Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 23:21:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514719.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_SRR5514719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 23:21:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	70,631,827
Mapped reads	66,212,298 / 93.74%
Unmapped reads	4,419,529 / 6.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,003,821 / 5.67%
Read min/max/mean length	30 / 100 / 101.07
Duplicated reads (estimated)	58,919,607 / 83.42%
Duplication rate	41.78%
Clipped reads	22,717,771 / 32.16%

2.2. ACGT Content

Number/percentage of A's	1,611,440,747 / 26.74%
Number/percentage of C's	1,348,424,753 / 22.37%
Number/percentage of T's	1,630,584,371 / 27.06%
Number/percentage of G's	1,361,816,968 / 22.6%
Number/percentage of N's	74,284,985 / 1.23%
GC Percentage	44.97%

2.3. Coverage

Mean	1.9496

Standard Deviation	282.3012

2.4. Mapping Quality

Mean Mapping Quality	48.26

2.5. Mismatches and indels

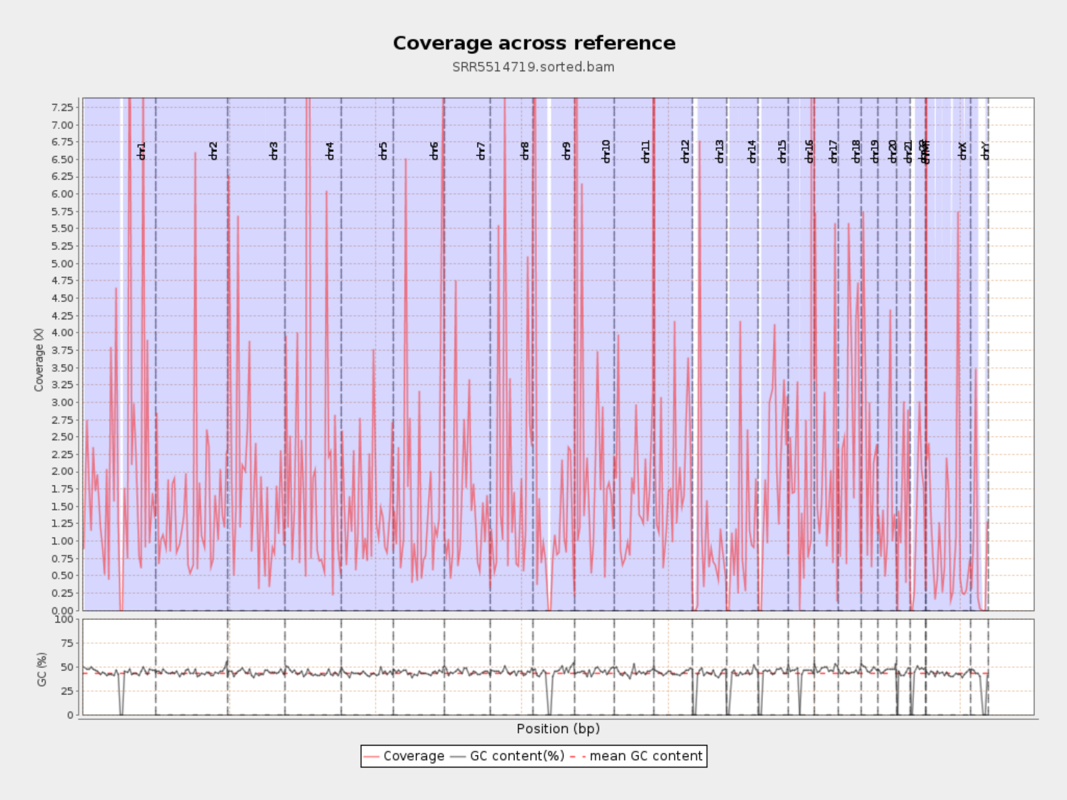
General error rate	1.18%
Mismatches	64,706,145
Insertions	3,278,034
Mapped reads with at least one insertion	4.55%
Deletions	2,992,008
Mapped reads with at least one deletion	4.03%
Homopolymer indels	29.61%

2.6. Chromosome stats

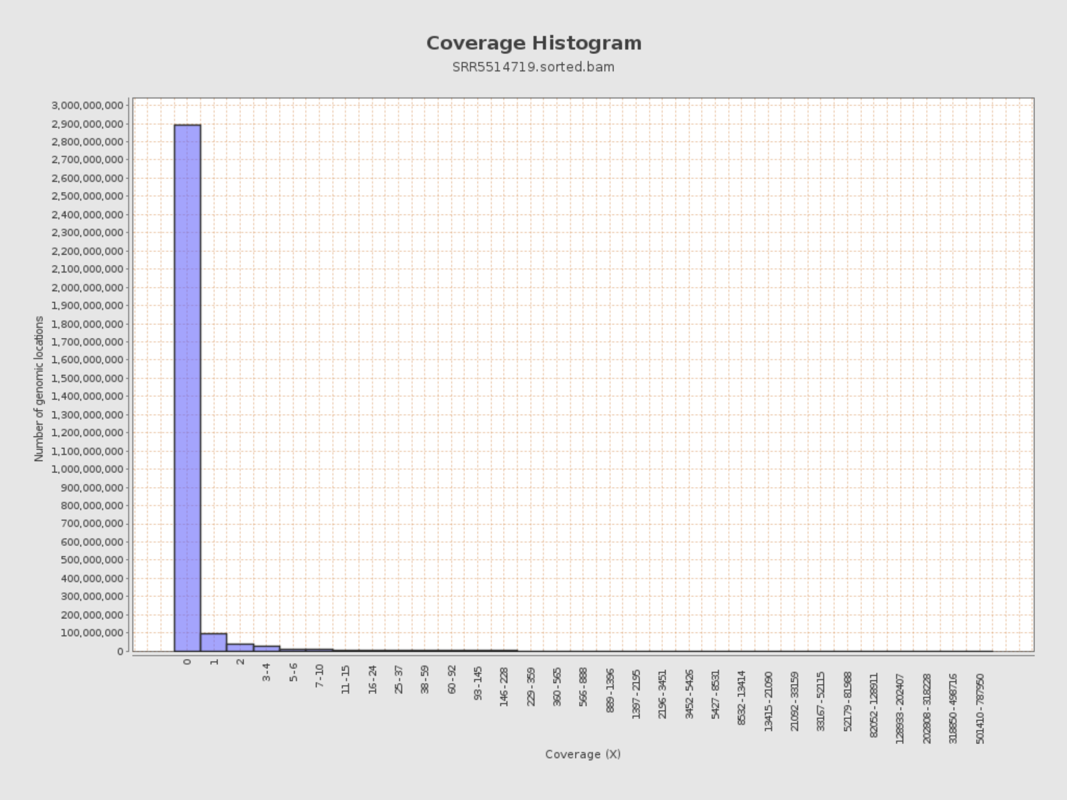
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	518255816	2.0793	81.0479
chr2	243199373	360893497	1.4839	97.0085
chr3	198022430	367084751	1.8538	74.4807
chr4	191154276	452956432	2.3696	266.5933
chr5	180915260	270544516	1.4954	71.7704
chr6	171115067	320933495	1.8755	83.3466
chr7	159138663	237544869	1.4927	48.5449

chr8	146364022	304808905	2.0825	209.8591
chr9	141213431	205085959	1.4523	95.2581
chr10	135534747	380966268	2.8108	227.3813
chr11	135006516	240526079	1.7816	52.9616
chr12	133851895	257501466	1.9238	74.0686
chr13	115169878	123806779	1.075	69.3888
chr14	107349540	122927468	1.1451	50.5082
chr15	102531392	206321568	2.0123	71.5683
chr16	90354753	673551435	7.4545	1,497.1083
chr17	81195210	181182176	2.2314	74.6067
chr18	78077248	214197859	2.7434	103.3345
chr19	59128983	144346544	2.4412	86.9444
chr20	63025520	92084496	1.4611	80.7453
chr21	48129895	69024405	1.4341	50.386
chr22	51304566	69667362	1.3579	58.9302
chrMT	16571	1364992	82.3723	78.4848
chrX	155270560	171192747	1.1025	63.1055
chrY	59373566	48505835	0.817	217.9311

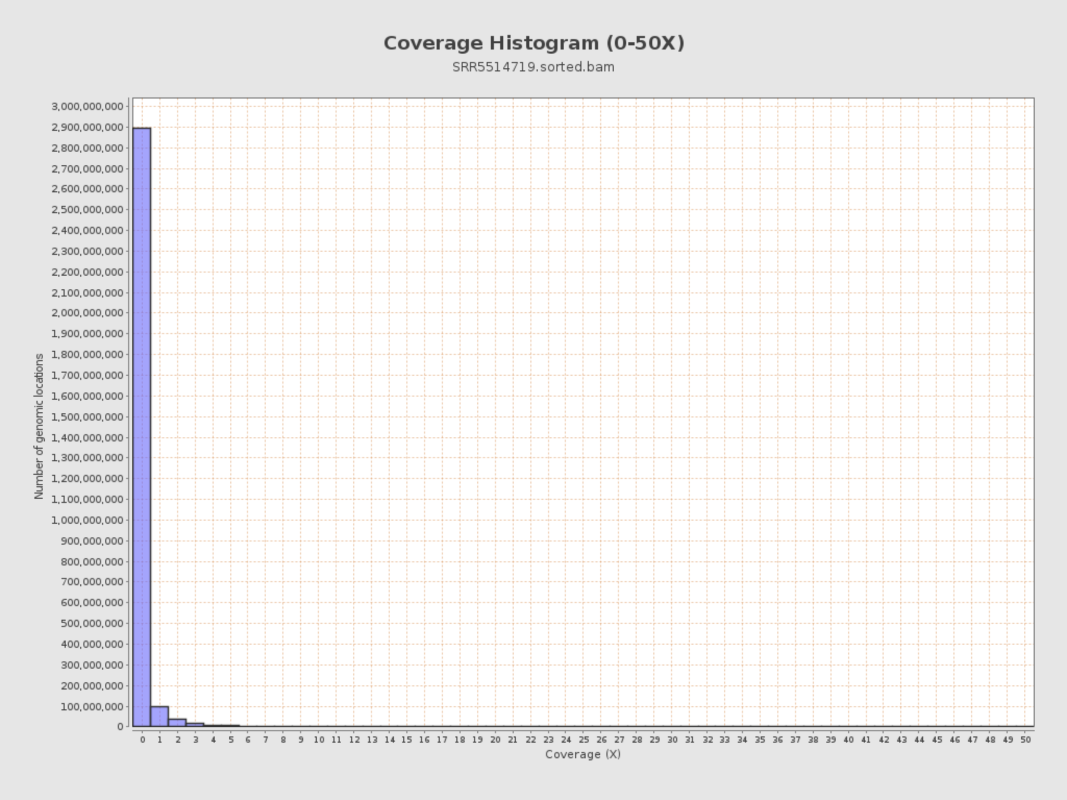
3. Results : Coverage across reference



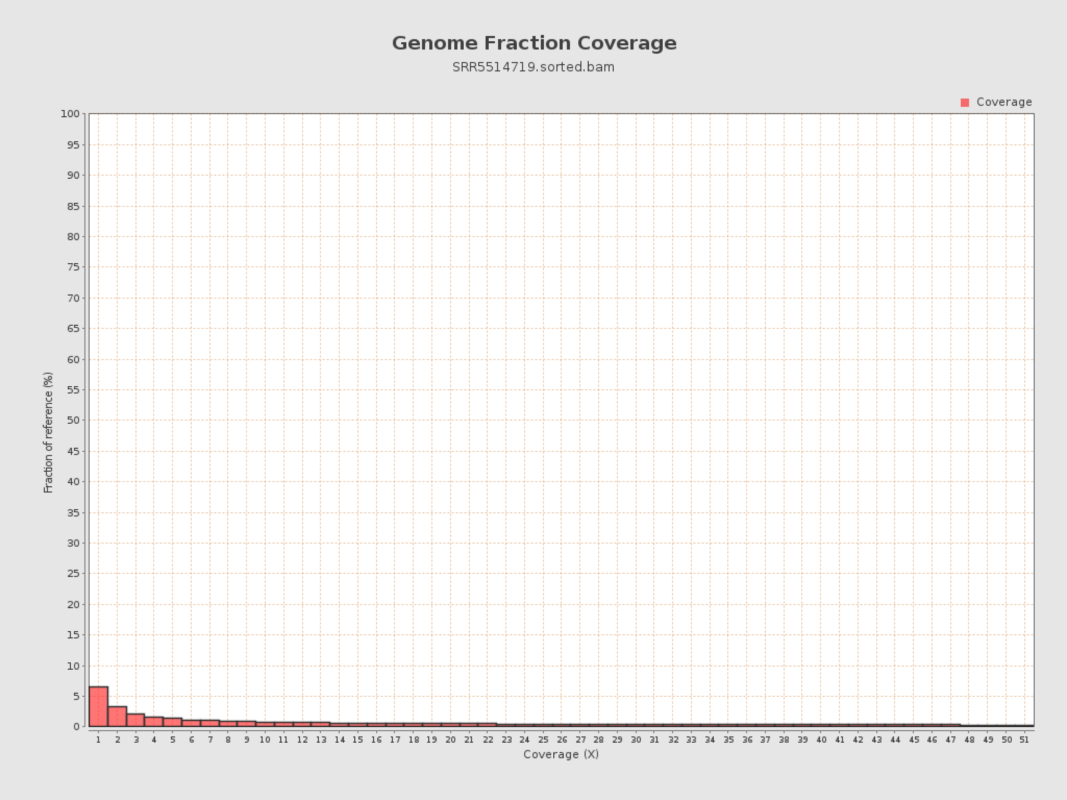
4. Results : Coverage Histogram



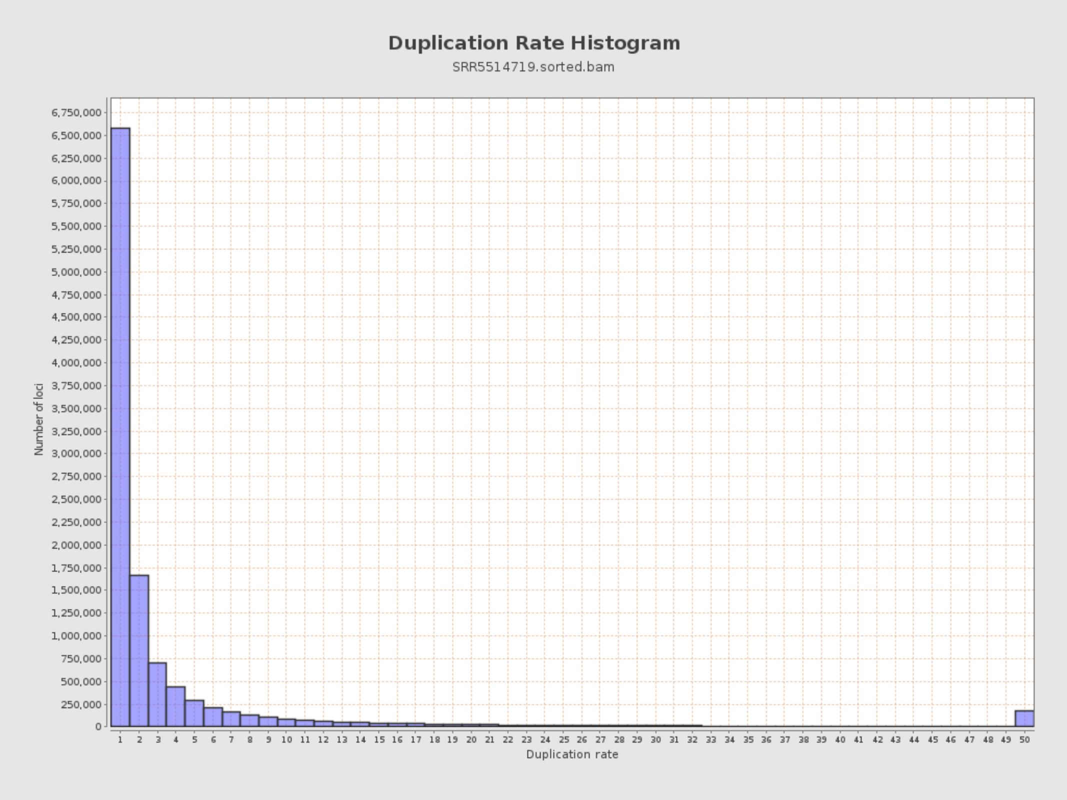
5. Results : Coverage Histogram (0-50X)



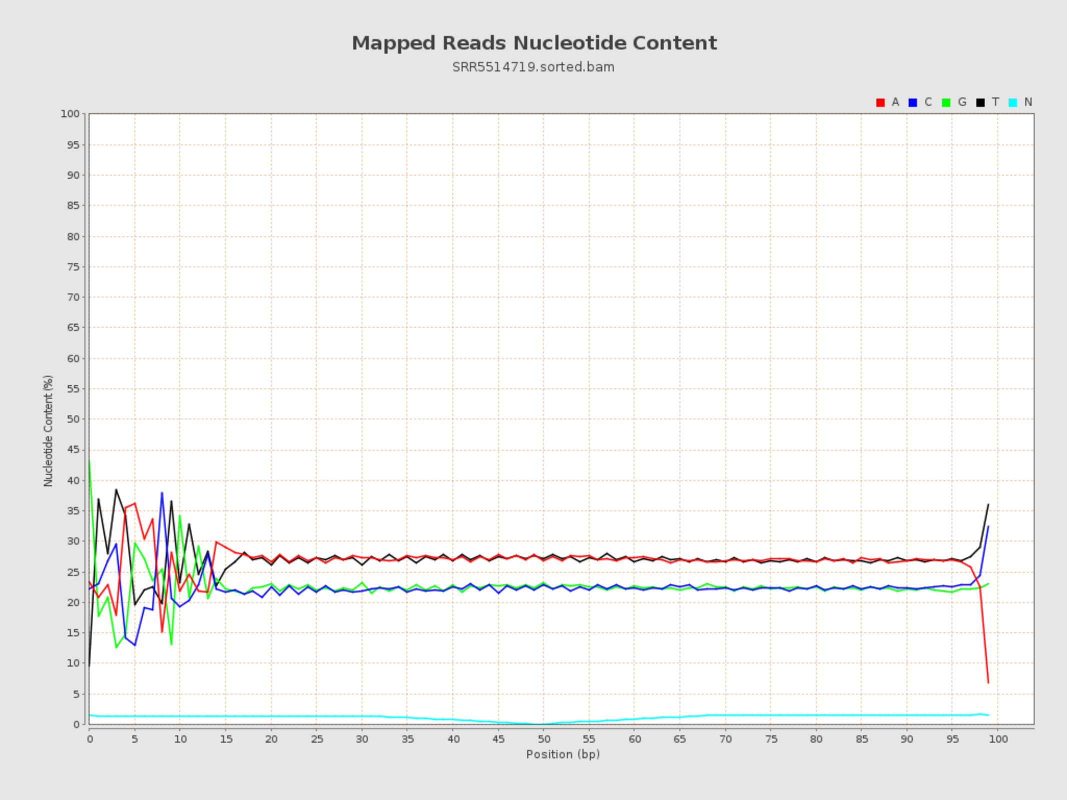
6. Results : Genome Fraction Coverage



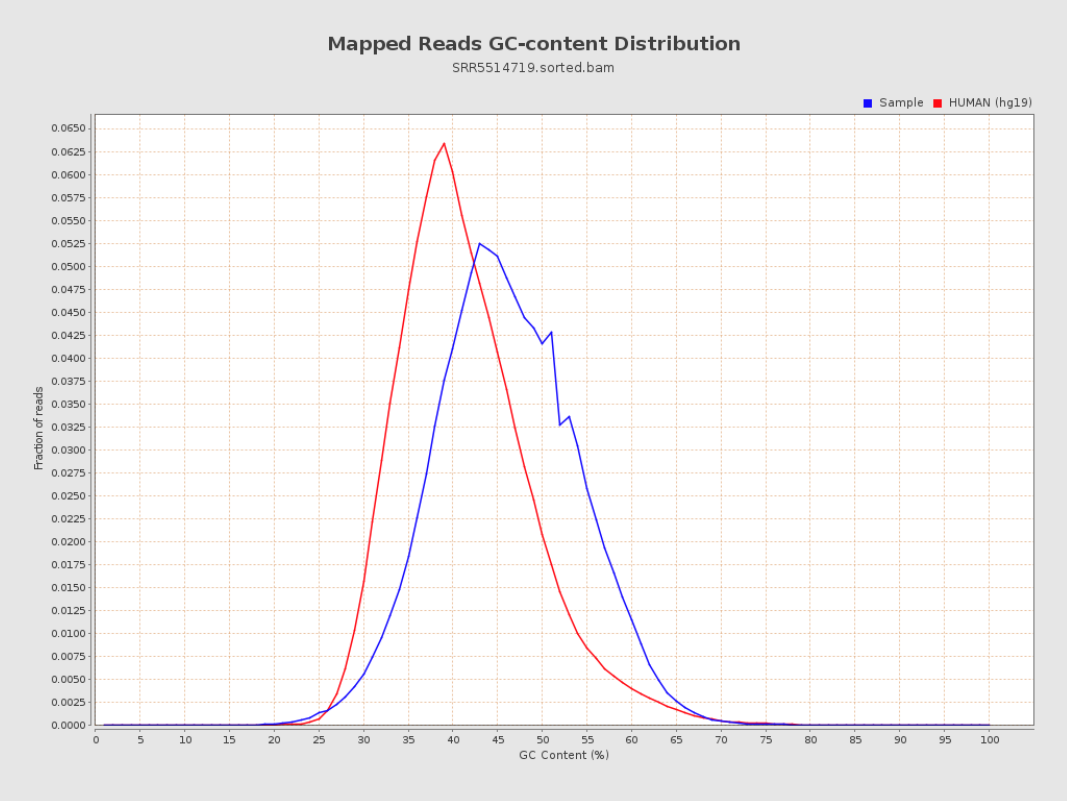
7. Results : Duplication Rate Histogram



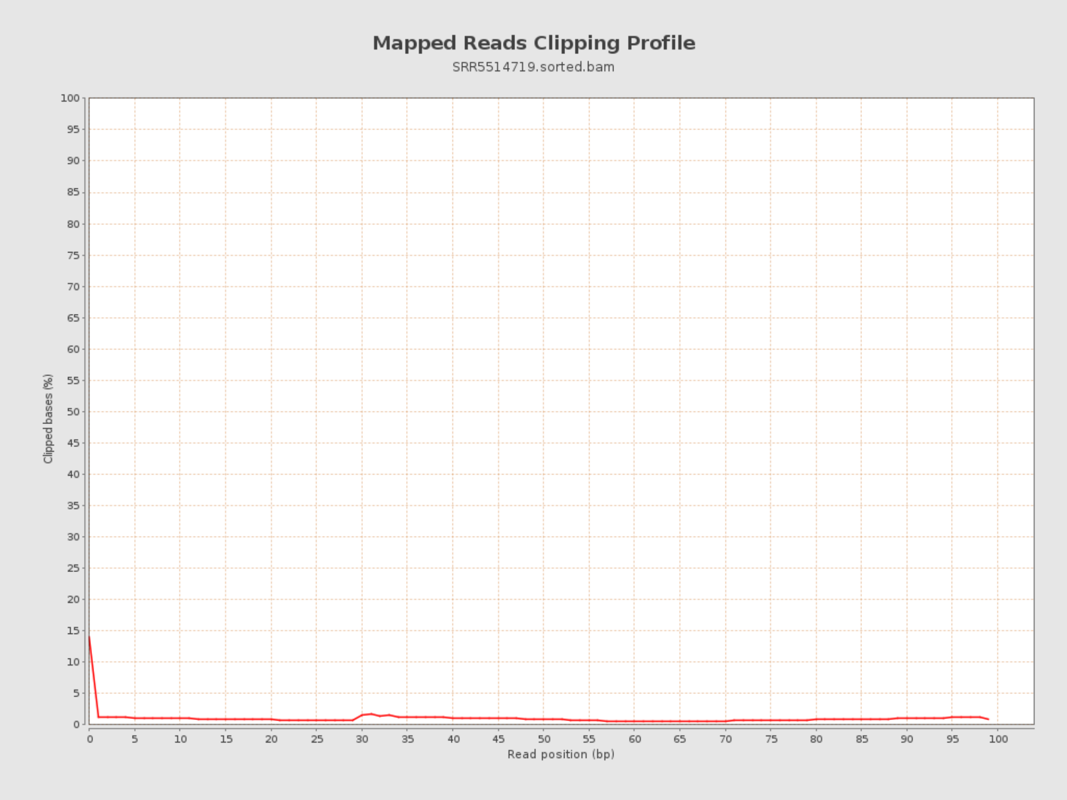
8. Results : Mapped Reads Nucleotide Content



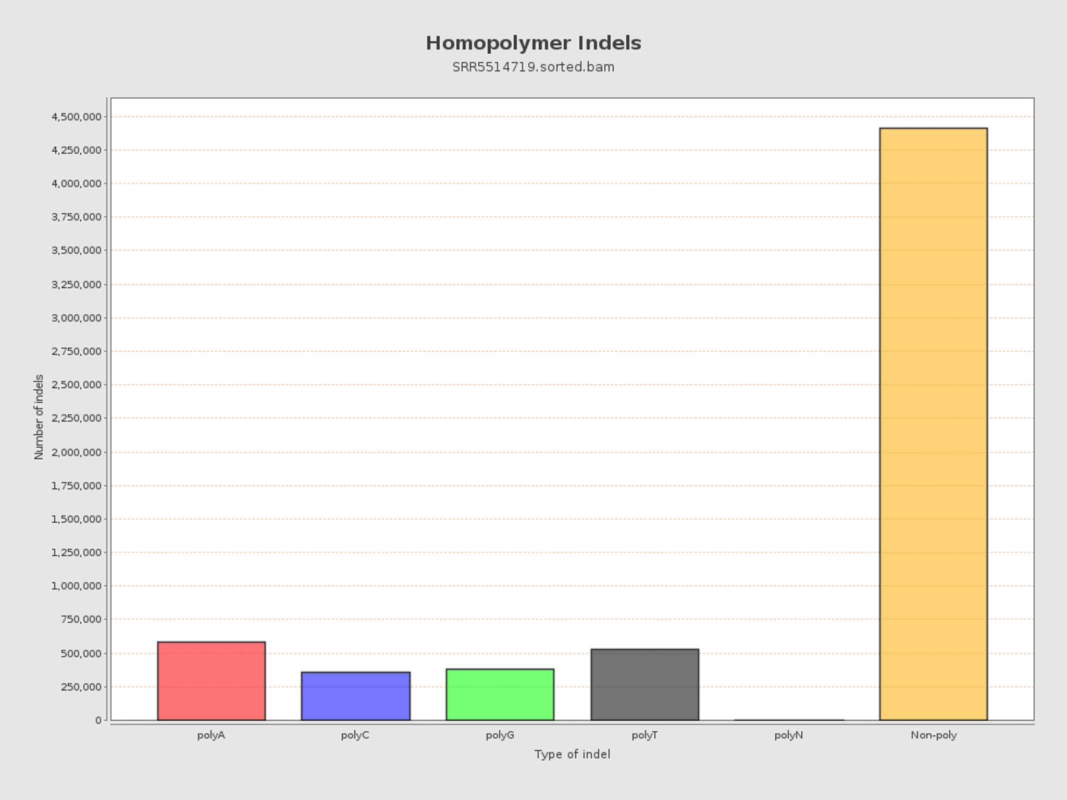
9. Results : Mapped Reads GC-content Distribution



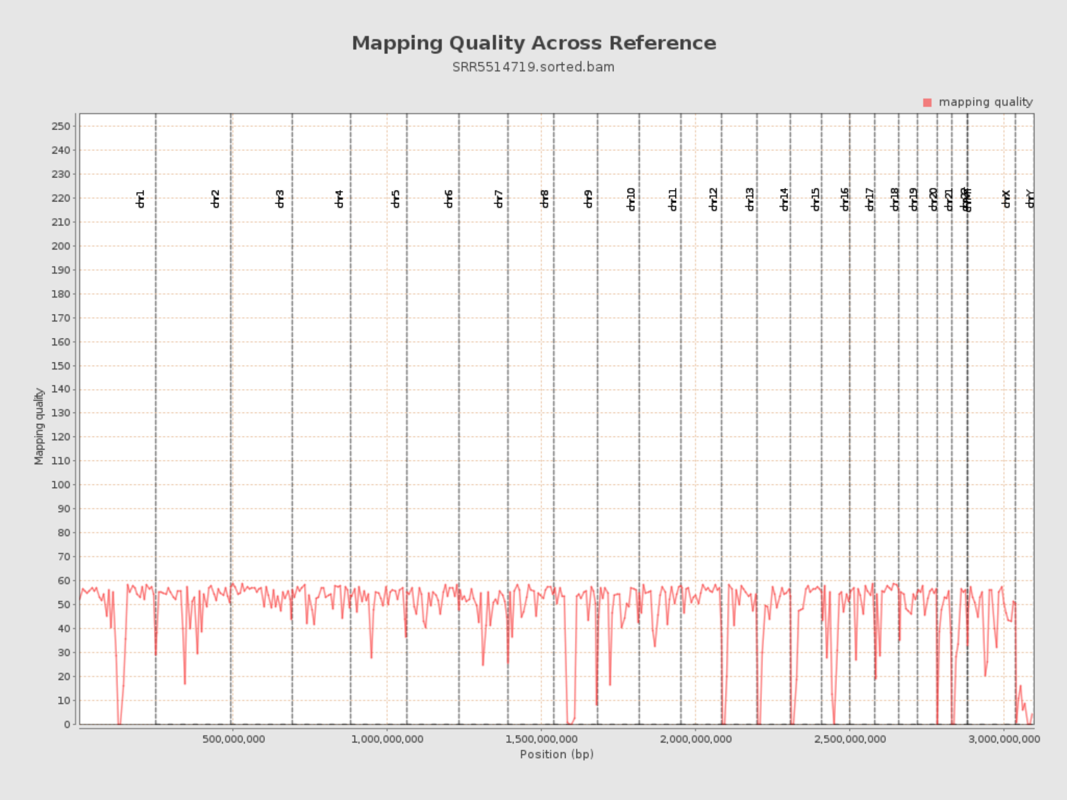
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram