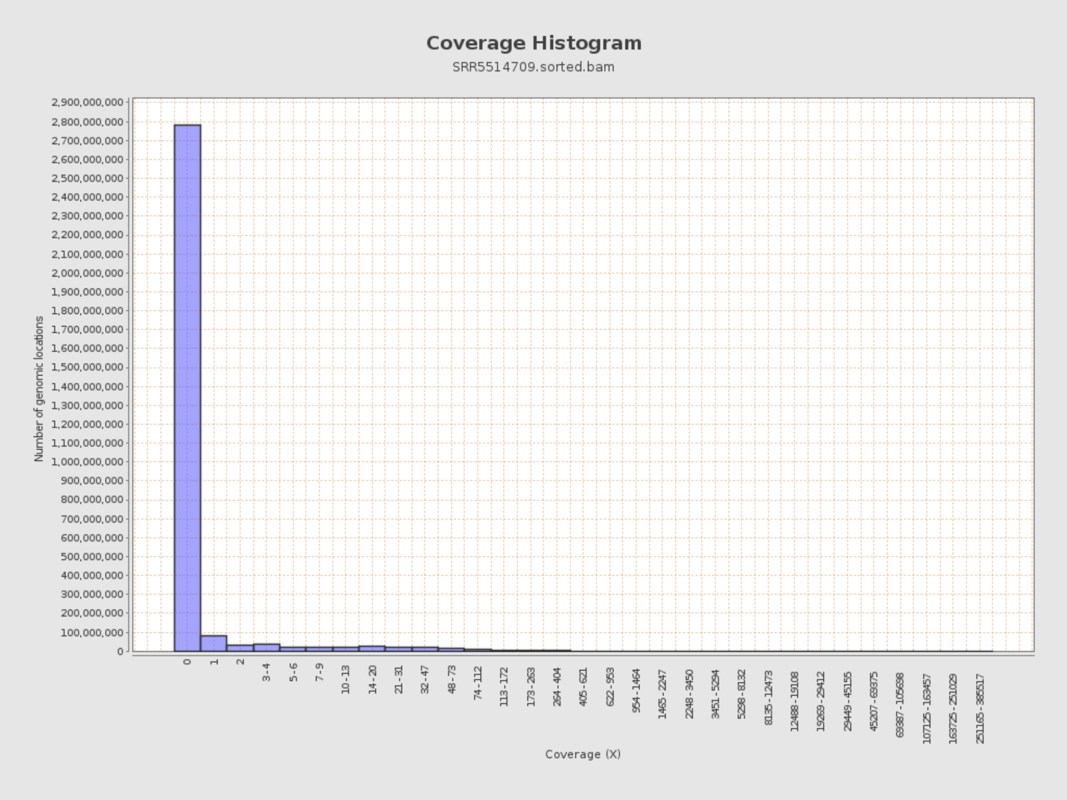
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	666878888	2.6755	67.6424
chr2	243199373	421383630	1.7327	18.3042
chr3	198022430	625425158	3.1584	26.7551
chr4	191154276	463908686	2.4269	16.6664
chr5	180915260	523950567	2.8961	21.1626
chr6	171115067	346812691	2.0268	18.6225
chr7	159138663	229508250	1.4422	13.22

chr8	146364022	387659000	2.6486	21.3521
chr9	141213431	512699192	3.6307	530.7412
chr10	135534747	305860554	2.2567	21.1001
chr11	135006516	331141171	2.4528	17.5335
chr12	133851895	622801641	4.6529	500.6701
chr13	115169878	127752047	1.1092	13.9948
chr14	107349540	184074736	1.7147	14.4602
chr15	102531392	124406363	1.2133	13.384
chr16	90354753	82222623	0.91	10.3875
chr17	81195210	147884811	1.8213	16.5897
chr18	78077248	183679511	2.3525	17.4115
chr19	59128983	157866591	2.6699	23.1596
chr20	63025520	139459599	2.2127	21.5487
chr21	48129895	156376740	3.2491	21.7206
chr22	51304566	42379301	0.826	9.9626
chrMT	16571	3408422	205.686	96.0565
chrX	155270560	139216514	0.8966	10.3116
chrY	59373566	31056958	0.5231	7.0634

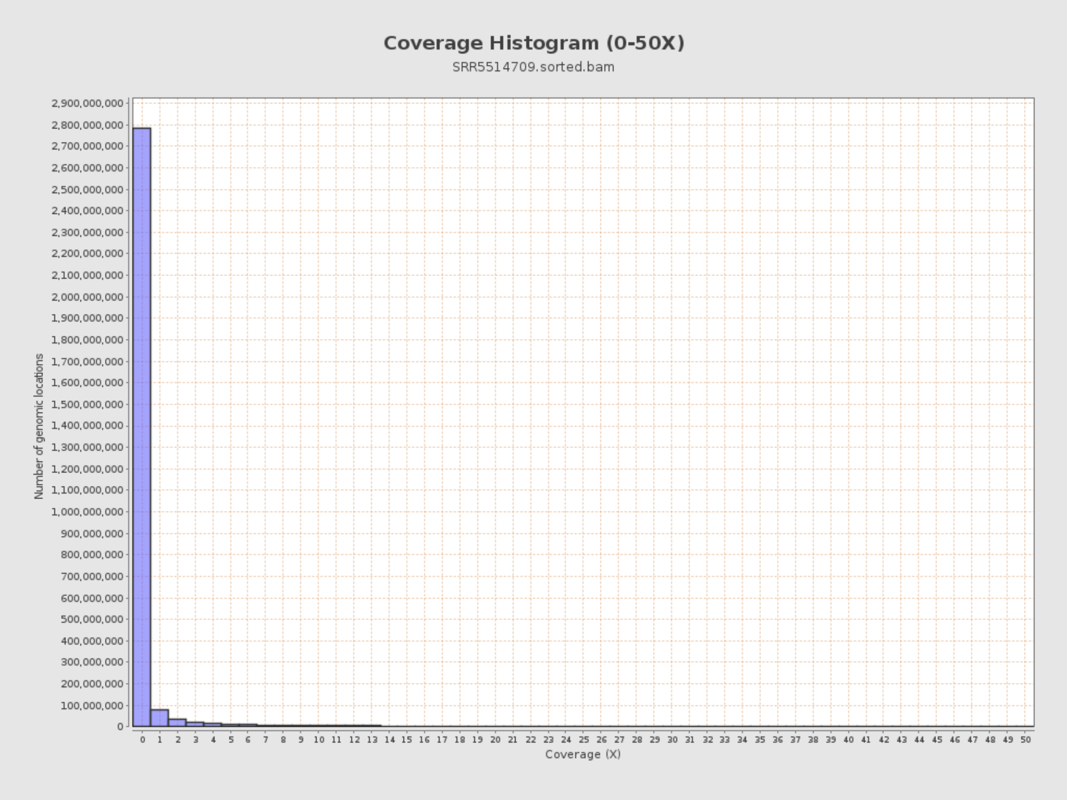
3. Results : Coverage across reference



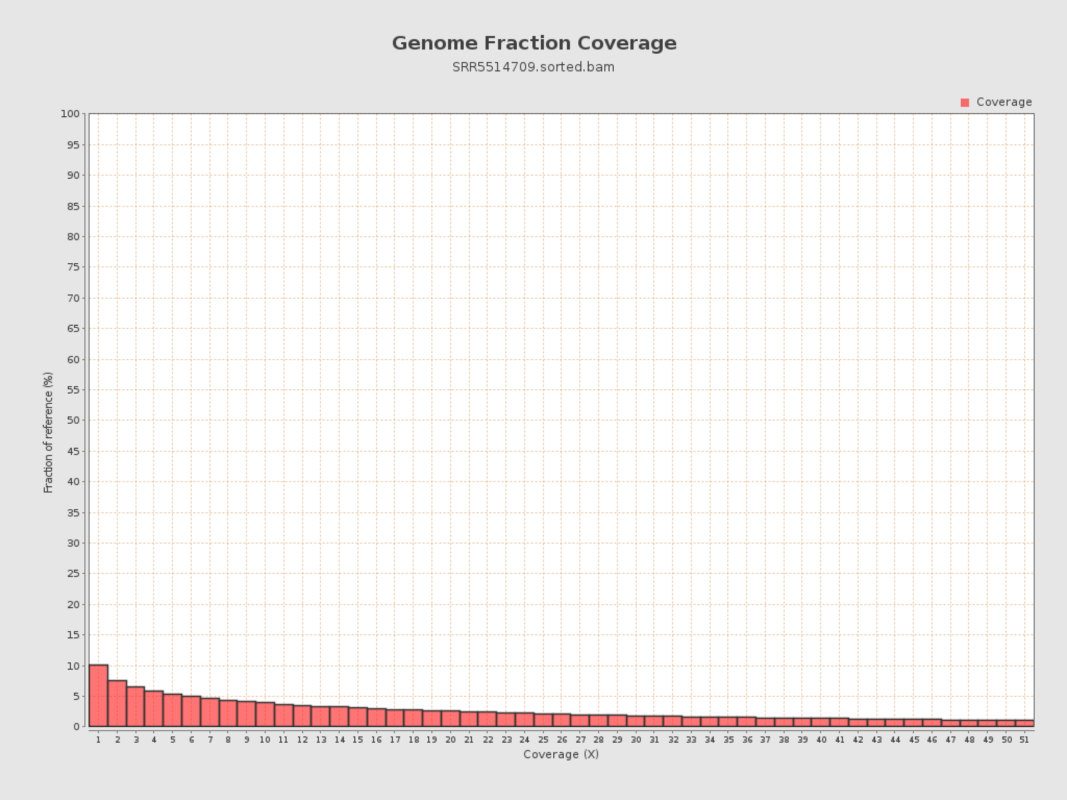
4. Results : Coverage Histogram



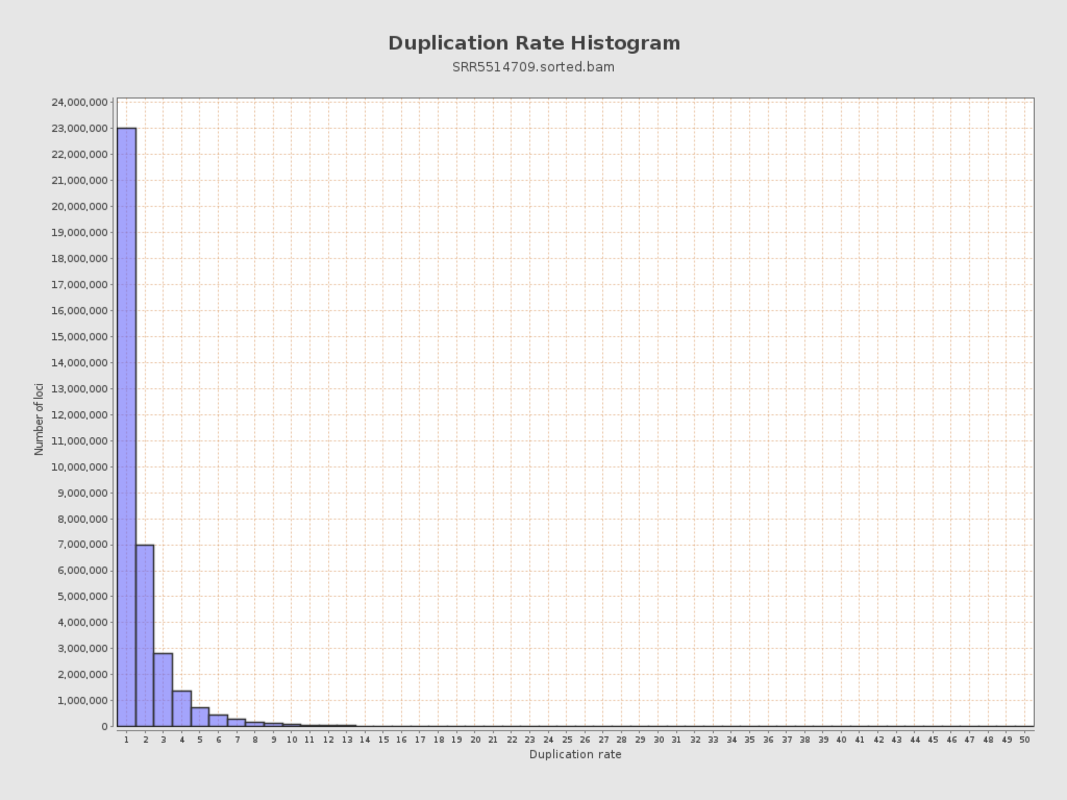
5. Results : Coverage Histogram (0-50X)



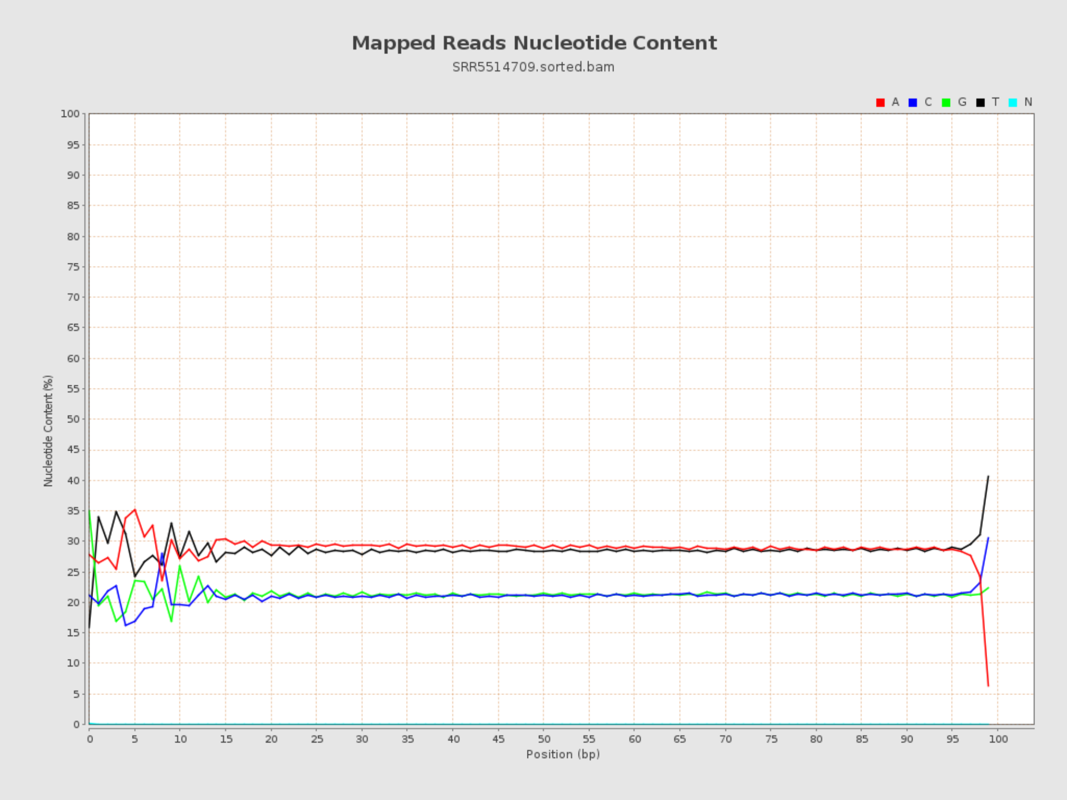
6. Results : Genome Fraction Coverage



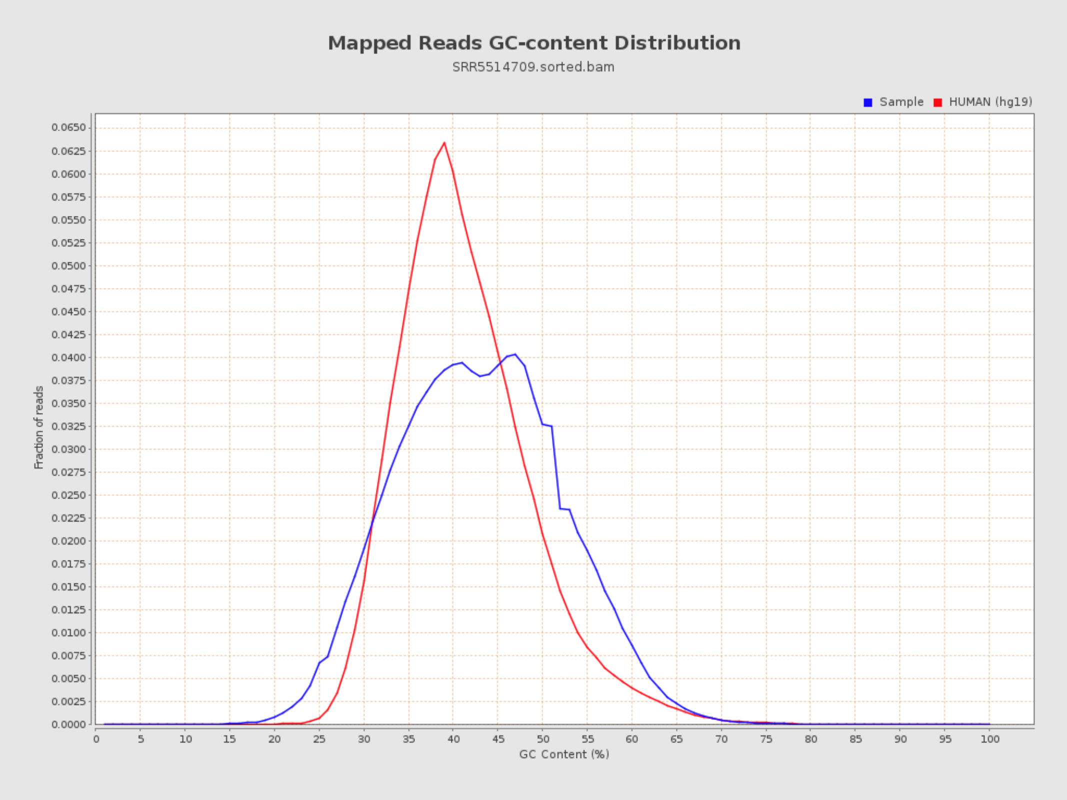
7. Results : Duplication Rate Histogram



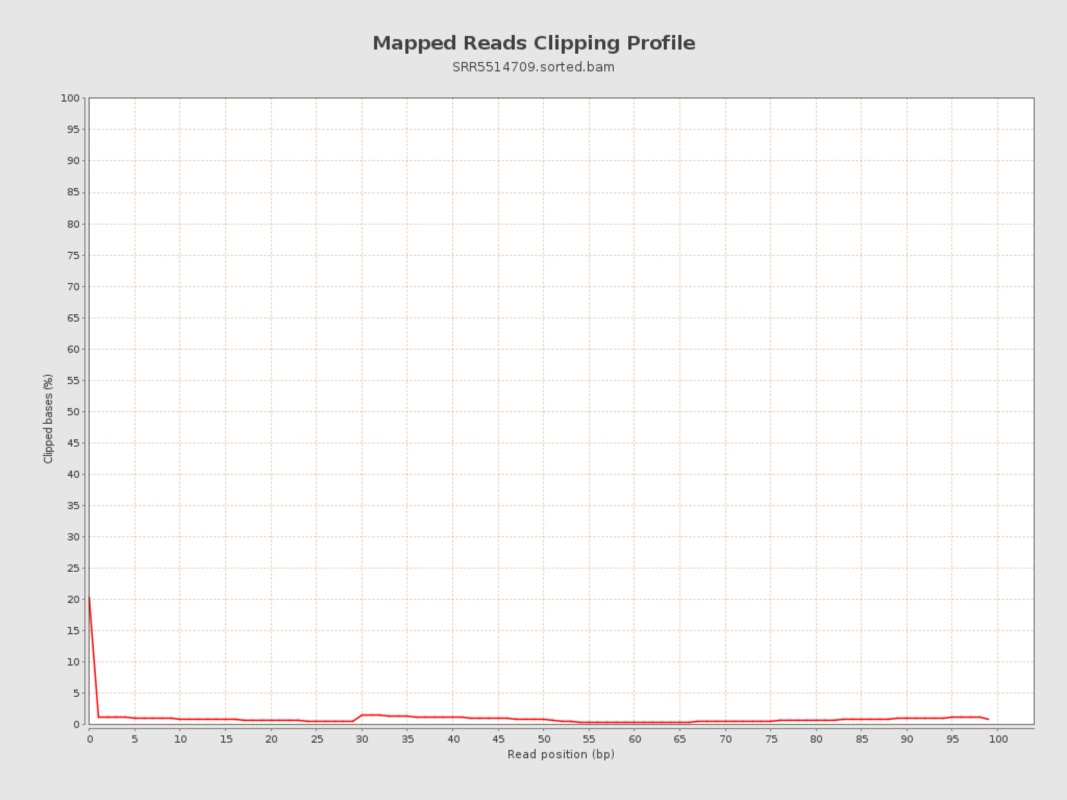
8. Results : Mapped Reads Nucleotide Content



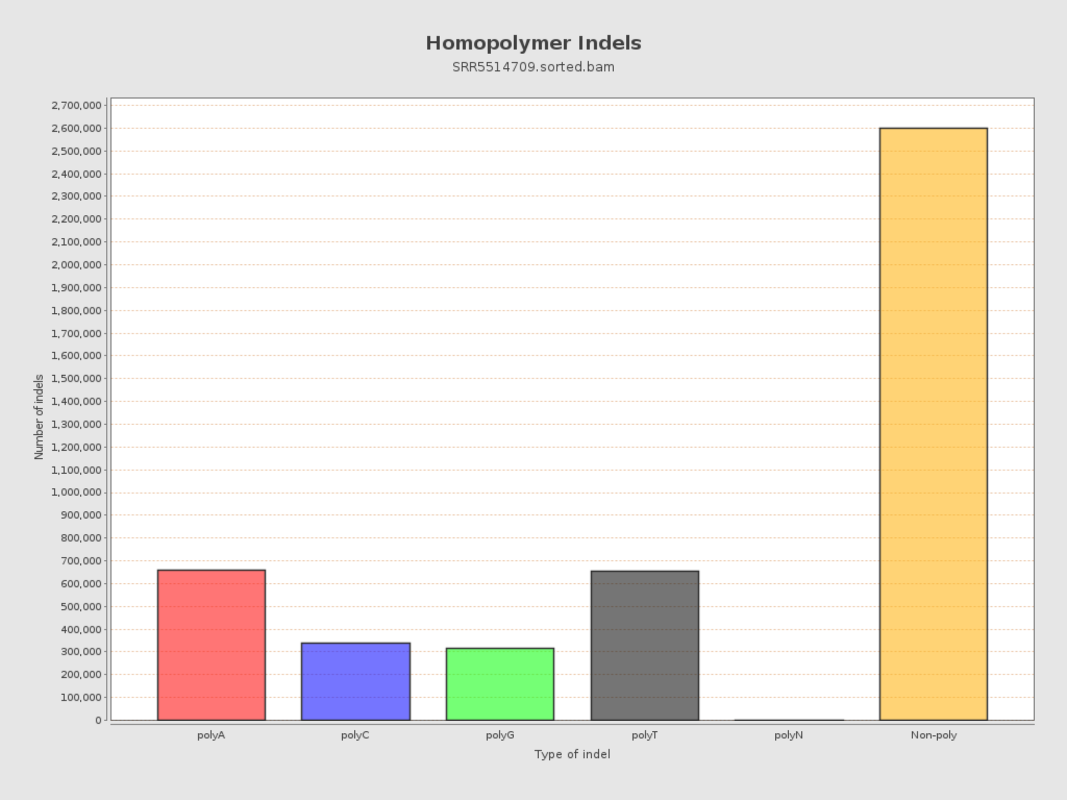
9. Results : Mapped Reads GC-content Distribution



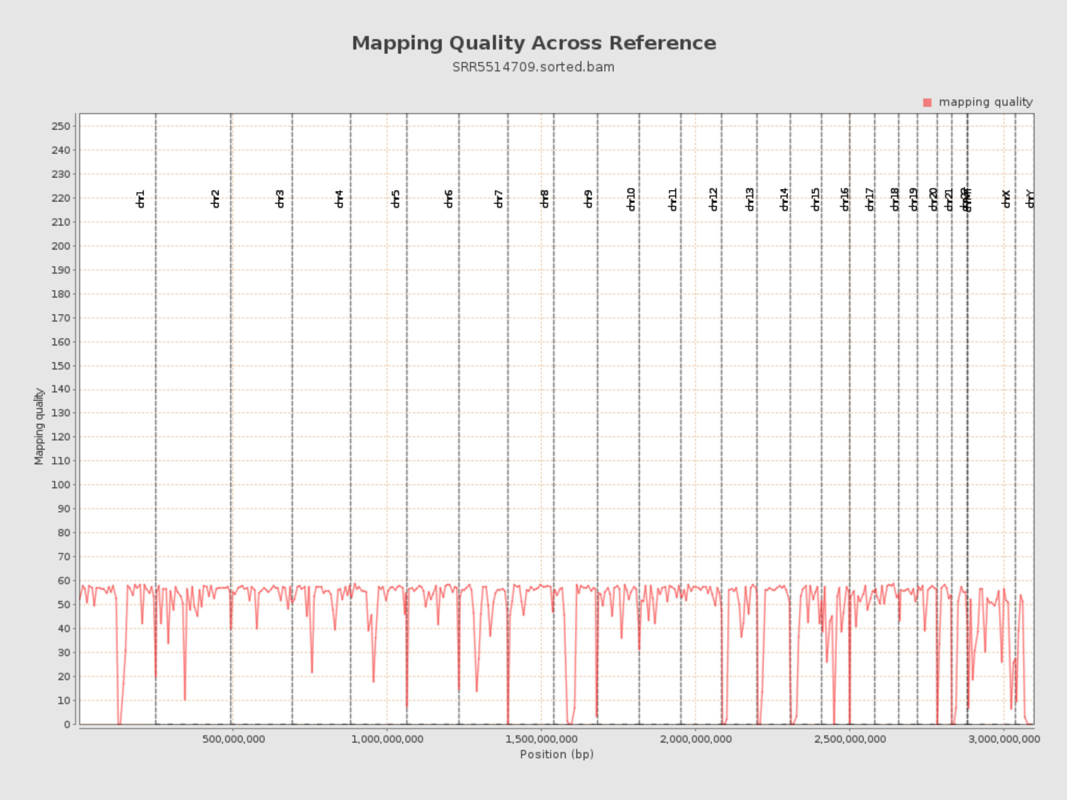
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram