Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 00:48:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514721.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_SRR5514721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514721.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 00:48:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	143,514,543
Mapped reads	115,699,644 / 80.62%
Unmapped reads	27,814,899 / 19.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,860,873 / 6.17%
Read min/max/mean length	30 / 100 / 101.3
Duplicated reads (estimated)	110,205,093 / 76.79%
Duplication rate	43.48%
Clipped reads	51,510,324 / 35.89%

2.2. ACGT Content

Number/percentage of A's	2,674,748,169 / 26.35%
Number/percentage of C's	2,319,606,731 / 22.85%
Number/percentage of T's	2,663,496,683 / 26.24%
Number/percentage of G's	2,304,818,690 / 22.7%
Number/percentage of N's	189,422,767 / 1.87%
GC Percentage	45.55%

2.3. Coverage

Mean	3.2855

Standard Deviation	712.3088

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Mismatches and indels

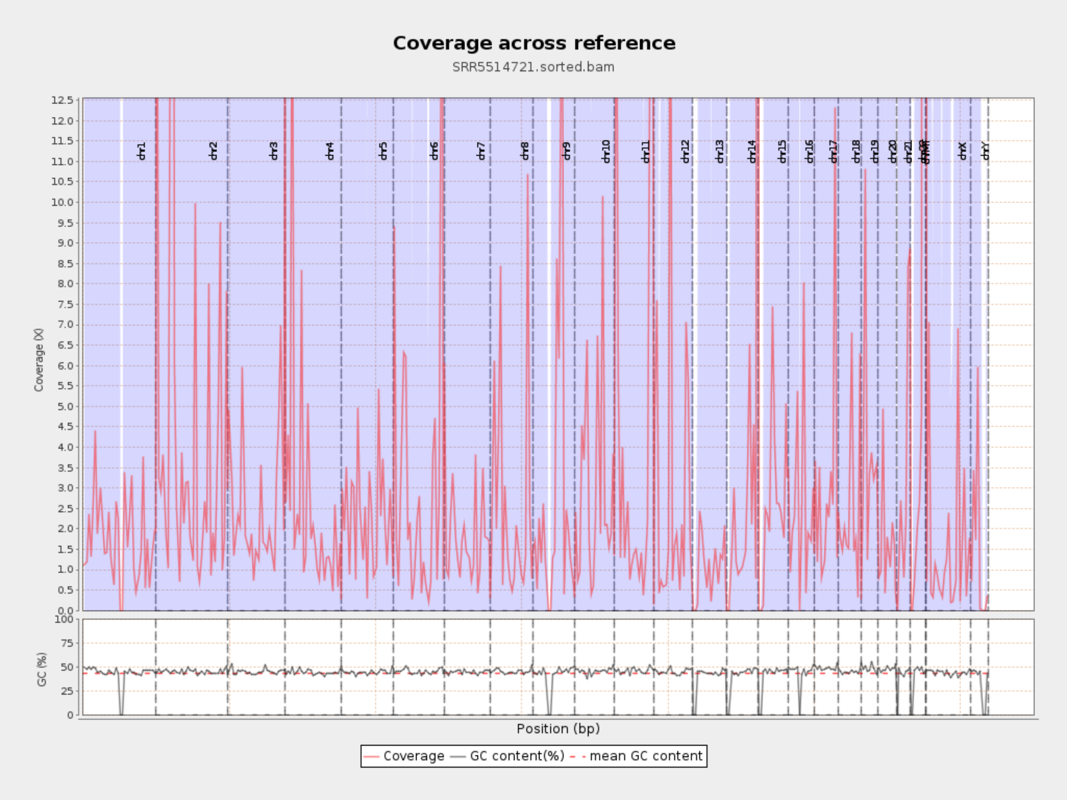
General error rate	1.28%
Mismatches	114,483,055
Insertions	7,413,942
Mapped reads with at least one insertion	5.96%
Deletions	5,943,861
Mapped reads with at least one deletion	4.7%
Homopolymer indels	27.66%

2.6. Chromosome stats

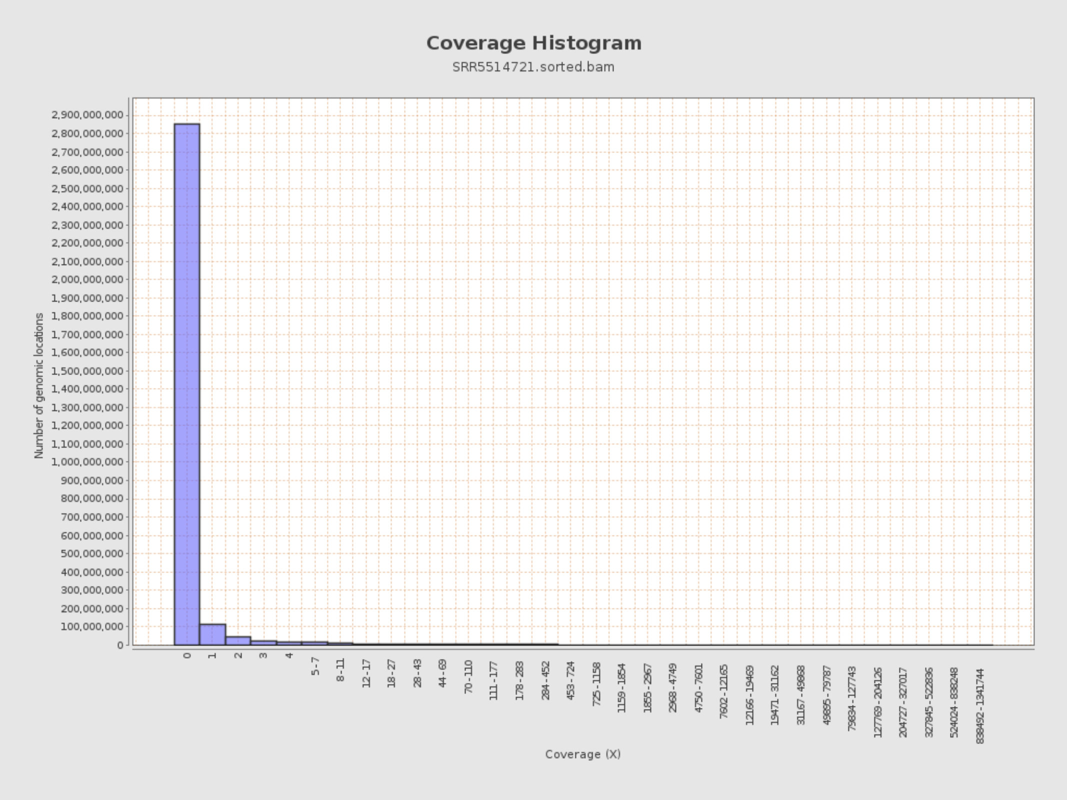
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	441681471	1.772	147.5668
chr2	243199373	1292227997	5.3135	614.1592
chr3	198022430	510196644	2.5765	89.4844
chr4	191154276	520013992	2.7204	176.838
chr5	180915260	427557462	2.3633	92.3563
chr6	171115067	552570808	3.2292	184.0744
chr7	159138663	287737702	1.8081	105.0014

chr8	146364022	381059196	2.6035	115.702
chr9	141213431	396933412	2.8109	341.6392
chr10	135534747	405912232	2.9949	140.484
chr11	135006516	620860133	4.5987	300.952
chr12	133851895	430751302	3.2181	133.6362
chr13	115169878	124378145	1.08	48.9329
chr14	107349540	262036909	2.441	86.0905
chr15	102531392	264421307	2.5789	82.0399
chr16	90354753	233274773	2.5818	102.3709
chr17	81195210	264192222	3.2538	310.0081
chr18	78077248	184088071	2.3578	74.363
chr19	59128983	230838889	3.904	215.5039
chr20	63025520	106224407	1.6854	88.8951
chr21	48129895	160036659	3.3251	159.0885
chr22	51304566	1732460941	33.7682	5,224.7801
chrMT	16571	3339942	201.5534	341.4375
chrX	155270560	245170177	1.579	156.0969
chrY	59373566	92976546	1.566	152.4204

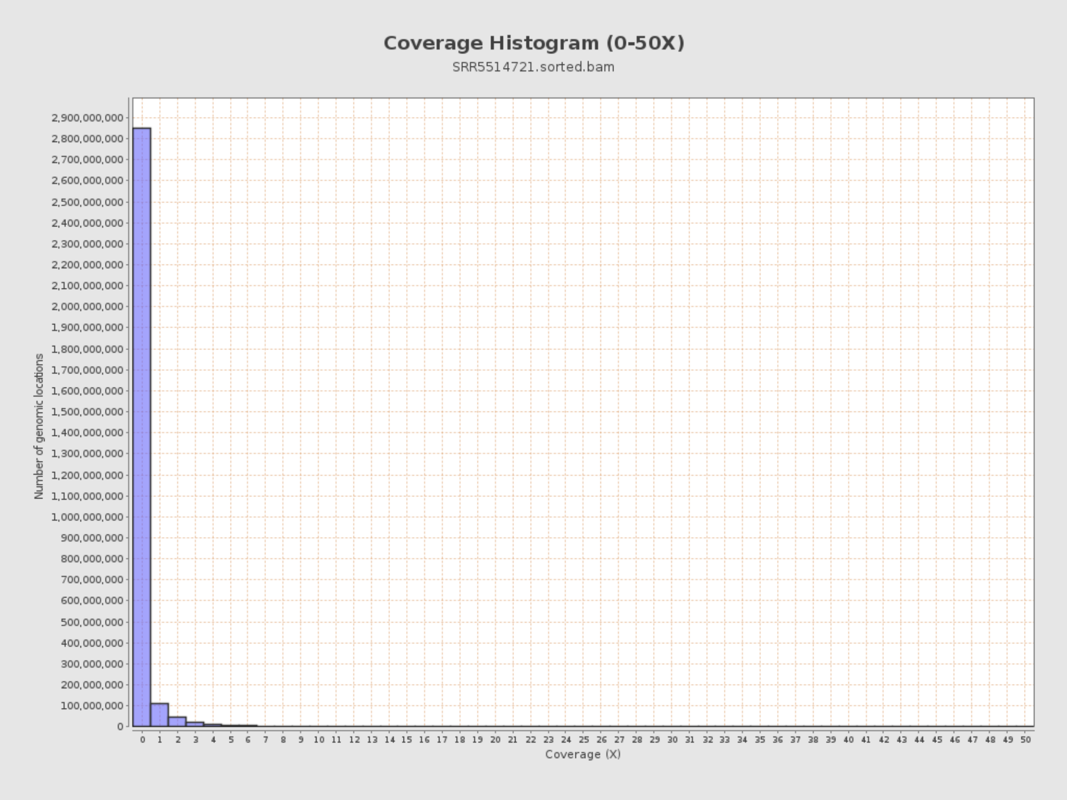
3. Results : Coverage across reference



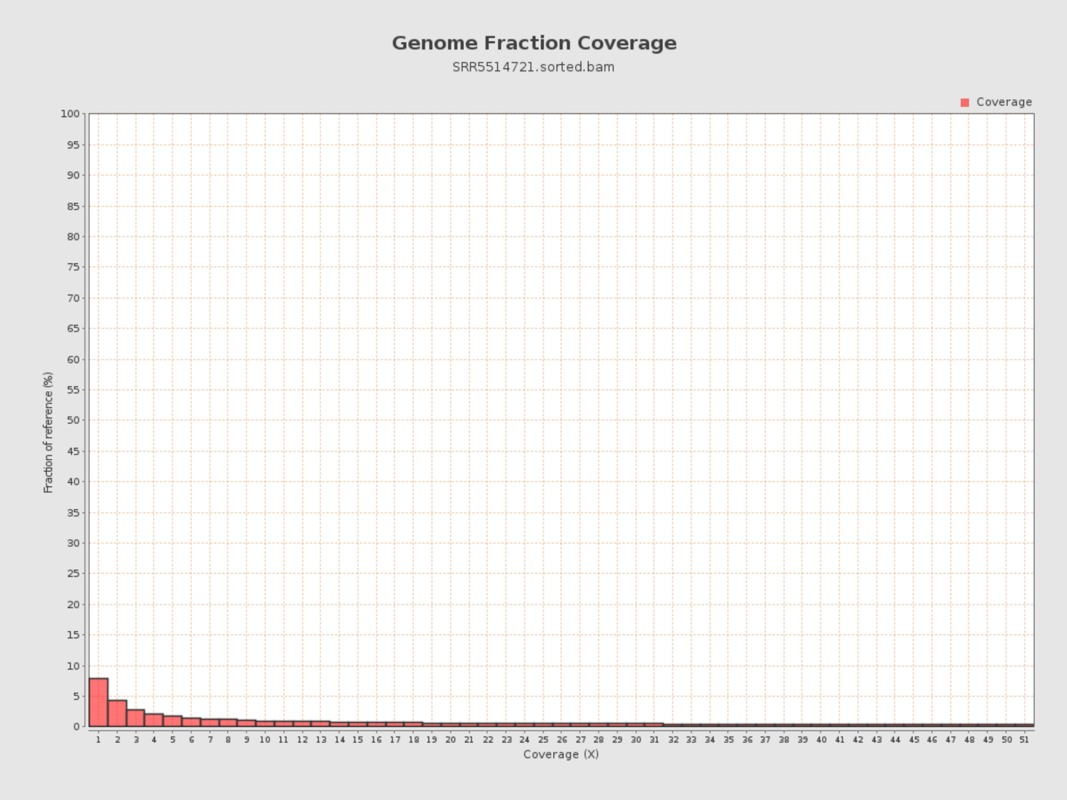
4. Results : Coverage Histogram



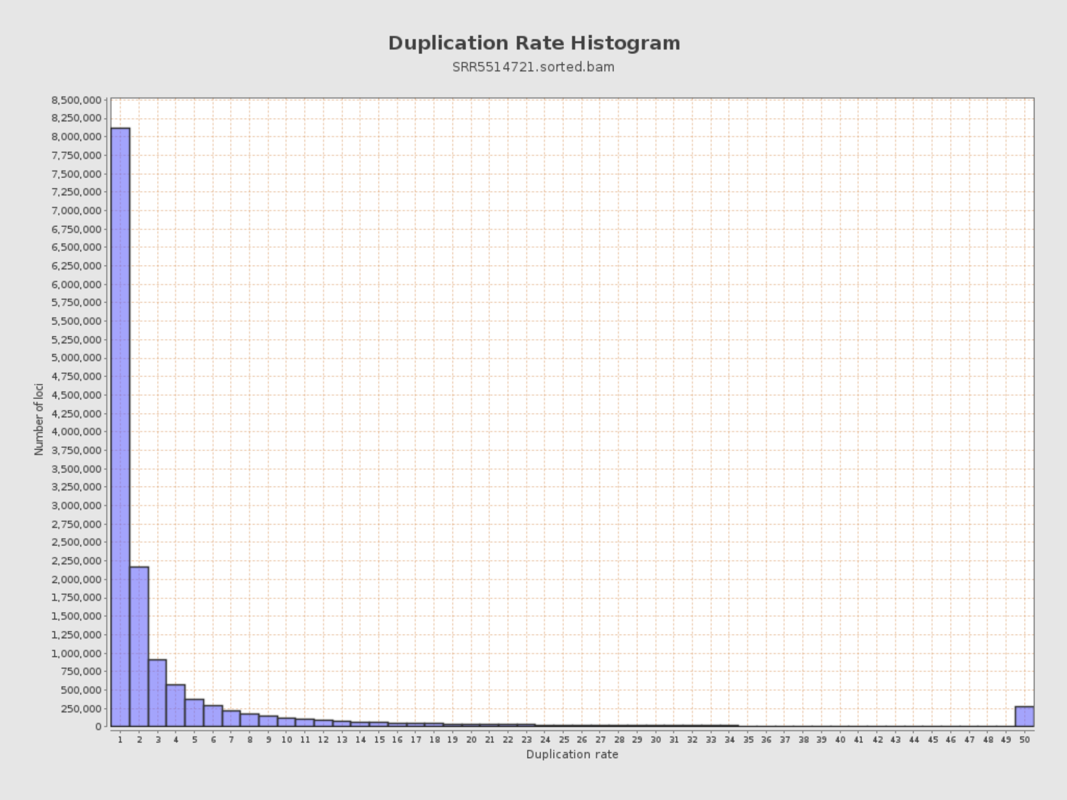
5. Results : Coverage Histogram (0-50X)



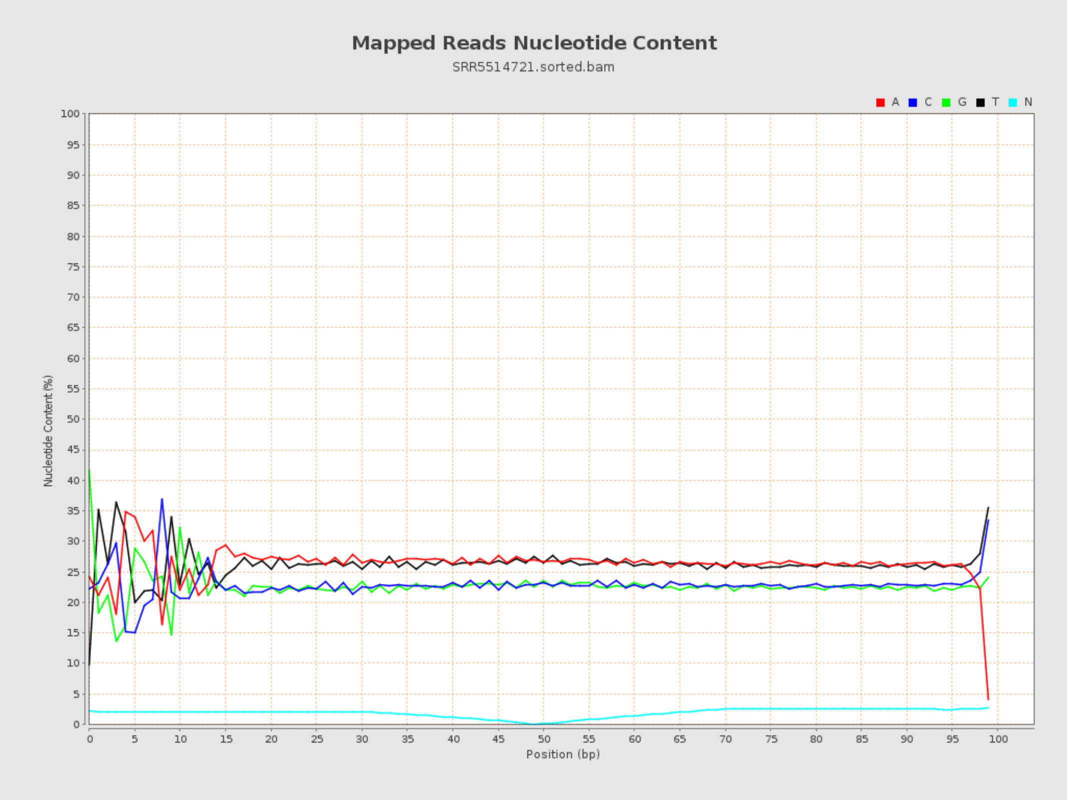
6. Results : Genome Fraction Coverage



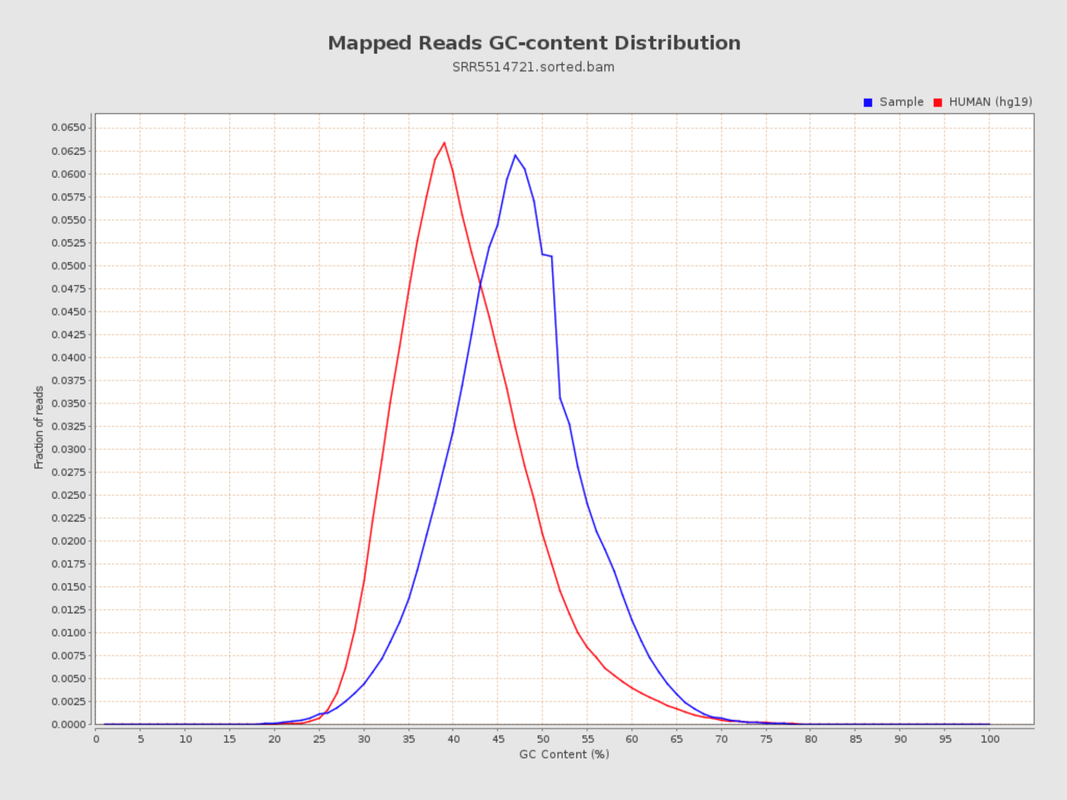
7. Results : Duplication Rate Histogram



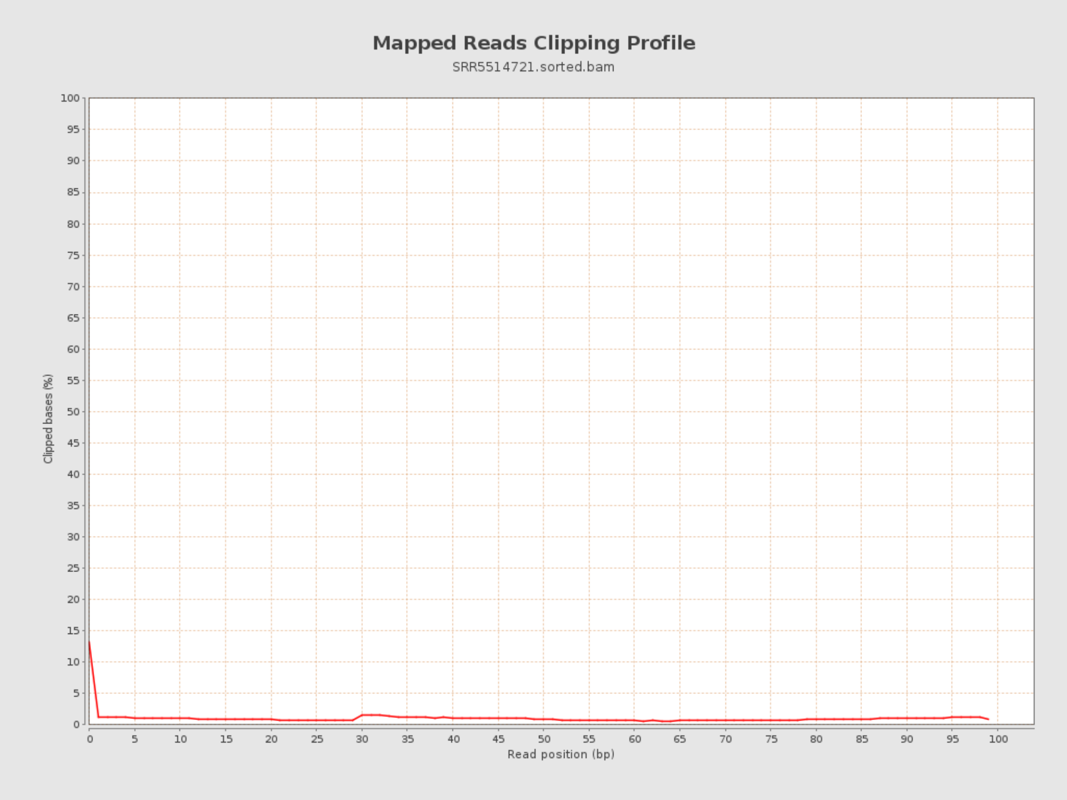
8. Results : Mapped Reads Nucleotide Content



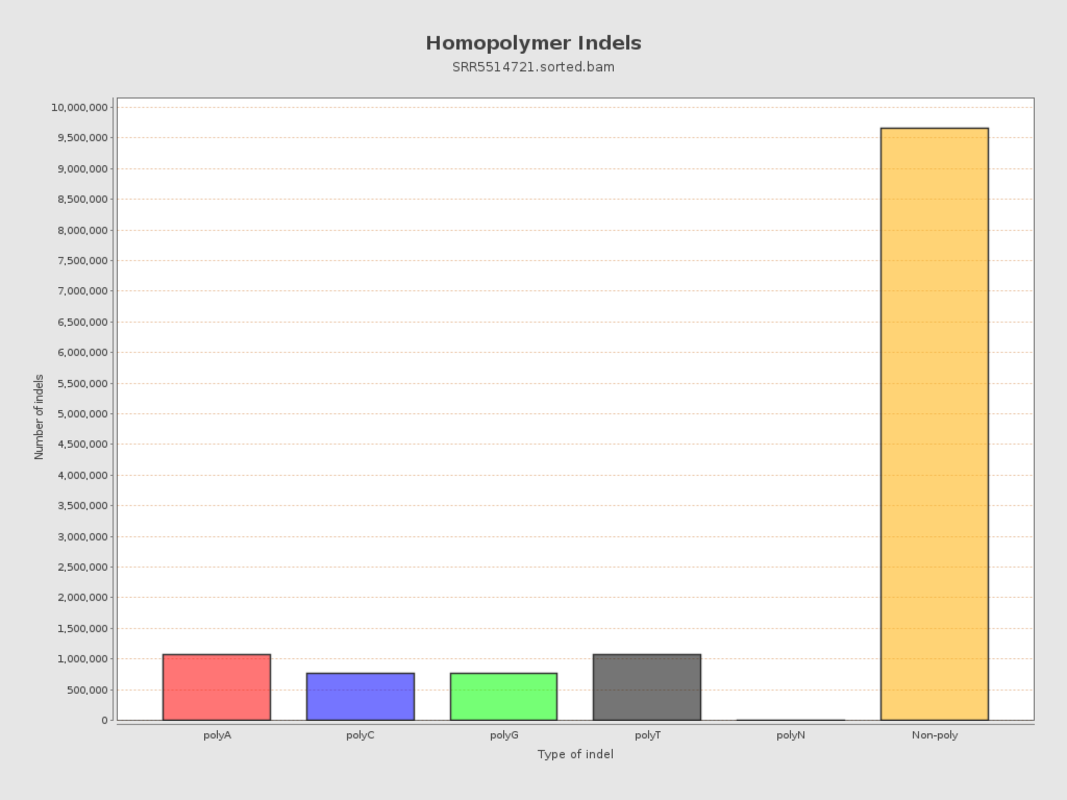
9. Results : Mapped Reads GC-content Distribution



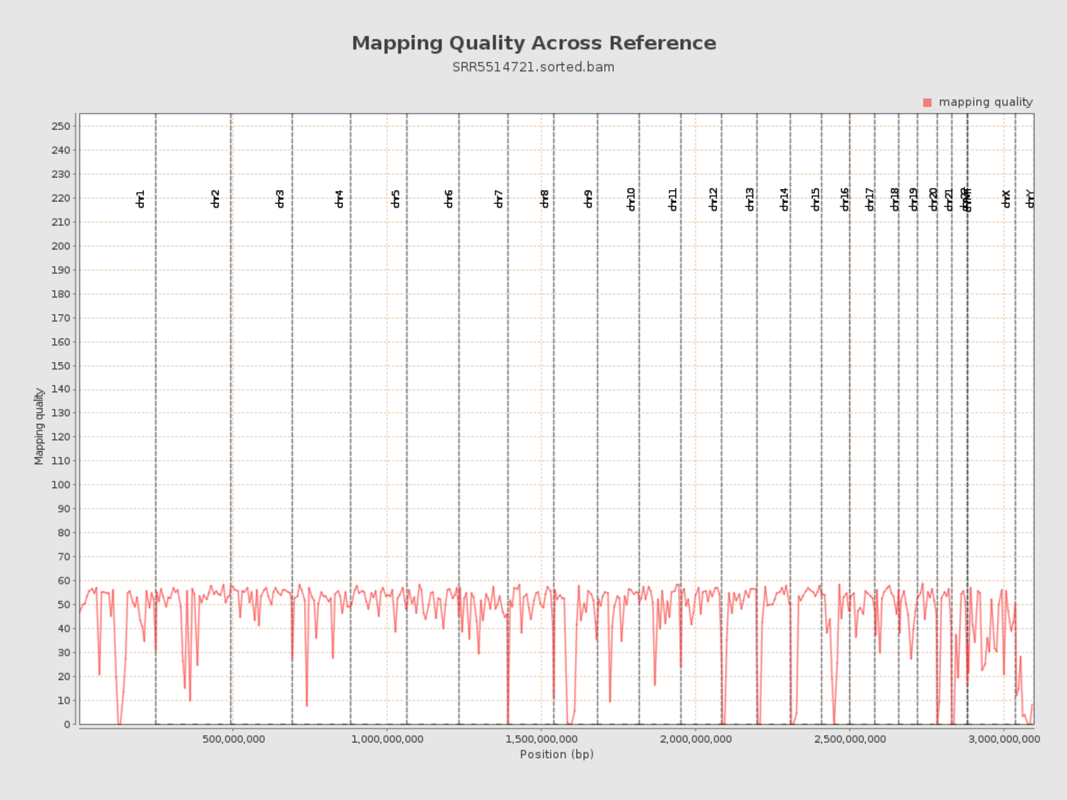
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram