Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 05:04:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514759.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_SRR5514759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 05:04:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,394,834
Mapped reads	44,894,947 / 92.77%
Unmapped reads	3,499,887 / 7.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,262,693 / 12.94%
Read min/max/mean length	30 / 100 / 104.39
Duplicated reads (estimated)	33,993,466 / 70.24%
Duplication rate	44.67%
Clipped reads	20,636,495 / 42.64%

2.2. ACGT Content

Number/percentage of A's	1,343,546,701 / 31.22%
Number/percentage of C's	809,099,433 / 18.8%
Number/percentage of T's	1,321,256,657 / 30.7%
Number/percentage of G's	829,962,084 / 19.28%
Number/percentage of N's	298,625 / 0.01%
GC Percentage	38.08%

2.3. Coverage

Mean	1.3911

Standard Deviation	45.2047

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

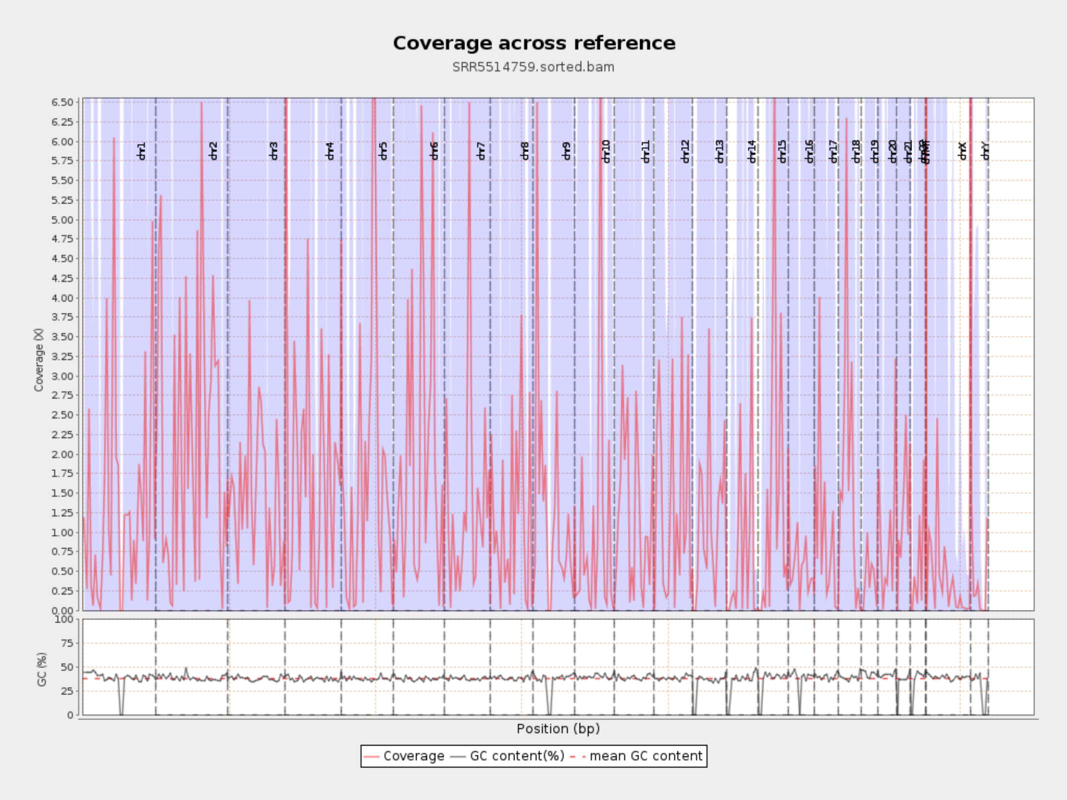
General error rate	0.57%
Mismatches	20,761,113
Insertions	2,416,410
Mapped reads with at least one insertion	5.2%
Deletions	870,391
Mapped reads with at least one deletion	1.86%
Homopolymer indels	55.66%

2.6. Chromosome stats

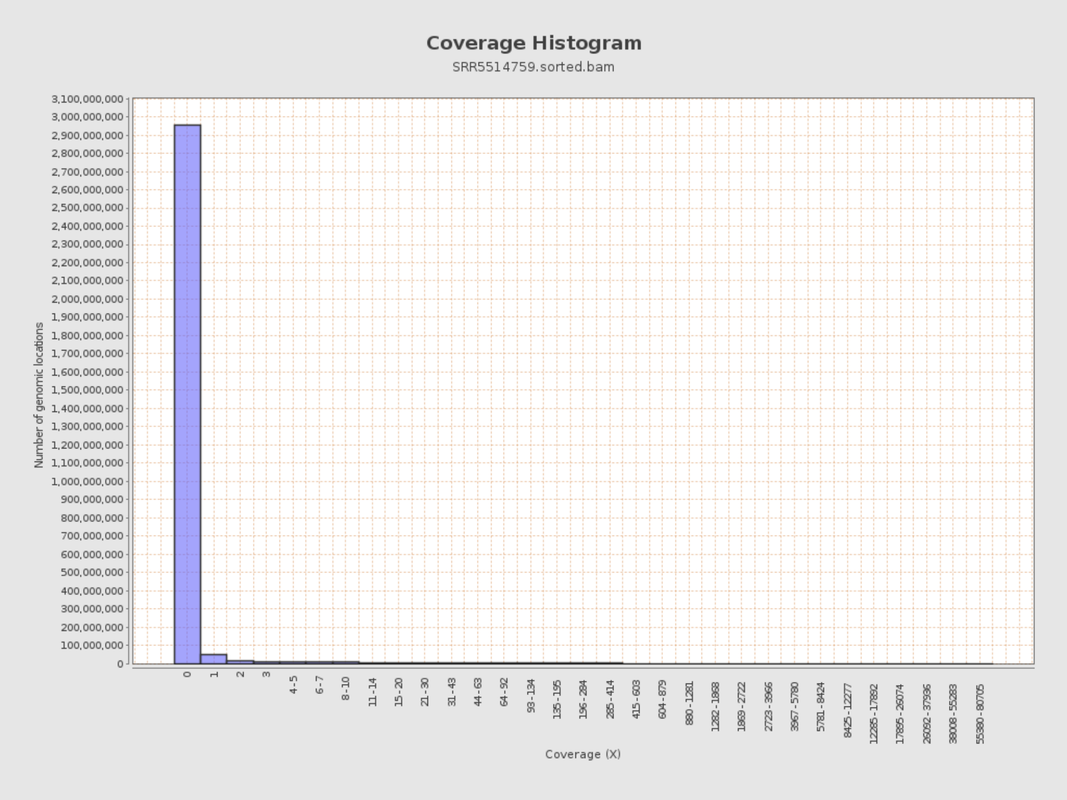
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	333093733	1.3364	33.8145
chr2	243199373	539121696	2.2168	68.3142
chr3	198022430	288547198	1.4571	25.9189
chr4	191154276	343308969	1.796	85.9815
chr5	180915260	306611892	1.6948	28.7771
chr6	171115067	349092271	2.0401	28.4995
chr7	159138663	221957333	1.3947	23.3263

chr8	146364022	173202301	1.1834	22.9335
chr9	141213431	185642141	1.3146	26.6367
chr10	135534747	135379393	0.9989	31.8841
chr11	135006516	161826469	1.1987	21.2198
chr12	133851895	185675584	1.3872	22.8965
chr13	115169878	137277985	1.192	24.4809
chr14	107349540	83650212	0.7792	13.3456
chr15	102531392	151881038	1.4813	22.7202
chr16	90354753	54396862	0.602	16.8821
chr17	81195210	86279870	1.0626	15.3156
chr18	78077248	138242014	1.7706	25.8463
chr19	59128983	25573988	0.4325	13.7087
chr20	63025520	56612410	0.8982	26.4937
chr21	48129895	61793899	1.2839	45.3677
chr22	51304566	29600482	0.577	38.5314
chrMT	16571	141213366	8,521.7166	7,064.2052
chrX	155270560	94716989	0.61	14.9278
chrY	59373566	21797838	0.3671	9.2478

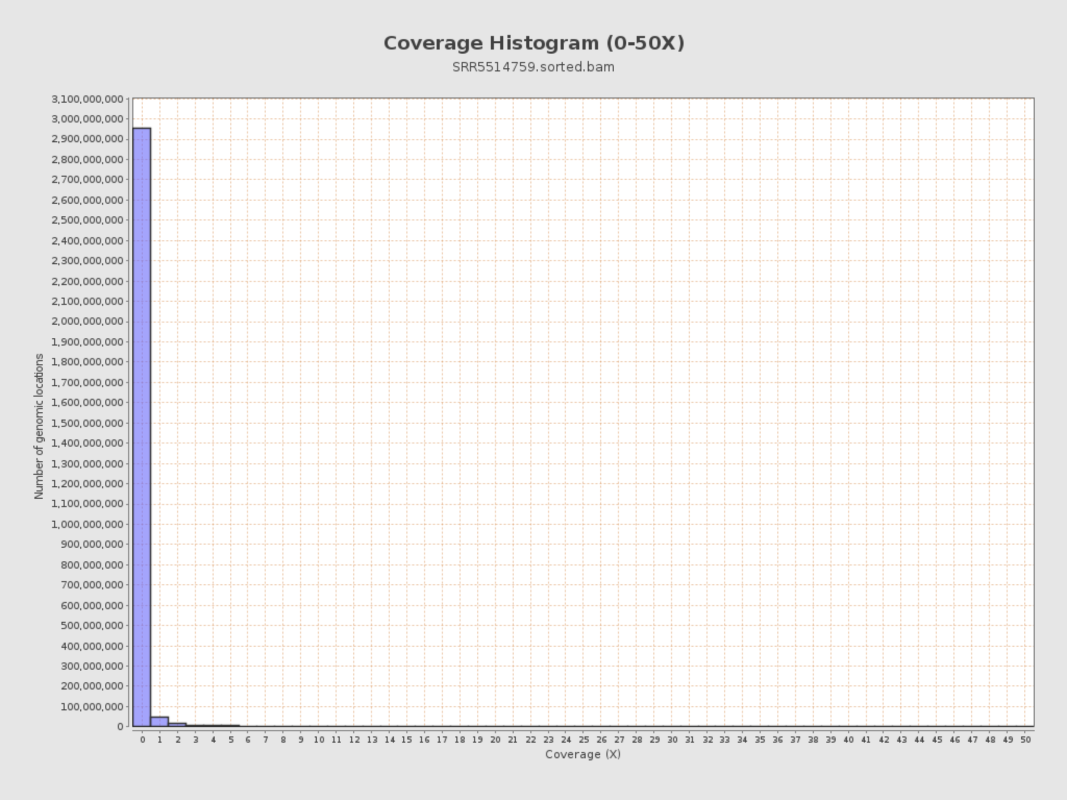
3. Results : Coverage across reference



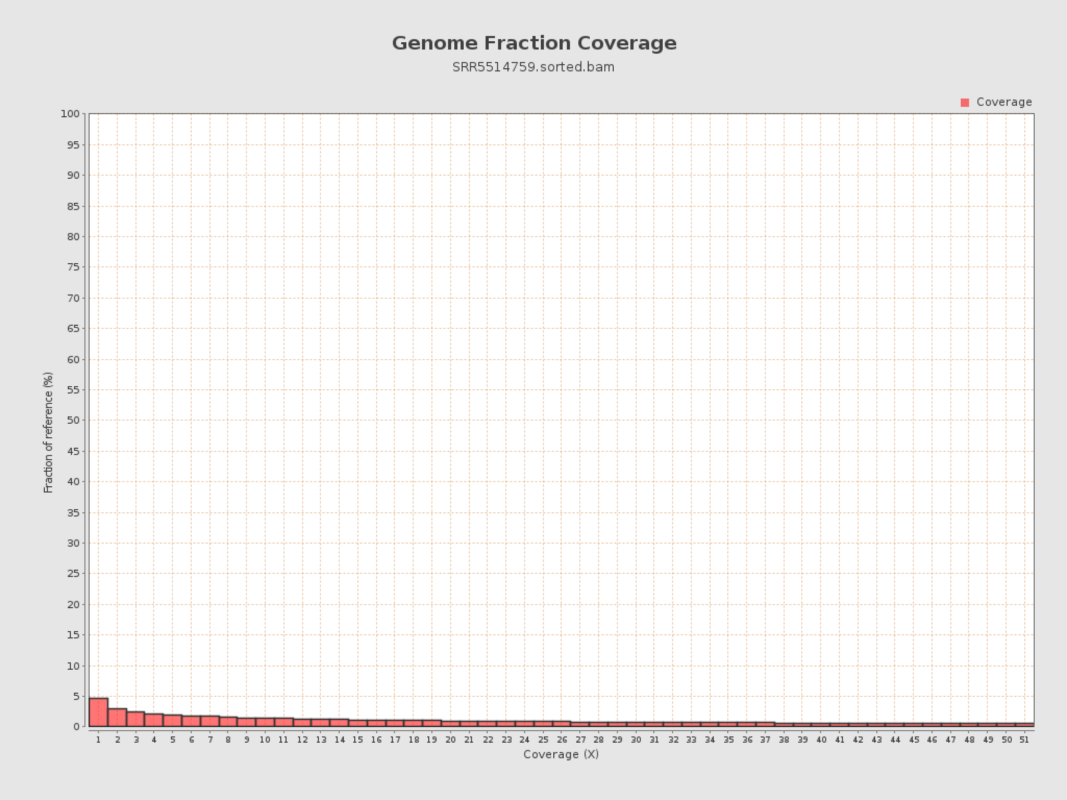
4. Results : Coverage Histogram



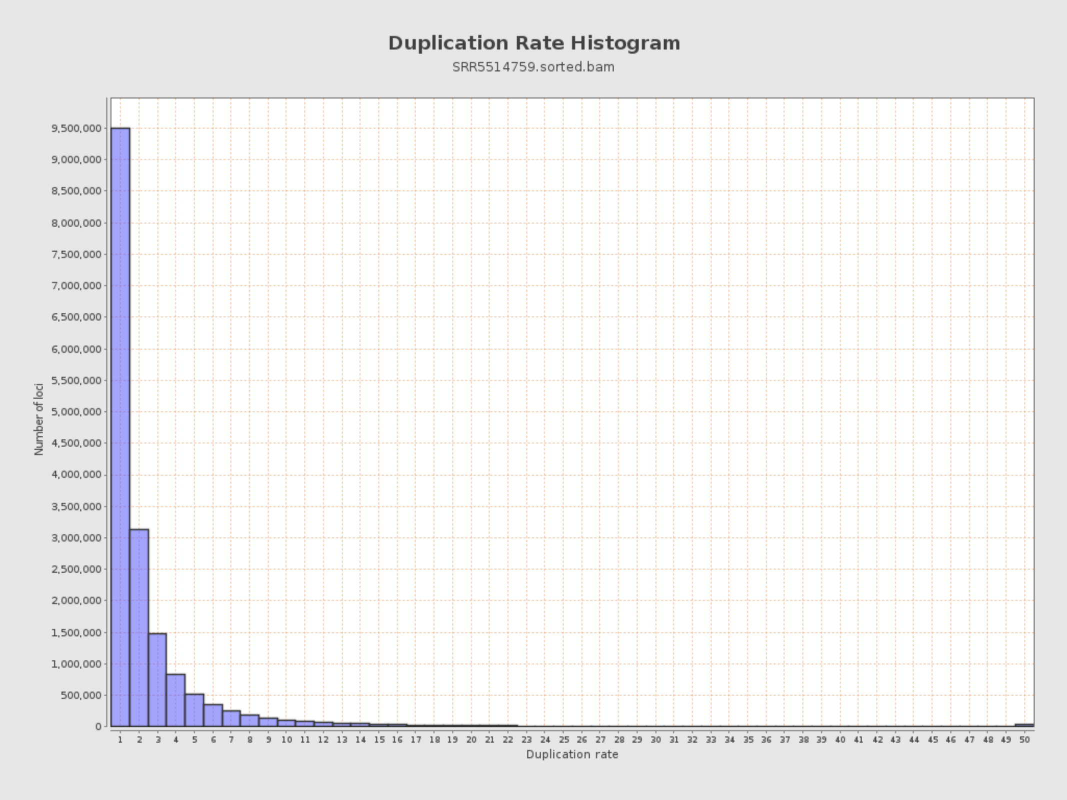
5. Results : Coverage Histogram (0-50X)



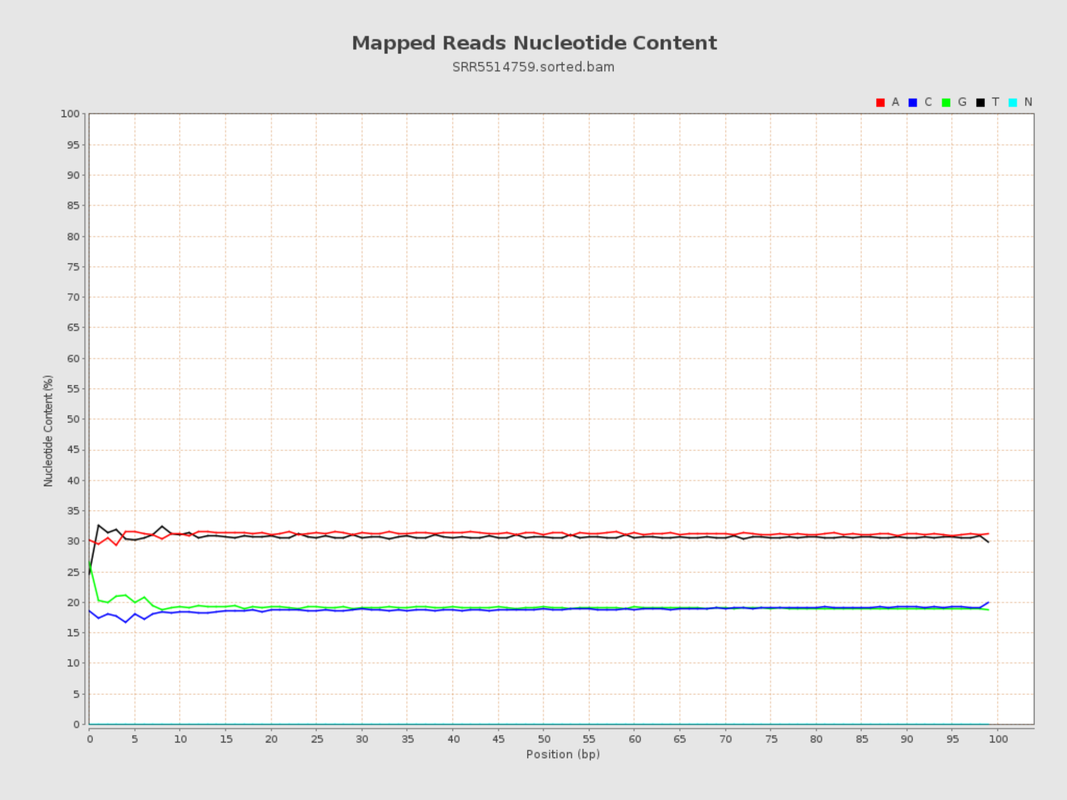
6. Results : Genome Fraction Coverage



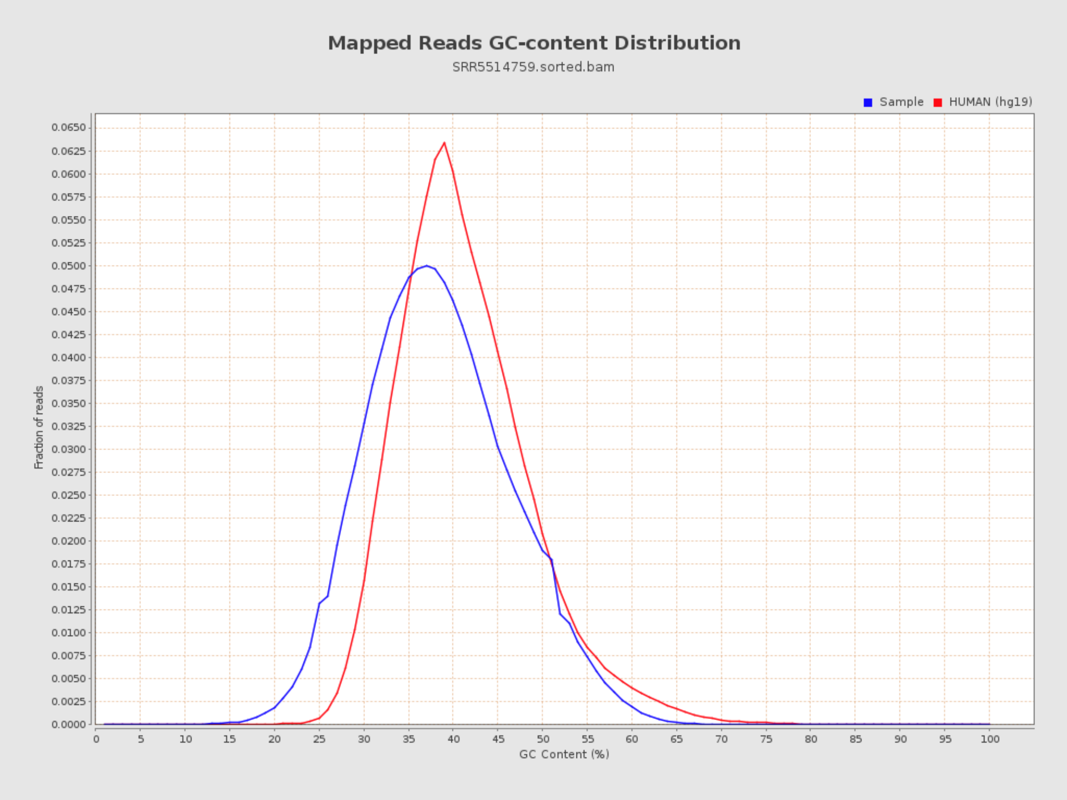
7. Results : Duplication Rate Histogram



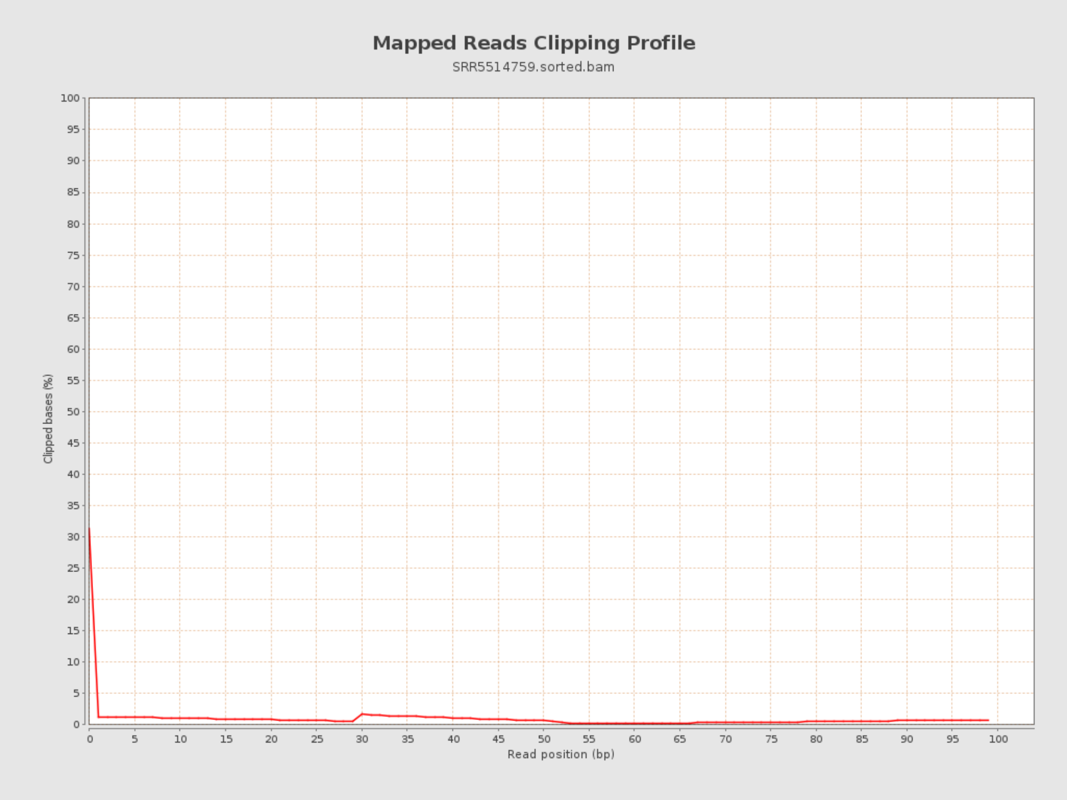
8. Results : Mapped Reads Nucleotide Content



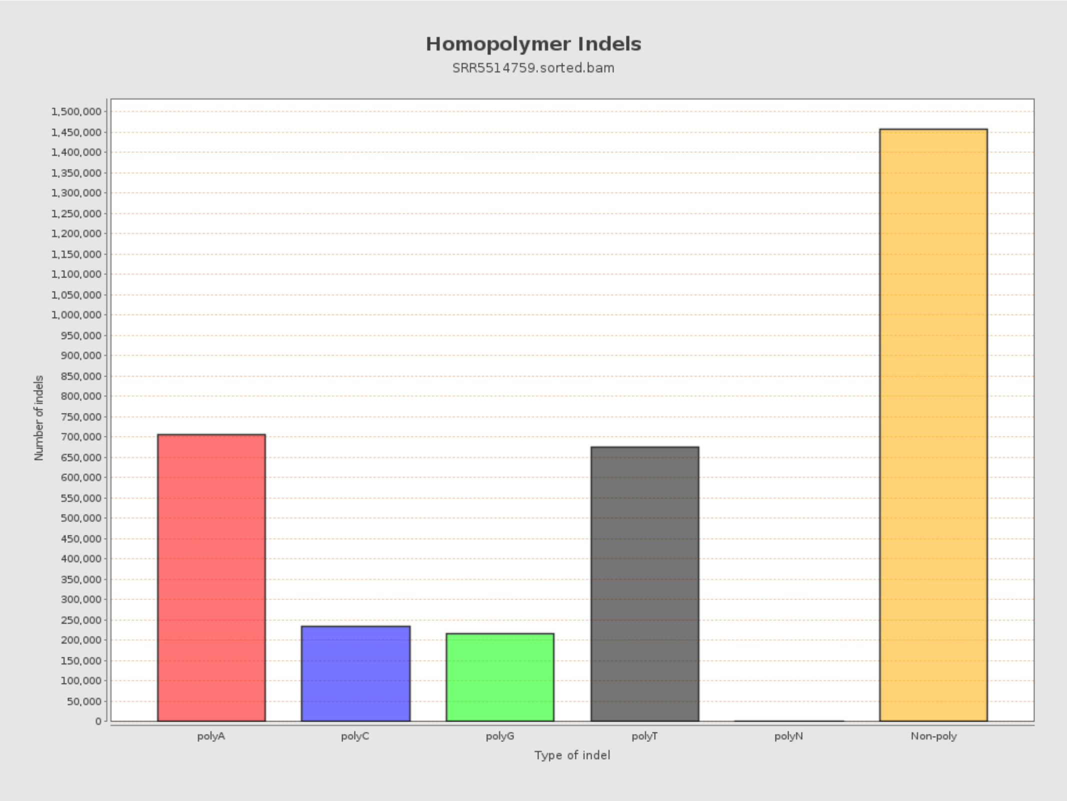
9. Results : Mapped Reads GC-content Distribution



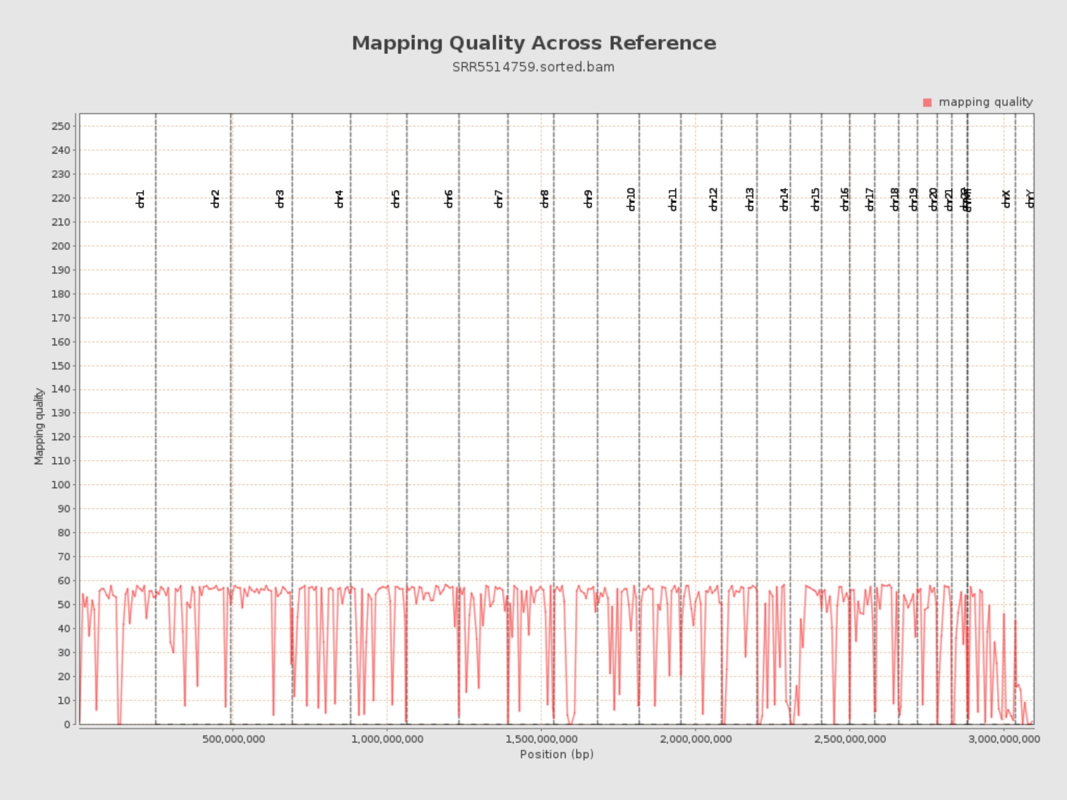
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram