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BUSCOMP Full Report

starling10xV5 BUSCOMP Analysis

2021-03-04

1 BUSCOMP Run Summary

BUSCOMP V0.11.0: run Thu Mar 4 16:10:40 2021

See the **run details appendix** end of this document for details of the **log file** (`/scratch/tmp/z3452659/projects/BUSCOMP-Jan19/analysis/2021-03-03.10xStarling/buscompV5/starling10xV5.log`), **commandline parameters** and runtime **BUSCOMP errors and warnings**.

NOTE: To edit this document, open `starling10xV5.N3L20ID0U.full.Rmd` in RStudio, edit and re-knit to HTML.

1.1 BUSCOMP Results Summary

Assemblies can be assessed on a number of criteria, but the main ones (in the absence of a reference “truth” genome) are either to judge contiguity or completeness. NG50 and LG50 values are based on a genome size of 1.1 Gb. If the `genomesize=X` parameter was not set (see command list in **appendix**), this will be based on the longest assembly (see sequence stats, below).

Of the 24 assemblies analysed (24 BUSCO; 24 fasta; 24 both), 23 genomes were rated as the “best” by at least one criterion:

- `starling10x.shuffle2` : MaxLength.
- `starling10x.pribusco` : MaxLength.
- `starling10x.dipnr` : MaxLength, Complete, Missing.
- `starling10x.pri` : MaxLength, Complete, Missing, BUSCO, NoBUSCO.
- `starling10x.shuffle3` : MaxLength.
- `starling10x.triplicate` : MaxLength.
- `starling10x.3n` : MaxLength.
- `starling10x.duplicate` : MaxLength.
- `starling10x.4n` : NG50Length, LG50Count, MaxLength.
- `starling10x.rep6` : MaxLength.
- `starling10x.rep7` : MaxLength.
- `starling10x.rep4` : MaxLength.
- `starling10x.rep5` : MaxLength.
- `starling10x.rep2` : MaxLength.
- `starling10x.rep3` : MaxLength.
- `starling10x.rep0` : MaxLength.
- `starling10x.rep1` : MaxLength.
- `starling10x.rep8` : MaxLength.
- `starling10x.rep9` : MaxLength.
- `starling10x.shuffle1` : MaxLength.
- `starling10x.revcomp` : MaxLength.
- `starling10x.2n` : MaxLength.
- `starling10x.copy` : MaxLength.

Best assemblies by assembly contiguity criteria:

- **NG50Length.** Longest NG50 contig/scaffold length (6,889,770 bp): `starling10x.4n`
- **LG50Count.** Smallest LG50 contig/scaffold count (67): `starling10x.4n`
- **MaxLength.** Maximum contig/scaffold length (12,884,419 bp): `starling10x.2n`, `starling10x.3n`, `starling10x.4n`, `starling10x.copy`, `starling10x.dipnr`, `starling10x.duplicate`, `starling10x.pri`, `starling10x.pribusco`, `starling10x.rep0`, `starling10x.rep1`, `starling10x.rep2`, `starling10x.rep3`, `starling10x.rep4`, `starling10x.rep5`, `starling10x.rep6`, `starling10x.rep7`, `starling10x.rep8`, `starling10x.rep9`, `starling10x.revcomp`, `starling10x.shuffle1`, `starling10x.shuffle2`, `starling10x.shuffle3`, `starling10x.triplicate`

Best assemblies by completeness criteria:

- **Complete.** Most Complete (Single & Duplicated) BUSCOMP sequences (99.9 %): `starling10x.dipnr`, `starling10x.pri`
- **Missing.** Fewest Missing BUSCOMP sequences (0.0 %): `starling10x.dipnr`, `starling10x.pri`
- **BUSCO.** Most Complete (Single & Duplicated) BUSCO sequences (94.8 %): `starling10x.pri`
- **NoBUSCO.** Fewest Missing BUSCO sequences (3.3 %): `starling10x.pri`

2 Genome Summary

The following genomes and BUSCO results were analysed by BUSCOMP:

- `starling10x.dipnr`. [[BUSCO](#) | [Fasta](#)] Pseudodiploid assembly
- `starling10x.pri`. [[BUSCO](#) | [Fasta](#)] Primary scaffolds

- **starling10x.alt.** [BUSCO | Fasta] Alternative scaffolds
- **starling10x.pribusco.** [BUSCO | Fasta] Primary BUSCO-containing scaffolds
- **starling10x.revcomp.** [BUSCO | Fasta] Reverse complemented BUSCO scaffolds
- **starling10x.copy.** [BUSCO | Fasta] Direct copy of primary BUSCO scaffolds
- **starling10x.duplicate.** [BUSCO | Fasta] Primary BUSCOs plus reverse complement
- **starling10x.triplicate.** [BUSCO | Fasta] Two primary BUSCO copies plus reverse complement
- **starling10x.shuffle1.** [Fasta] Randomly shuffled primary BUSCO scaffolds (1)
- **starling10x.shuffle2.** [Fasta] Randomly shuffled primary BUSCO scaffolds (2)
- **starling10x.shuffle3.** [Fasta] Randomly shuffled primary BUSCO scaffolds (3)
- **starling10x.2n.** [BUSCO | Fasta] Primary BUSCO scaffolds plus one shuffled copy
- **starling10x.3n.** [BUSCO | Fasta] Primary BUSCO scaffolds plus two shuffled copies
- **starling10x.4n.** [BUSCO | Fasta] Primary BUSCO scaffolds plus three shuffled copies
- **starling10x.rep0.** [BUSCO | Fasta] Primary BUSCO replication 0
- **starling10x.rep1.** [BUSCO | Fasta] Primary BUSCO replication 1
- **starling10x.rep2.** [BUSCO | Fasta] Primary BUSCO replication 2
- **starling10x.rep3.** [BUSCO | Fasta] Primary BUSCO replication 3
- **starling10x.rep4.** [BUSCO | Fasta] Primary BUSCO replication 4
- **starling10x.rep5.** [BUSCO | Fasta] Primary BUSCO replication 5
- **starling10x.rep6.** [BUSCO | Fasta] Primary BUSCO replication 6
- **starling10x.rep7.** [BUSCO | Fasta] Primary BUSCO replication 7
- **starling10x.rep8.** [BUSCO | Fasta] Primary BUSCO replication 8
- **starling10x.rep9.** [BUSCO | Fasta] Primary BUSCO replication 9

Details of the directories and files are below:

Directory	>
<chr>	
1	./busco5/run_00_starling10x.dipnr
2	./busco5/run_01_starling10x.pri
3	./busco5/run_02_starling10x.alt
5	./busco5/run_04_starling10x.pribusco
6	./busco5/run_05_starling10x.revcomp
8	./busco5/run_11_starling10x.copy
9	./busco5/run_12_starling10x.duplicate
10	./busco5/run_13_starling10x.triplicate
12	
13	
1-10 of 24 rows 1-2 of 6 columns	Previous 1 2 3 Next

Genomes with a **Directory** listed had BUSCO results available. If **Sequences** is `True`, these would have been compiled to generate the BUSCOMP sequence set (unless `buscompseq=F`, or alternative sequences were provided with `buscofas=FASFILE`). Genomes with a **Fasta** listed had sequence data available for BUSCOMP searches.

2.1 Genome statistics

The following genome statistics were also calculated by `RJE_SeqList` for each genome (table, below):

- **SeqNum:** The total number of scaffolds/contigs in the assembly.
- **TotLength:** The total combined length of scaffolds/contigs in the assembly.
- **MinLength:** The length of the shortest scaffold/contig in the assembly.
- **MaxLength:** The length of the longest scaffold/contig in the assembly.
- **MeanLength:** The mean length of scaffolds/contigs in the assembly.
- **MedLength:** The median length of scaffolds/contigs in the assembly.
- **N50Length:** At least half of the assembly is contained on scaffolds/contigs of this length or greater.
- **L50Count:** The smallest number scaffolds/contigs needed to cover half the the assembly.
- **CtgNum:** Number of contigs (`SeqNum` + `GapCount`).
- **N50Ctg:** At least half of the assembly is contained on contigs of this length or greater.
- **L50Ctg:** The smallest number contigs needed to cover half the the assembly.
- **NG50Length:** At least half of the genome is contained on scaffolds/contigs of this length or greater. This is based on `genomysize=x`. If no genome size is given, it will be relative to the biggest assembly.
- **LG50Count:** The smallest number scaffolds/contigs needed to cover half the the genome. This is based on `genomysize=x`. If no genome size is given, it will be relative to the biggest assembly.
- **GapLength:** The total number of undefined "gap" (`N`) nucleotides in the assembly.
- **GapCount:** The total number of undefined "gap" (`N`) regions in the assembly.
- **GC:** The %GC content of the assembly.

Genome	Description	SeqNum	TotLength	MinLength	MaxLength	MeanLength	MedLength	N50Length	L50Count	CtgNum	N50Ctg
starling10x.dipnr	Pseudodiploid assembly	19346	1887443050	1000	12884419	97562.44	2307.5	1907593	245	49415	142122
starling10x.pri	Primary scaffolds	18439	1040106492	1000	12884419	56407.97	2153.0	1764435	146	37354	132973

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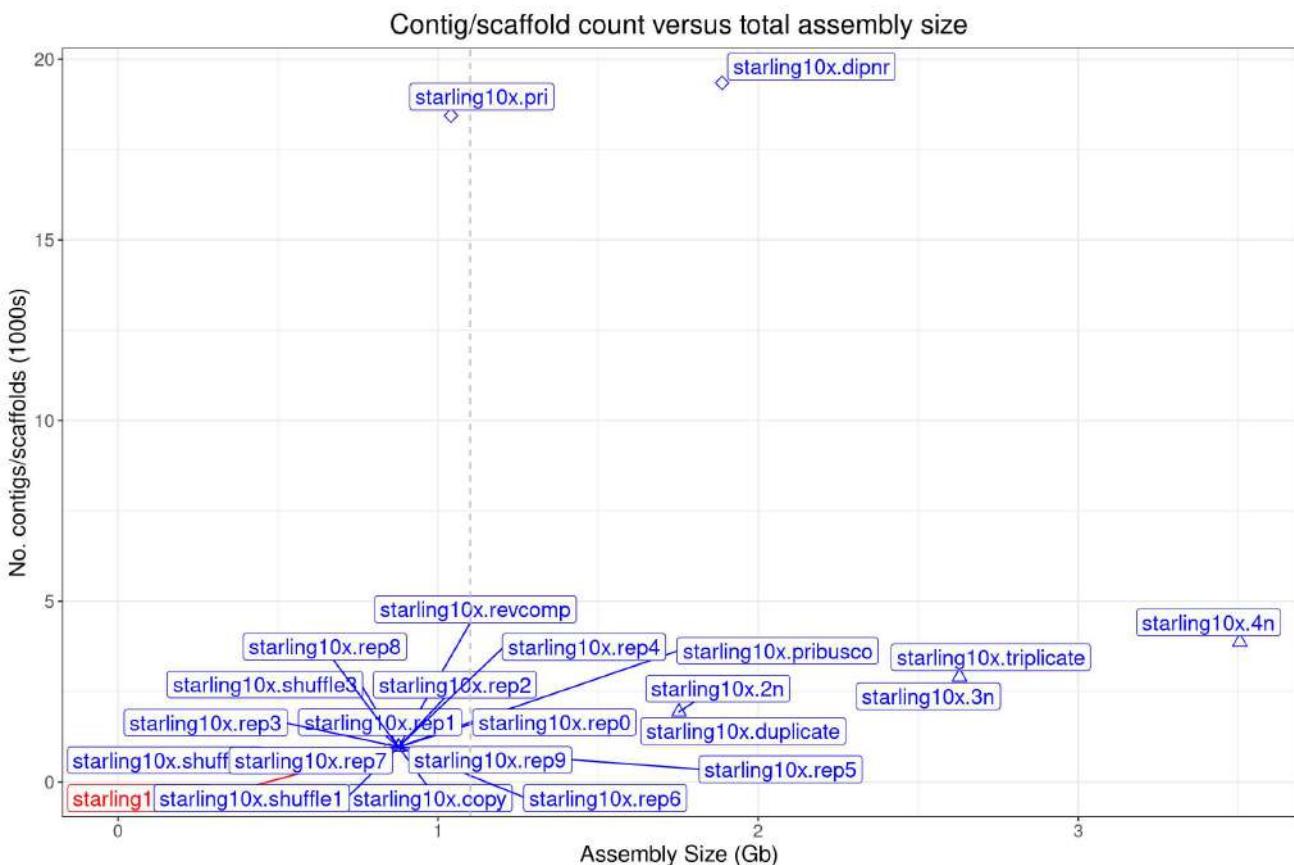
Genome	Description	SeqNum	TotLength	MinLength	MaxLength	MeanLength	MedLength	N50Length	L50Count	CtgNum	N50Ctg
starling10x.alt	Alternative scaffolds	907	847336558	1620	12880535	934218.92	450476.0	2203301	102	12061	152010
starling10x.pribusco	Primary BUSCO-containing scaffolds	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.revcomp	Reverse complemented BUSCO scaffolds	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.copy	Direct copy of primary BUSCO scaffolds	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.duplicate	Primary BUSCOs plus reverse complement	1936	1752696430	1833	12884419	905318.40	409882.5	2277667	208	23158	154535
starling10x.triplicate	Two primary BUSCO copies plus reverse complement	2904	2629044645	1833	12884419	905318.40	409882.5	2277667	312	34737	154535
starling10x.shuffle1	Randomly shuffled primary BUSCO scaffolds (1)	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	971	2277667
starling10x.shuffle2	Randomly shuffled primary BUSCO scaffolds (2)	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	973	2277667
starling10x.shuffle3	Randomly shuffled primary BUSCO scaffolds (3)	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	969	2277667
starling10x.2n	Primary BUSCO scaffolds plus one shuffled copy	1936	1752696430	1833	12884419	905318.40	409882.5	2277667	208	12550	436368
starling10x.3n	Primary BUSCO scaffolds plus two shuffled copies	2904	2629044645	1833	12884419	905318.40	409882.5	2277667	312	13523	1002636
starling10x.4n	Primary BUSCO scaffolds plus three shuffled copies	3872	3505392860	1833	12884419	905318.40	409882.5	2277667	416	14492	1397823
starling10x.rep0	Primary BUSCO replication 0	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep1	Primary BUSCO replication 1	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep2	Primary BUSCO replication 2	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep3	Primary BUSCO replication 3	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535

Genome	Description	SeqNum	TotLength	MinLength	MaxLength	MeanLength	MedLength	N50Length	L50Count	CtgNum	N50Ctg
starling10x.rep4	Primary BUSCO replication 4	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep5	Primary BUSCO replication 5	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep6	Primary BUSCO replication 6	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep7	Primary BUSCO replication 7	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep8	Primary BUSCO replication 8	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535
starling10x.rep9	Primary BUSCO replication 9	968	876348215	1833	12884419	905318.40	409882.5	2277667	104	11579	154535

NOTE: `NG50Length` and `LG50Count` statistics use `genomesize=x` or the biggest assembly loaded (1.10 Gb). If BUSCOMP has been run more than once on the same data (e.g. to update descriptions or sorting), please make sure that a consistent genome size is used, or these values may be wrong. If in doubt, run with `force=T` and force regeneration of statistics.

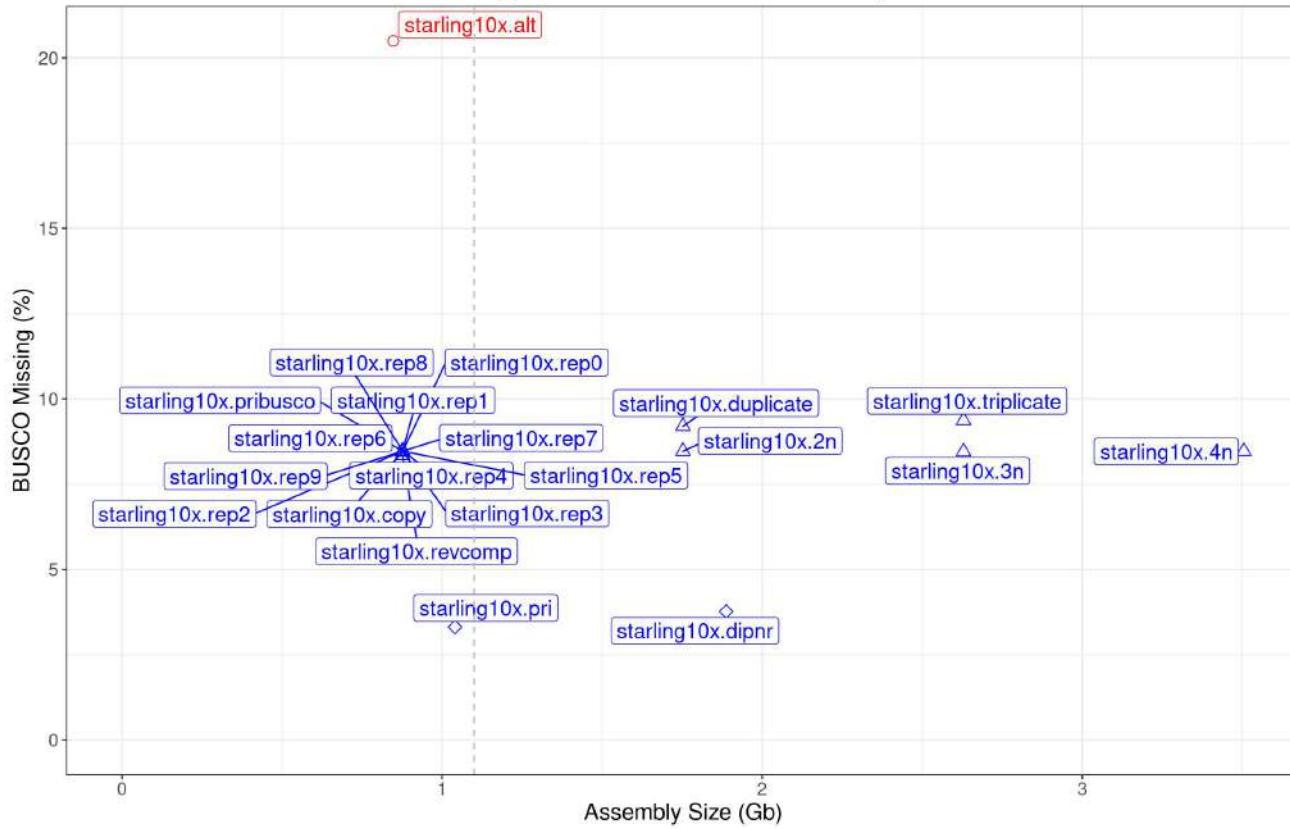
2.2 Genome coverage assessment plots

In general, a good assembly will be approx. the same size as the genome and in as few pieces as possible. Any assembly smaller than the predicted genome size is clearly missing coverage. Assemblies bigger than the genome size might still be missing chunks of the genome if redundancy/duplication is a problem. In the following plot, the grey line marks the given genome size of 1.1 Gb.

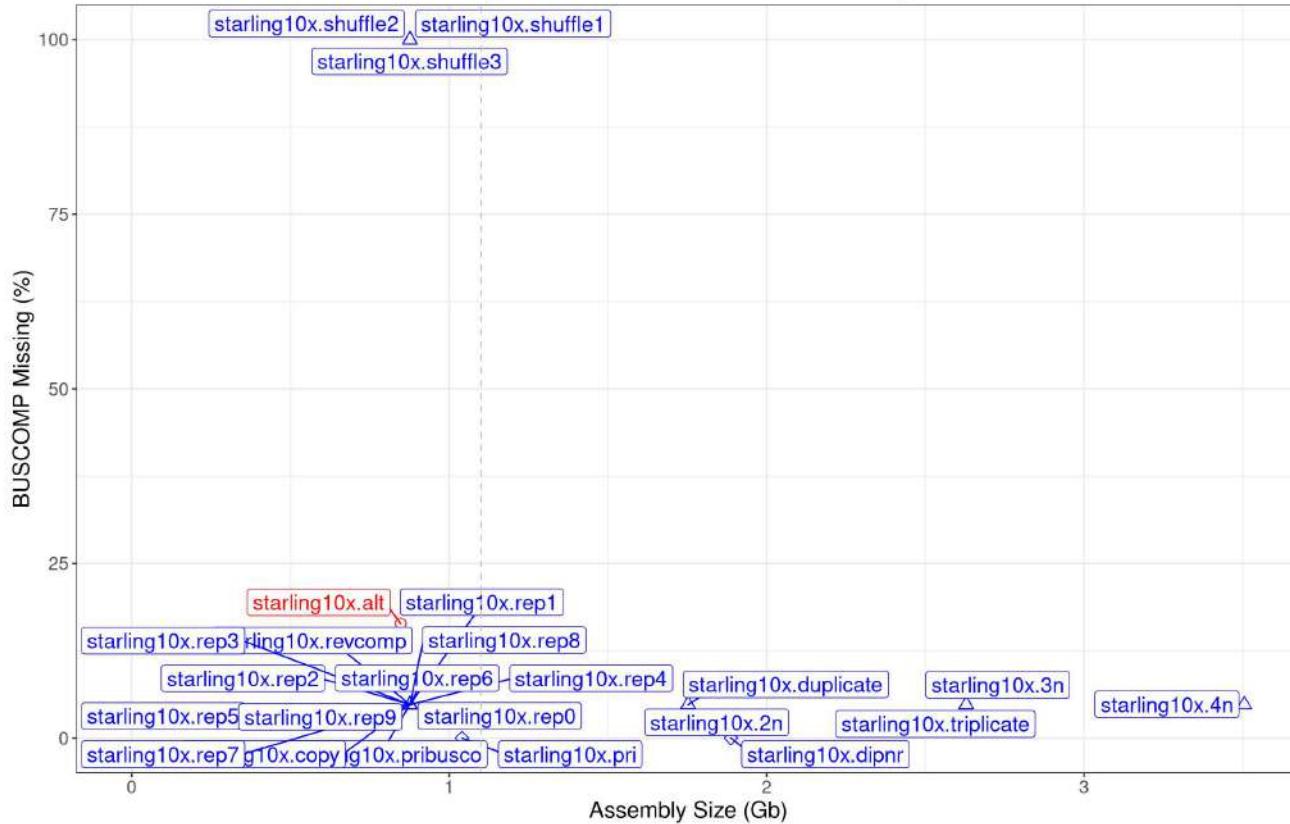


A better indicator of the overall coverage of the genome is the number of **Missing** BUSCO genes. As BUSCO is highly dependent on the accuracy of the sequence and the gene models it makes, the **Missing** BUSCOMP ratings arguably give a more consistent proxy for genome completeness. NOTE: this says nothing about the fragmentation or completeness of the genes themselves.

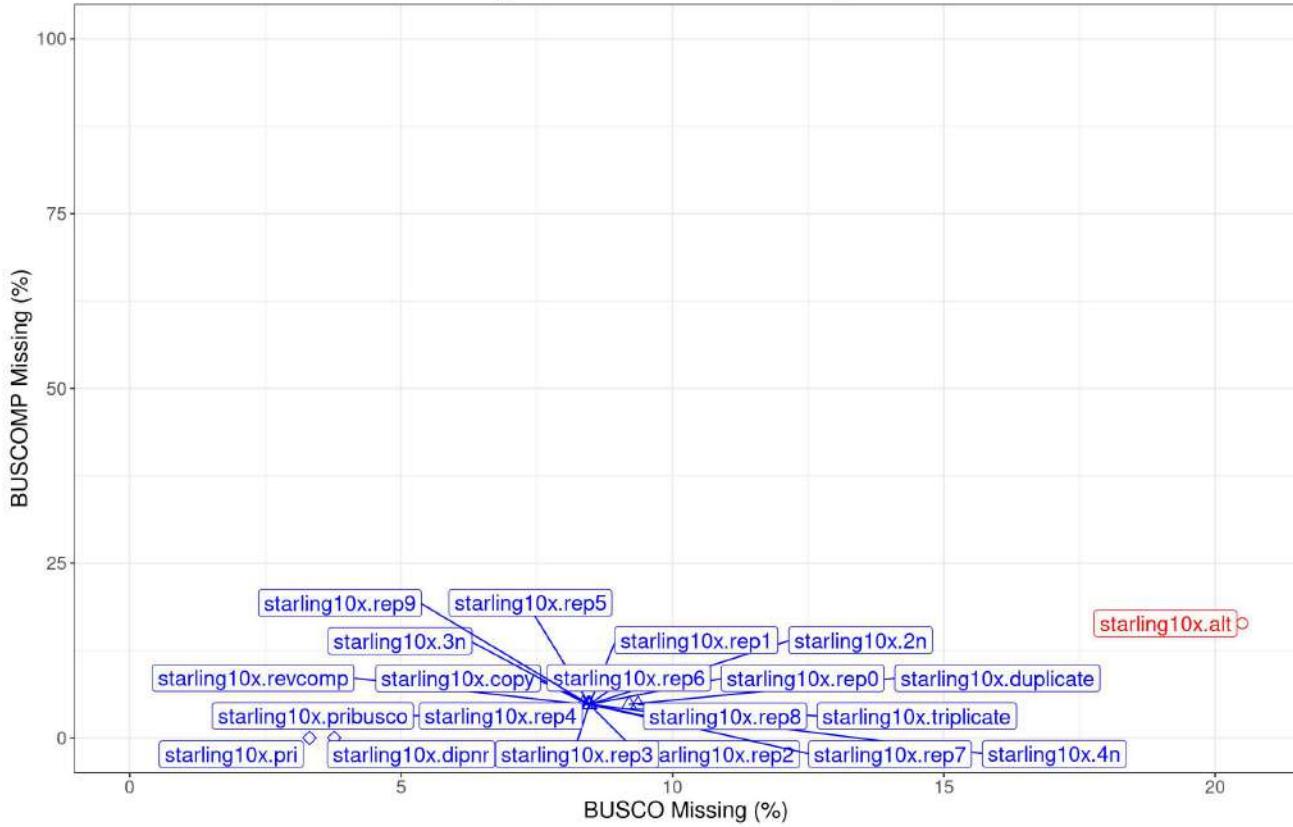
Missing BUSCO versus total assembly size



Missing BUSCOMP versus total assembly size

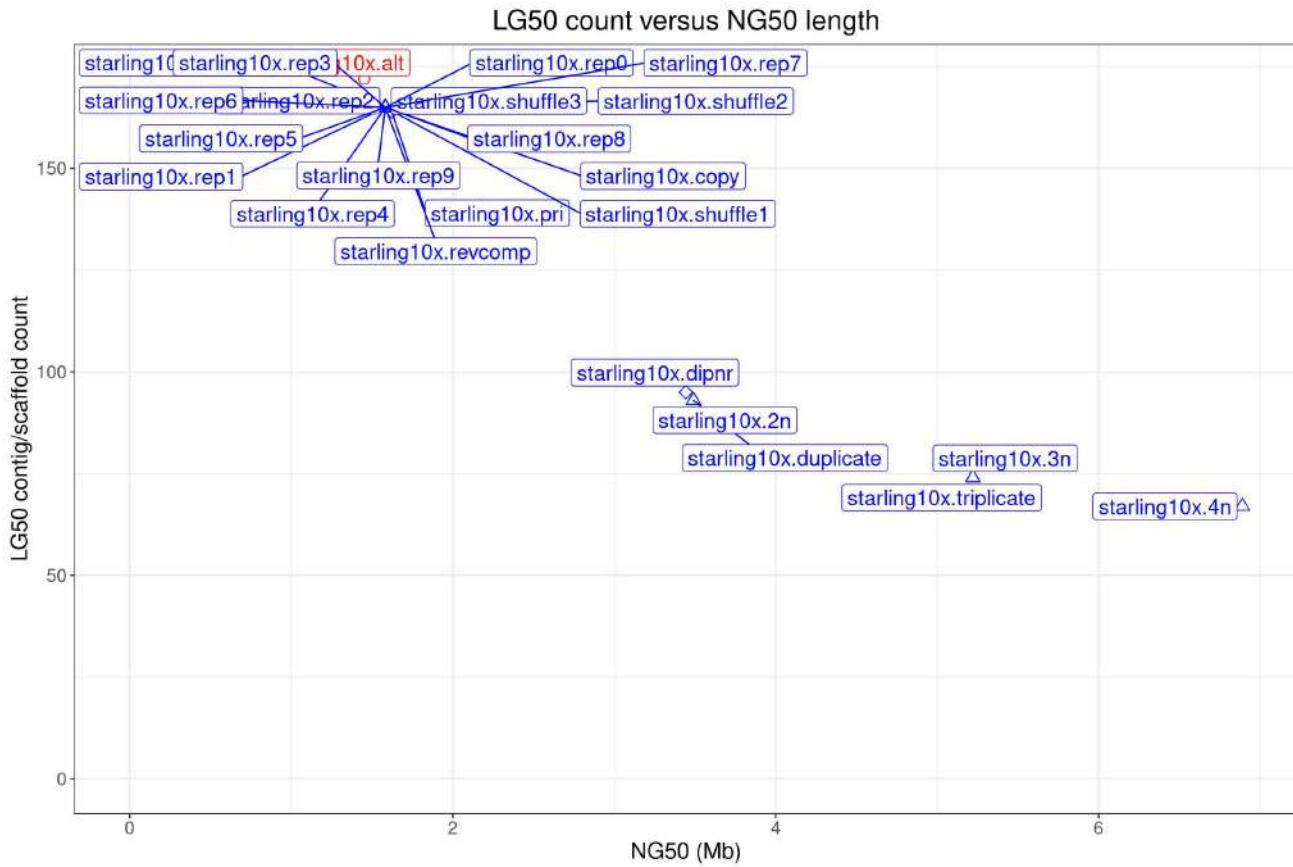


Missing BUSCOMP versus Missing BUSCO

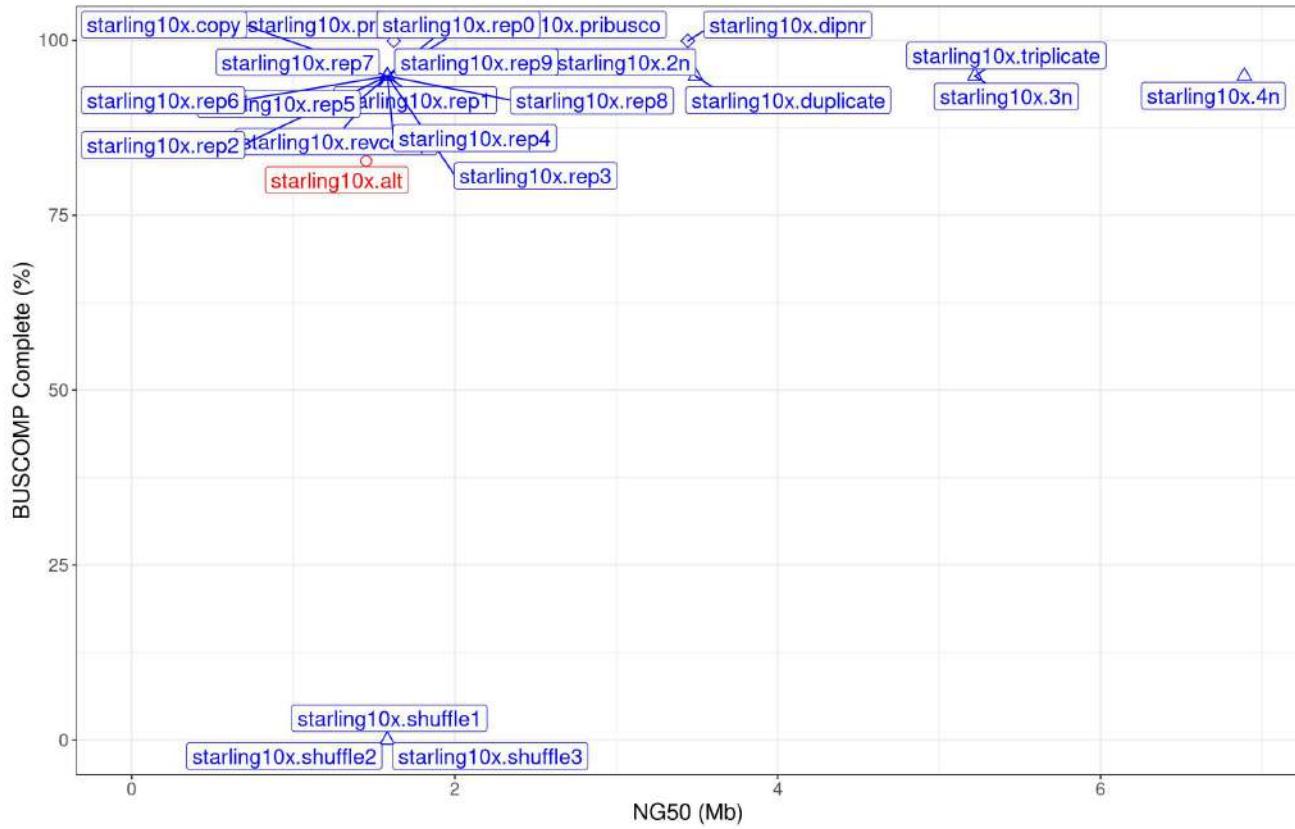


2.3 Genome contiguity assessment plots

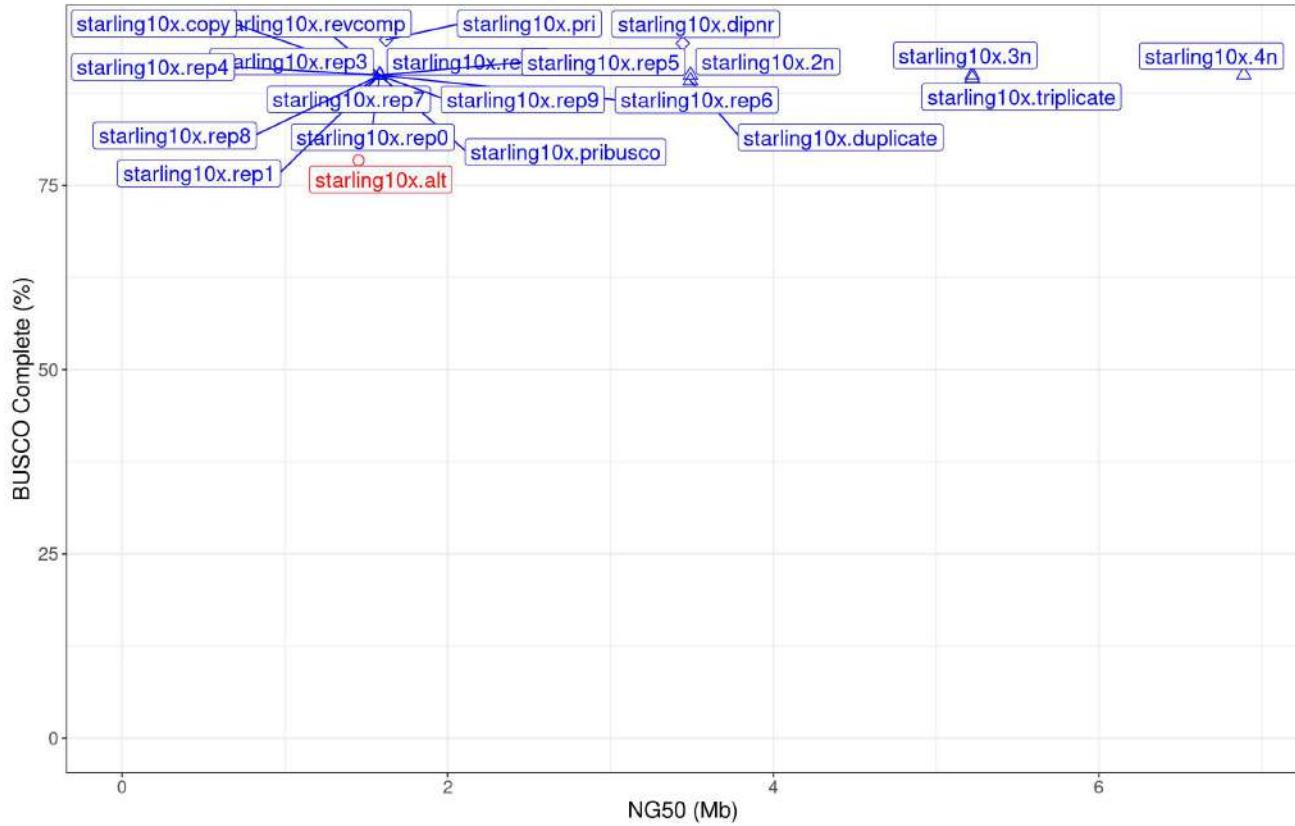
In general, a good assembly will be in fewer, bigger pieces. This is approximated using NG50 and LG50, which are the min. length and number of contigs/scaffolds required to cover at least half the genome. These stats use the given genome size of 1.1 Gb.



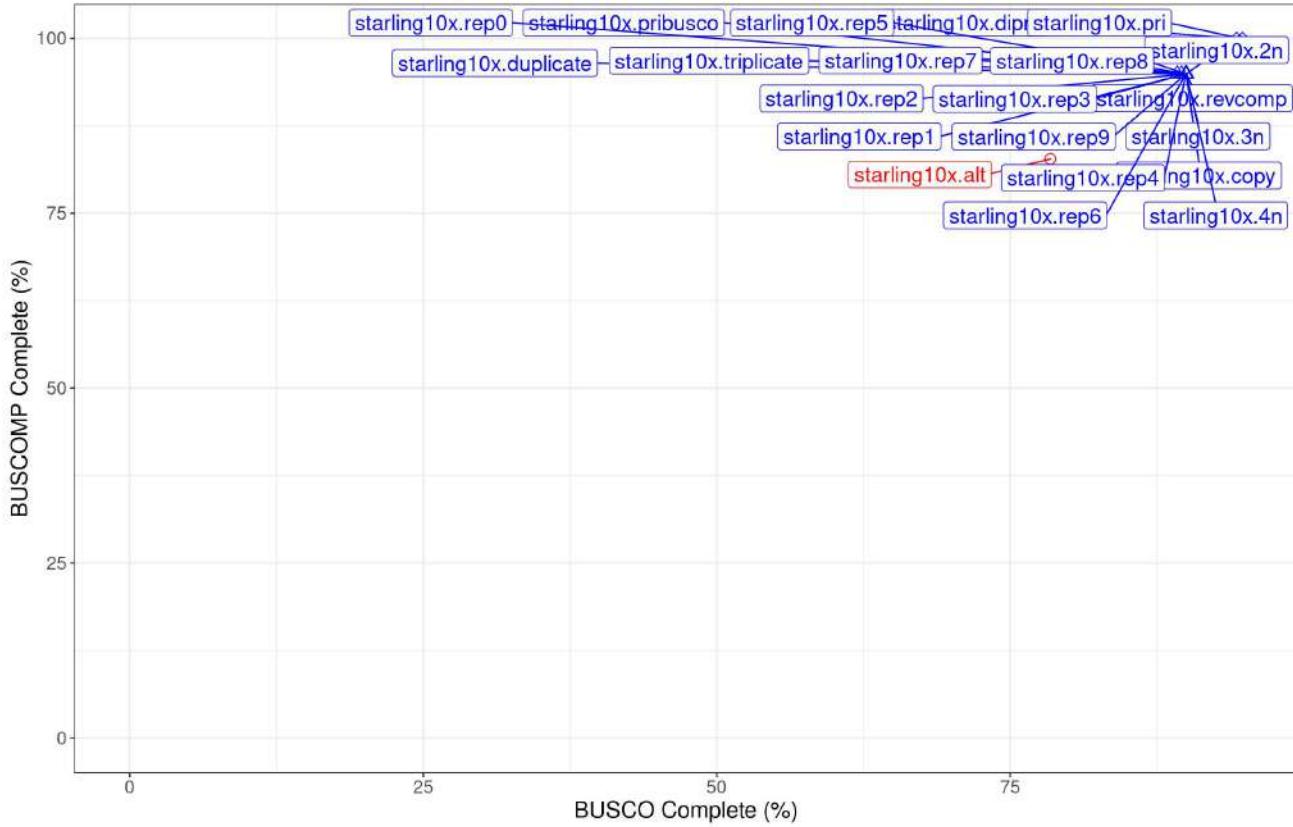
Complete BUSCOMP versus NG50



Complete BUSCO versus NG50



Complete BUSCOMP versus Complete BUSCO



NOTE: To modify these plots and tables, edit the `*.genomes.tdt` and `*.NxLxxIDxx.rdata.tdt` files and re-knit the `*.NxLxxIDxx.Rmd` file.

3 BUSCO Ratings

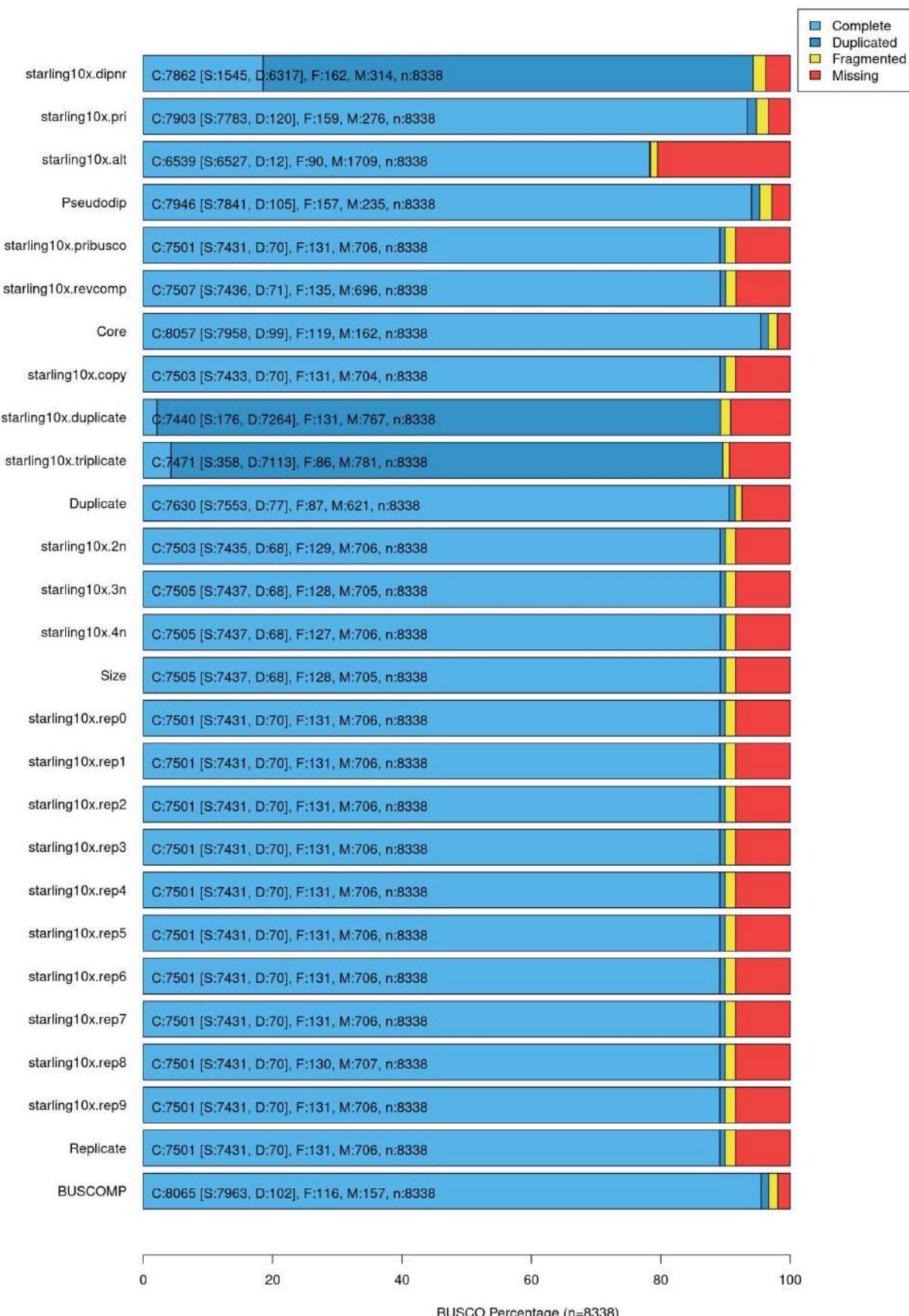
Compiled BUSCO results for 24 assemblies and 6 groups have been saved in `starling10xV5.genomes.tdt`. BUSCO ratings are defined (quoting from the **BUSCO v3 User Guide** (http://gitlab.com/ezlab/busco/raw/master/BUSCO_v3_userguide.pdf) as:

- Complete** : Single-copy hits where "BUSCO matches have scored within the expected range of scores and within the expected range of length alignments to the BUSCO profile."
- Duplicated** : As **Complete** but 2+ copies.
- Fragmented** : "BUSCO matches ... within the range of scores but not within the range of length alignments to the BUSCO profile."
- Missing** : "Either no significant matches at all, or the BUSCO matches scored below the range of scores for the BUSCO profile."

Genome	N	Complete	Single	Duplicated	Fragmented	Missing
starling10x.dipnr	8338	7862	1545	6317	162	314
starling10x.pri	8338	7903	7783	120	159	276
starling10x.alt	8338	6539	6527	12	90	1709
Pseudodip	8338	7946	7841	105	157	235
starling10x.pribusco	8338	7501	7431	70	131	706
starling10x.revcomp	8338	7507	7436	71	135	696
Core	8338	8057	7958	99	119	162
starling10x.copy	8338	7503	7433	70	131	704
starling10x.duplicate	8338	7440	176	7264	131	767
starling10x.triplicate	8338	7471	358	7113	86	781
Duplicate	8338	7630	7553	77	87	621
starling10x.shuffle1	0	0	0	0	0	0
starling10x.shuffle2	0	0	0	0	0	0
starling10x.shuffle3	0	0	0	0	0	0
starling10x.2n	8338	7503	7435	68	129	706
starling10x.3n	8338	7505	7437	68	128	705
starling10x.4n	8338	7505	7437	68	127	706
Size	8338	7505	7437	68	128	705
starling10x.rep0	8338	7501	7431	70	131	706
starling10x.rep1	8338	7501	7431	70	131	706

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Genome	N	Complete	Single	Duplicated	Fragmented	Missing
starling10x.rep2	8338	7501	7431	70	131	706
starling10x.rep3	8338	7501	7431	70	131	706
starling10x.rep4	8338	7501	7431	70	131	706
starling10x.rep5	8338	7501	7431	70	131	706
starling10x.rep6	8338	7501	7431	70	131	706
starling10x.rep7	8338	7501	7431	70	131	706
starling10x.rep8	8338	7501	7431	70	130	707
starling10x.rep9	8338	7501	7431	70	131	706
Replicate	8338	7501	7431	70	131	706
BUSCOMP	8338	8065	7963	102	116	157

BUSCO Rating Summary**3.1 Genome Groups**

BUSCOMP compiled the following groups of genomes (where BUSCO data was loaded), keeping the “best” rating for each BUSCO gene across the group:

- **Pseudodip:** starling10x.dipnr | starling10x.pri | starling10x.alt
- **Core:** starling10x.dipnr | starling10x.pri | starling10x.alt | starling10x.pribusco | starling10x.revcomp
- **Duplicate:** starling10x.copy | starling10x.duplicate | starling10x.triplicate
- **Size:** (starling10x.shuffle1)(starling10x.shuffle2)(starling10x.shuffle3) | starling10x.2n | starling10x.3n | starling10x.4n

- **Replicate:** starling10x.rep0 starling10x.rep1 starling10x.rep2 starling10x.rep3 starling10x.rep4 starling10x.rep5
starling10x.rep6 starling10x.rep7 starling10x.rep8 starling10x.rep9
- **BUSCOMP:** starling10x.dipnr starling10x.pri starling10x.alt starling10x.pribusco starling10x.revcomp starling10x.copy
starling10x.duplicate starling10x.triplicate (starling10x.shuffle1)(starling10x.shuffle2)(starling10x.shuffle3)
starling10x.2n starling10x.3n starling10x.4n starling10x.rep0 starling10x.rep1 starling10x.rep2 starling10x.rep3
starling10x.rep4 starling10x.rep5 starling10x.rep6 starling10x.rep7 starling10x.rep8 starling10x.rep9

3.2 BUSCO Summary

```

starling10x.dipnr BUSCO Results:
C:94.3%[S:18.5%,D:75.8%],F:1.9%,M:3.8%,n:8338

starling10x.pri BUSCO Results:
C:94.8%[S:93.3%,D:1.4%],F:1.9%,M:3.3%,n:8338

starling10x.alt BUSCO Results:
C:78.4%[S:78.3%,D:0.1%],F:1.1%,M:20.5%,n:8338

Pseudodip BUSCO Results:
C:95.3%[S:94.0%,D:1.3%],F:1.9%,M:2.8%,n:8338

starling10x.pribusco BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.revcomp BUSCO Results:
C:90.0%[S:89.2%,D:0.9%],F:1.6%,M:8.3%,n:8338

Core BUSCO Results:
C:96.6%[S:95.4%,D:1.2%],F:1.4%,M:1.9%,n:8338

starling10x.copy BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.4%,n:8338

starling10x.duplicate BUSCO Results:
C:89.2%[S:2.1%,D:87.1%],F:1.6%,M:9.2%,n:8338

starling10x.triplicate BUSCO Results:
C:89.6%[S:4.3%,D:85.3%],F:1.0%,M:9.4%,n:8338

Duplicate BUSCO Results:
C:91.5%[S:90.6%,D:0.9%],F:1.0%,M:7.4%,n:8338

starling10x.shuffle1 BUSCO Results:
C:0.0%[S:0.0%,D:0.0%],F:0.0%,M:0.0%,n:0

starling10x.shuffle2 BUSCO Results:
C:0.0%[S:0.0%,D:0.0%],F:0.0%,M:0.0%,n:0

starling10x.shuffle3 BUSCO Results:
C:0.0%[S:0.0%,D:0.0%],F:0.0%,M:0.0%,n:0

starling10x.2n BUSCO Results:
C:90.0%[S:89.2%,D:0.8%],F:1.5%,M:8.5%,n:8338

starling10x.3n BUSCO Results:
C:90.0%[S:89.2%,D:0.8%],F:1.5%,M:8.5%,n:8338

starling10x.4n BUSCO Results:
C:90.0%[S:89.2%,D:0.8%],F:1.5%,M:8.5%,n:8338

Size BUSCO Results:
C:90.0%[S:89.2%,D:0.8%],F:1.5%,M:8.5%,n:8338

starling10x.rep0 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep1 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep2 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep3 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep4 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep5 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep6 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep7 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep8 BUSCO Results:
C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

starling10x.rep9 BUSCO Results:

```

C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

Replicate BUSCO Results:

C:90.0%[S:89.1%,D:0.8%],F:1.6%,M:8.5%,n:8338

BUSCOMP BUSCO Results:

C:96.7%[S:95.5%,D:1.2%],F:1.4%,M:1.9%,n:8338

3.3 BUSCO Gene Details

Full BUSCO results with ratings for each gene have been compiled in `starling10xV5.busco.tdt`:

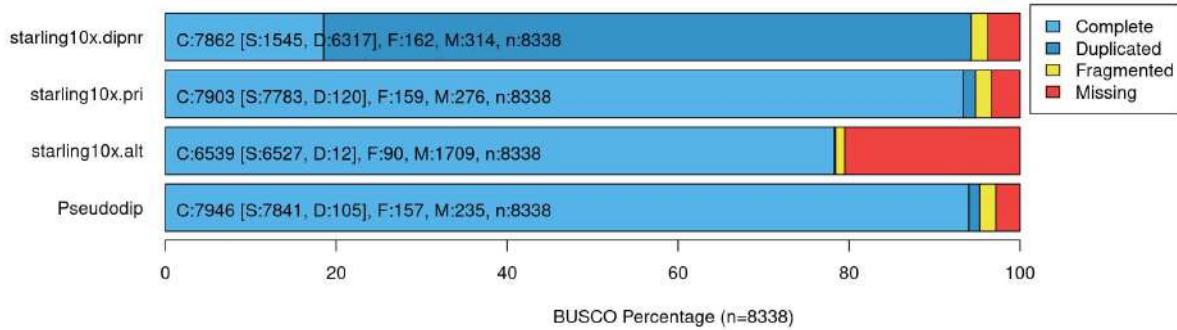
BuscoID <chr>	starling10x.dipnr <chr>	starling10x.pri <chr>
10004at8782	Duplicated	Complete
10005at8782	Duplicated	Complete
10020at8782	Duplicated	Complete
10021at8782	Duplicated	Complete
10029at8782	Complete	Complete
10031at8782	Duplicated	Complete
10032at8782	Duplicated	Complete
10042at8782	Duplicated	Complete
10045at8782	Duplicated	Complete
10049at8782	Duplicated	Complete

1-10 of 8,338 rows | 1-3 of 28 columns

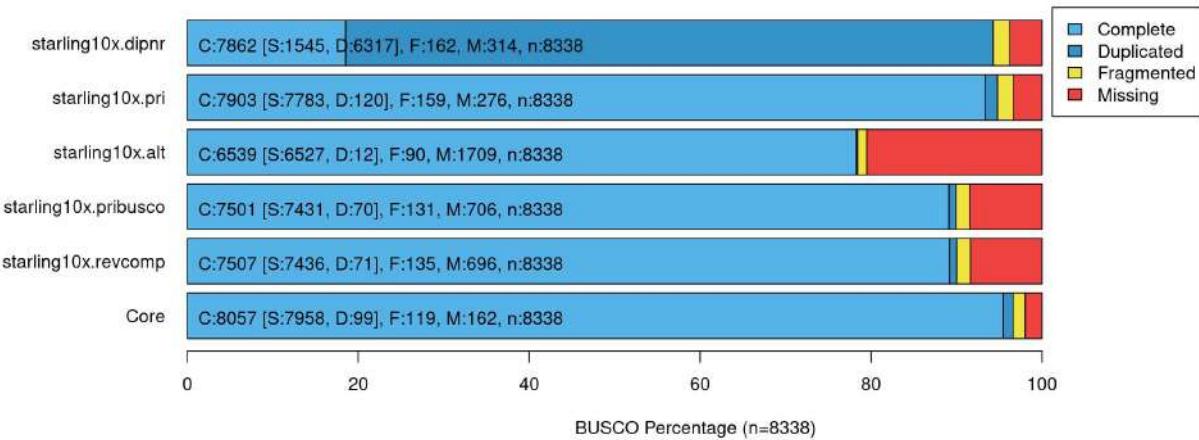
Previous 1 2 3 4 5 6 ... 834 Next ▶

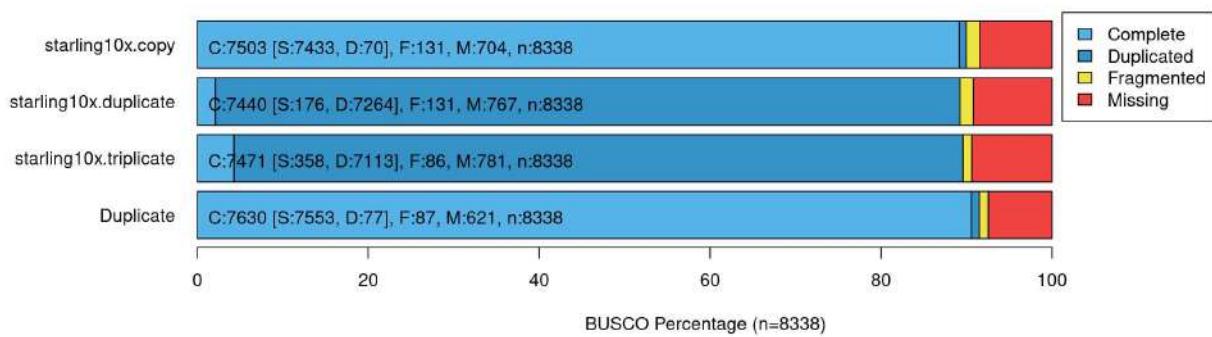
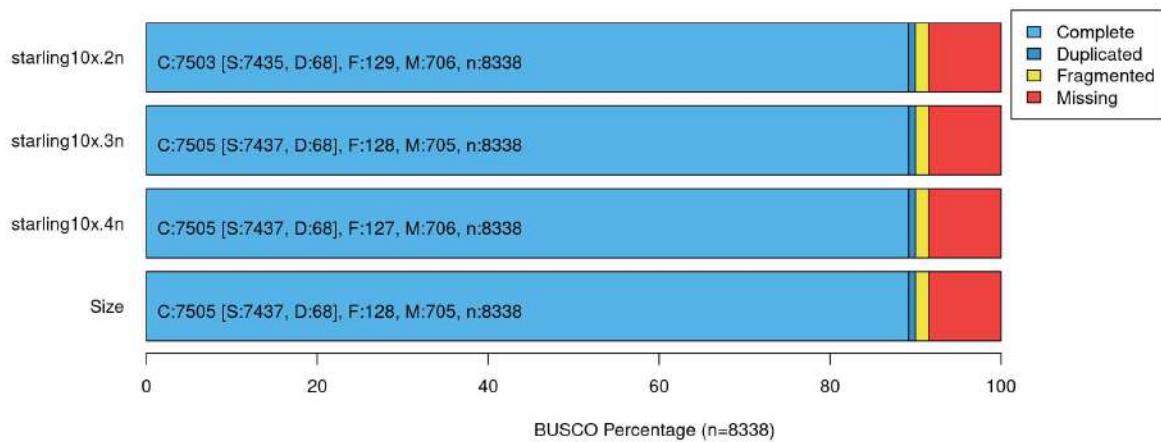
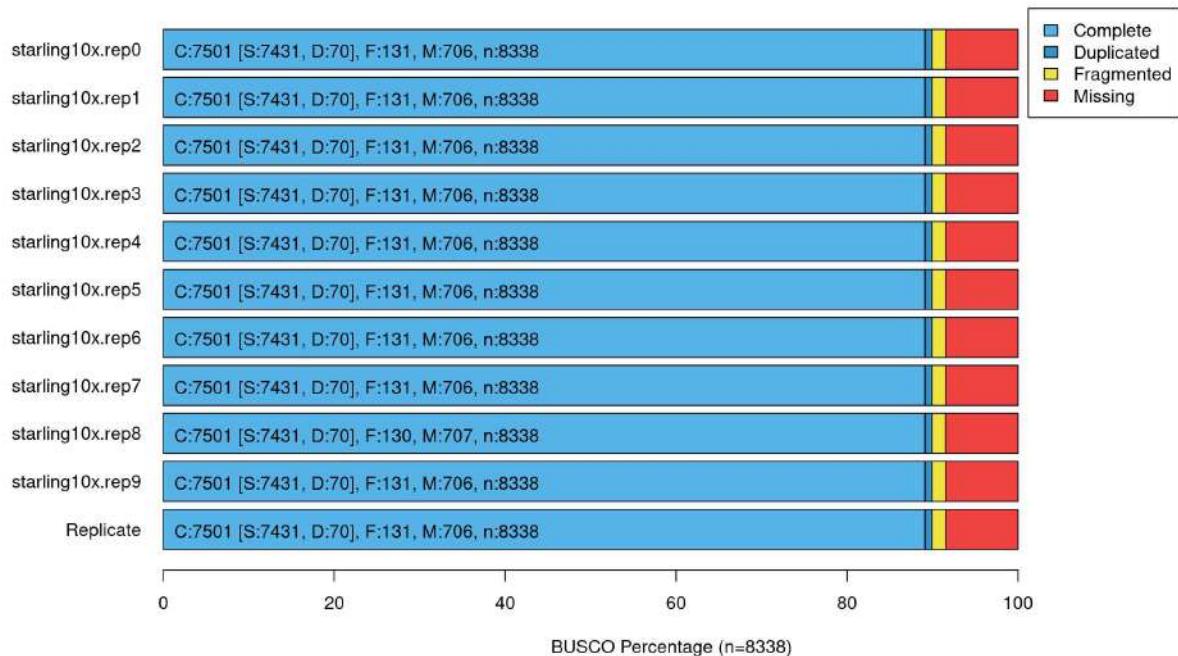
3.4 Genome Group BUSCO charts

Pseudodip BUSCO Rating Summary

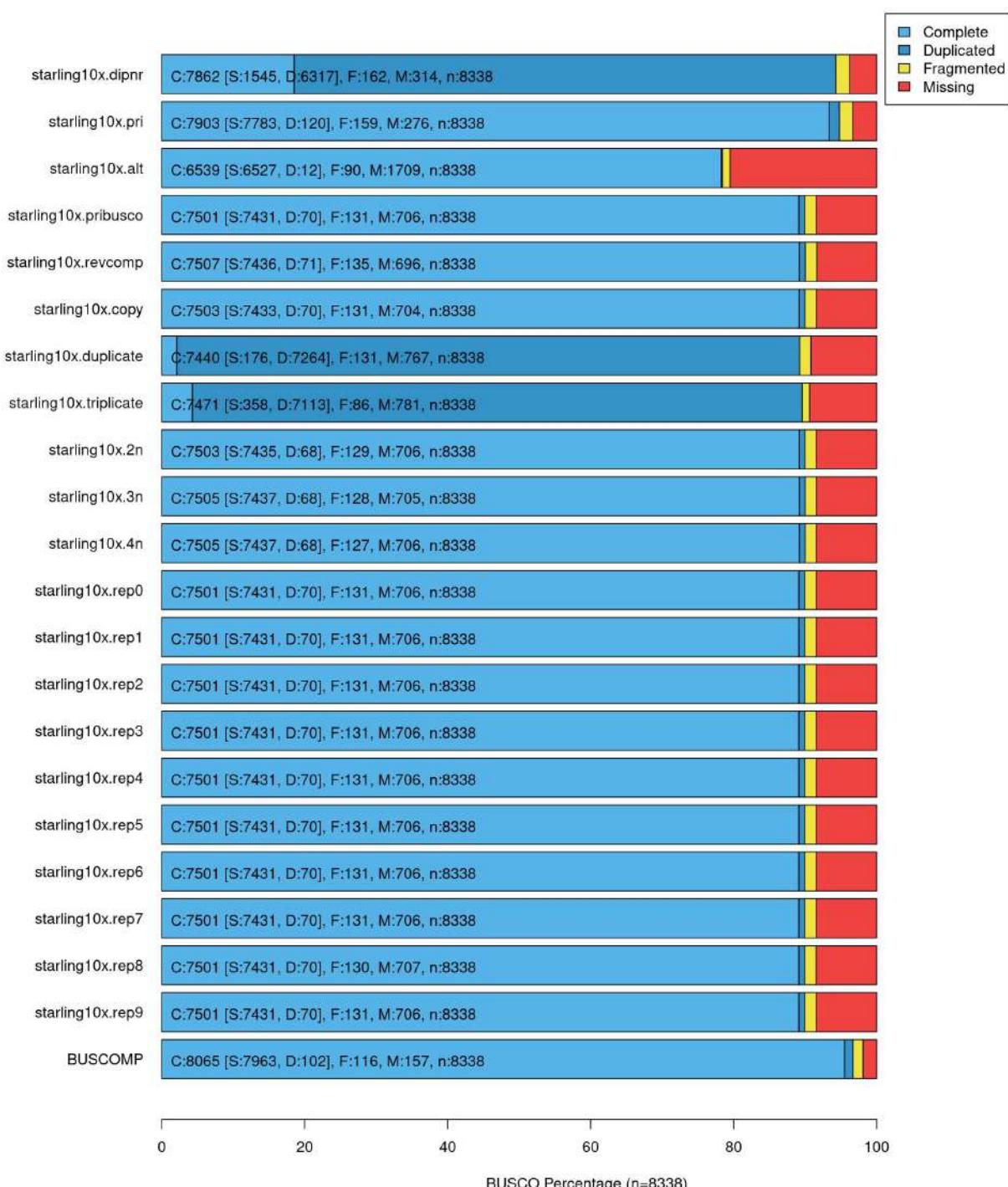


Core BUSCO Rating Summary



Duplicate BUSCO Rating Summary**Size BUSCO Rating Summary****Replicate BUSCO Rating Summary**

BUSCOMP BUSCO Rating Summary



4 BUSCOMP Ratings

The best complete BUSCO hit results (based on `Score` and `Length`) have been compiled in `starling10xV5.buscoseq.tdt`. The `Genome` field indicates the assembly with the best hit, which is followed by details of that hit (`Contig`, `Start`, `End`, `Score`, `Length`). BUSCOMP ratings for each assembly are then given in subsequent fields:

- * `Identical`: 100% coverage and 100% identity in at least one contig/scaffold.
- * `Complete`: 95% Coverage in a single contig/scaffold. (Note: accuracy/identity is not considered.)
- * `Duplicated`: 95%+ Coverage in 2+ contigs/scaffolds.
- * `Fragmented`: 95%+ combined coverage but not in any single contig/scaffold.
- * `Partial`: 40-95% combined coverage.
- * `Ghost`: Hits meeting local cutoff but <40% combined coverage.
- * `Missing`: No hits meeting local cutoff.

Genome	BuscoID	Status
<chr>	<chr>	<chr>
starling10x.2n	10004at8782	Complete
starling10x.2n	10005at8782	Complete

Genome <chr>	BuscID <chr>	Status <chr>	▶
starling10x.alt	10020at8782	Complete	
starling10x.revcomp	10021at8782	Complete	
starling10x.2n	10029at8782	Complete	
starling10x.alt	10031at8782	Complete	
starling10x.alt	10032at8782	Complete	
starling10x.revcomp	10042at8782	Complete	
starling10x.2n	10045at8782	Complete	
starling10x.revcomp	10049at8782	Complete	

1-10 of 8,338 rows | 1-3 of 11 columns

Previous 1 2 3 4 5 6 ... 834 Next

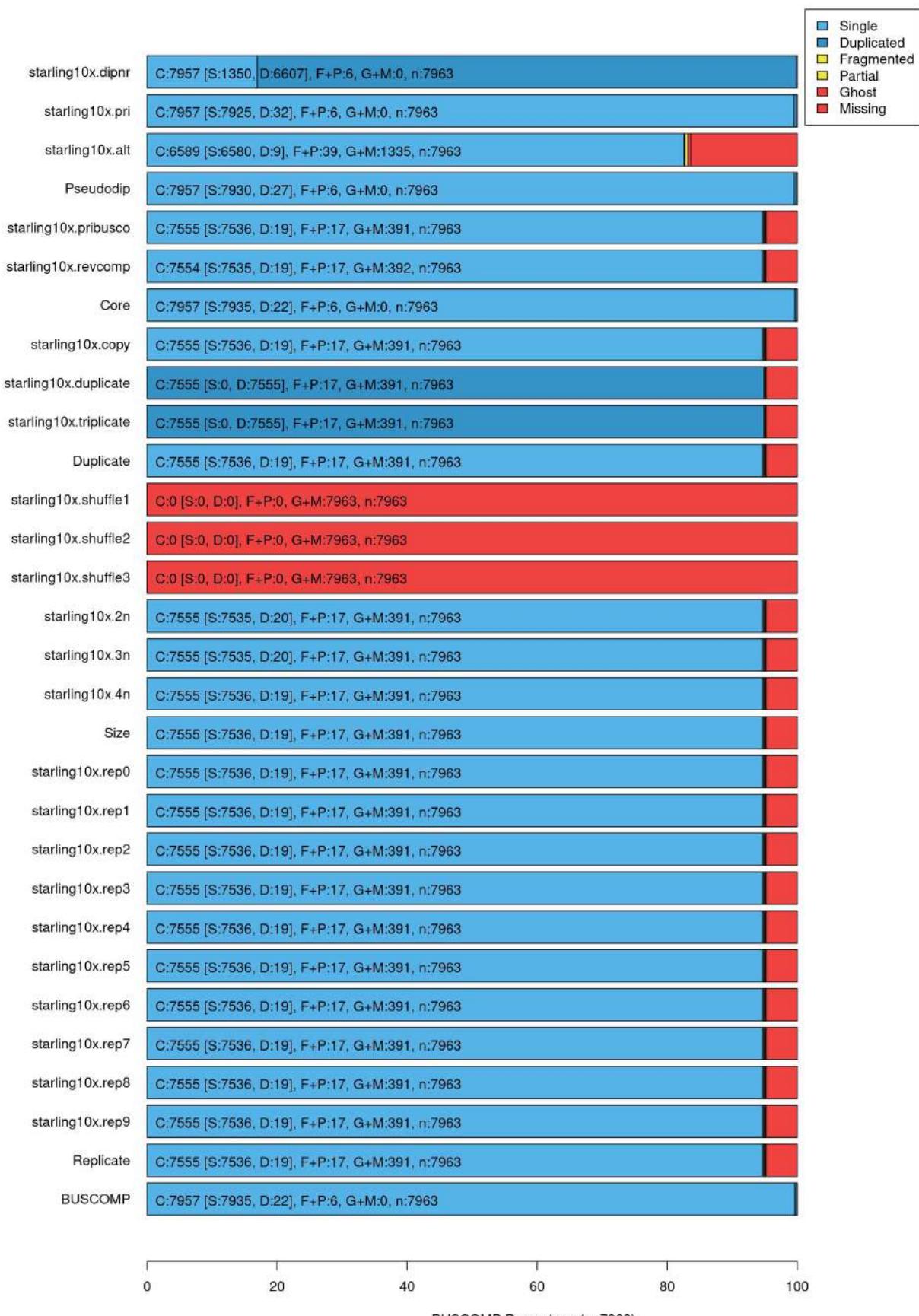
4.1 BUSCOSeq Rating Summary

BUSCOMP ratings (see above) are compiled to summary statistics in `starling10xV5.N3L20ID0U.ratings.tdt`. Note that `Identical` ratings in this table will also be rated as `Complete`, which in turn are `Single` or `Duplicated`. Percentage summaries are plotted below, along with a BUSCO-style one-line summary per assembly/group.

NOTE: Group summaries do not include `Identical` ratings.

X.	Genome	N	Identical	Complete	Single	Duplicated	Fragmented	Partial	Ghost	Missing
1	starling10x.dipnr	7963	6847	7957	1350	6607	0	6	0	0
2	starling10x.pri	7963	5972	7957	7925	32	0	6	0	0
3	starling10x.alt	7963	2629	6589	6580	9	0	39	29	1306
4	Pseudodip	7963	0	7957	7930	27	0	6	0	0
5	starling10x.pribusco	7963	5720	7555	7536	19	0	17	9	382
6	starling10x.revcomp	7963	5714	7554	7535	19	1	16	9	383
7	Core	7963	0	7957	7935	22	0	6	0	0
8	starling10x.copy	7963	5720	7555	7536	19	0	17	9	382
9	starling10x.duplicate	7963	5720	7555	0	7555	0	17	9	382
10	starling10x.triplicate	7963	5729	7555	0	7555	0	17	9	382
11	Duplicate	7963	0	7555	7536	19	0	17	9	382
12	starling10x.shuffle1	7963	0	0	0	0	0	0	0	7963
13	starling10x.shuffle2	7963	0	0	0	0	0	0	0	7963
14	starling10x.shuffle3	7963	0	0	0	0	0	0	0	7963
15	starling10x.2n	7963	5720	7555	7535	20	0	17	9	382
16	starling10x.3n	7963	5720	7555	7535	20	0	17	9	382
17	starling10x.4n	7963	5720	7555	7536	19	0	17	9	382
18	Size	7963	0	7555	7536	19	0	17	9	382
19	starling10x.rep0	7963	5720	7555	7536	19	0	17	9	382
20	starling10x.rep1	7963	5720	7555	7536	19	0	17	9	382
21	starling10x.rep2	7963	5720	7555	7536	19	0	17	9	382
22	starling10x.rep3	7963	5720	7555	7536	19	0	17	9	382
23	starling10x.rep4	7963	5720	7555	7536	19	0	17	9	382
24	starling10x.rep5	7963	5720	7555	7536	19	0	17	9	382
25	starling10x.rep6	7963	5720	7555	7536	19	0	17	9	382
26	starling10x.rep7	7963	5720	7555	7536	19	0	17	9	382
27	starling10x.rep8	7963	5720	7555	7536	19	0	17	9	382
28	starling10x.rep9	7963	5720	7555	7536	19	0	17	9	382
29	Replicate	7963	0	7555	7536	19	0	17	9	382
30	BUSCOMP	7963	0	7957	7935	22	0	6	0	0

BUSCOSeq Rating Summary



BUSCOMP BUSCOMP Results [8065 (96.73%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:99.9%[S:99.6%,D:0.3%],F:0.0%,P:0.1%,G:0.0%,M:0.0%,n:7963

Core BUSCOMP Results [8057 (96.63%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:99.9%[S:99.6%,D:0.3%],F:0.0%,P:0.1%,G:0.0%,M:0.0%,n:7963

Duplicate BUSCOMP Results [7630 (91.51%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

Pseudodip BUSCOMP Results [7946 (95.30%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:99.9%[S:99.6%,D:0.3%],F:0.0%,P:0.1%,G:0.0%,M:0.0%,n:7963

Replicate BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

Size BUSCOMP Results [7505 (90.01%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.2n BUSCOMP Results [7503 (89.99%) Complete BUSCOs; 5191 (65.19%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.3%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.3n BUSCOMP Results [7505 (90.01%) Complete BUSCOs; 1 (0.01%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.3%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.4n BUSCOMP Results [7505 (90.01%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.alt BUSCOMP Results [6539 (78.42%) Complete BUSCOs; 1159 (14.55%) BUSCOMP Seqs]:
C:82.7%[S:82.6%,D:0.1%,I:33.0%],F:0.0%,P:0.5%,G:0.4%,M:16.4%,n:7963

starling10x.copy BUSCOMP Results [7503 (89.99%) Complete BUSCOs; 59 (0.74%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.dipnr BUSCOMP Results [7862 (94.29%) Complete BUSCOs; 238 (2.99%) BUSCOMP Seqs]:
C:99.9%[S:17.0%,D:83.0%,I:86.0%],F:0.0%,P:0.1%,G:0.0%,M:0.0%,n:7963

starling10x.duplicate BUSCOMP Results [7440 (89.23%) Complete BUSCOs; 5 (0.06%) BUSCOMP Seqs]:
C:94.9%[S:0.0%,D:94.9%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.pri BUSCOMP Results [7903 (94.78%) Complete BUSCOs; 44 (0.55%) BUSCOMP Seqs]:
C:99.9%[S:99.5%,D:0.4%,I:75.0%],F:0.0%,P:0.1%,G:0.0%,M:0.0%,n:7963

starling10x.pribusco BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 3 (0.04%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep0 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep1 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep2 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep3 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep4 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep5 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep6 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep7 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep8 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.rep9 BUSCOMP Results [7501 (89.96%) Complete BUSCOs; 0 (0.00%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.revcomp BUSCOMP Results [7507 (90.03%) Complete BUSCOs; 1251 (15.71%) BUSCOMP Seqs]:
C:94.9%[S:94.6%,D:0.2%,I:71.8%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

starling10x.shuffle1 BUSCOMP Results [No BUSCO analysis]:
C:0.0%[S:0.0%,D:0.0%,I:0.0%],F:0.0%,P:0.0%,G:0.0%,M:100.0%,n:7963

starling10x.shuffle2 BUSCOMP Results [No BUSCO analysis]:

C:0.0%[S:0.0%,D:0.0%,I:0.0%],F:0.0%,P:0.0%,G:0.0%,M:100.0%,n:7963

starling10x.shuffle3 BUSCOMP Results [No BUSCO analysis]:
C:0.0%[S:0.0%,D:0.0%,I:0.0%],F:0.0%,P:0.0%,G:0.0%,M:100.0%,n:7963starling10x.triplicate BUSCOMP Results [7471 (89.60%) Complete BUSCOs; 12 (0.15%) BUSCOMP Seqs]:
C:94.9%[S:0.0%,D:94.9%,I:71.9%],F:0.0%,P:0.2%,G:0.1%,M:4.8%,n:7963

4.2 BUSCOSeq Full Results Table

Full BUSCOMP results with ratings for each gene in every assembly and group have been compiled in [starling10xV5.N3L20ID0U.buscomp.tdt](#):

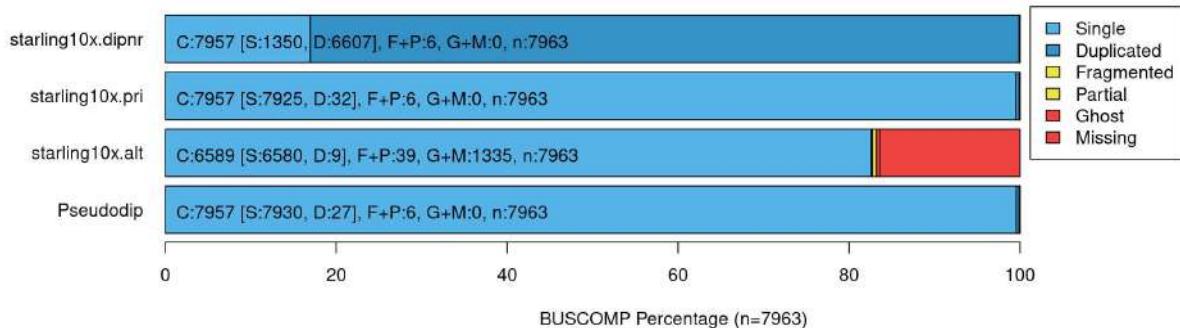
BuscoID <chr>	Genome <chr>	starling10x.dipnr <chr>	starling10x.pri <chr>
10004at8782	BUSCOFas	Duplicated	Complete
10005at8782	BUSCOFas	Duplicated	Complete
10020at8782	BUSCOFas	Duplicated	Complete
10021at8782	BUSCOFas	Duplicated	Complete
10029at8782	BUSCOFas	Complete	Complete
10031at8782	BUSCOFas	Duplicated	Complete
10032at8782	BUSCOFas	Duplicated	Complete
10042at8782	BUSCOFas	Duplicated	Complete
10045at8782	BUSCOFas	Duplicated	Complete
10049at8782	BUSCOFas	Duplicated	Complete

1-10 of 7,963 rows | 1-4 of 32 columns

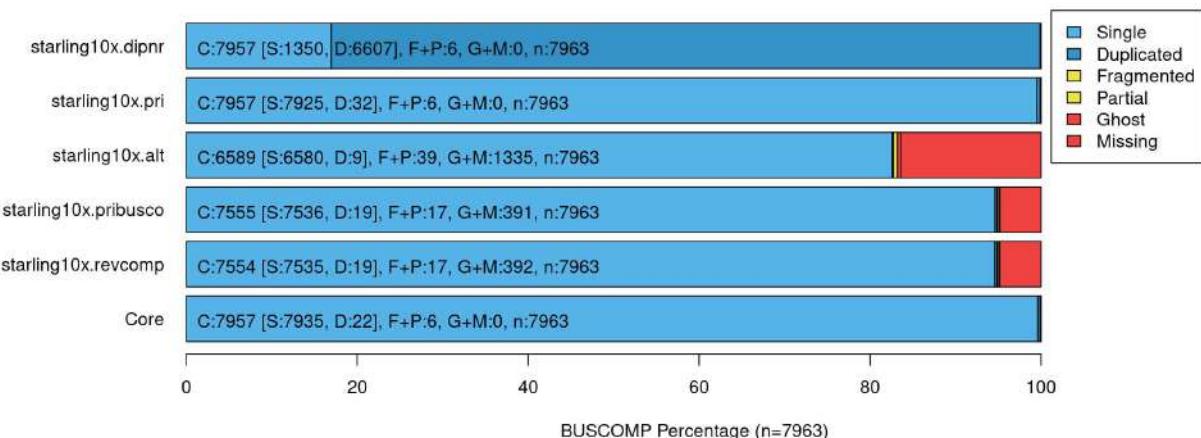
[Previous](#) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) ... [797](#) [Next](#)

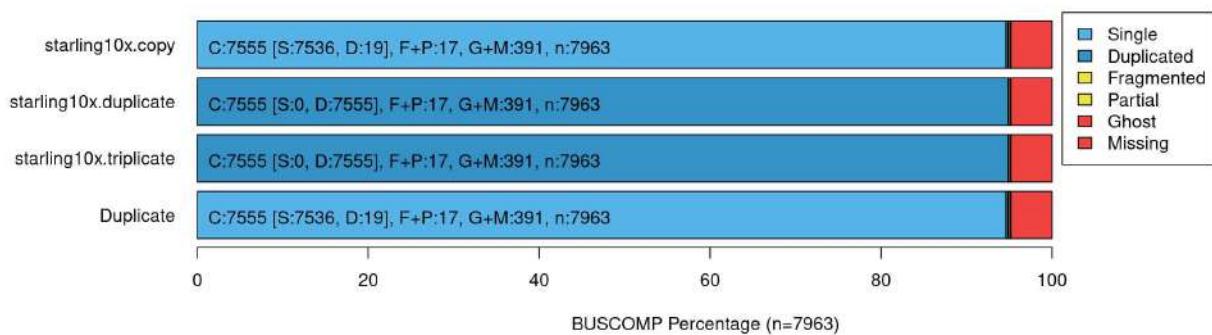
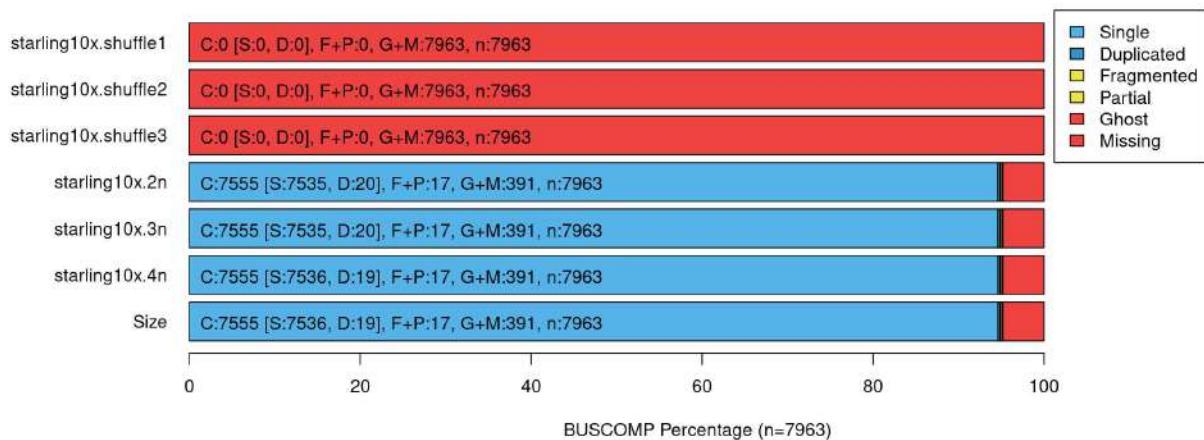
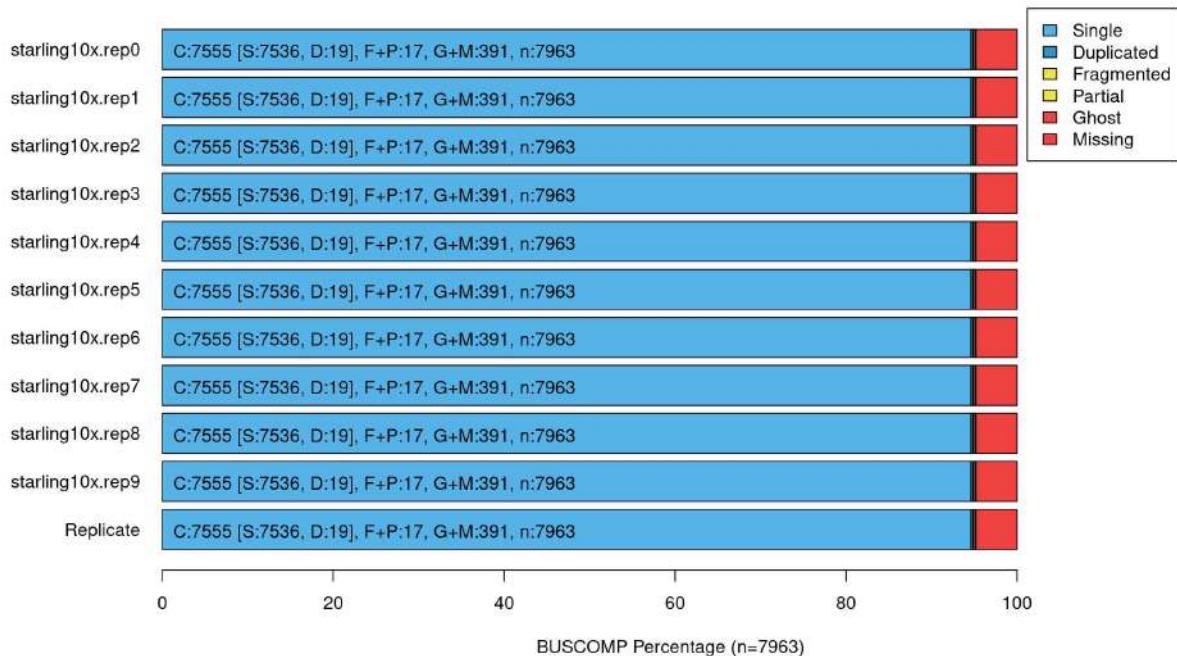
4.3 Genome Group BUSCOMP charts

Pseudodip BUSCOSeq Rating Summary

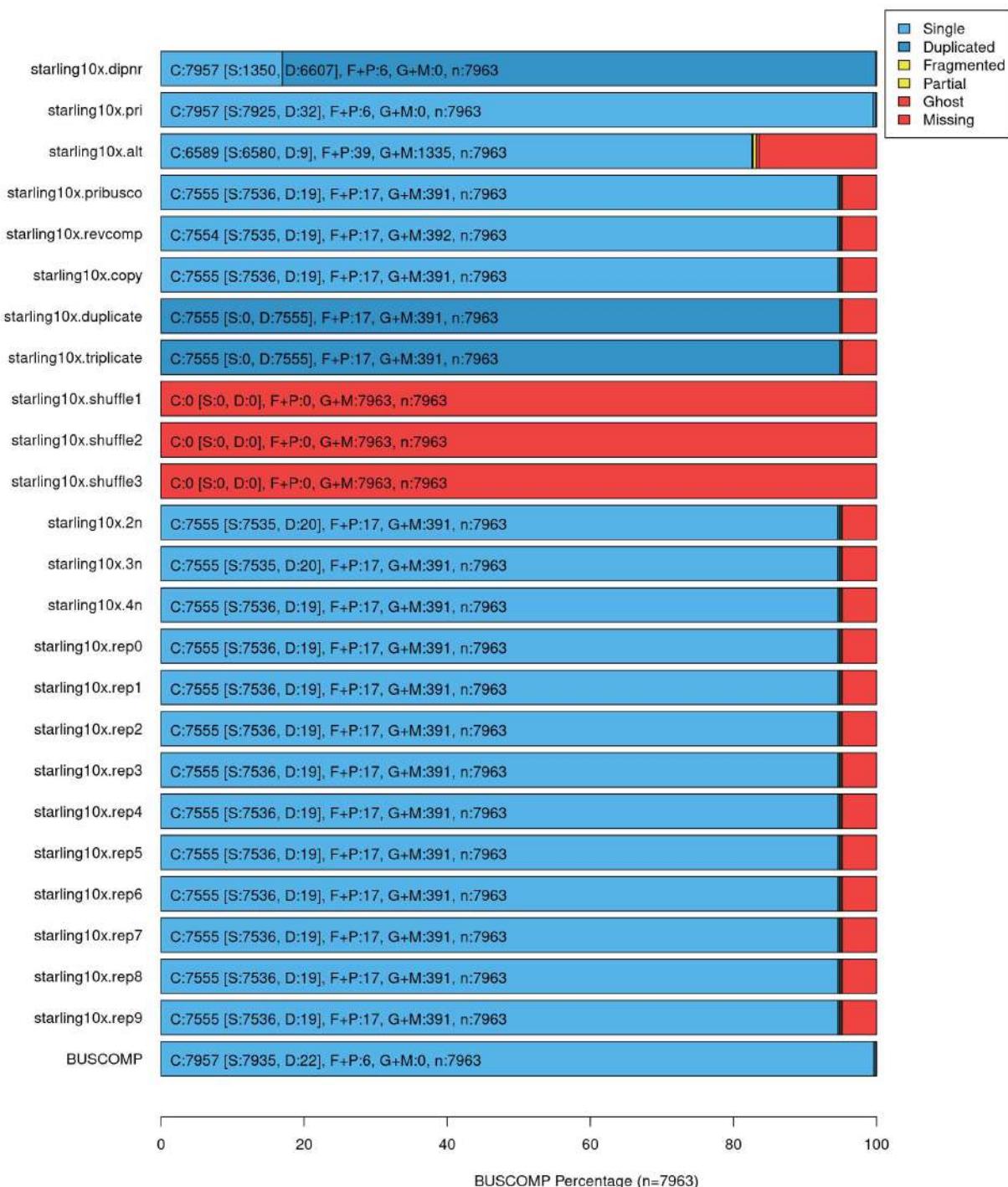


Core BUSCOSeq Rating Summary



Duplicate BUSCOSeq Rating Summary**Size BUSCOSeq Rating Summary****Replicate BUSCOSeq Rating Summary**

BUSCOMP BUSCOSeq Rating Summary



5 BUSCO and BUSCOMP Comparisons

5.1 BUSCO to BUSCOMP Rating Changes

Ratings changes from BUSCO to BUSCOMP (where `NULL` ratings indicate no BUSCOMP sequence):

BUSCO	BUSCOMP	starling10x.dipnr	starling10x.pri	starling10x.alt	starling10x.pribusco	starling10x.revcomp	starling10x.copy	starling10x.dup
Complete	Complete	1314	7760	6465	7402	7403	7404	
Complete	Duplicated	230	17	7	11	13	11	
Complete	Fragmented	0	0	0	0	1	0	
Complete	Ghost	0	0	1	0	0	0	
Complete	Missing	0	0	43	12	12	12	
Complete	Partial	1	6	11	6	7	6	
Duplicated	Complete	3	12	2	5	6	5	
Duplicated	Duplicated	6213	12	0	6	6	6	

BUSCO	BUSCOMP	starling10x.dipnr	starling10x.pri	starling10x.alt	starling10x.pribusco	starling10x.revcomp	starling10x.copy	starling10x.dup
Duplicated	Missing	0	0	4	2	2	2	
Duplicated	NULL	96	96	5	57	57	57	
Duplicated	Partial	5	0	1	0	0	0	
Fragmented	Complete	14	51	40	50	53	50	
Fragmented	Duplicated	40	0	0	0	0	0	
Fragmented	Missing	0	0	6	3	4	3	
Fragmented	NULL	108	108	44	77	78	77	
Fragmented	Partial	0	0	0	1	0	1	
Missing	Complete	19	102	73	79	73	77	
Missing	Duplicated	124	3	2	2	0	2	
Missing	Ghost	0	0	28	9	9	9	
Missing	Missing	0	0	1253	365	365	365	
Missing	NULL	171	171	326	241	240	241	
Missing	Partial	0	0	27	10	9	10	

Full table of Ratings changes from by gene:

Buscold <chr>	starling10x.dipnr <chr>	starling10x.pri <chr>
10004at8782	DD	CC
10005at8782	DD	CC
10020at8782	DD	CC
10021at8782	DD	CC
10029at8782	CC	CC
10031at8782	DD	CC
10032at8782	DD	CC
10042at8782	DD	CC
10045at8782	DD	CC
10049at8782	DD	CC

1-10 of 8,338 rows | 1-3 of 22 columns

Previous 1 2 3 4 5 6 ... 834 Next ▶

Complete, Duplicated, Fragmented, Partial, Ghost, Missing, NULL (no BUSCOMP sequence)

5.1.1 BUSCOMP Gain test

There is a risk that performing a low stringency search will identify homologues or pseudogenes of the desired BUSCO gene in error. If there is a second copy of a gene in the genome that is detectable by the search then we would expect the same genes that go from `Missing` to `Complete` in some genomes to go from `Single` to `Duplicated` in others.

To test this, data is reduced for each pair of genomes to BUSCO-BUSCOMP rating pairs of:

- `Single - Single`
- `Single - Duplicated`
- `Missing - Missing`
- `Missing - Single`

This is then converted in to `Gain` ratings (`Single - Duplicated` & `Missing - Single`) or `No Gain` ratings (`Single - Single` & `Missing - Missing`). The `Single - Duplicated` shift in one genome is then used to set the expected `Missing - Single` shift in the other, and assess the probability of observing the `Missing - Single` shift using a cumulative binomial distribution, where:

- k is the number of observed `GG` pairs (`Single - Duplicated` and `Missing - Single`)
- n is the number of `Missing - Single` Gains in the focal genome (`NG + GG`)
- p is the proportion of `Single - Duplicated` Gains in the background genome ($(GN + GG) / (GN + GG + NN + NG)$)
- pB is the probability of observing $k+1$ `Missing - Single` gains, given p and n

This is output to `*.gain.tdt`, where each row is a Genome and each field gives the probability of the row genome's `Missing - Single` gains, given the column genome's `Single - Duplicated` gains:

Genome <chr>	starling10x.dipnr <dbl>
starling10x.2n	4.23e-05
starling10x.3n	4.23e-05
starling10x.4n	4.23e-05
starling10x.alt	1.60e-14

Genome	starling10x.dipnr	>
<chr>	<dbl>	
starling10x.copy	4.02e-06	
starling10x.dipnr	1.00e+00	
starling10x.duplicate	1.00e+00	
starling10x.pri	7.38e-01	
starling10x.pribusco	4.16e-07	
starling10x.rep0	4.16e-07	

1-10 of 21 rows | 1-2 of 22 columns

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Low probabilities indicate that BUSCOMP might be rating paralogues or pseudogenes and not functional orthologues of the BUSCO gene. Note that there is no correction for multiple testing, nor any adjustment for lack of independence between samples.

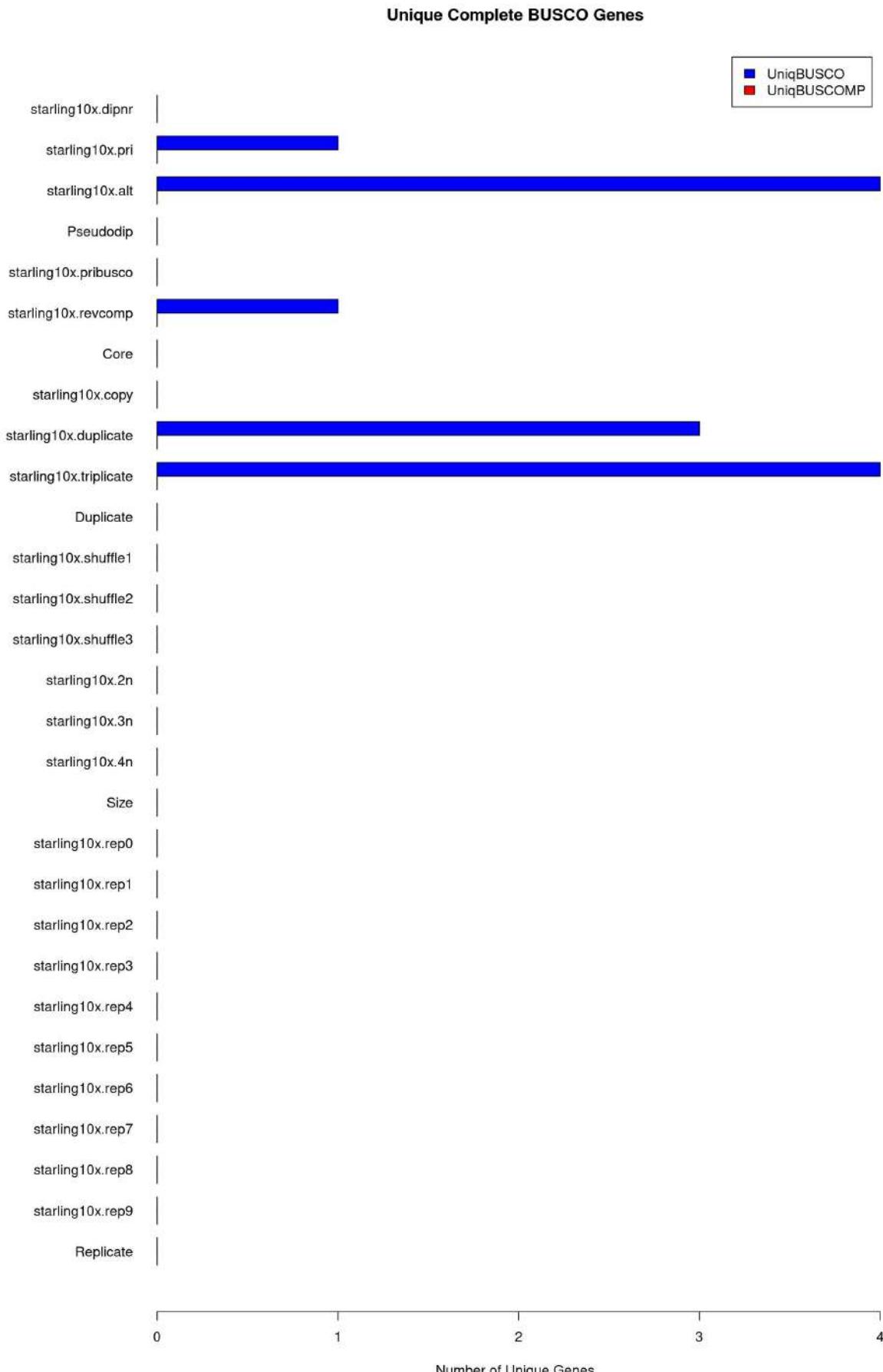
5.2 Unique BUSCO and BUSCOMP Complete Genes

BUSCO and BUSCOMP `Complete` ratings were compared for each BUSCO gene to identify those genes unique to either a single assembly or a group of assemblies. The `buscomp` group is excluded from this analysis, as (typically) are other redundant groups wholly contained within another group. (Inclusion of such groups is guaranteed to result in 2+ groups containing any `Complete` BUSCOs they have.)

```

starling10x.dipnr unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.pri unique Complete genes: 1 BUSCO; 0 BUSCOMP
starling10x.alt unique Complete genes: 4 BUSCO; 0 BUSCOMP
starling10x.pribusco unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.revcomp unique Complete genes: 1 BUSCO; 0 BUSCOMP
starling10x.copy unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.duplicate unique Complete genes: 3 BUSCO; 0 BUSCOMP
starling10x.triplicate unique Complete genes: 4 BUSCO; 0 BUSCOMP
starling10x.shuffle1 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.shuffle2 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.shuffle3 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.2n unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.3n unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.4n unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep0 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep1 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep2 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep3 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep4 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep5 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep6 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep7 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep8 unique Complete genes: 0 BUSCO; 0 BUSCOMP
starling10x.rep9 unique Complete genes: 0 BUSCO; 0 BUSCOMP
Core unique Complete genes: 0 BUSCO; 0 BUSCOMP
Duplicate unique Complete genes: 0 BUSCO; 0 BUSCOMP
Pseudodip unique Complete genes: 0 BUSCO; 0 BUSCOMP
Replicate unique Complete genes: 0 BUSCO; 0 BUSCOMP
Size unique Complete genes: 0 BUSCO; 0 BUSCOMP

```



5.3 Ratings for Missing BUSCO genes

In addition to the unique ratings (above), it can be useful to know how genes `Missing` from one assembly/group are rated in the others. These plots are generated for each assembly/group in turn. The full BUSCO (`*.busco.tdt`) and BUSCOMP (`*.LnnIDxx.buscomp.tdt`) tables are reduced to the subset of genes that are missing in the assembly/group of interest, and then the summary ratings recalculated for that subset.

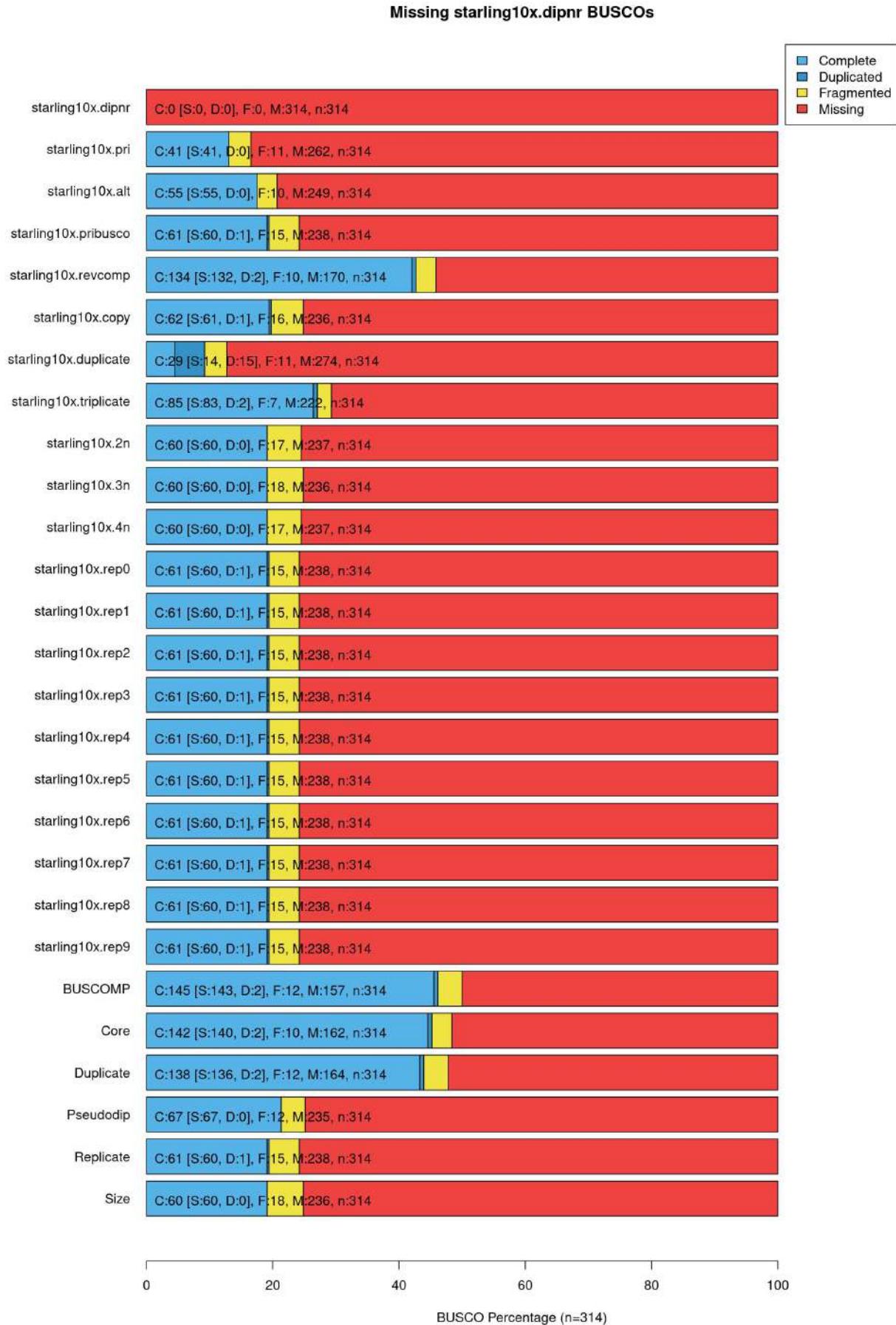
In each case, three plots are made (assuming both BUSCO and BUSCOMP data is available):

1. BUSCO ratings for missing BUSCO genes.

2. BUSCOMP ratings for missing BUSCO genes. As well as being more relaxed than pure BUSCO results, this will indicate when BUSCOMP has found a gene in the focal assembly/group where BUSCO did not.
3. BUSCOMP ratings for missing BUSCOMP genes. It is expected that assemblies will be much more similar in terms of BUSCOMP coverage.

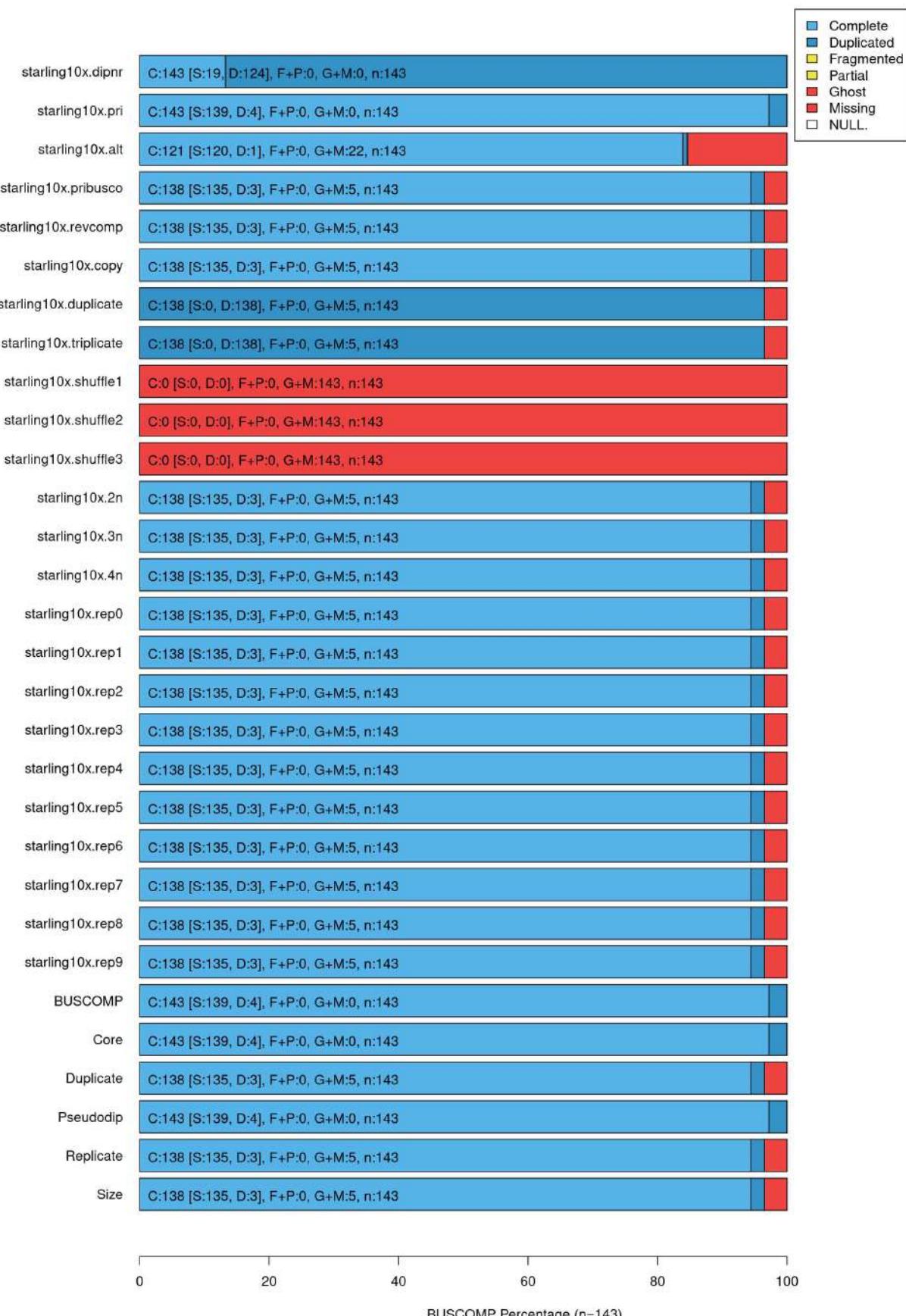
5.4 Missing starling10x.dipnr BUSCO genes

BUSCO ratings for **Missing** starling10x.dipnr BUSCO genes:



BUSCOMP ratings for **Missing** starling10x.dipnr BUSCO genes:

Missing starling10x.dipnr BUSCOs: BUSCOMP ratings

BUSCOMP ratings for **Missing** starling10x.dipnr BUSCOMP genes:

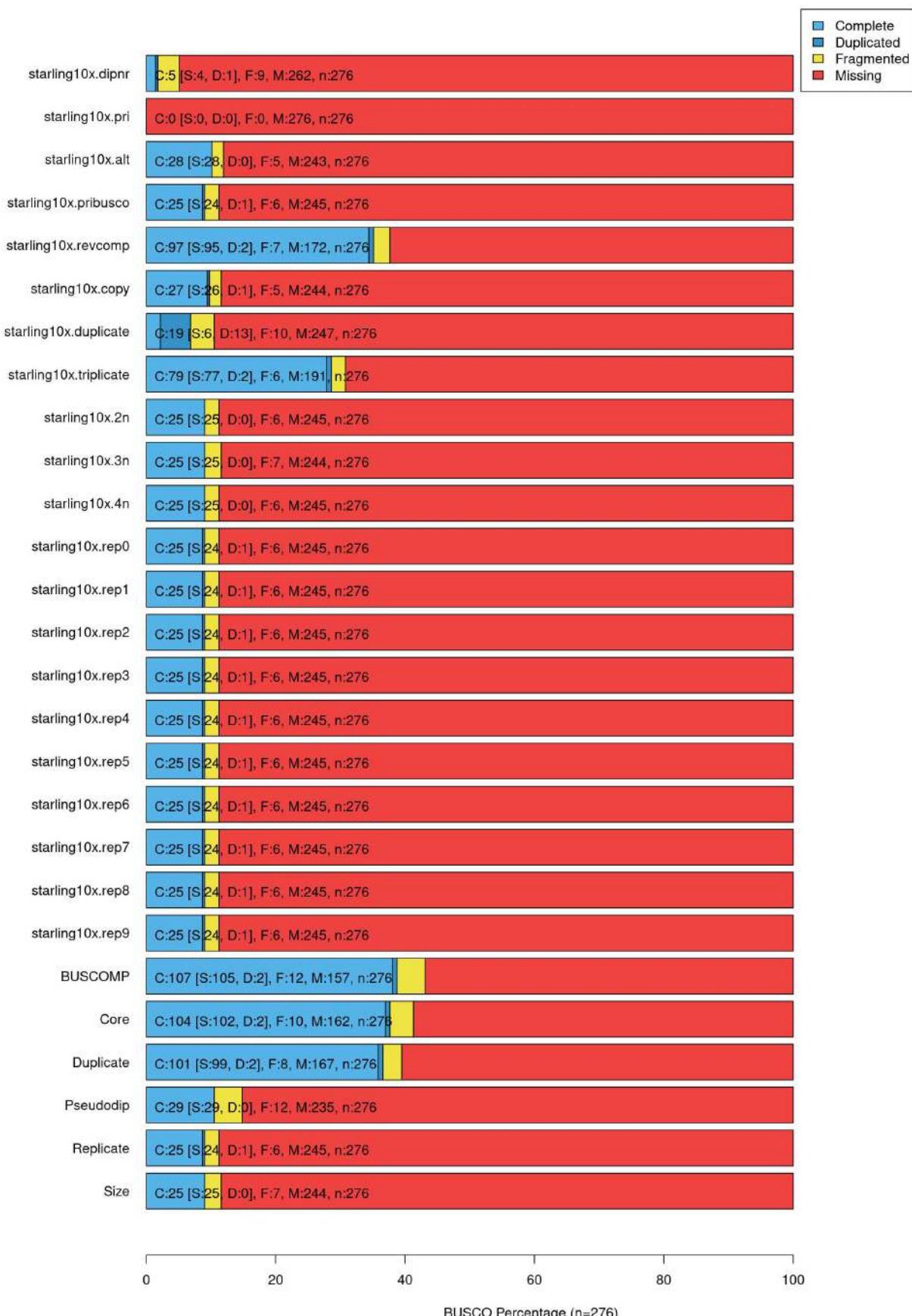
Missing starling10x.dipnr BUSCOMPs

	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0

**5.5 Missing starling10x.pri BUSCO genes**

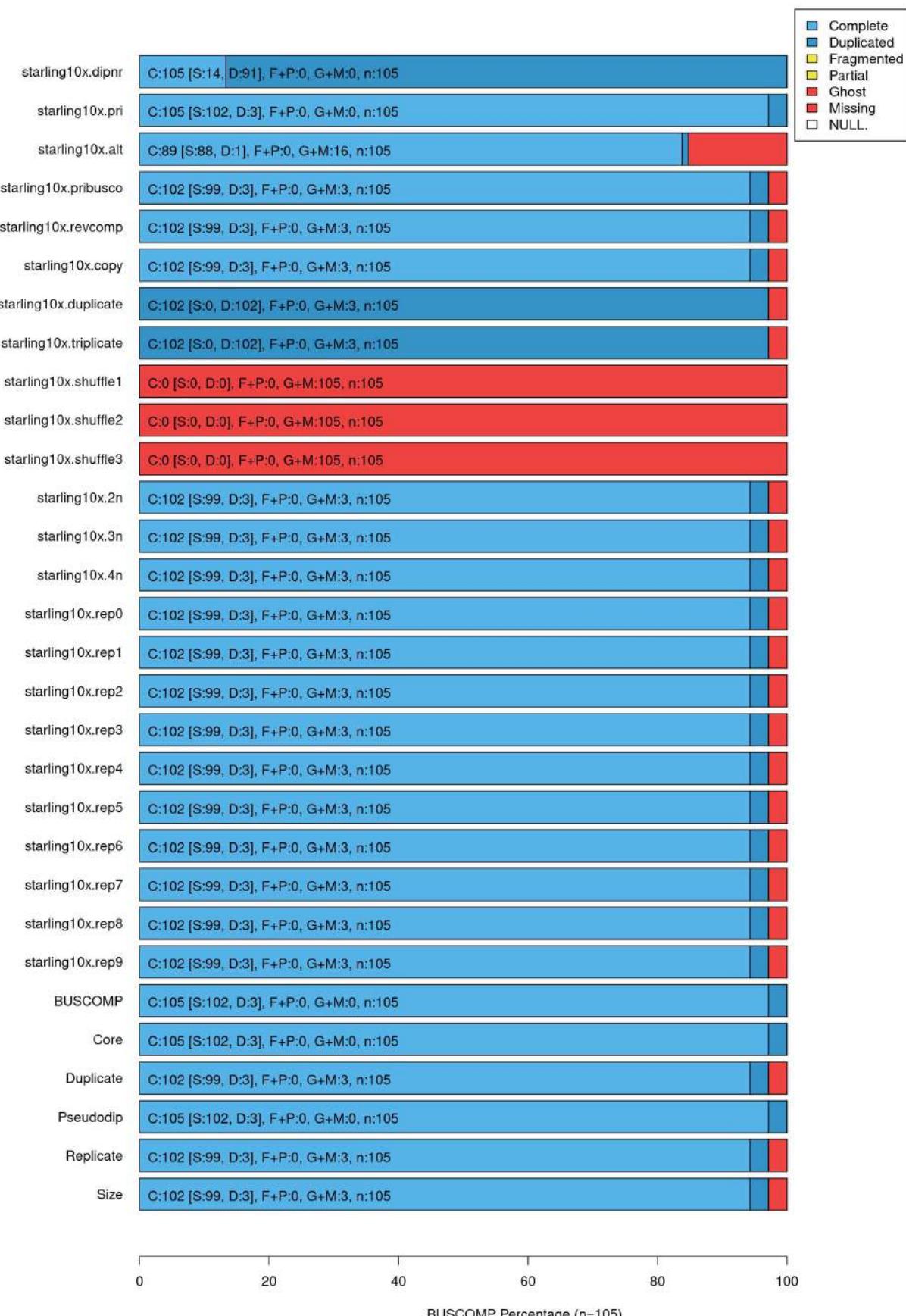
BUSCO ratings for **Missing** starling10x.pri BUSCO genes:

Missing starling10x.pri BUSCOs



BUSCOMP ratings for [Missing] starling10x.pri BUSCO genes:

Missing starling10x.pri BUSCOs: BUSCOMP ratings



BUSCOMP ratings for [Missing] starling10x.pri BUSCOMP genes:

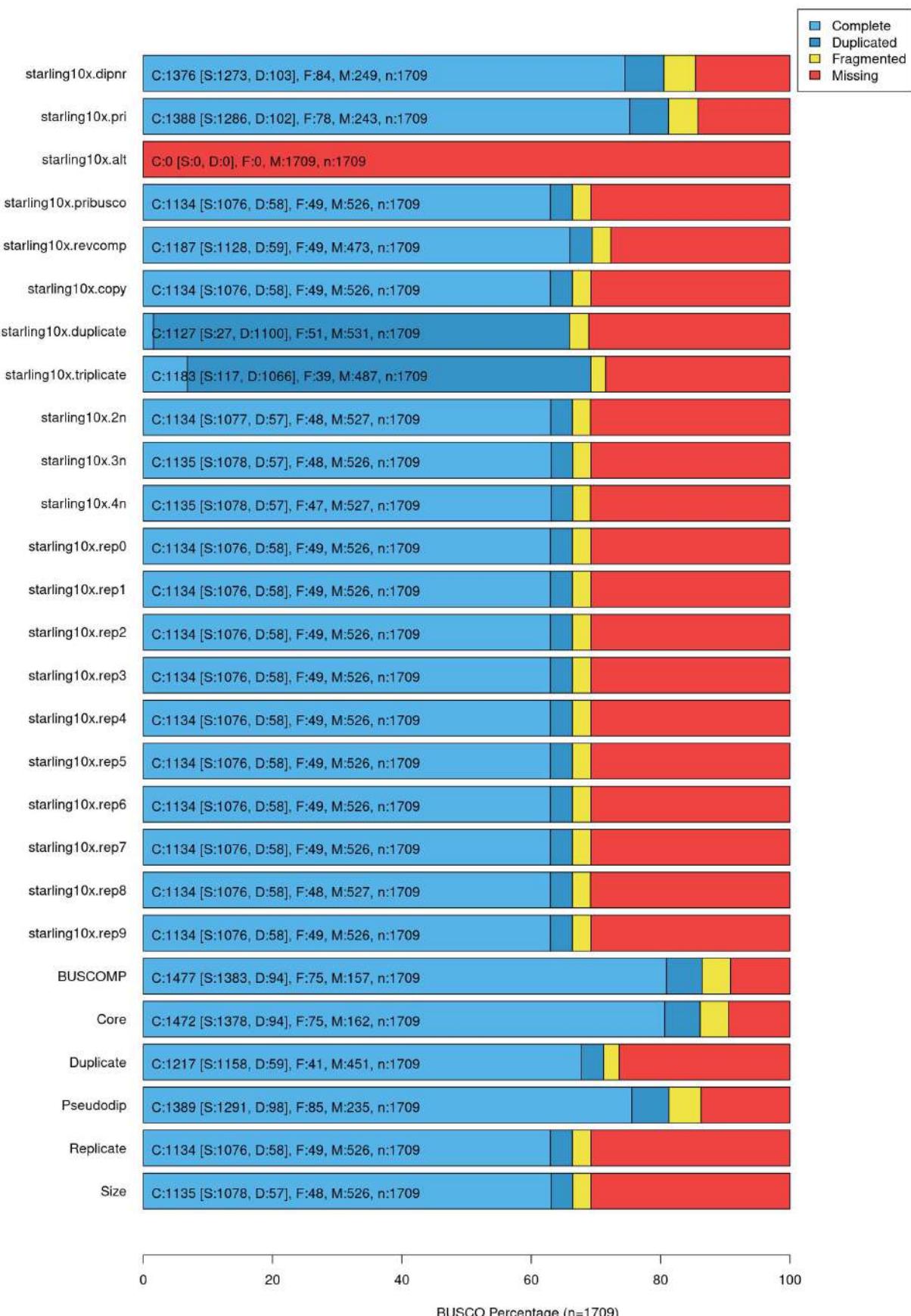
Missing starling10x.pri BUSCOMPs

	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0

**5.6 Missing starling10x.alt BUSCO genes**

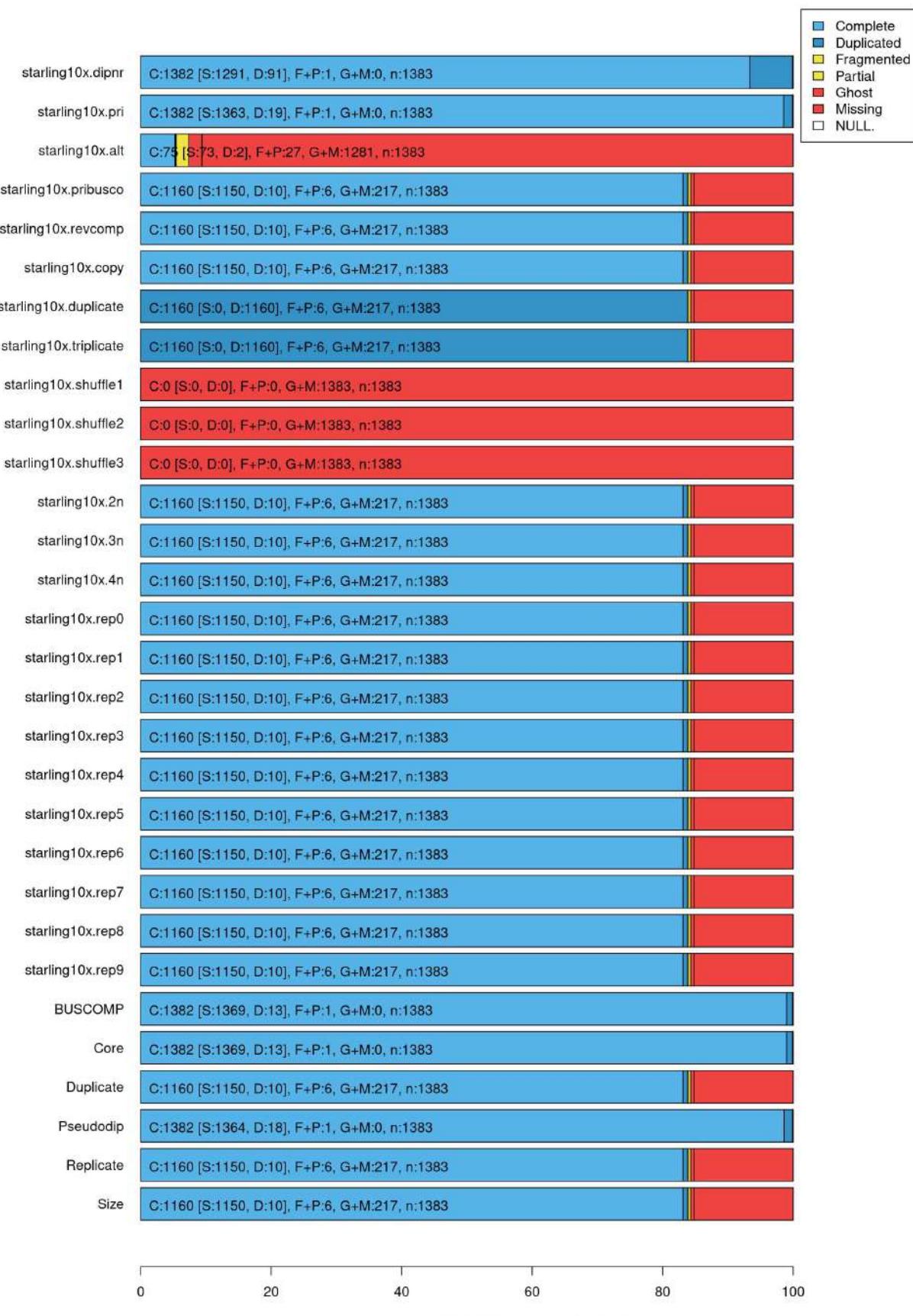
BUSCO ratings for **Missing** starling10x.alt BUSCO genes:

Missing starling10x.alt BUSCOs

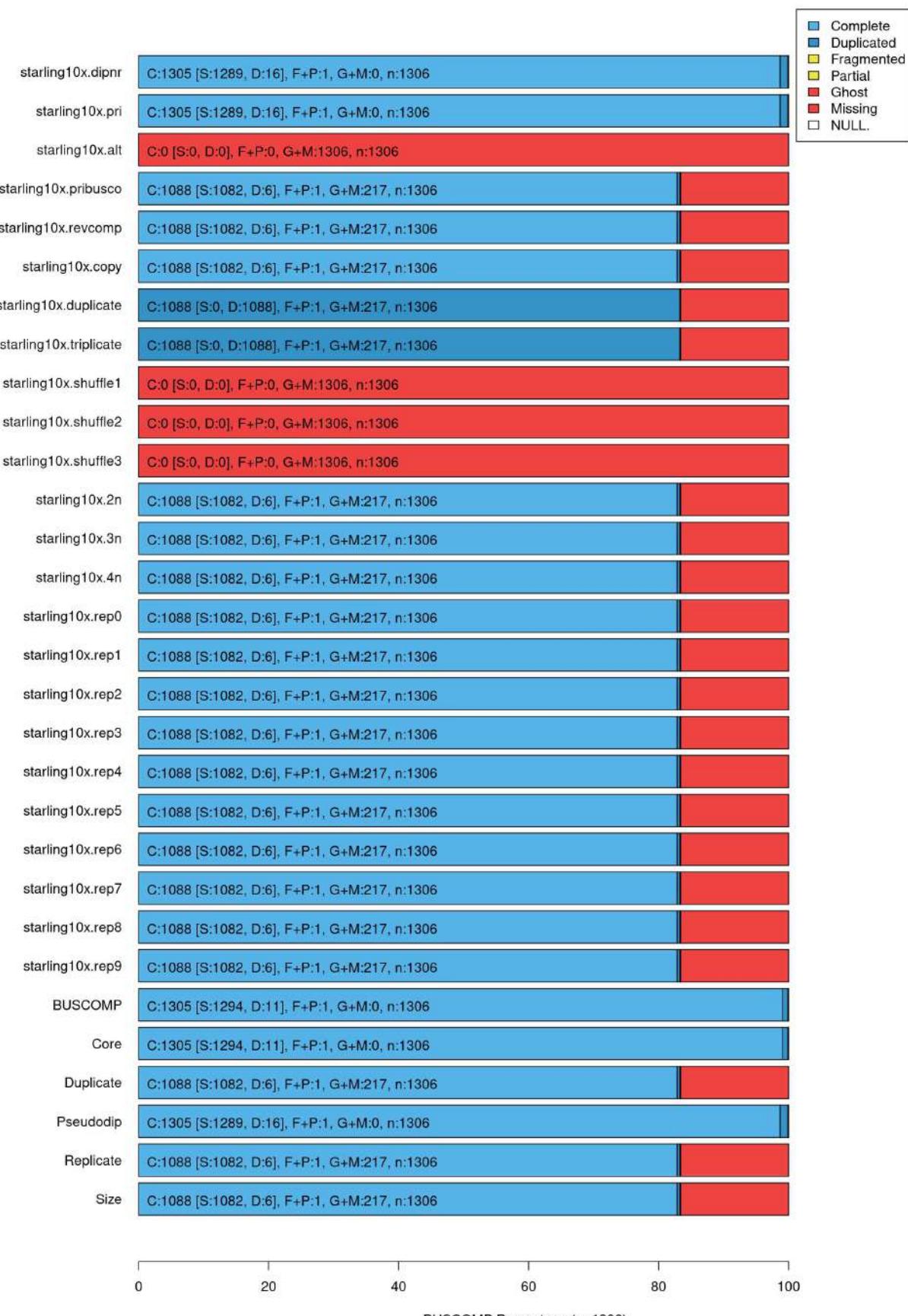


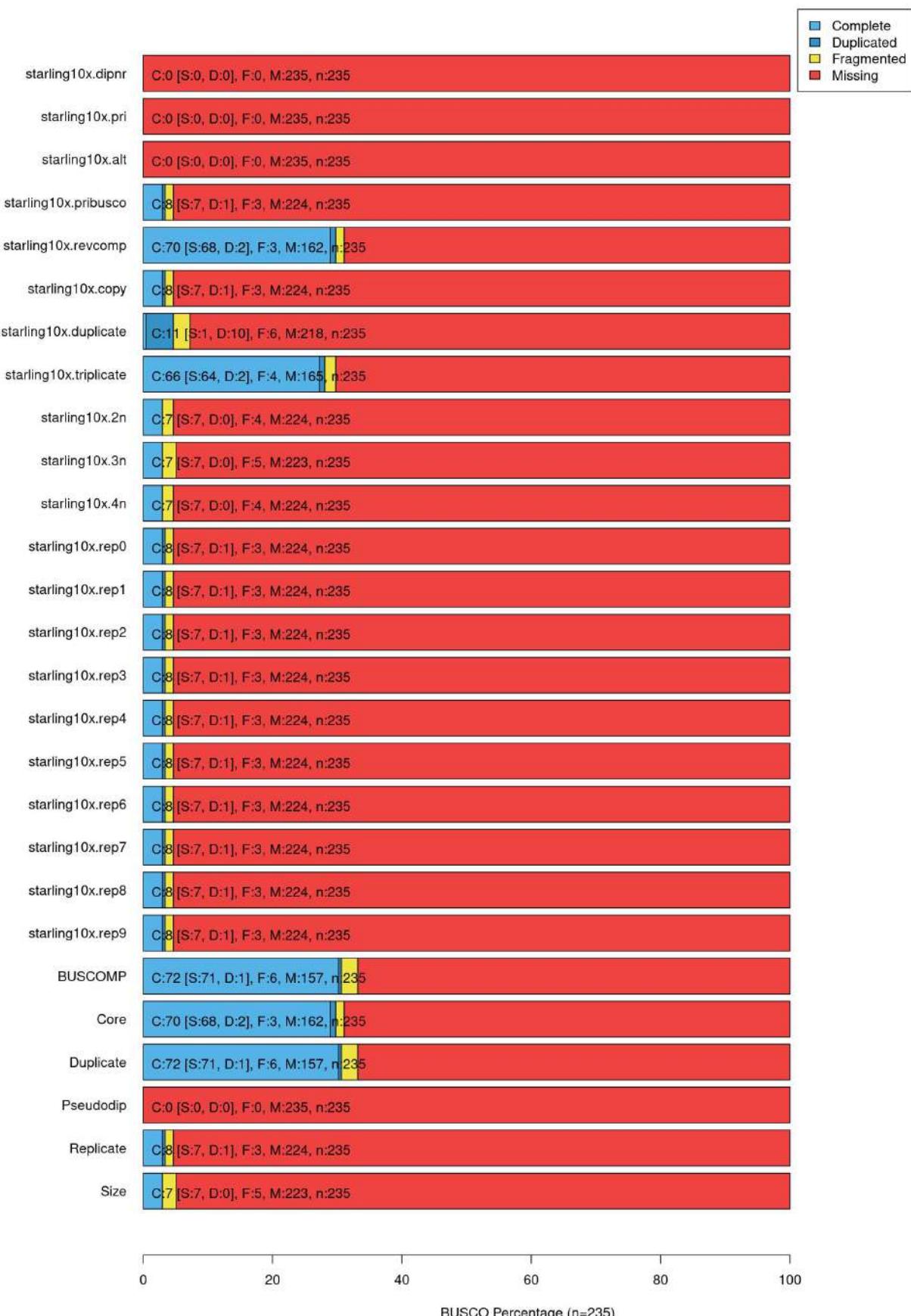
BUSCOMP ratings for [Missing] starling10x.alt BUSCO genes:

Missing starling10x.alt BUSCOs: BUSCOMP ratings



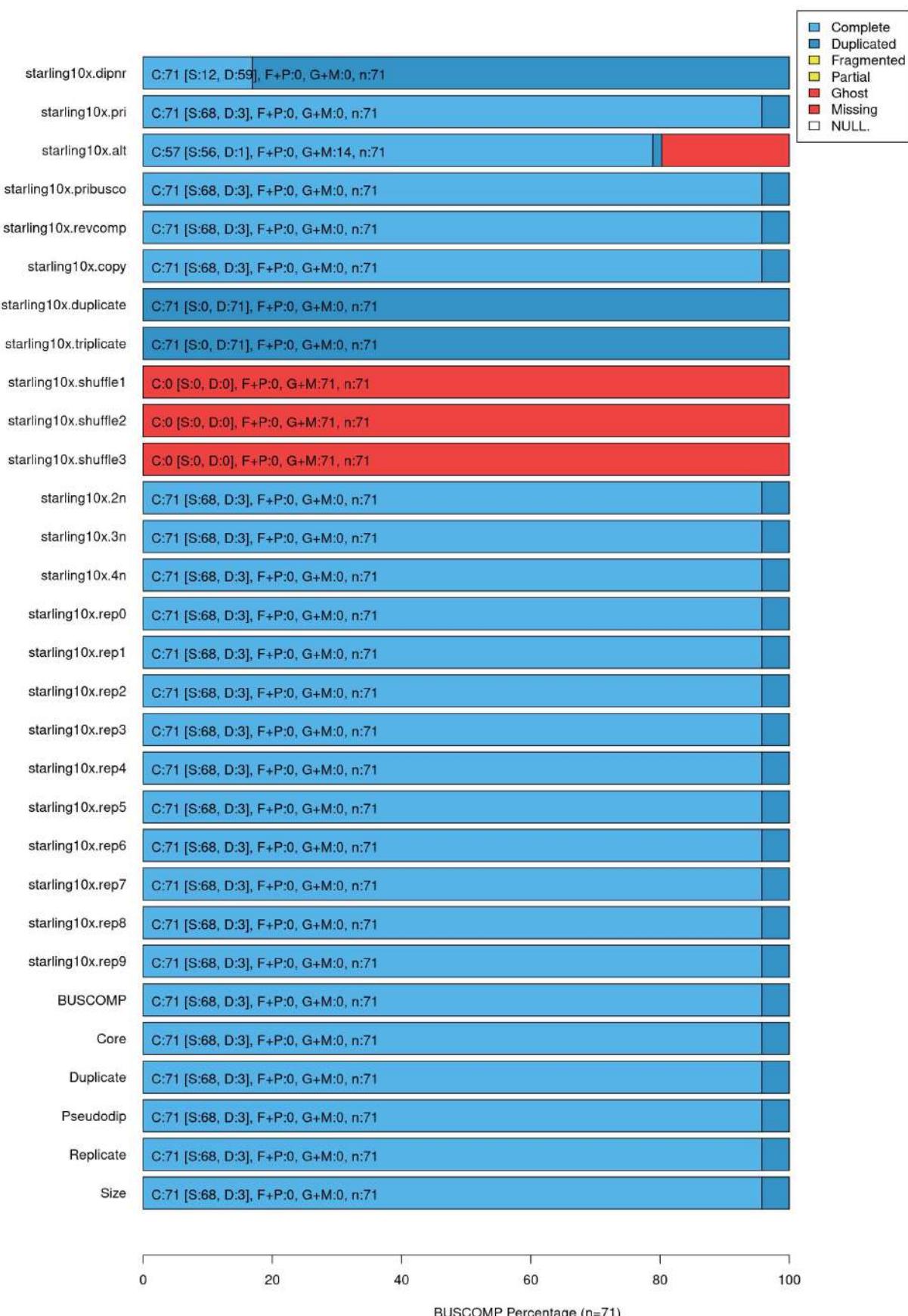
BUSCOMP ratings for [Missing] starling10x.alt BUSCOMP genes:

Missing starling10x.alt BUSCOMPs**5.7 Missing Pseudodip BUSCO genes**BUSCO ratings for Missing Pseudodip BUSCO genes:

Missing Pseudodip BUSCOs

BUSCOMP ratings for **[Missing]** Pseudodip BUSCO genes:

Missing Pseudodip BUSCOs: BUSCOMP ratings

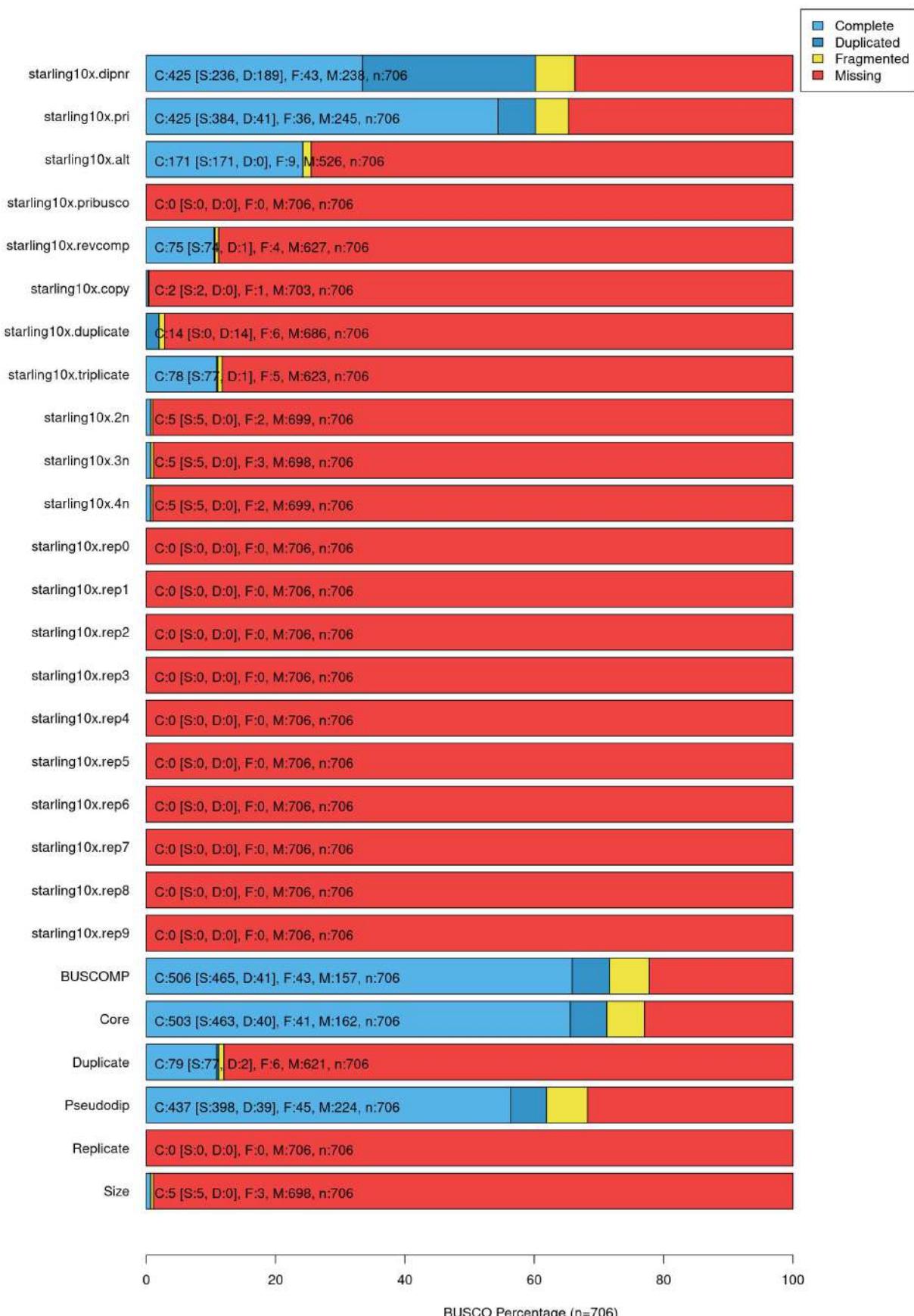
BUSCOMP ratings for **[Missing]** Pseudodip BUSCOMP genes:

Missing Pseudodip BUSCOMPs

starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0

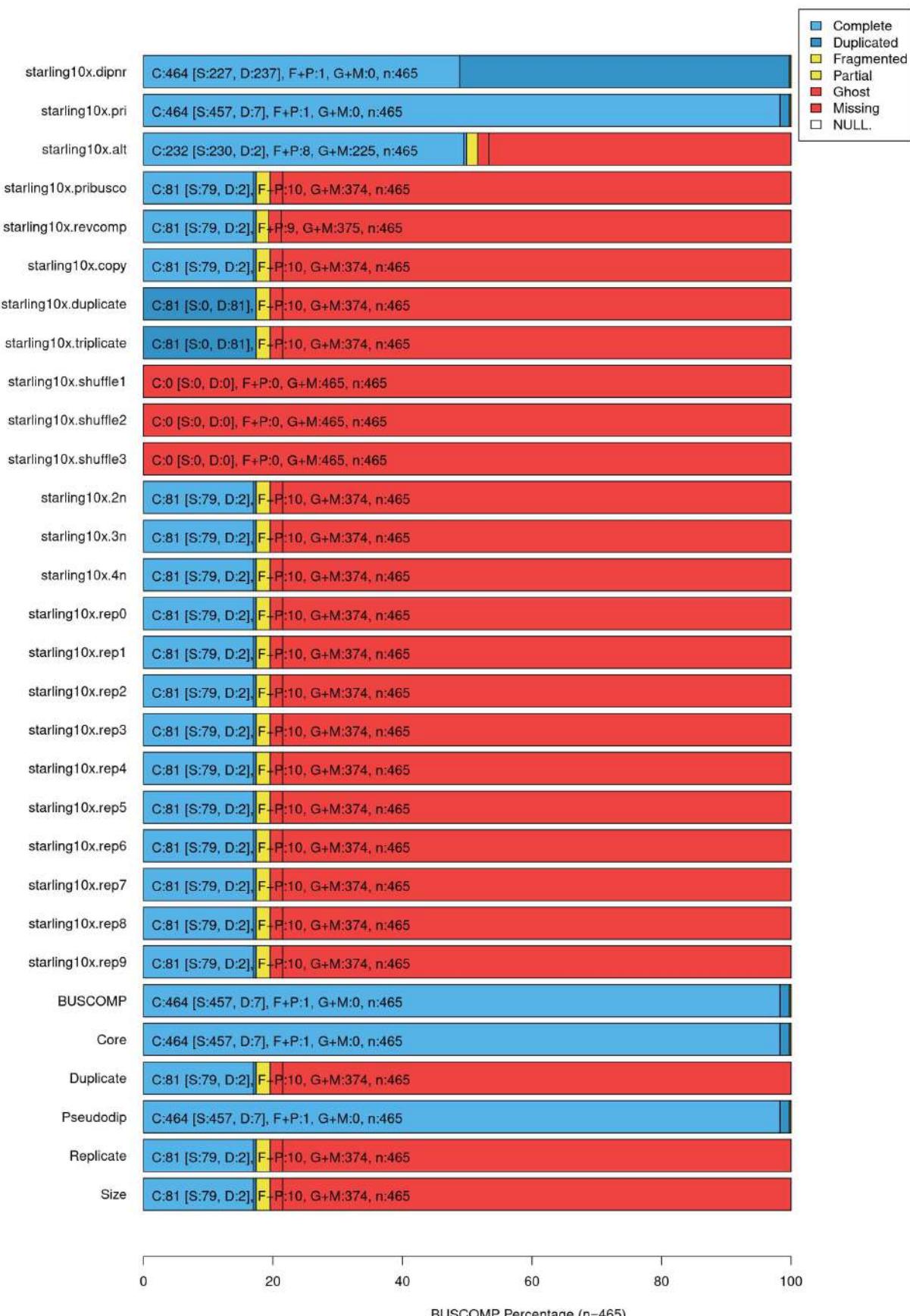
**5.8 Missing starling10x.pribusco BUSCO genes**

BUSCO ratings for Missing starling10x.pribusco BUSCO genes:

Missing starling10x.pribusco BUSCOs

BUSCOMP ratings for **[Missing]** starling10x.pribusco BUSCO genes:

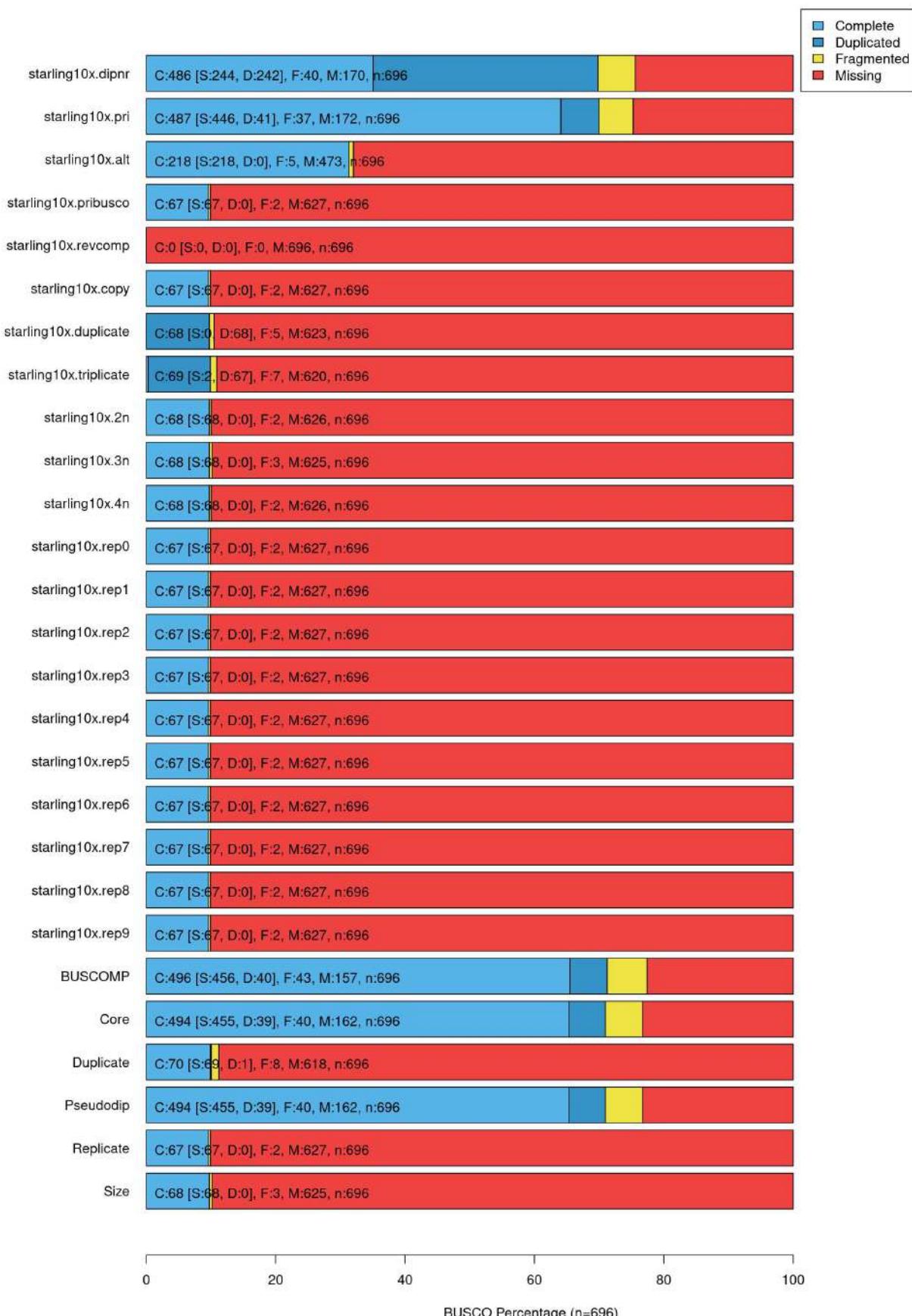
Missing starling10x.pribusco BUSCOs: BUSCOMP ratings

BUSCOMP ratings for **Missing** starling10x.pribusco BUSCOMP genes:

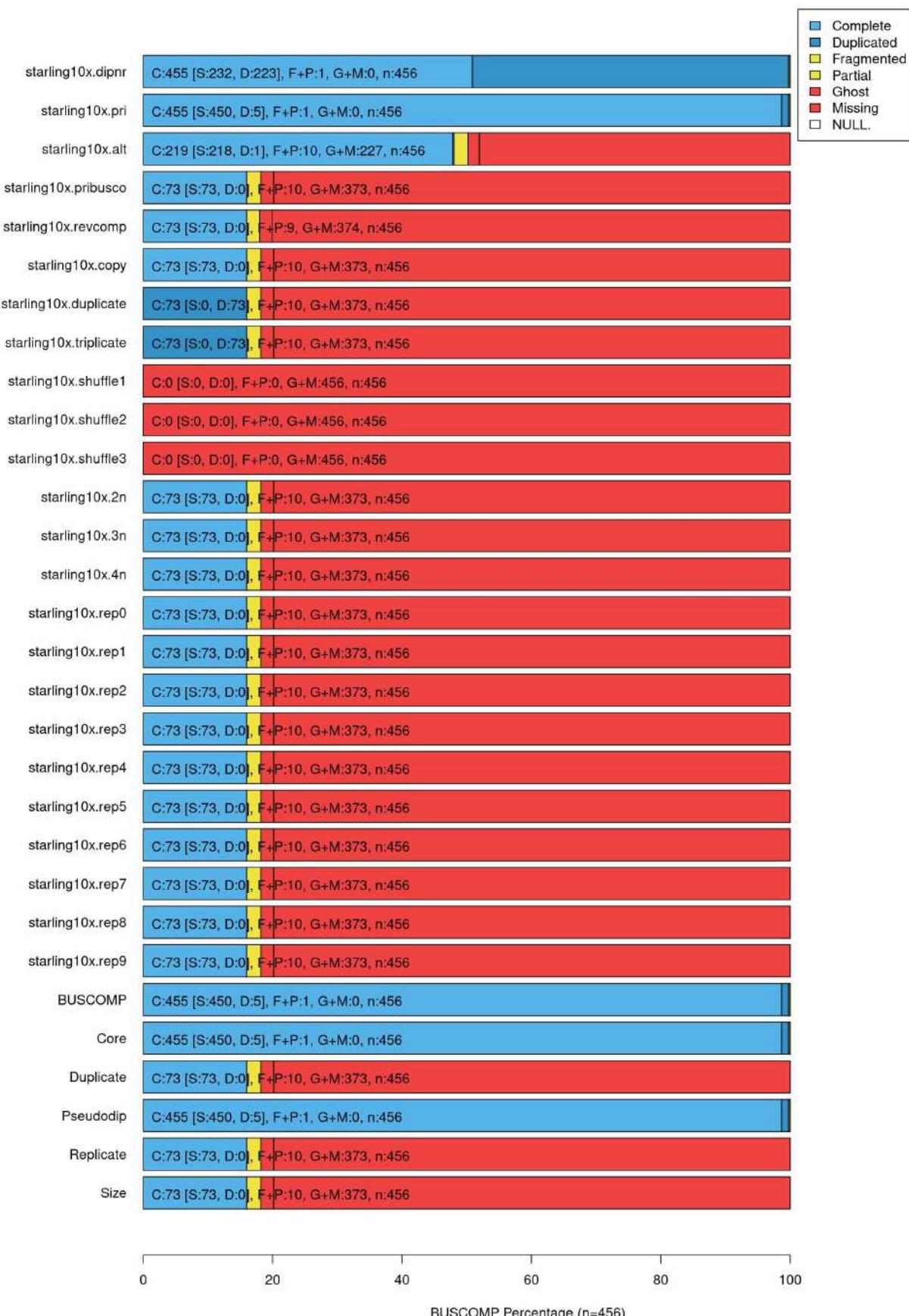
Missing starling10x.pribusco BUSCOMPs**5.9 Missing starling10x.revcomp BUSCO genes**

BUSCO ratings for **Missing** starling10x.revcomp BUSCO genes:

Missing starling10x.revcomp BUSCOs

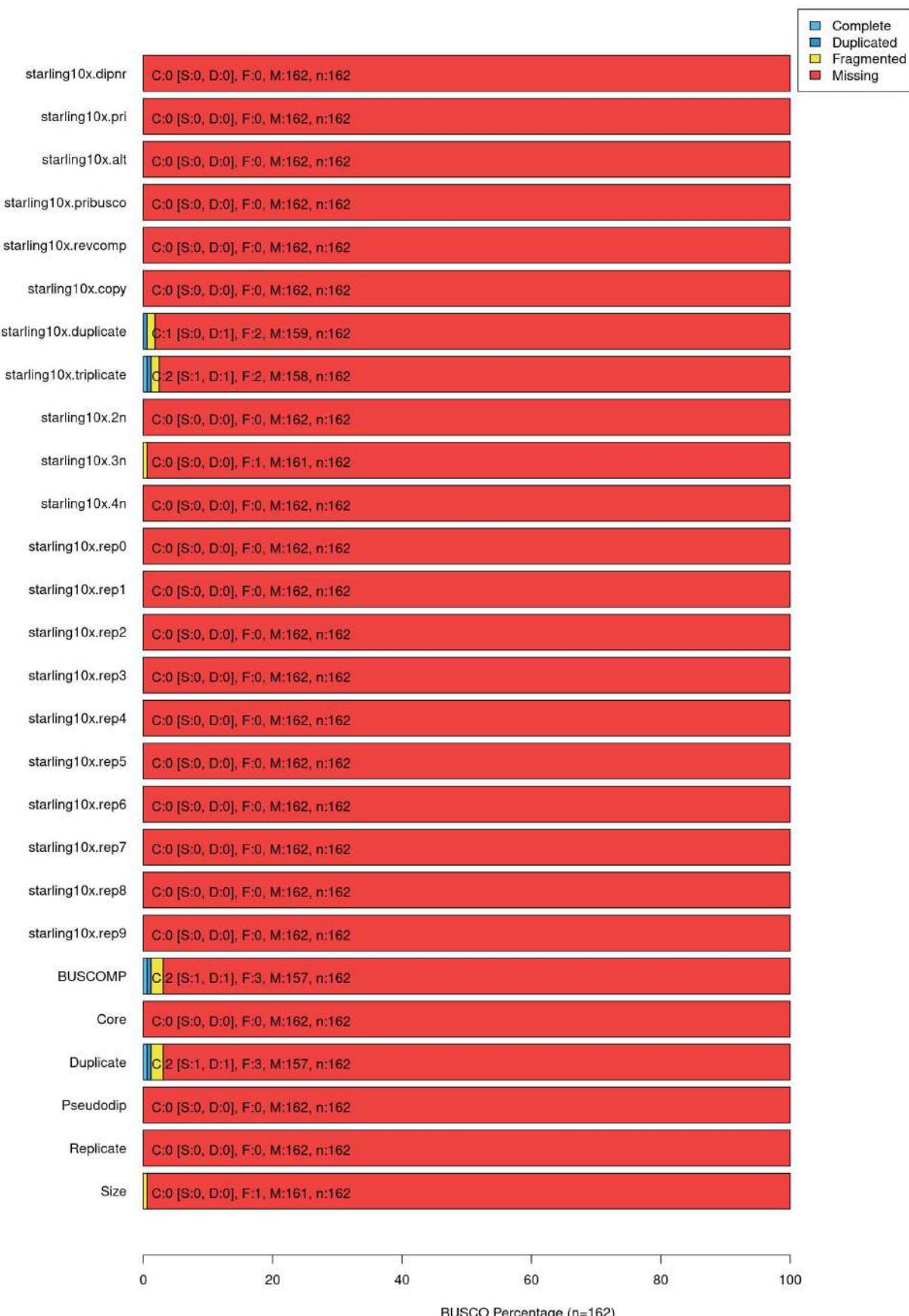
BUSCOMP ratings for **Missing** starling10x.revcomp BUSCO genes:

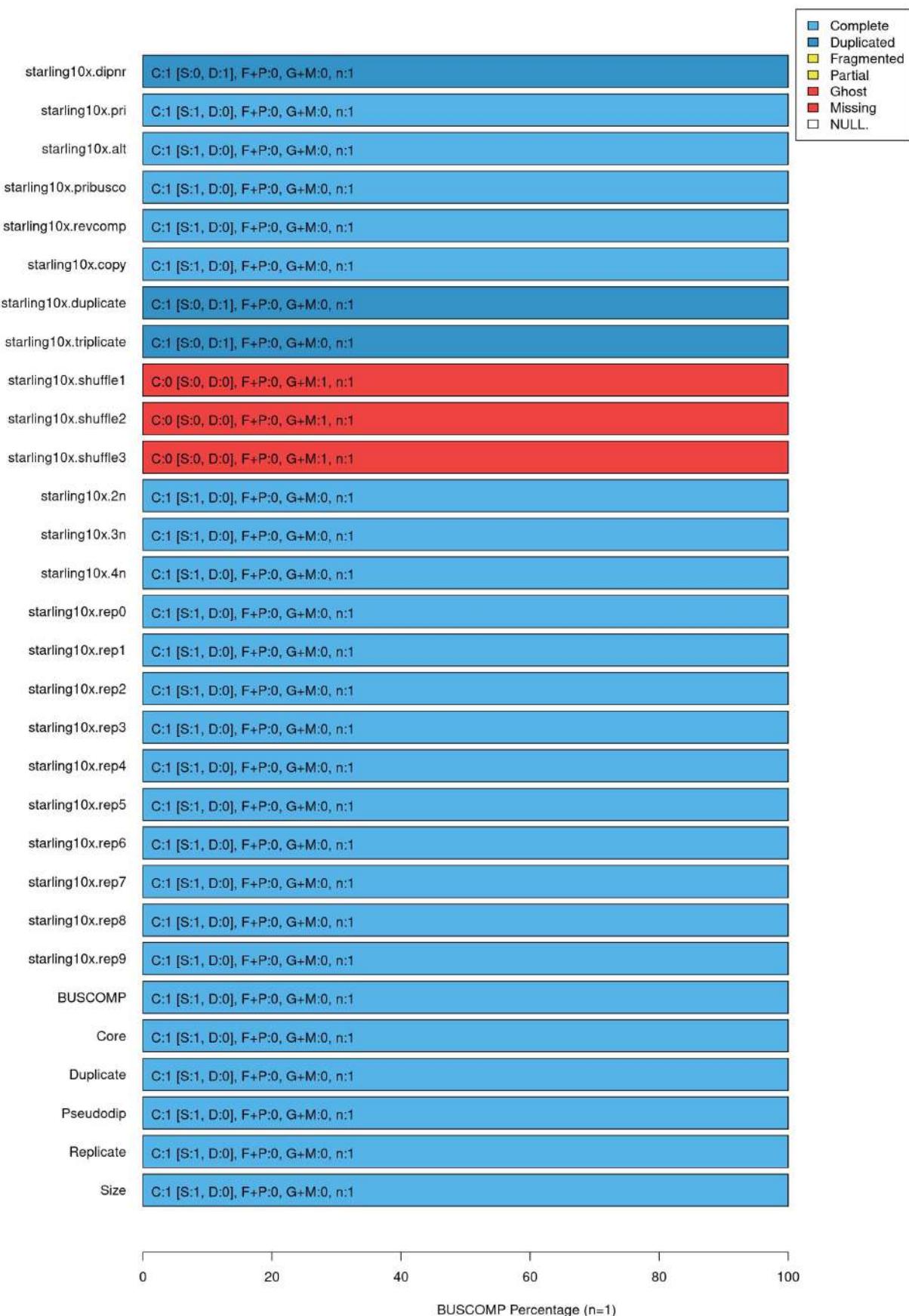
Missing starling10x.revcomp BUSCOs: BUSCOMP ratings

BUSCOMP ratings for **Missing** starling10x.revcomp BUSCOMP genes:

Missing starling10x.revcomp BUSCOMPs

**5.10 Missing Core BUSCO genes**BUSCO ratings for Missing Core BUSCO genes:

Missing Core BUSCOsBUSCOMP ratings for **Missing** Core BUSCO genes:

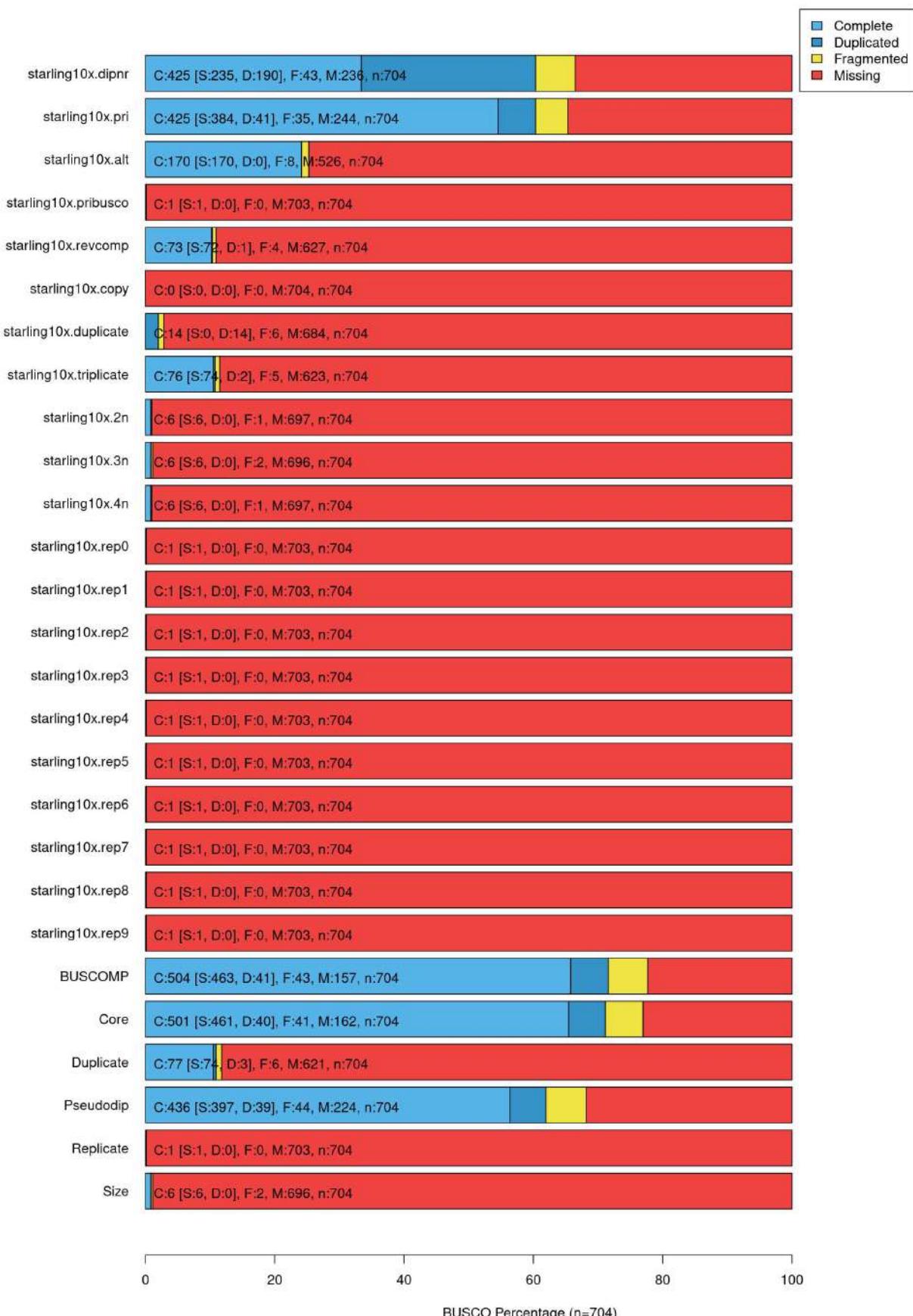
Missing Core BUSCOs: BUSCOMP ratingsBUSCOMP ratings for **Missing** Core BUSCOMP genes:

Missing Core BUSCOMPs

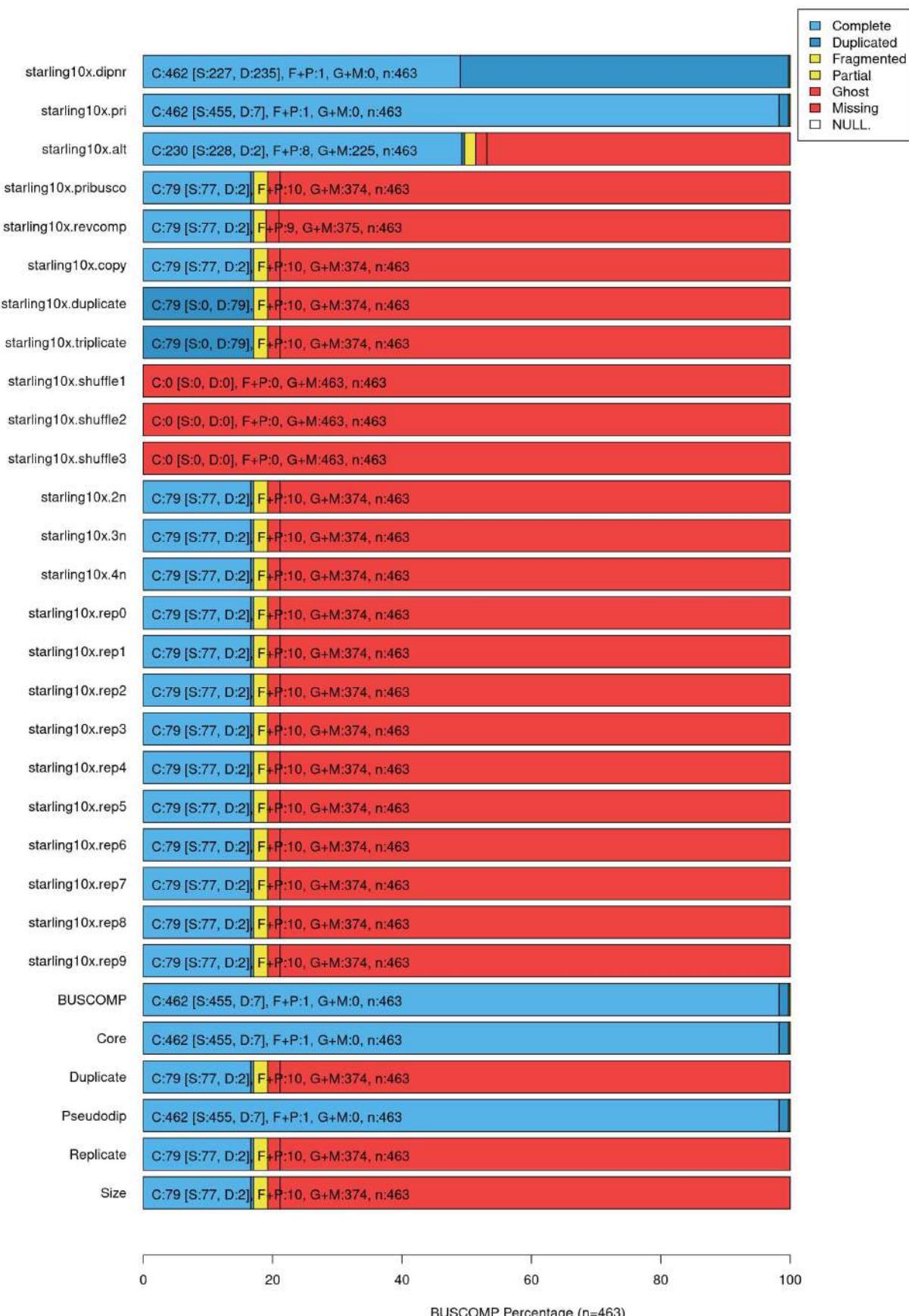
starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0

**5.11 Missing starling10x.copy BUSCO genes**

BUSCO ratings for Missing starling10x.copy BUSCO genes:

Missing starling10x.copy BUSCOsBUSCOMP ratings for **Missing** starling10x.copy BUSCO genes:

Missing starling10x.copy BUSCOs: BUSCOMP ratings

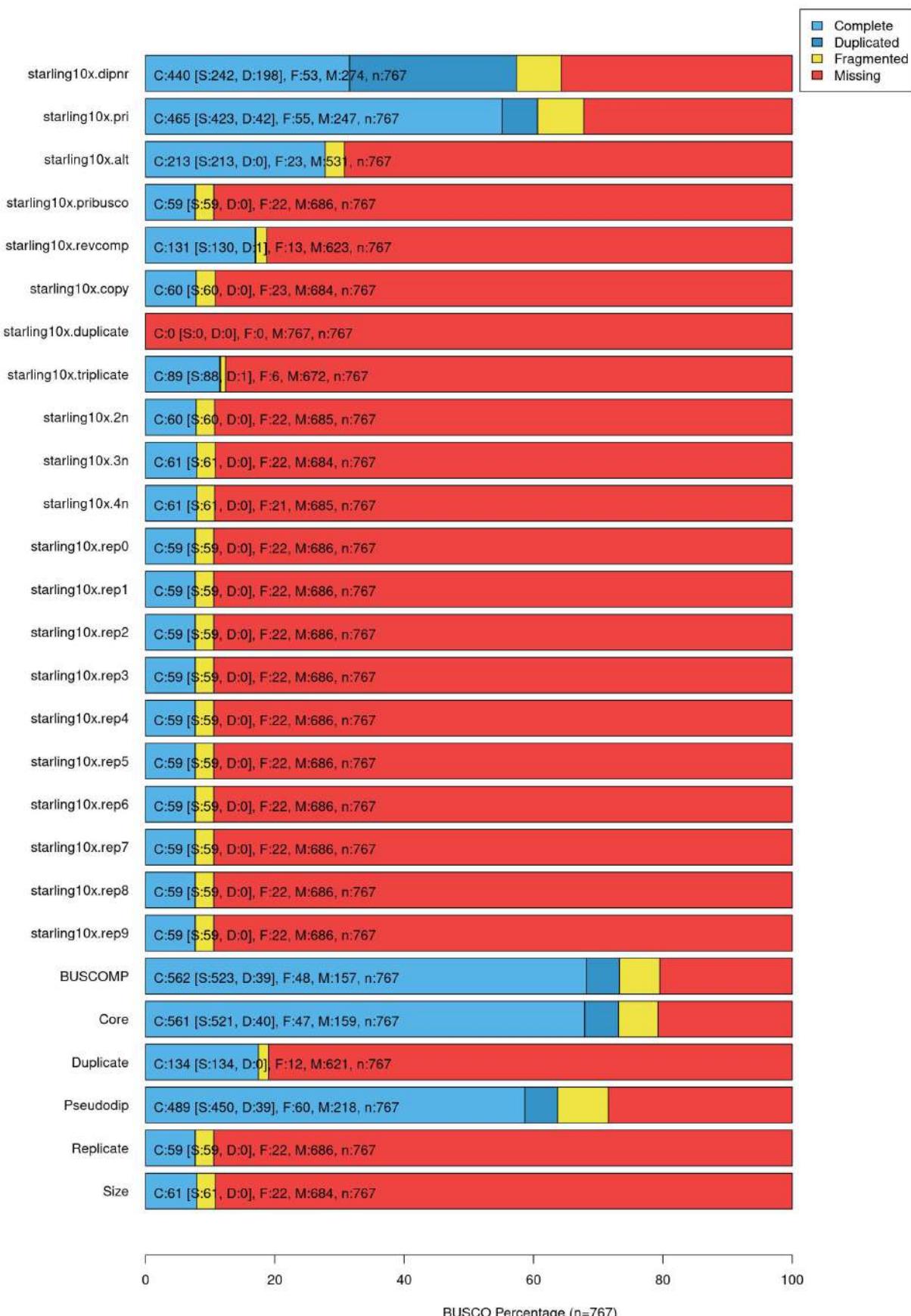


BUSCOMP ratings for [Missing] starling10x.copy BUSCOMP genes:

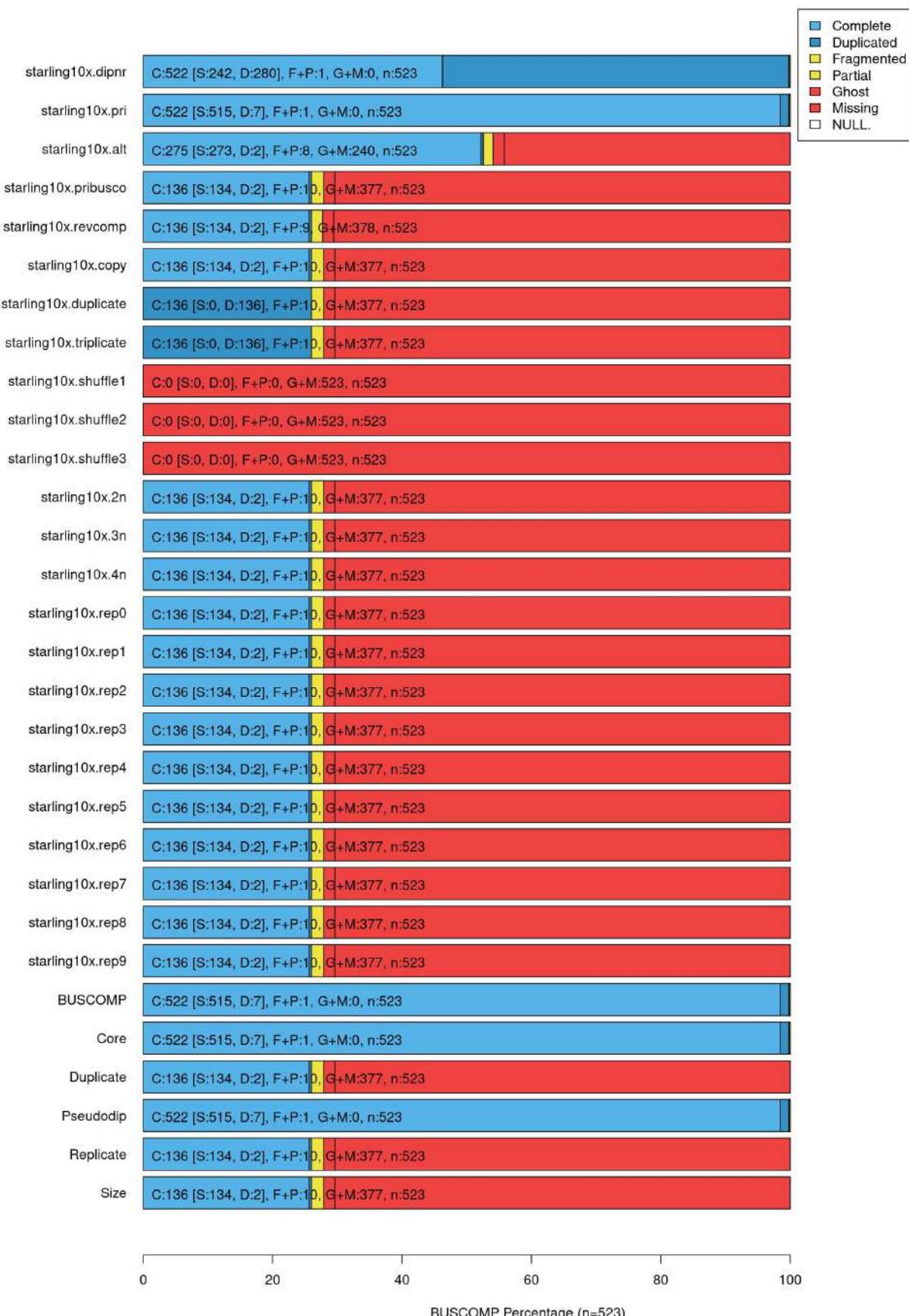
Missing starling10x.copy BUSCOMPs**5.12 Missing starling10x.duplicate BUSCO genes**

BUSCO ratings for Missing starling10x.duplicate BUSCO genes:

Missing starling10x.duplicate BUSCOs

BUSCOMP ratings for **Missing** starling10x.duplicate BUSCO genes:

Missing starling10x.duplicate BUSCOs: BUSCOMP ratings

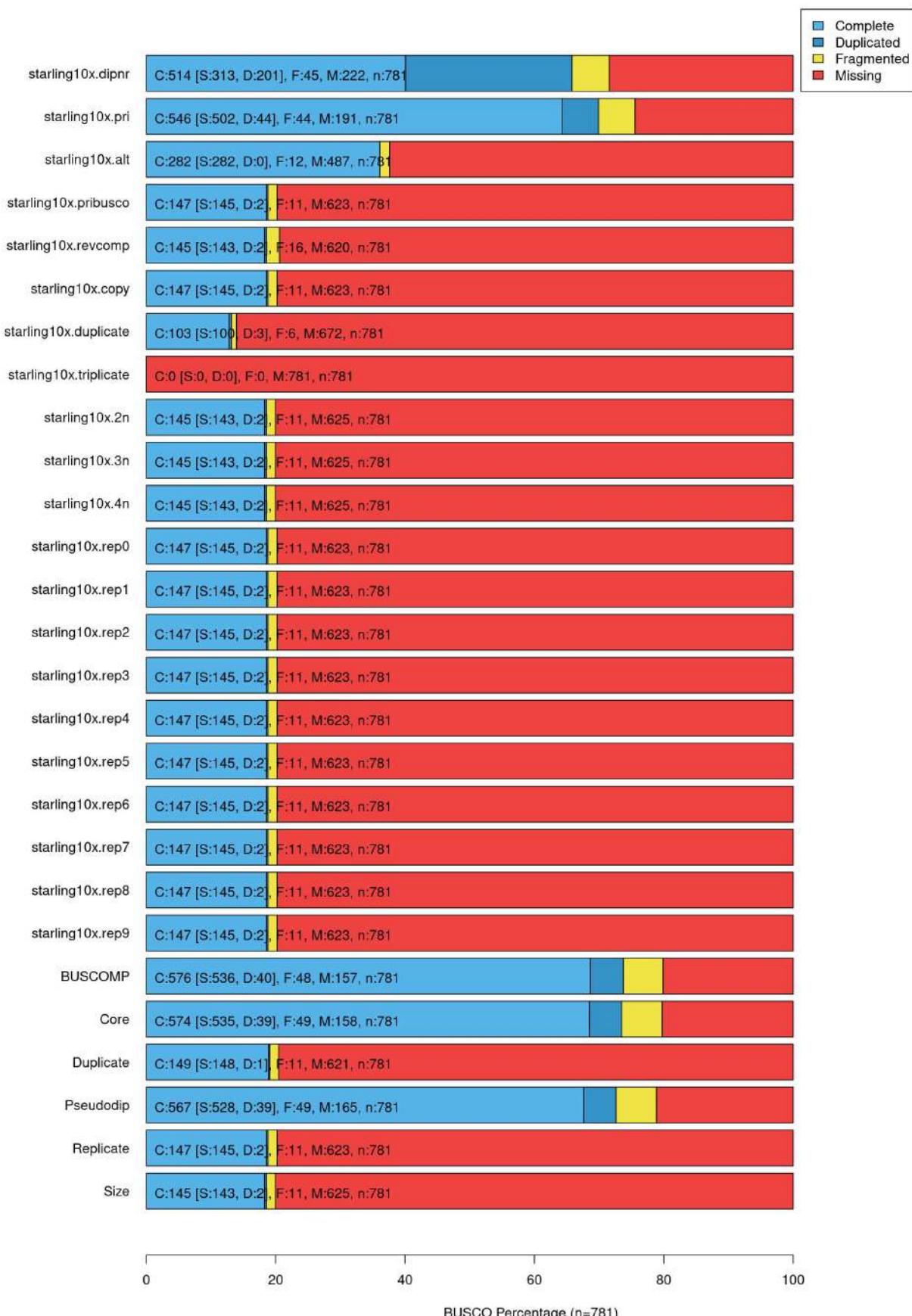


BUSCOMP ratings for [Missing] starling10x.duplicate BUSCOMP genes:

Missing starling10x.duplicate BUSCOMPs**5.13 Missing starling10x.triplicate BUSCO genes**

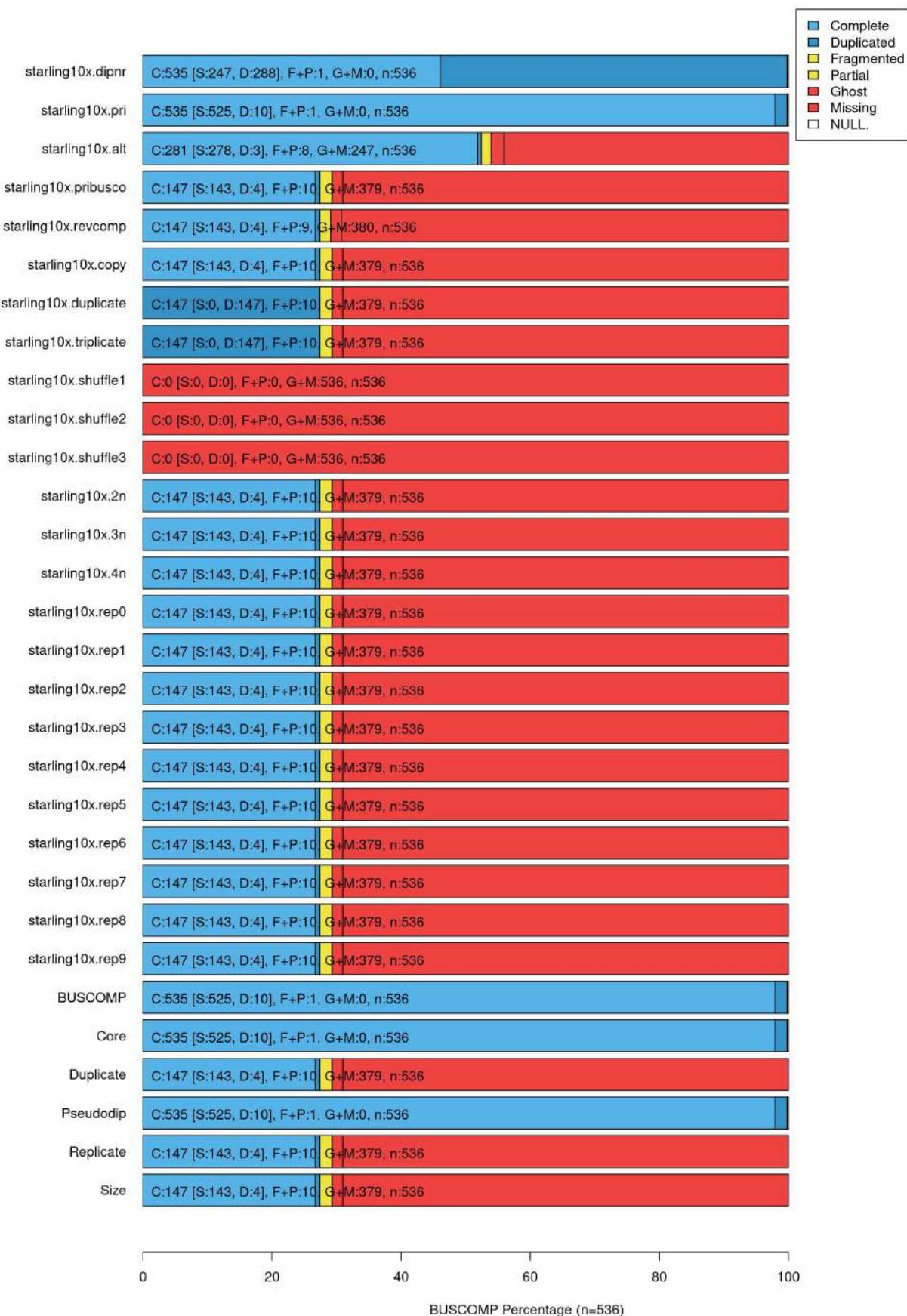
BUSCO ratings for Missing starling10x.triplicate BUSCO genes:

Missing starling10x.triplicate BUSCOs



BUSCOMP ratings for [Missing] starling10x.triplicate BUSCO genes:

Missing starling10x.triplicate BUSCOs: BUSCOMP ratings



BUSCOMP ratings for [Missing] starling10x.triplicate BUSCOMP genes:

Missing starling10x.triplicate BUSCOMPs**5.14 Missing Duplicate BUSCO genes**BUSCO ratings for Missing Duplicate BUSCO genes:

Missing Duplicate BUSCOs

BUSCOMP ratings for **[Missing]** Duplicate BUSCO genes:

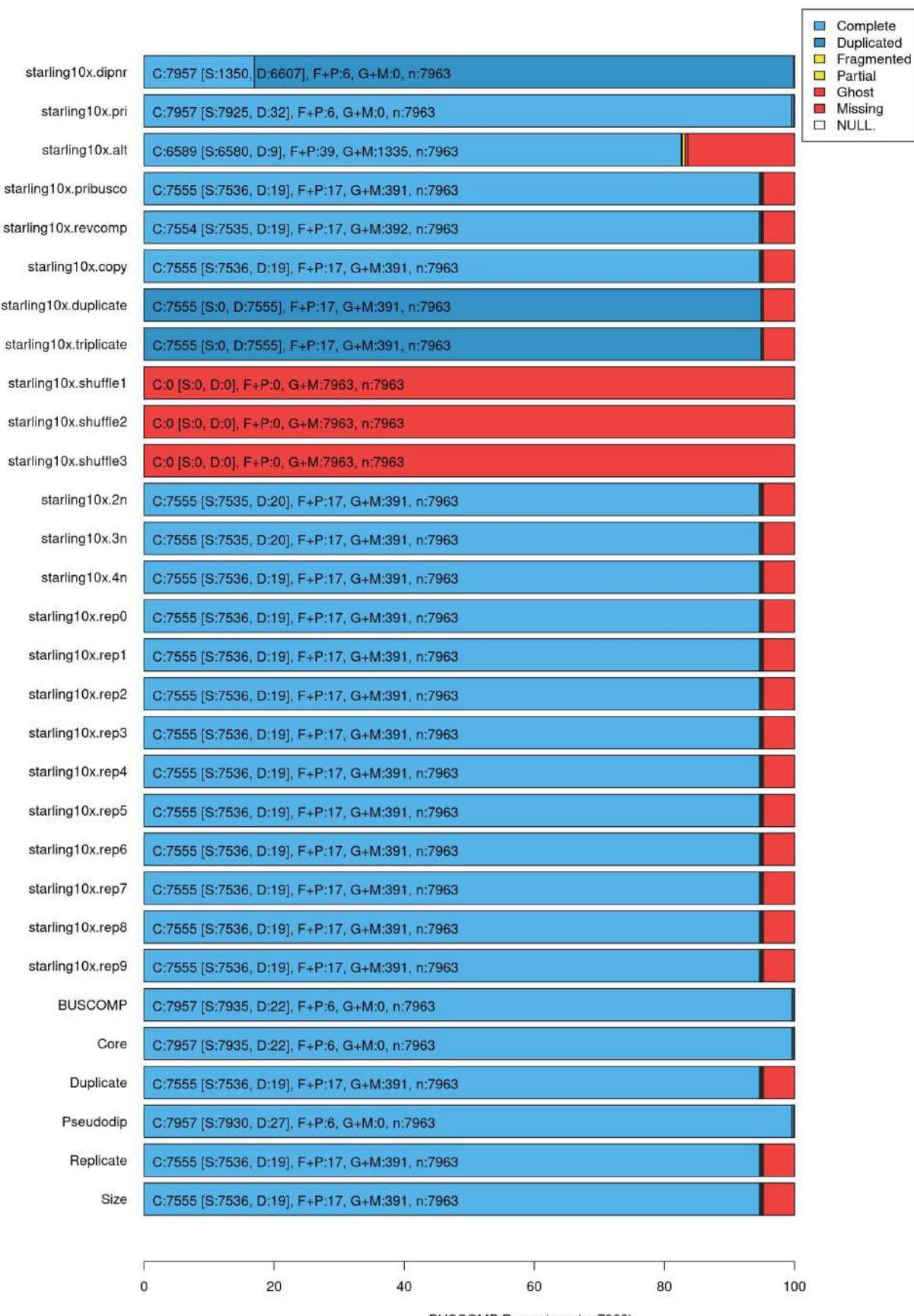
Missing Duplicate BUSCOs: BUSCOMP ratings



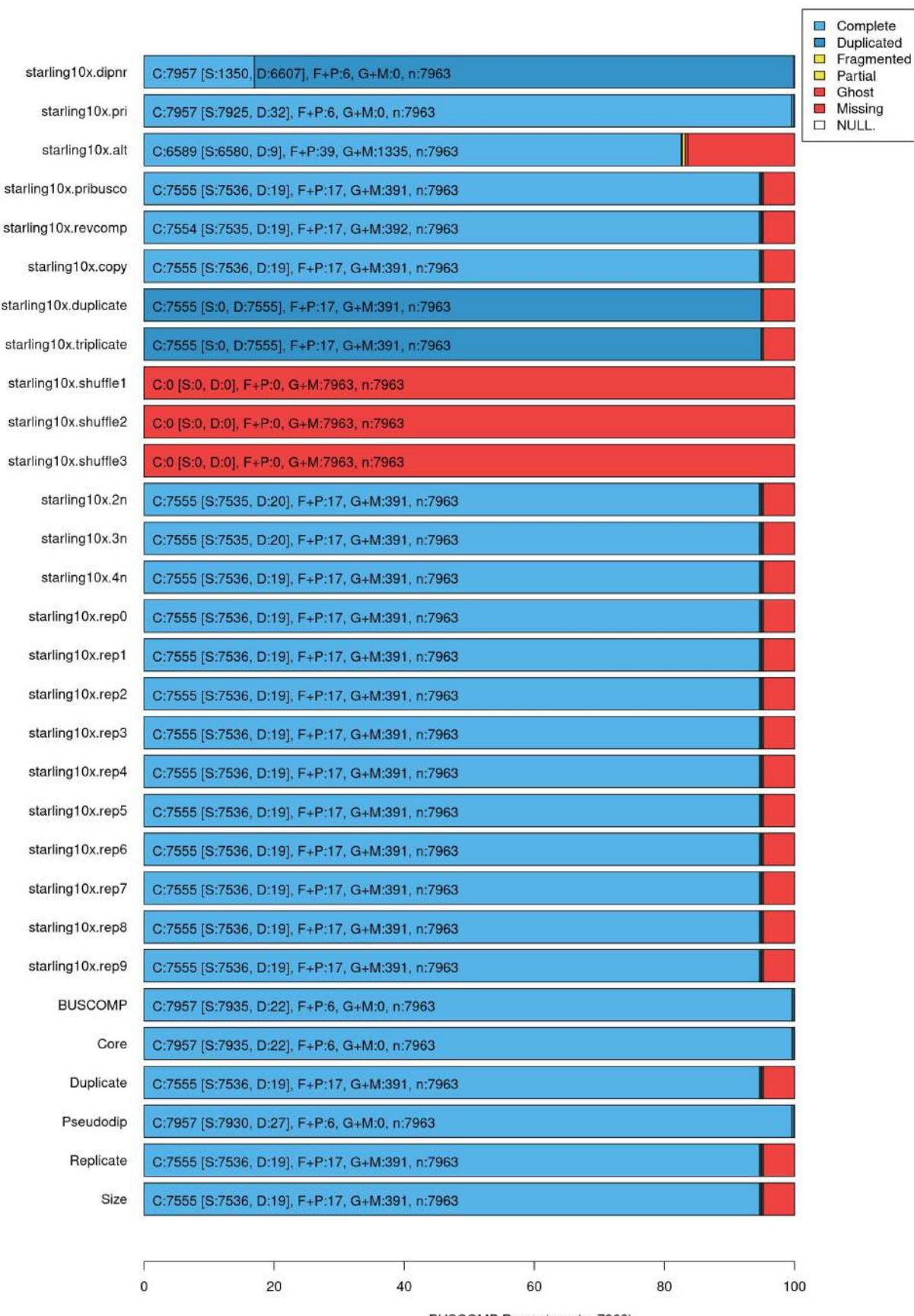
BUSCOMP ratings for [Missing] Duplicate BUSCOMP genes:

Missing Duplicate BUSCOMPs**5.15 Missing starling10x.shuffle1 BUSCO genes**

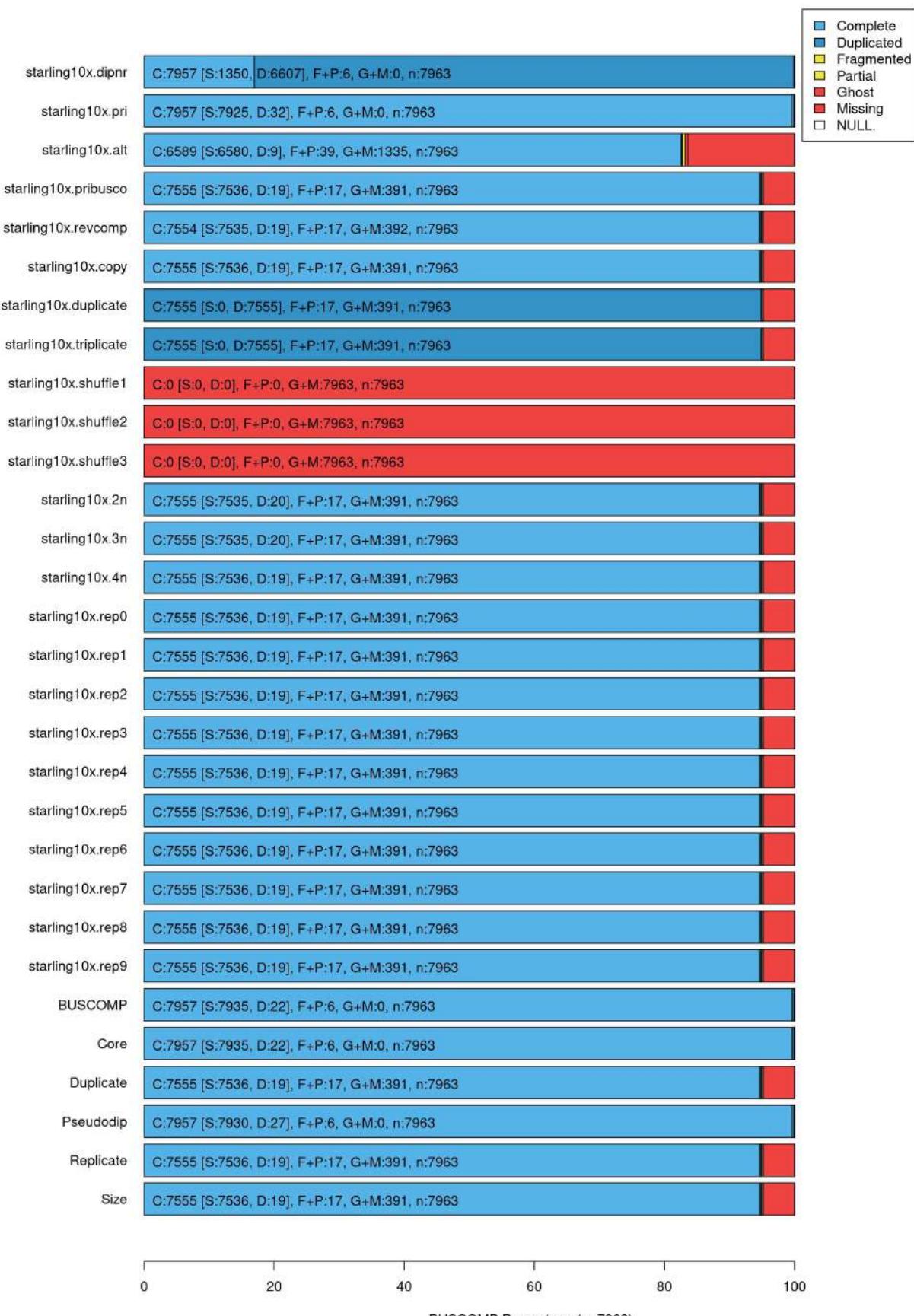
BUSCOMP ratings for **Missing** starling10x.shuffle1 BUSCO genes:

Missing starling10x.shuffle1 BUSCOMPs**5.16 Missing starling10x.shuffle2 BUSCO genes**

BUSCOMP ratings for Missing starling10x.shuffle2 BUSCOMP genes:

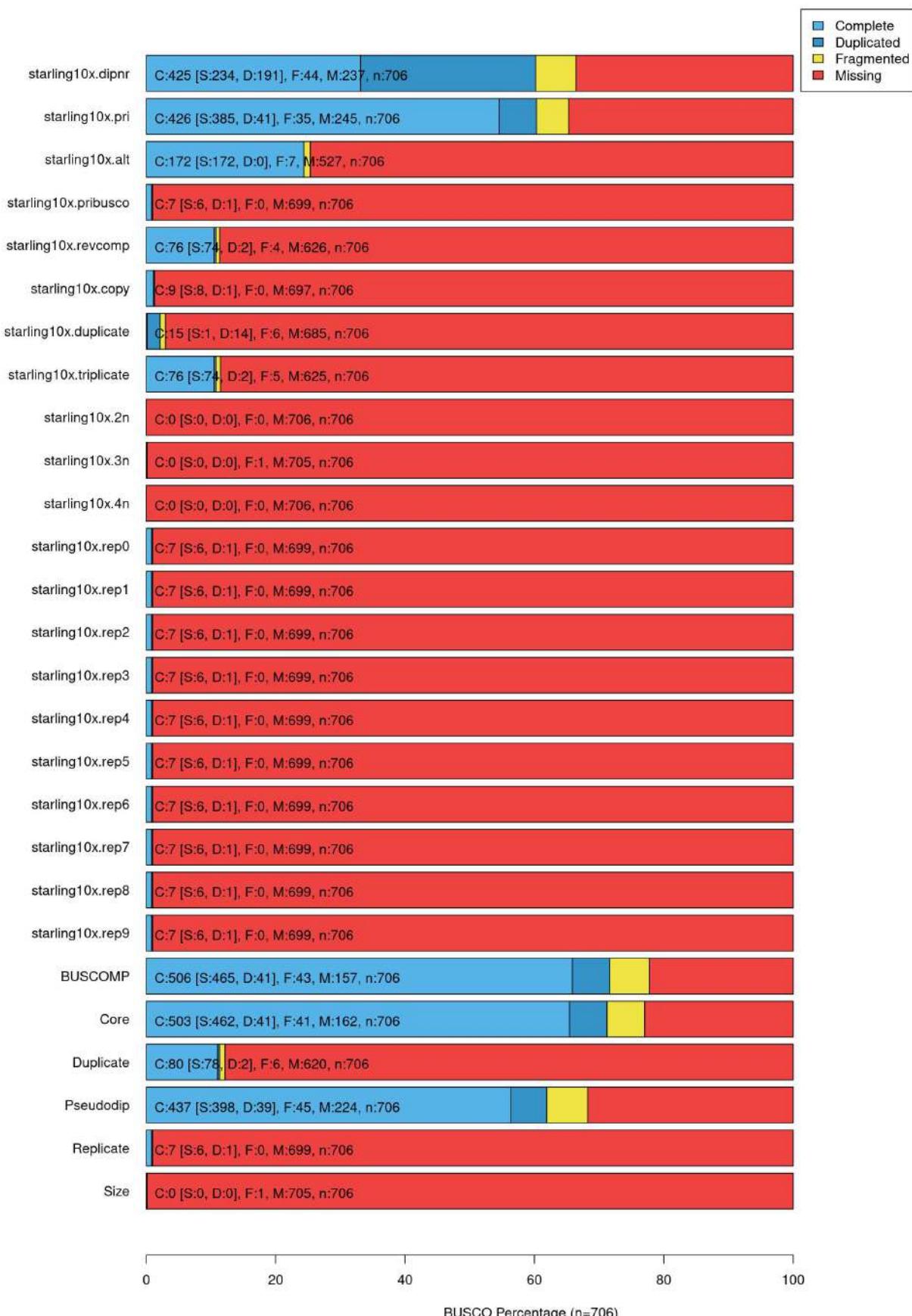
Missing starling10x.shuffle2 BUSCOMPs**5.17 Missing starling10x.shuffle3 BUSCO genes**

BUSCOMP ratings for Missing starling10x.shuffle3 BUSCO genes:

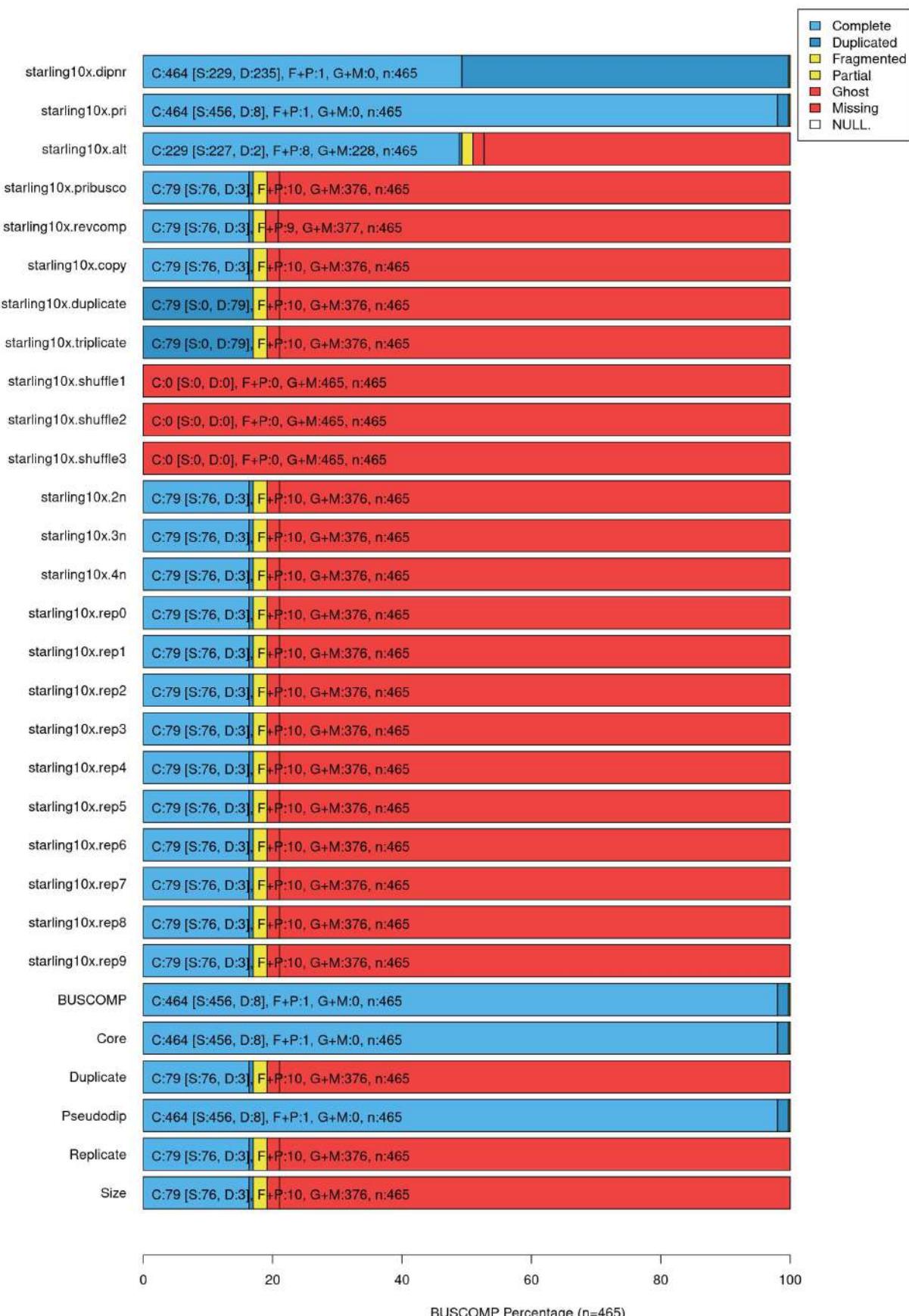
Missing starling10x.shuffle3 BUSCOMPs**5.18 Missing starling10x.2n BUSCO genes**

BUSCO ratings for Missing starling10x.2n BUSCO genes:

Missing starling10x.2n BUSCOs

BUSCOMP ratings for **Missing** starling10x.2n BUSCO genes:

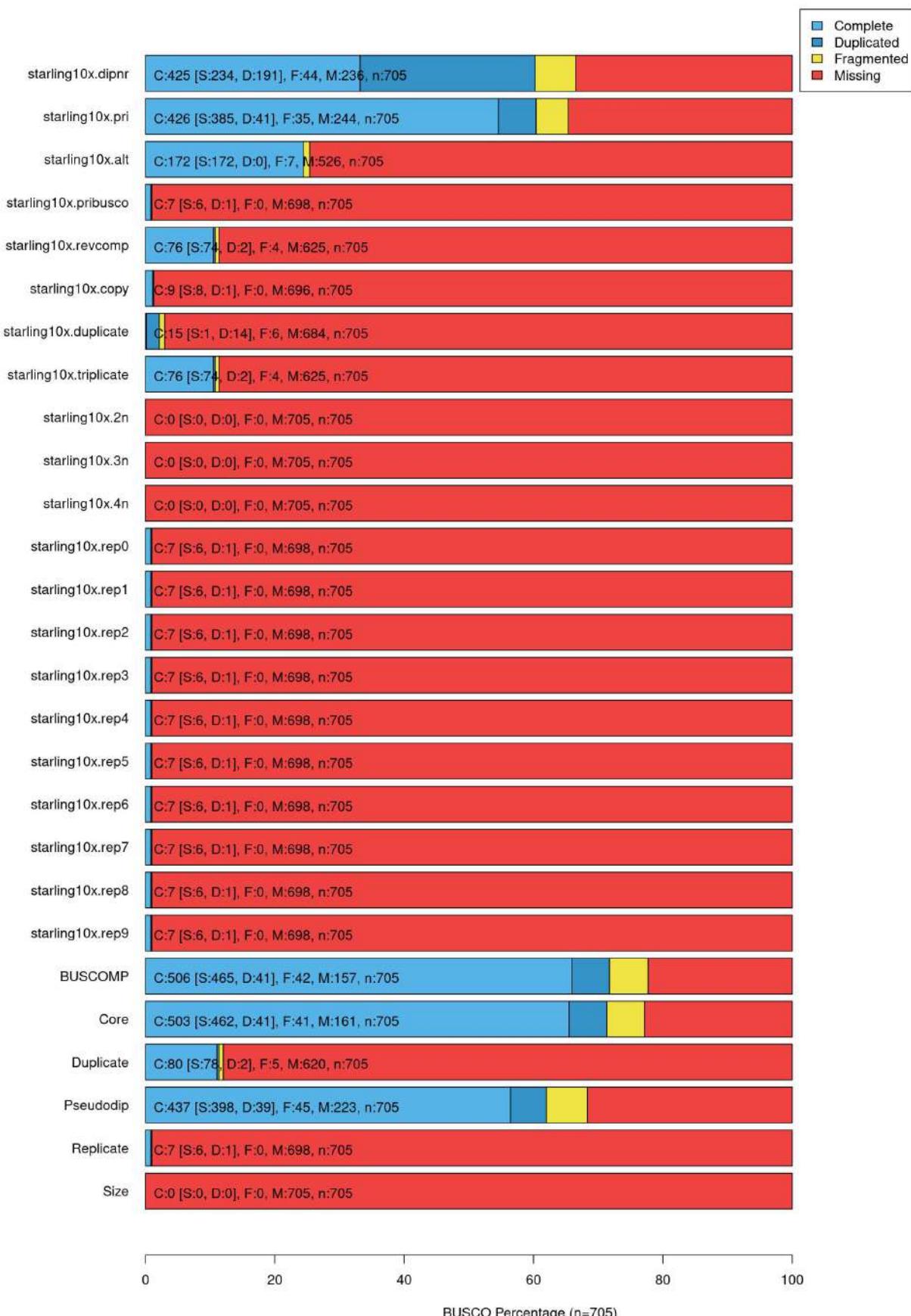
Missing starling10x.2n BUSCOs: BUSCOMP ratings



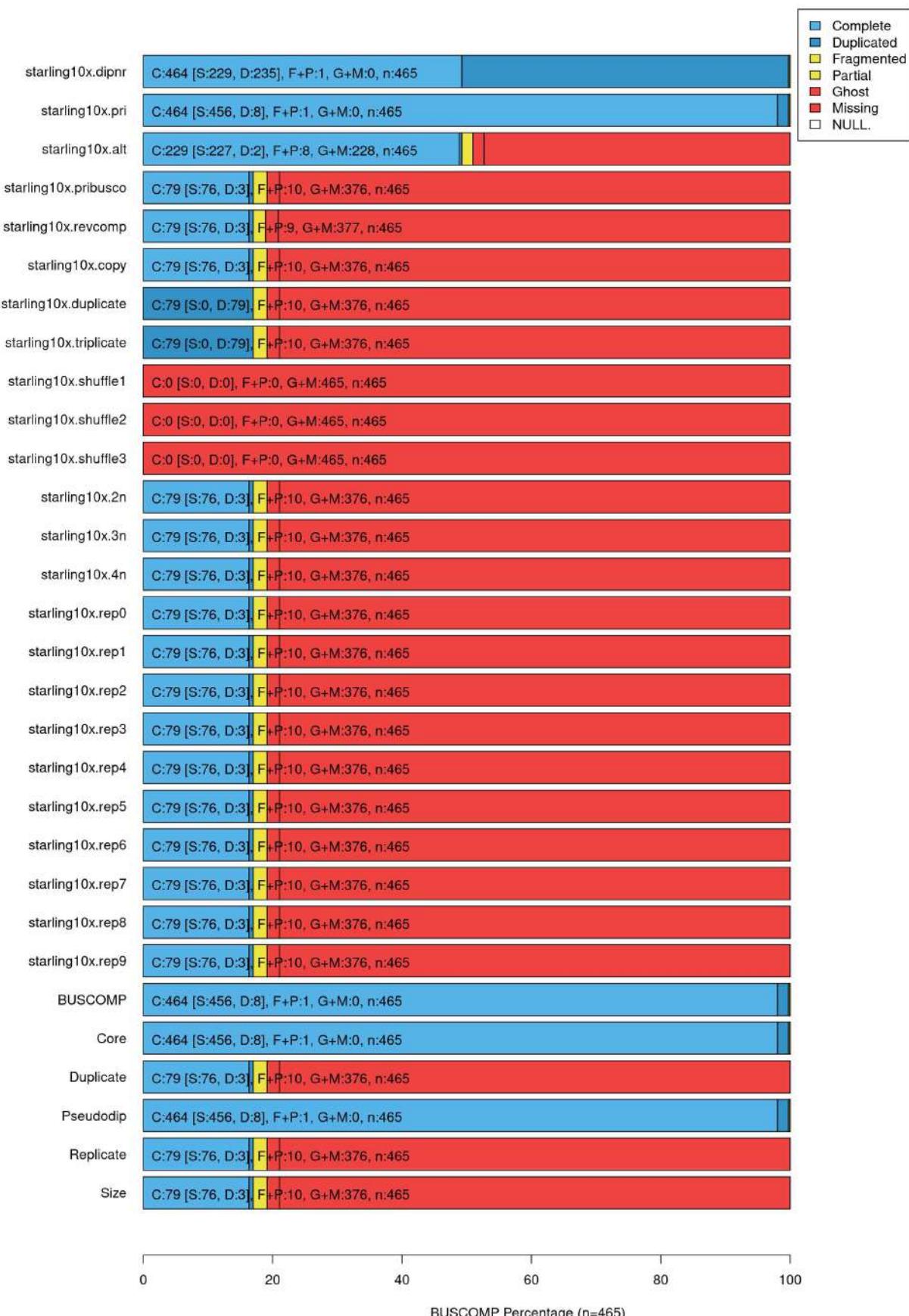
BUSCOMP ratings for [Missing] starling10x.2n BUSCO genes:

Missing starling10x.2n BUSCOMPs**5.19 Missing starling10x.3n BUSCO genes**BUSCO ratings for Missing starling10x.3n BUSCO genes:

Missing starling10x.3n BUSCOs

BUSCOMP ratings for **Missing** starling10x.3n BUSCO genes:

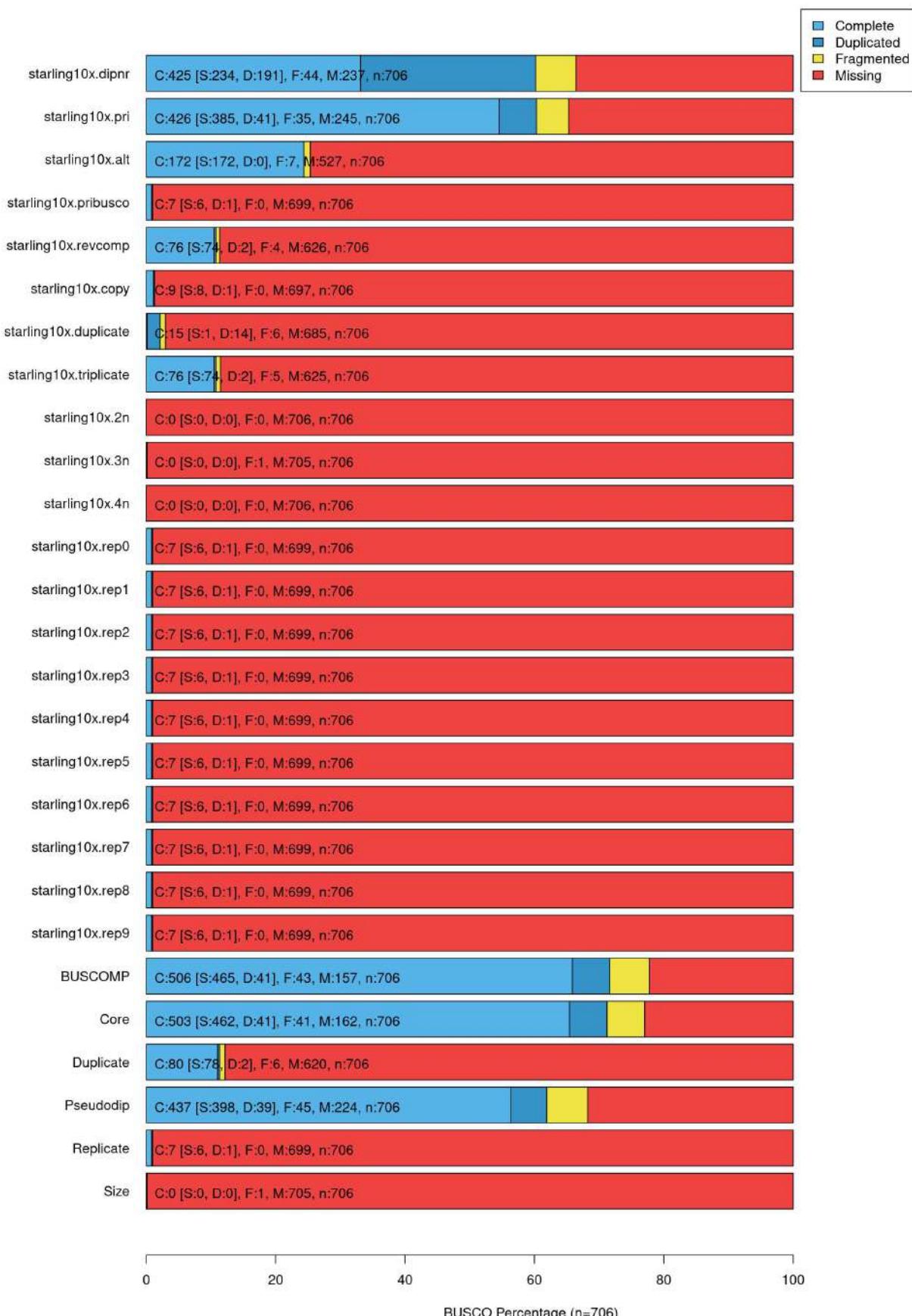
Missing starling10x.3n BUSCOs: BUSCOMP ratings



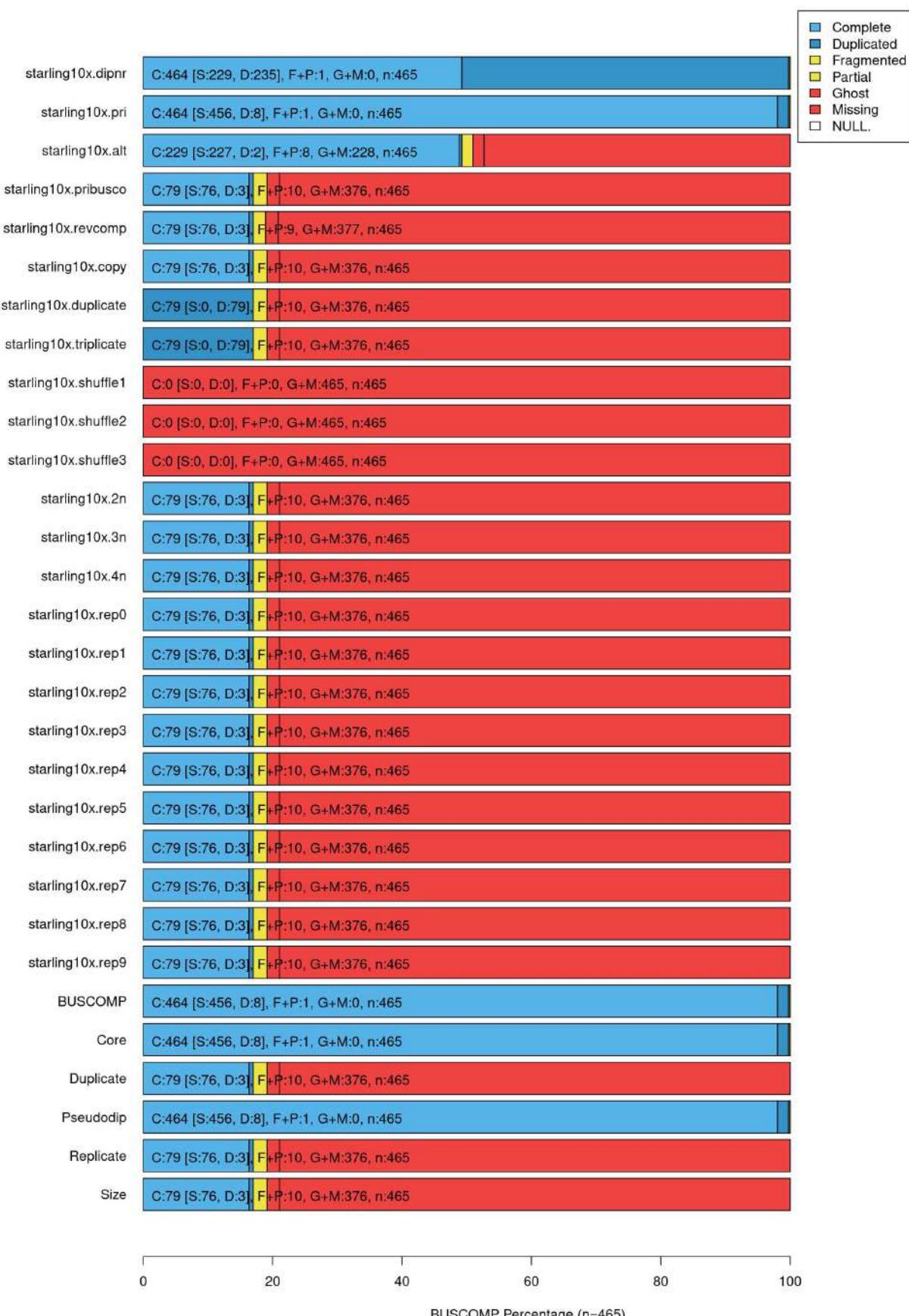
BUSCOMP ratings for [Missing] starling10x.3n BUSCOMP genes:

Missing starling10x.3n BUSCOMPs**5.20 Missing starling10x.4n BUSCO genes**BUSCO ratings for Missing starling10x.4n BUSCO genes:

Missing starling10x.4n BUSCOs

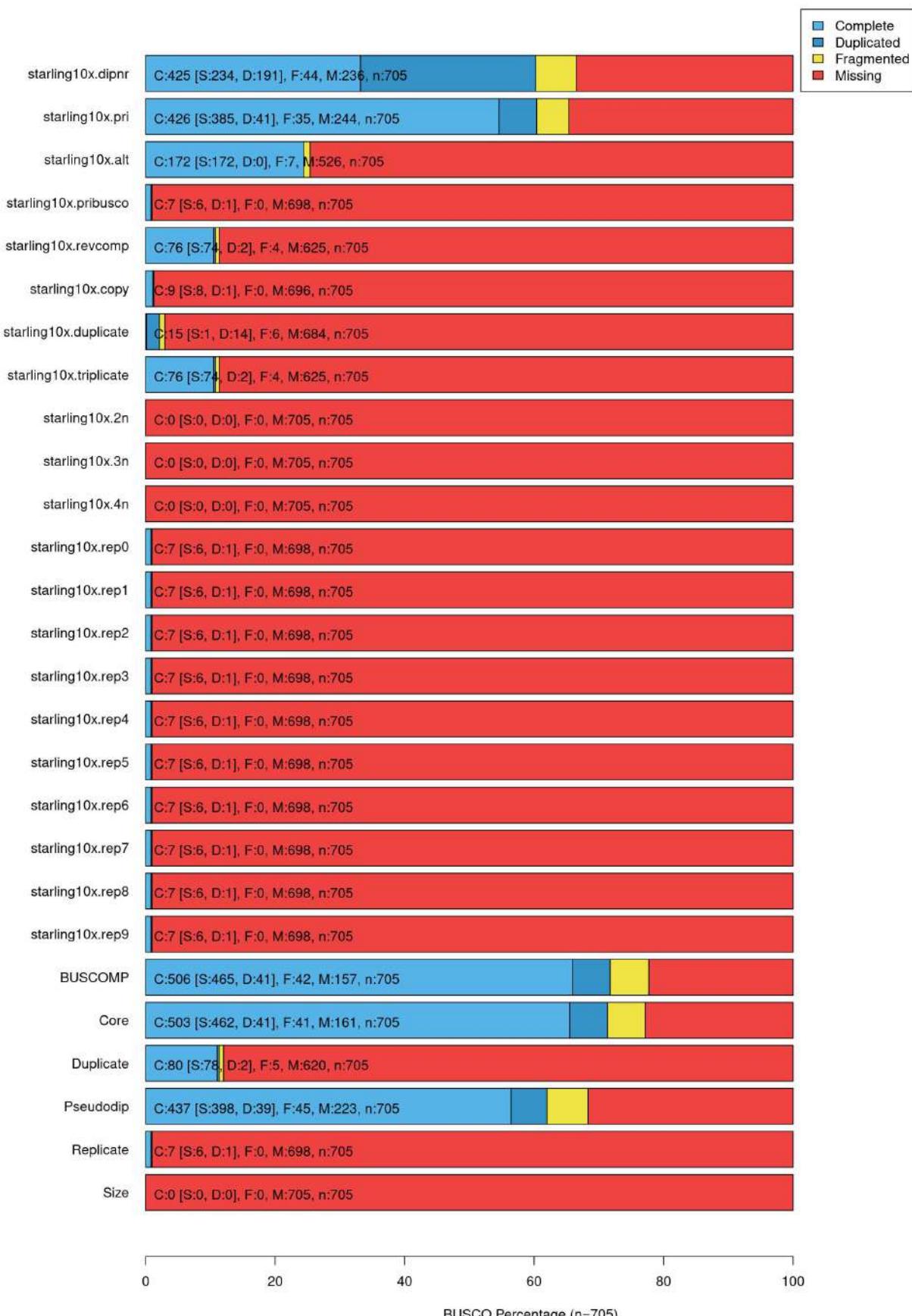
BUSCOMP ratings for **Missing** starling10x.4n BUSCO genes:

Missing starling10x.4n BUSCOs: BUSCOMP ratings

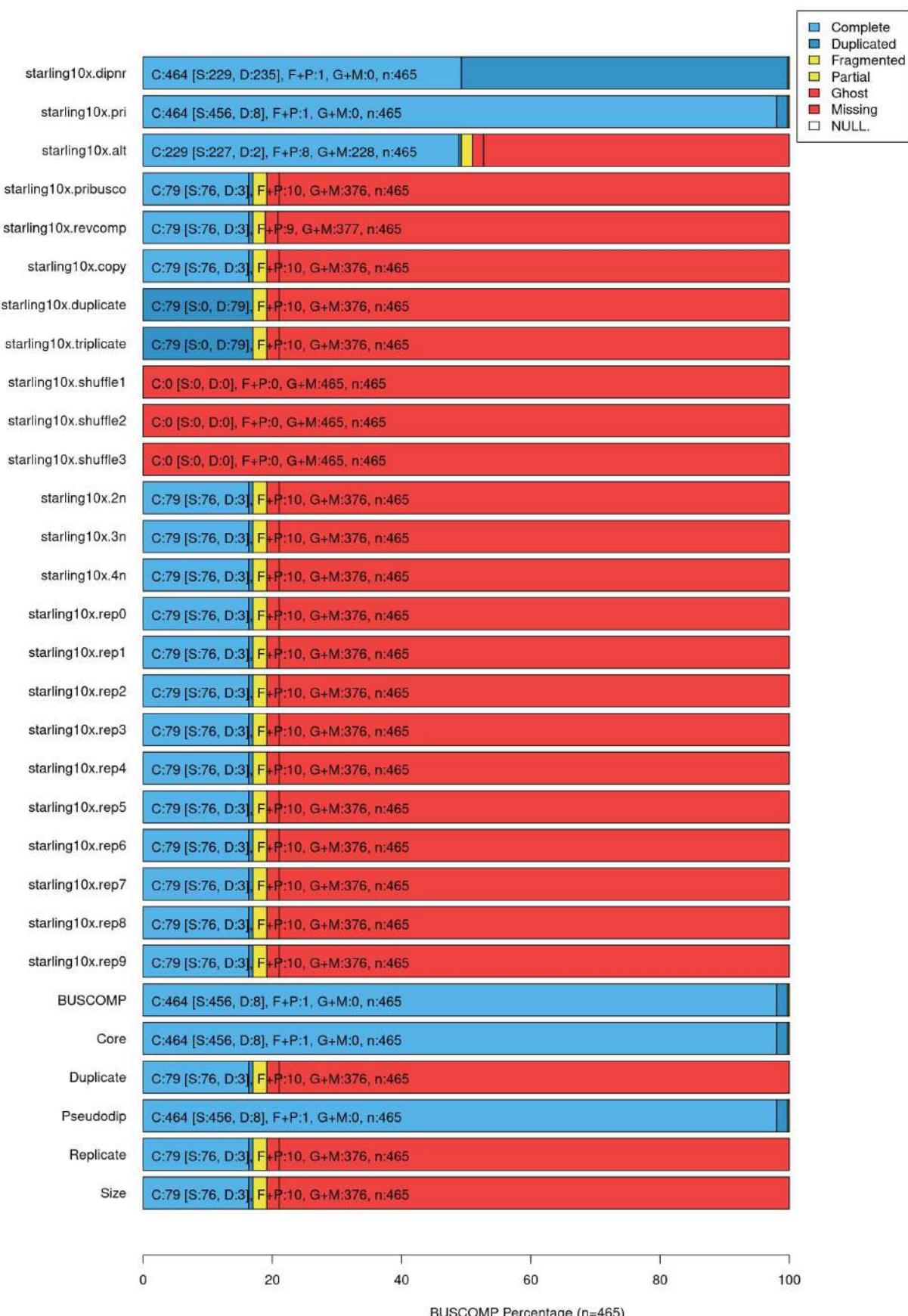


BUSCOMP ratings for [Missing] starling10x.4n BUSCOMP genes:

Missing starling10x.4n BUSCOMPs**5.21 Missing Size BUSCO genes**BUSCO ratings for Missing Size BUSCO genes:

Missing Size BUSCOsBUSCOMP ratings for **Missing** Size BUSCO genes:

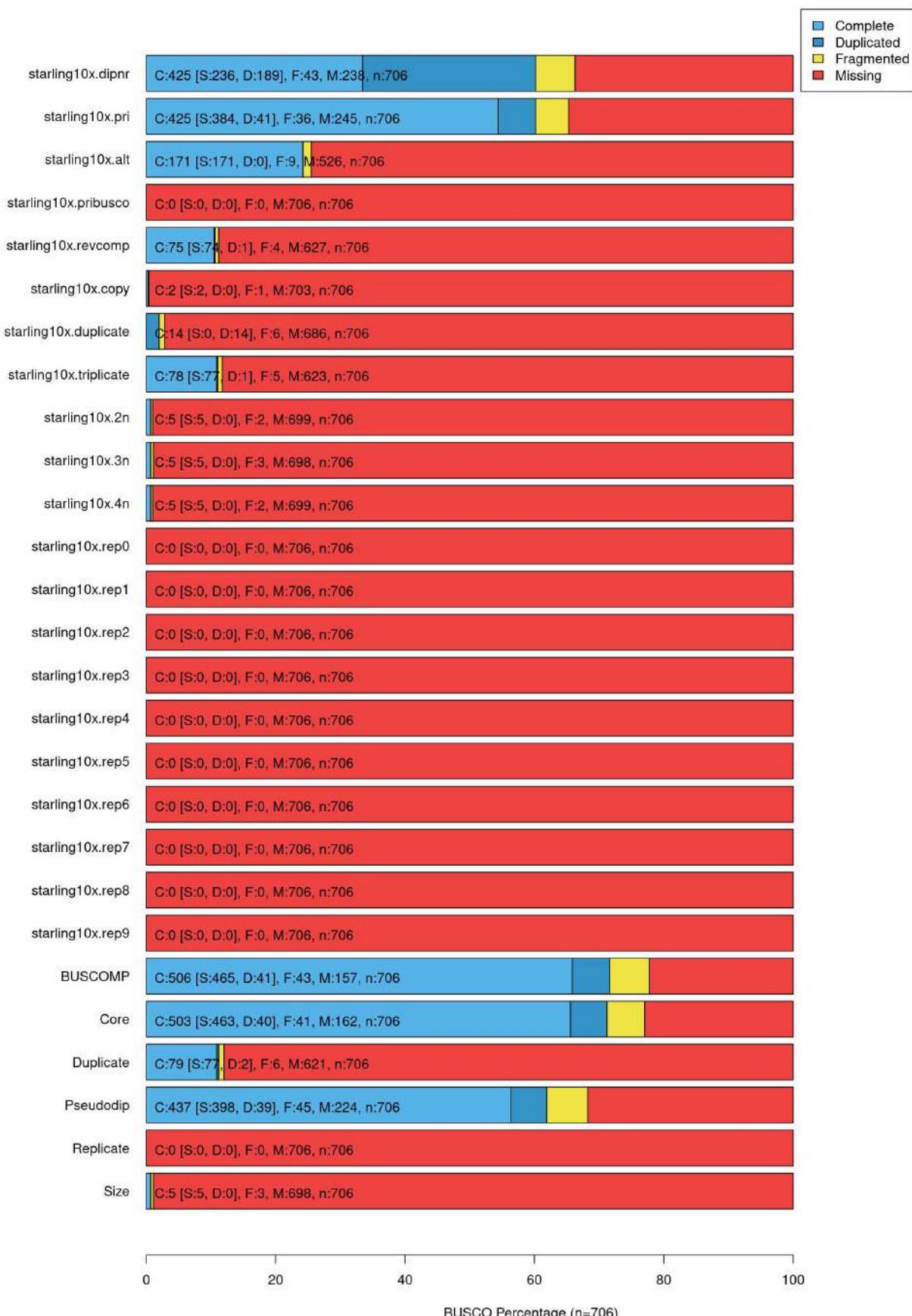
Missing Size BUSCOs: BUSCOMP ratings

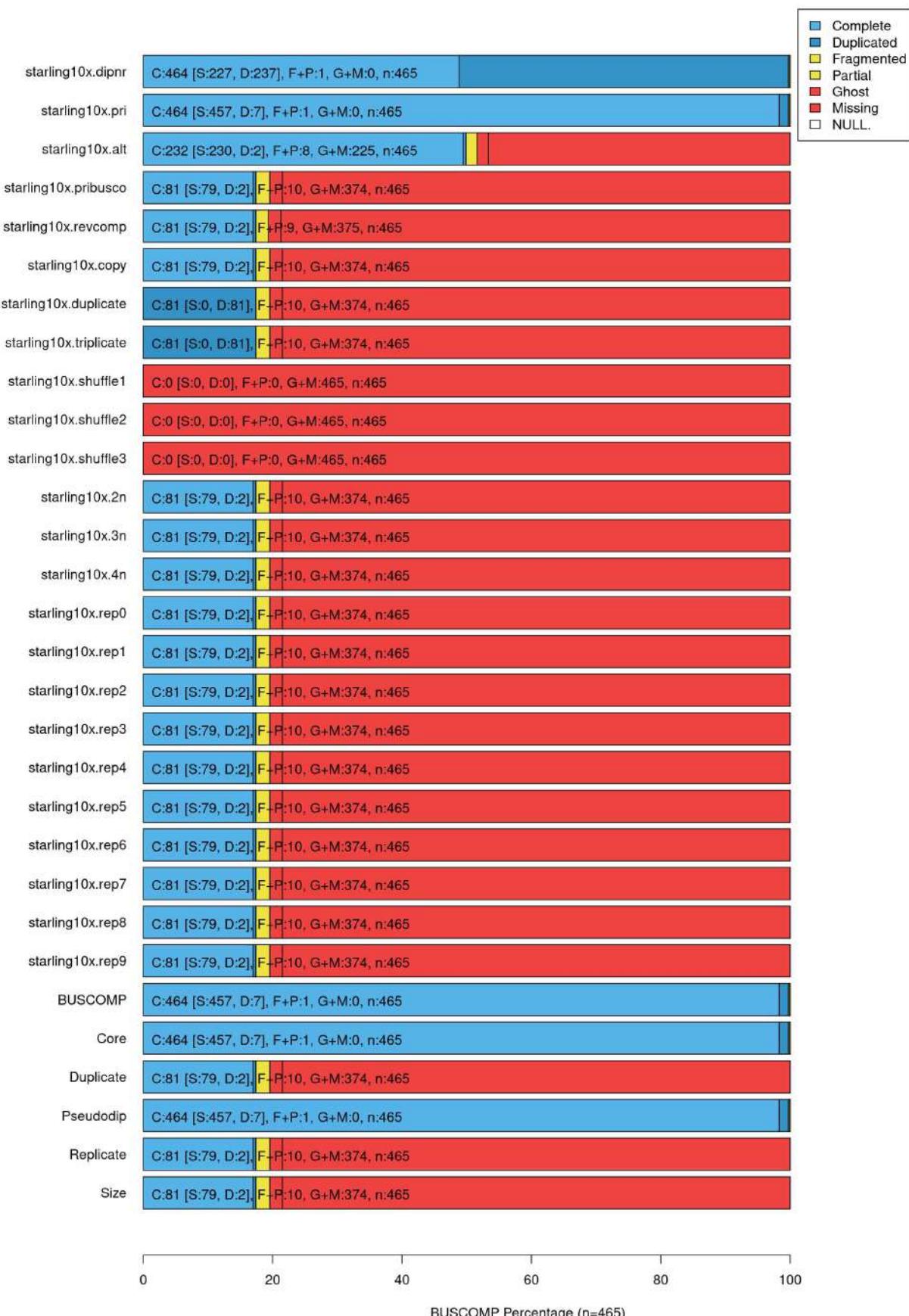
BUSCOMP ratings for **Missing** Size BUSCOMP genes:

Missing Size BUSCOMPs

**5.22 Missing starling10x.rep0 BUSCO genes**BUSCO ratings for Missing starling10x.rep0 BUSCO genes:

Missing starling10x.rep0 BUSCOs

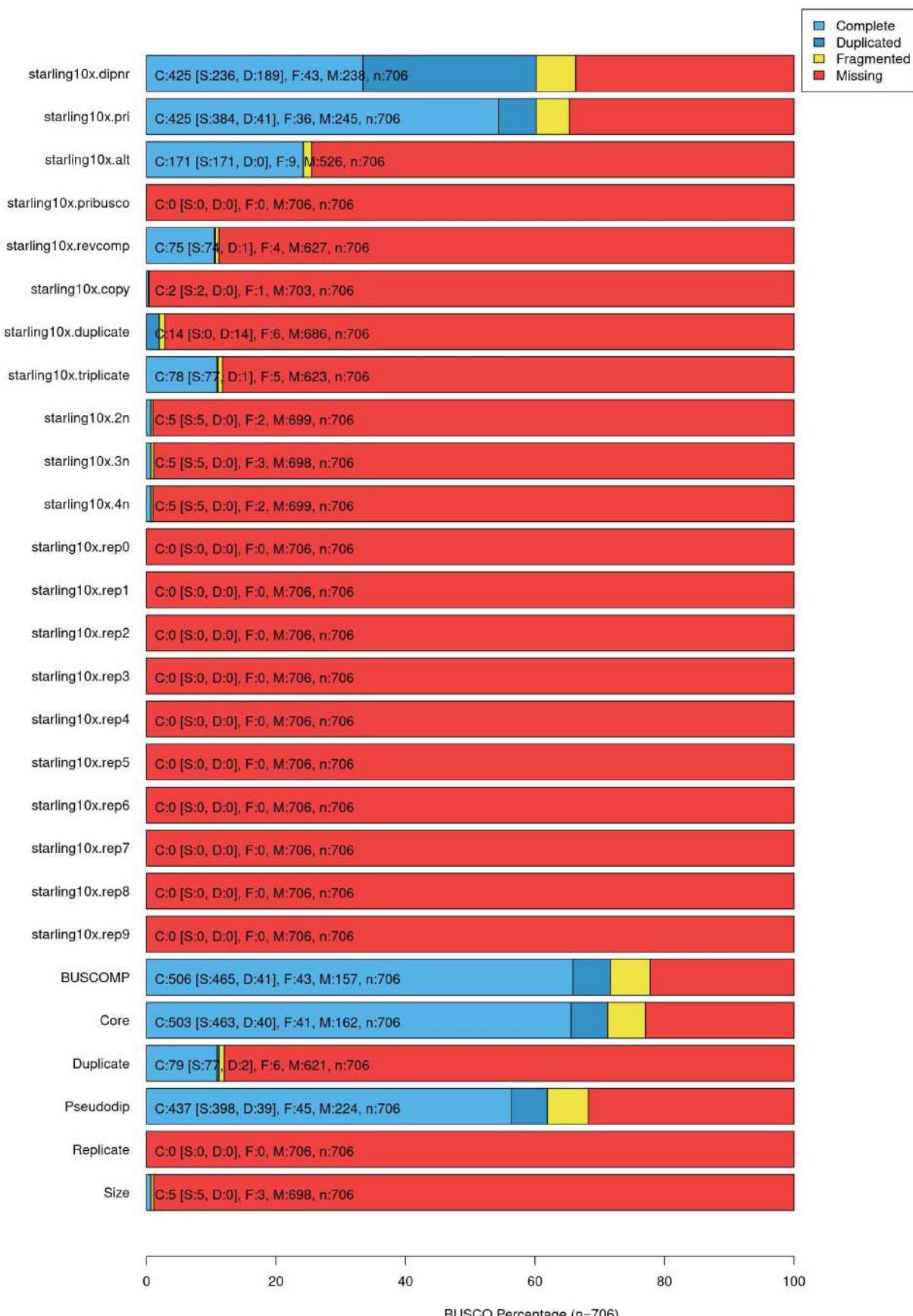
BUSCOMP ratings for **Missing** starling10x.rep0 BUSCO genes:

Missing starling10x.rep0 BUSCOs: BUSCOMP ratingsBUSCOMP ratings for **Missing** starling10x.rep0 BUSCOMP genes:

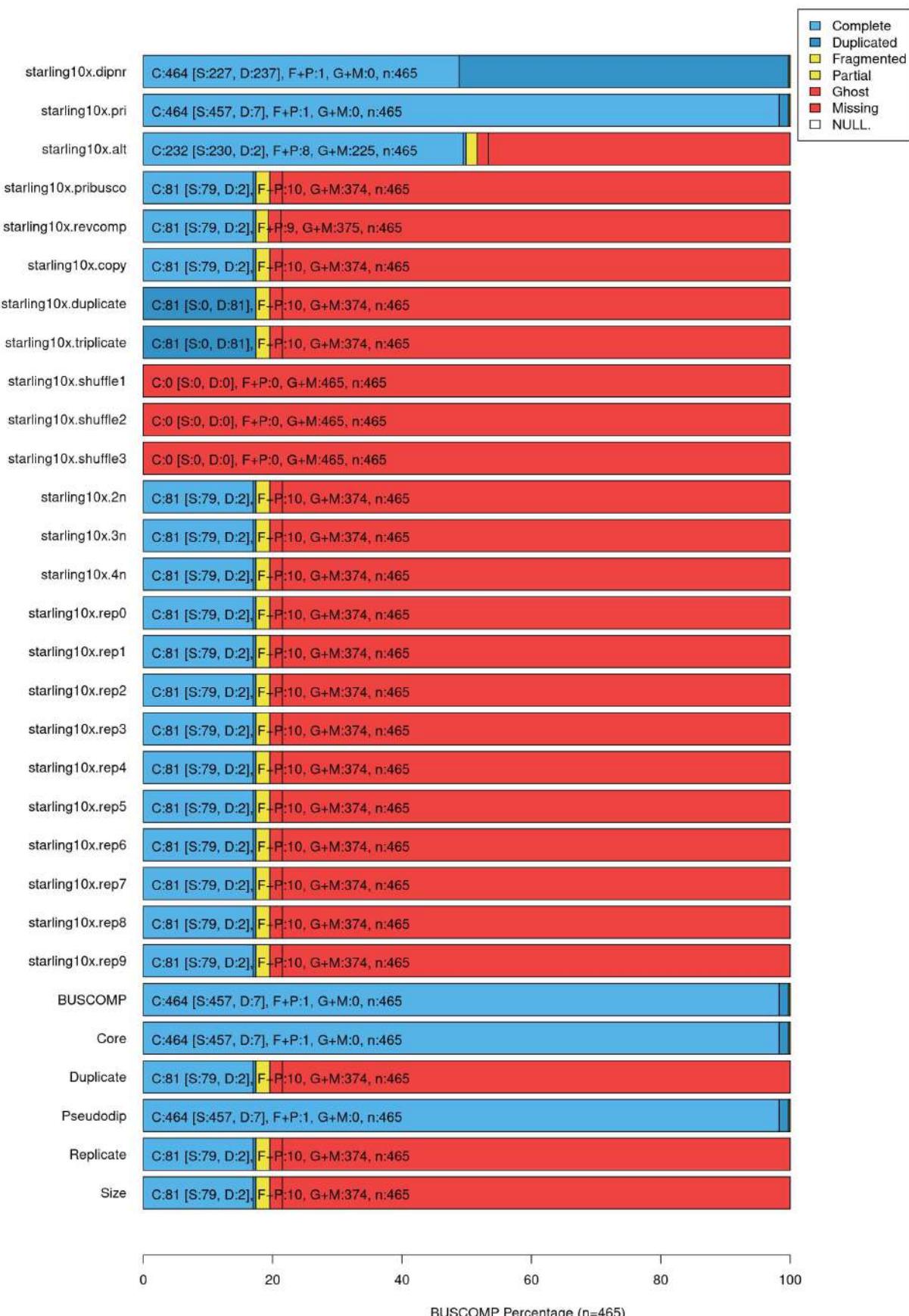
Missing starling10x.rep0 BUSCOMPs**5.23 Missing starling10x.rep1 BUSCO genes**

BUSCO ratings for Missing starling10x.rep1 BUSCO genes:

Missing starling10x.rep1 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep1 BUSCO genes:

Missing starling10x.rep1 BUSCOs: BUSCOMP ratings

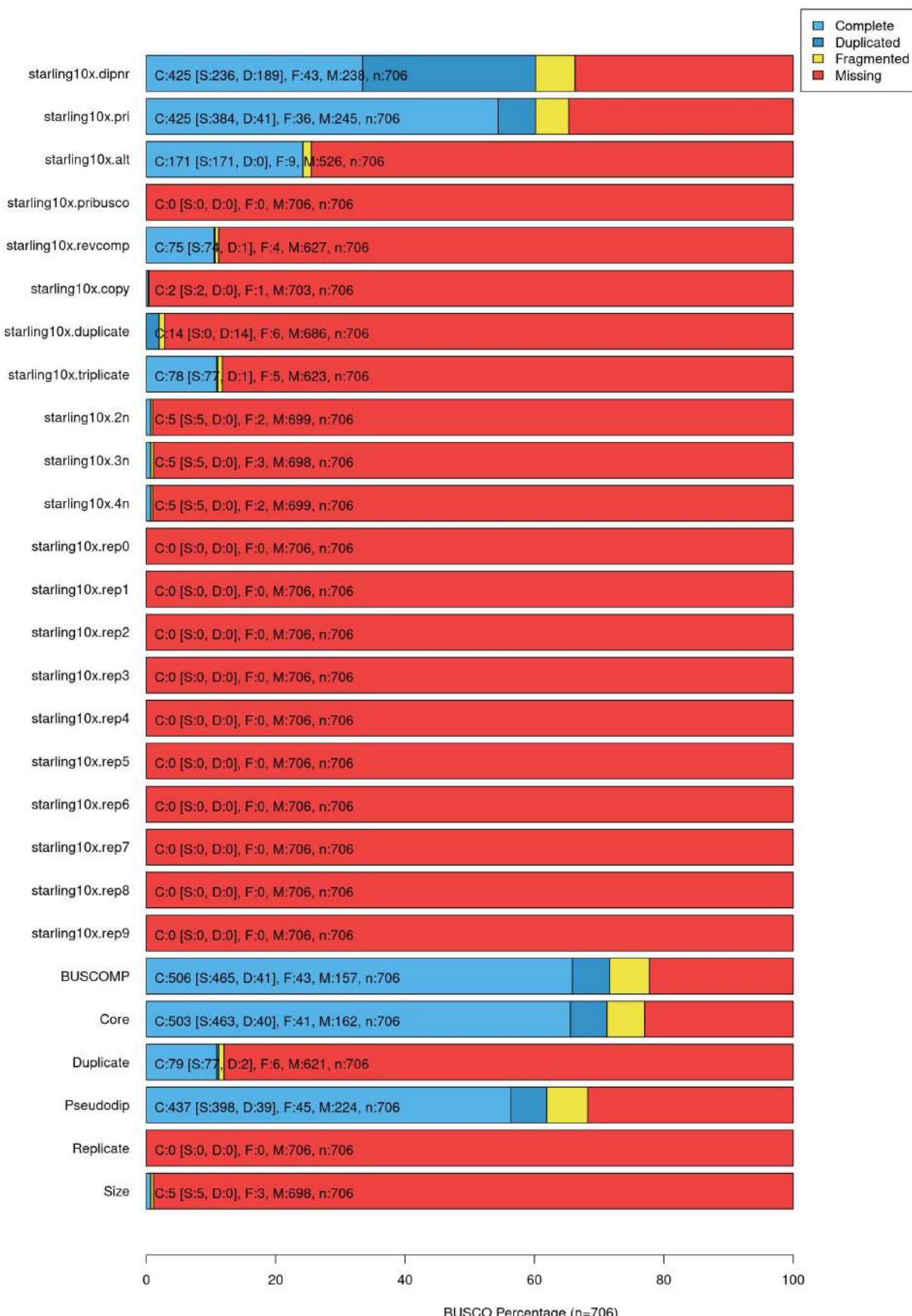


BUSCOMP ratings for [Missing] starling10x.rep1 BUSCOMP genes:

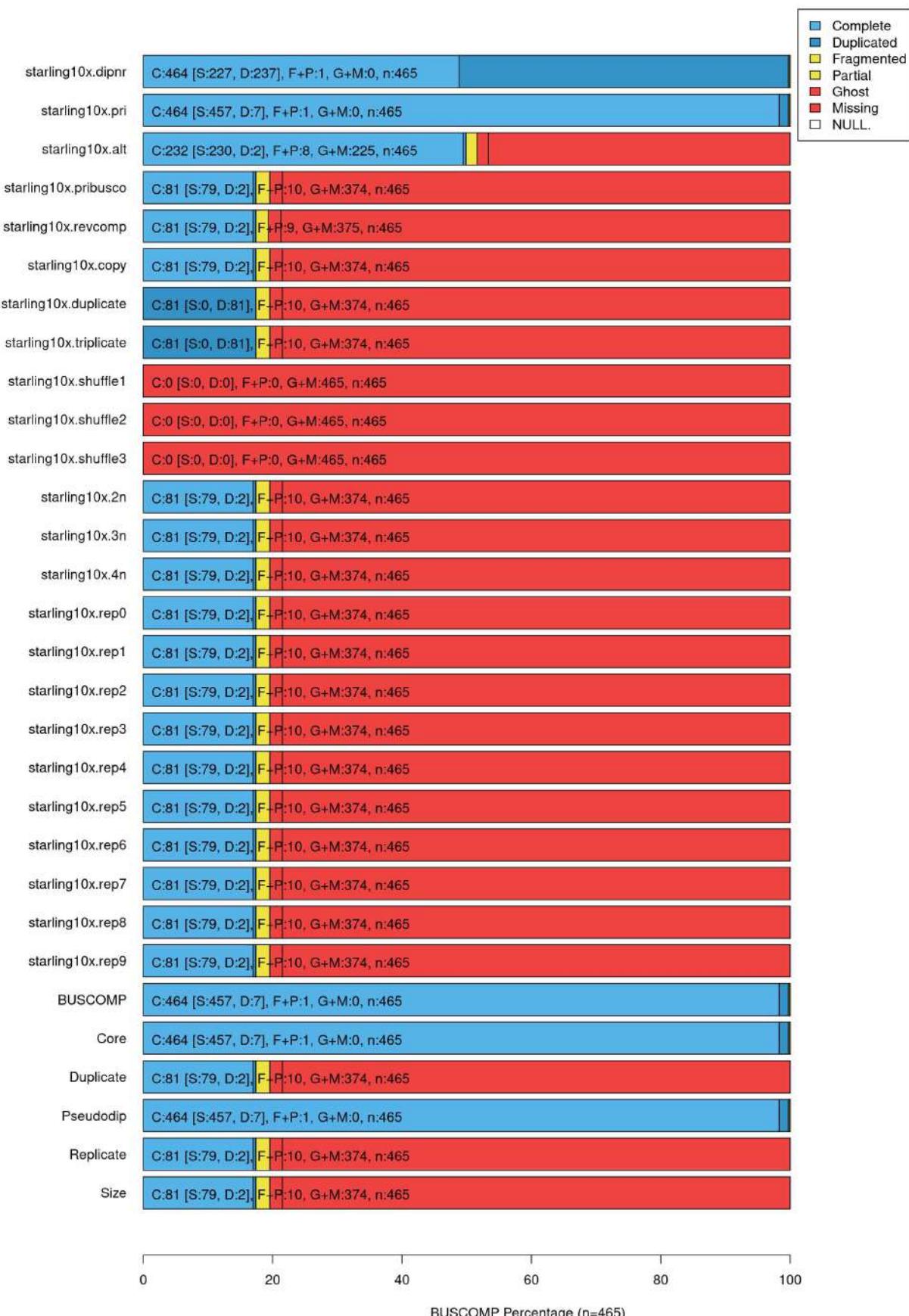
Missing starling10x.rep1 BUSCOMPs**5.24 Missing starling10x.rep2 BUSCO genes**

BUSCO ratings for Missing starling10x.rep2 BUSCO genes:

Missing starling10x.rep2 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep2 BUSCO genes:

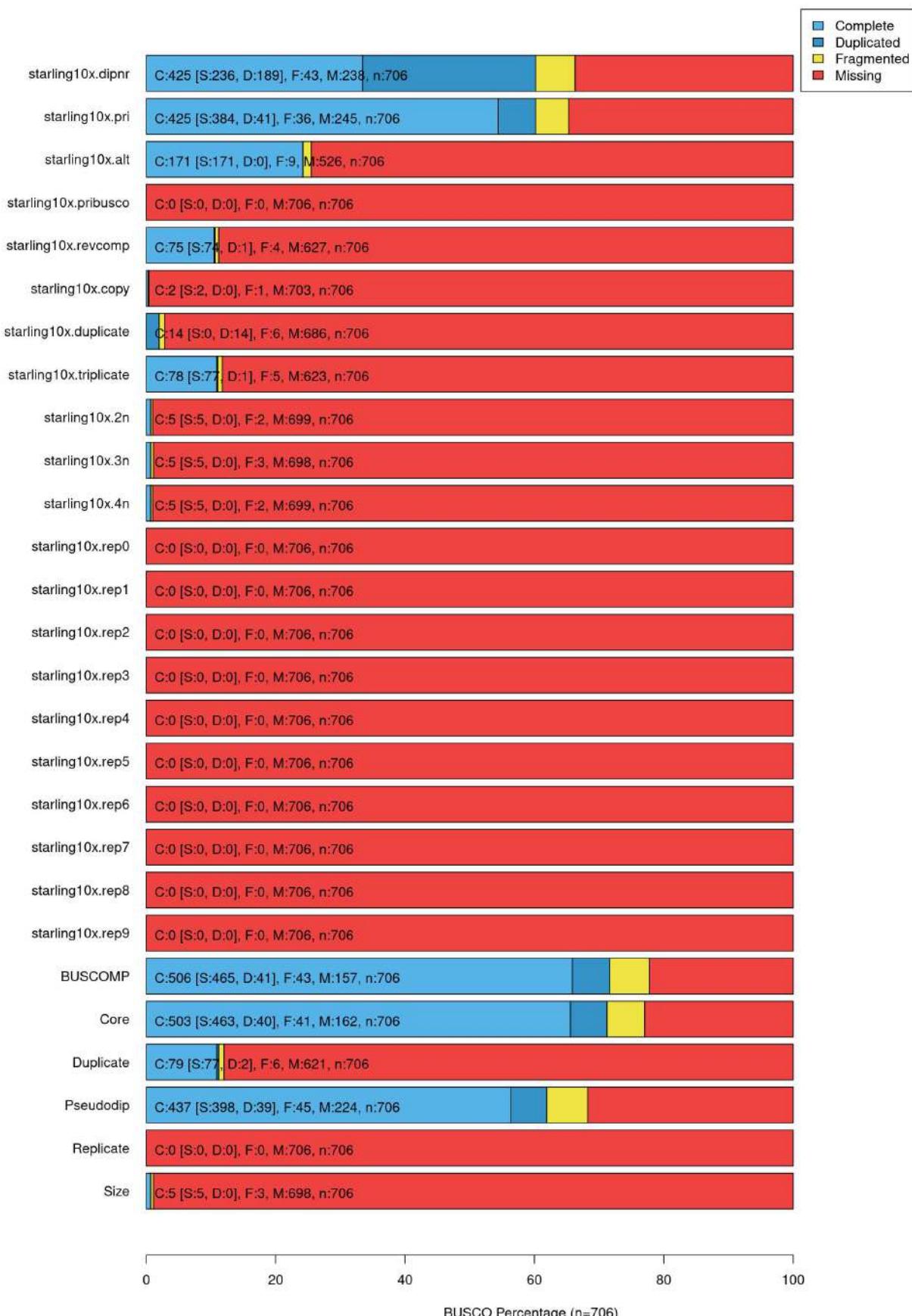
Missing starling10x.rep2 BUSCOs: BUSCOMP ratings



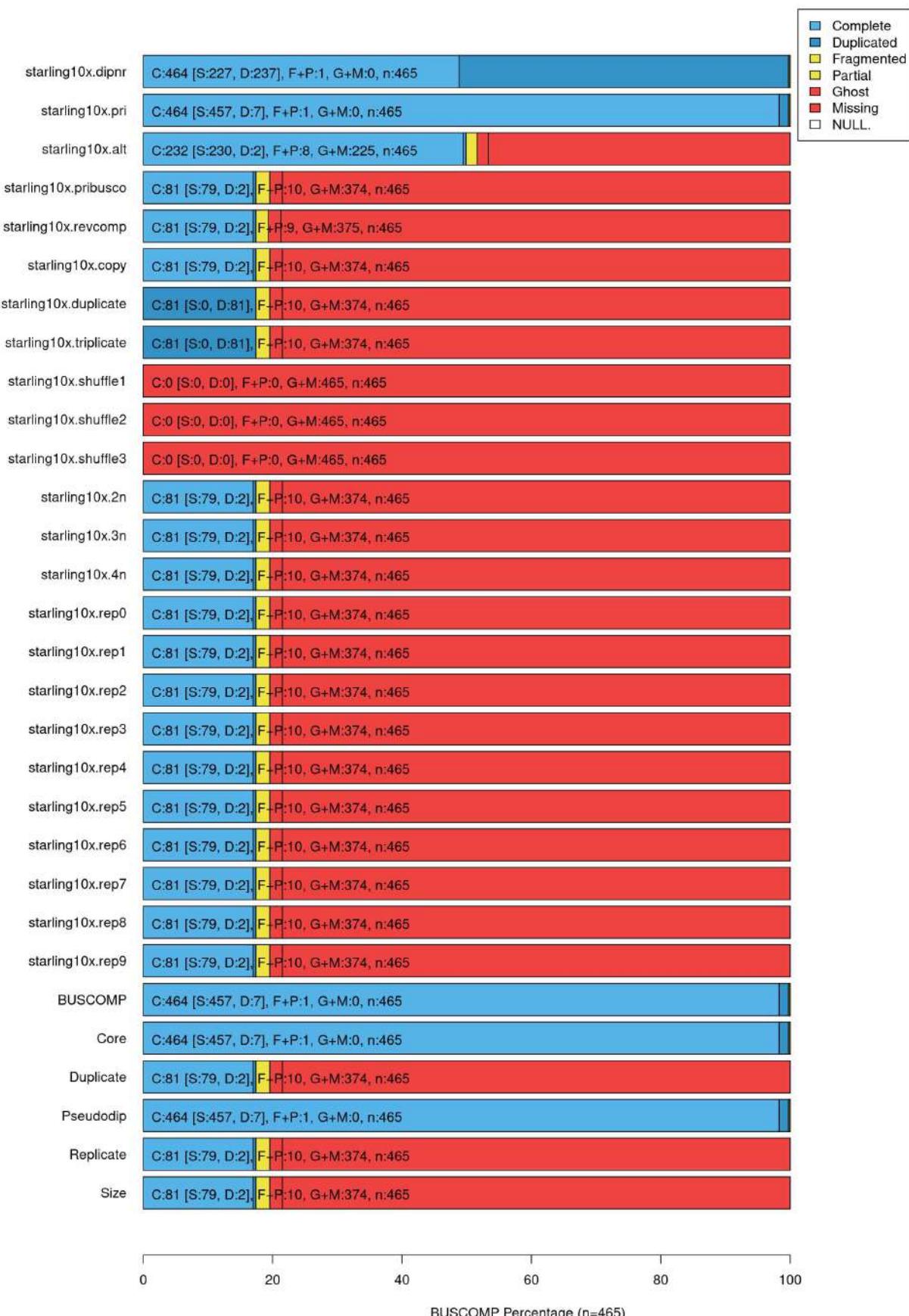
BUSCOMP ratings for [Missing] starling10x.rep2 BUSCOMP genes:

Missing starling10x.rep2 BUSCOMPs**5.25 Missing starling10x.rep3 BUSCO genes**BUSCO ratings for Missing starling10x.rep3 BUSCO genes:

Missing starling10x.rep3 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep3 BUSCO genes:

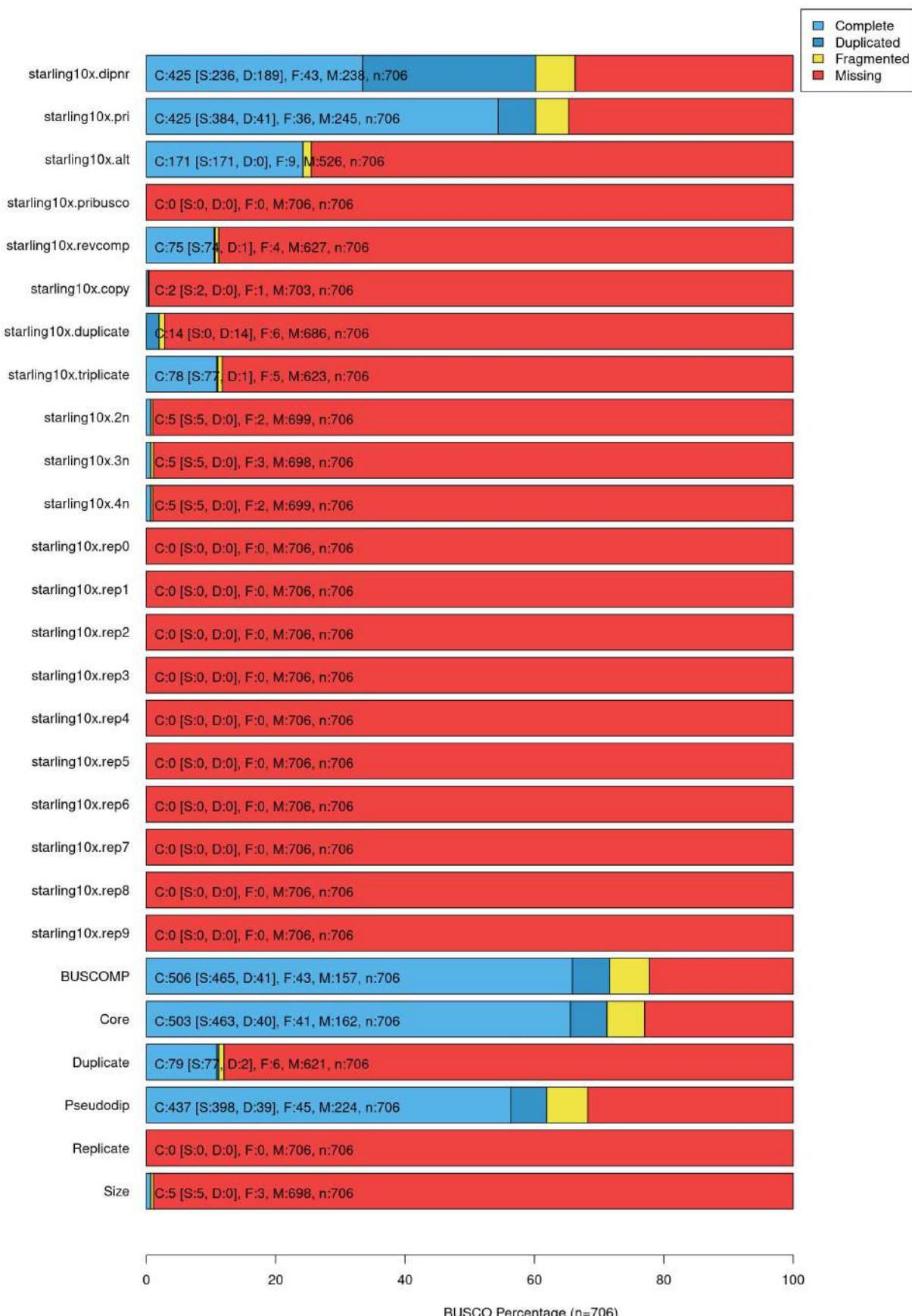
Missing starling10x.rep3 BUSCOs: BUSCOMP ratings



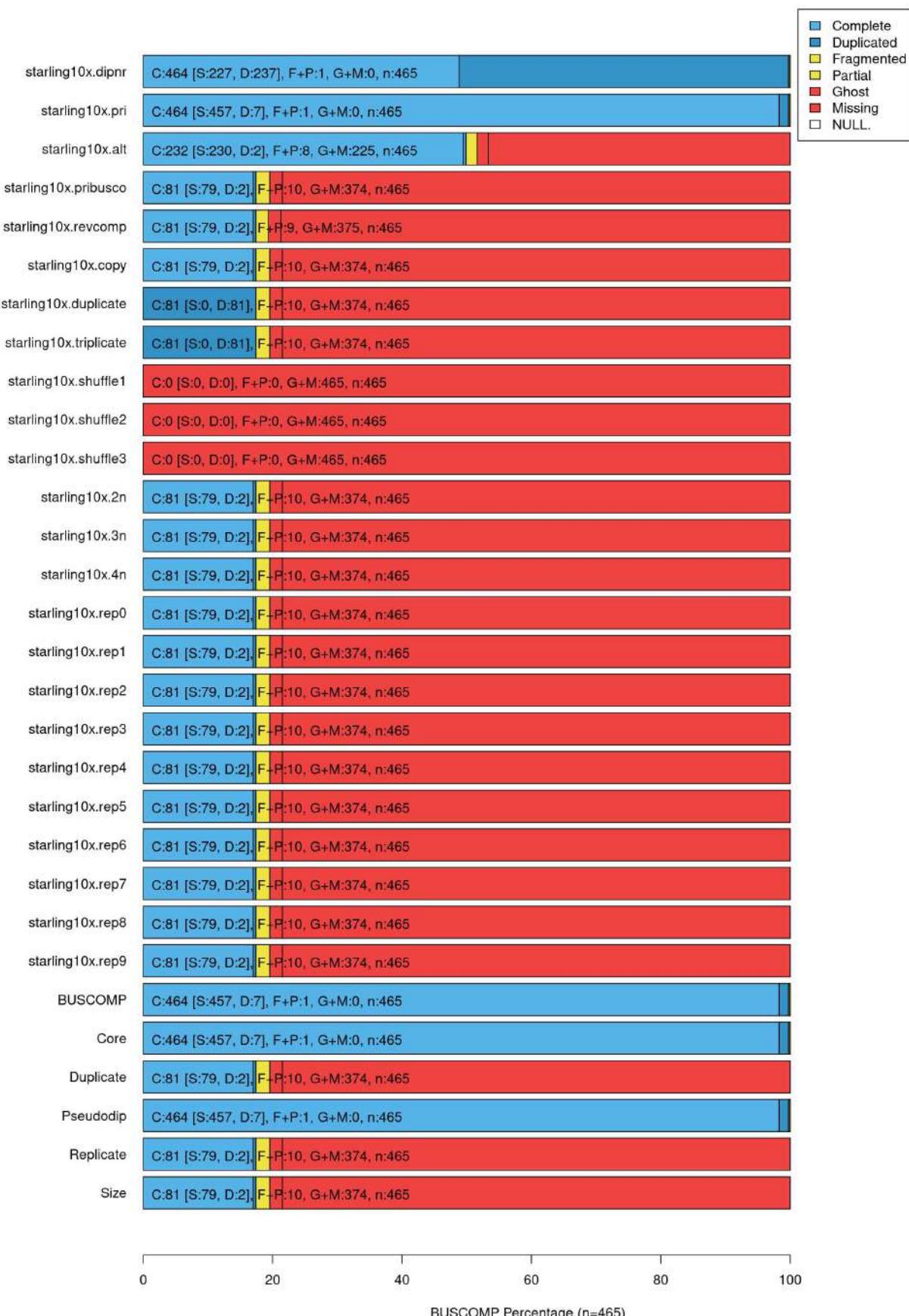
BUSCOMP ratings for [Missing] starling10x.rep3 BUSCOMP genes:

Missing starling10x.rep3 BUSCOMPs**5.26 Missing starling10x.rep4 BUSCO genes**BUSCO ratings for Missing starling10x.rep4 BUSCO genes:

Missing starling10x.rep4 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep4 BUSCO genes:

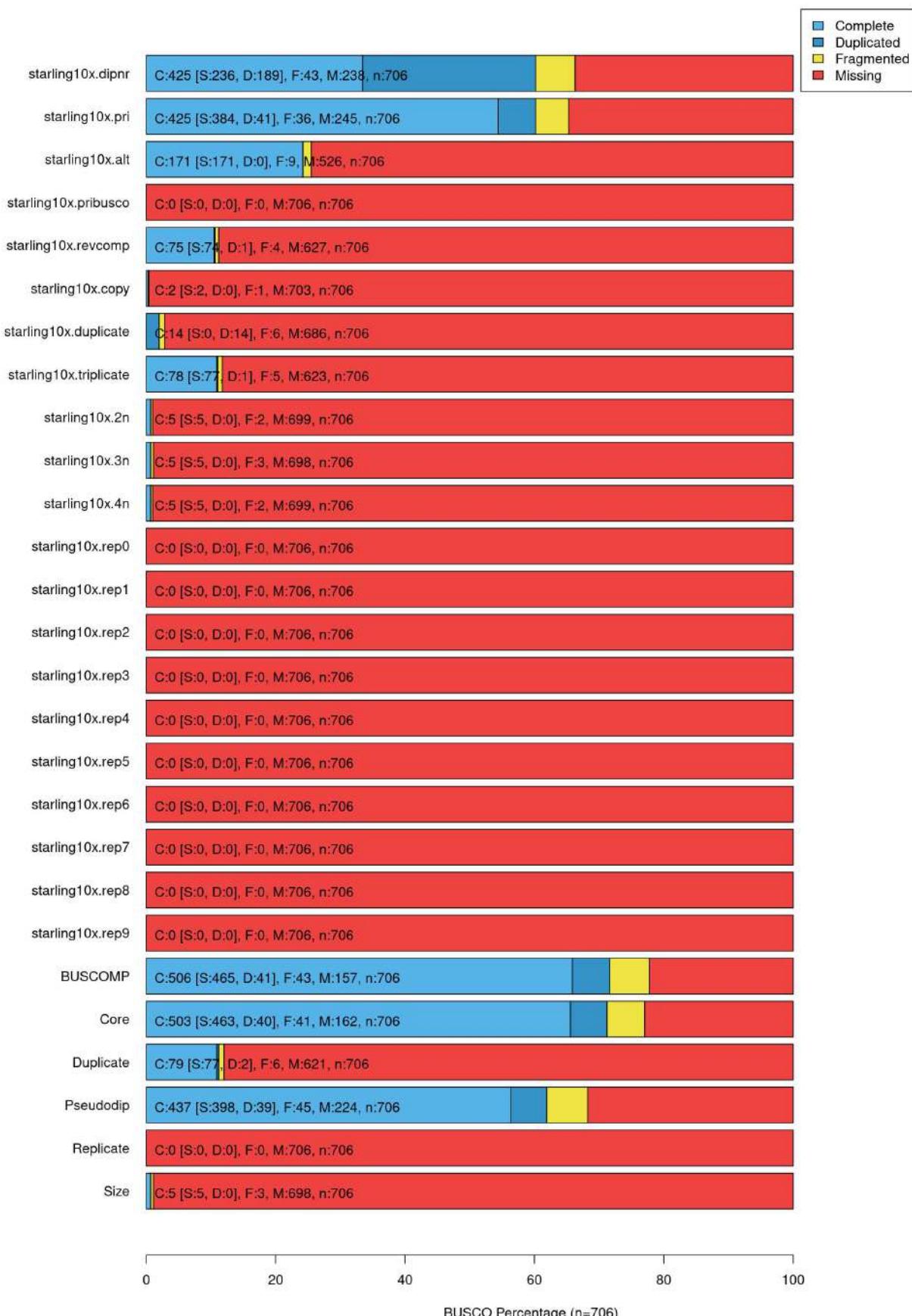
Missing starling10x.rep4 BUSCOs: BUSCOMP ratings

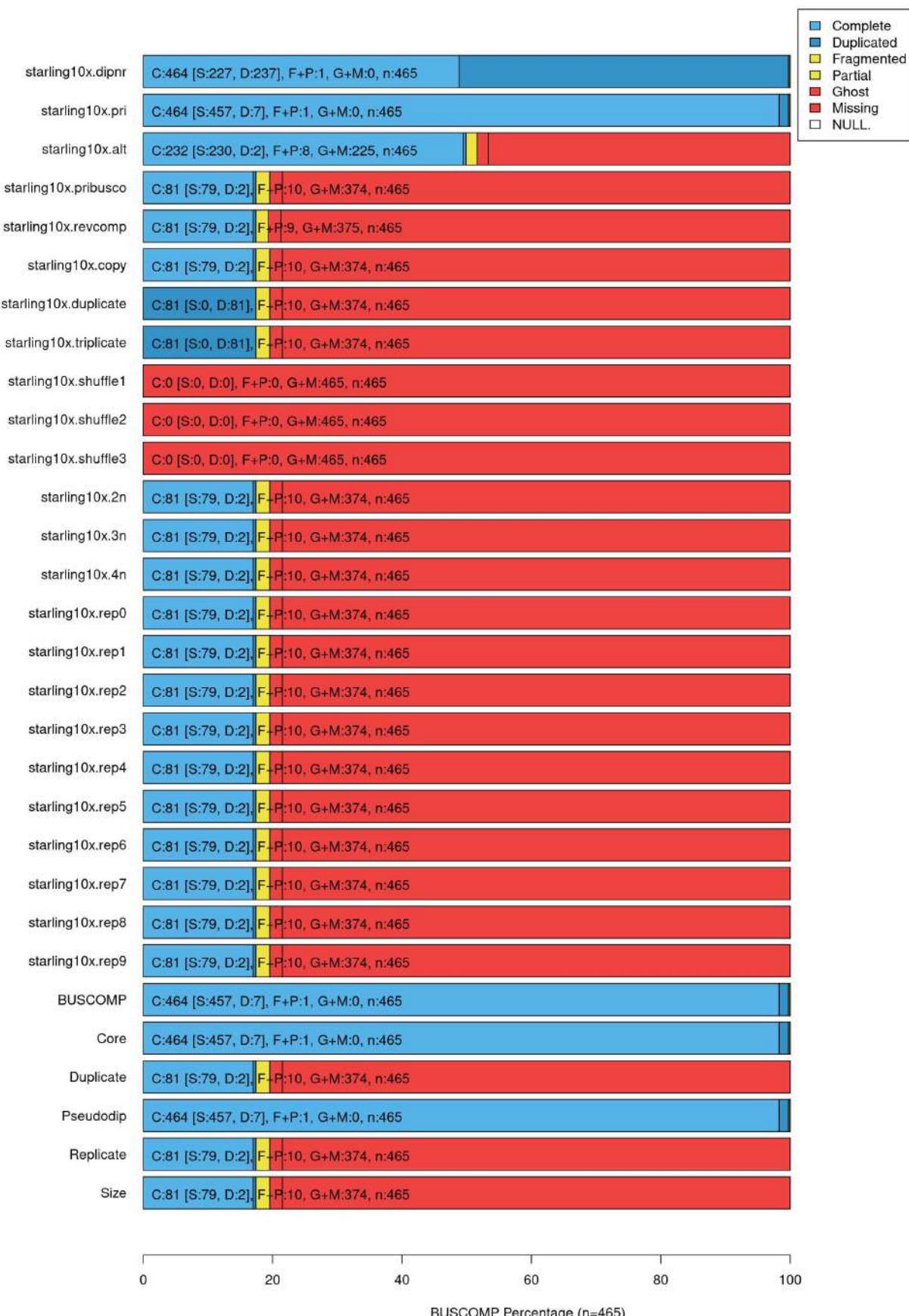


BUSCOMP ratings for [Missing] starling10x.rep4 BUSCOMP genes:

Missing starling10x.rep4 BUSCOMPs**5.27 Missing starling10x.rep5 BUSCO genes**BUSCO ratings for Missing starling10x.rep5 BUSCO genes:

Missing starling10x.rep5 BUSCOs

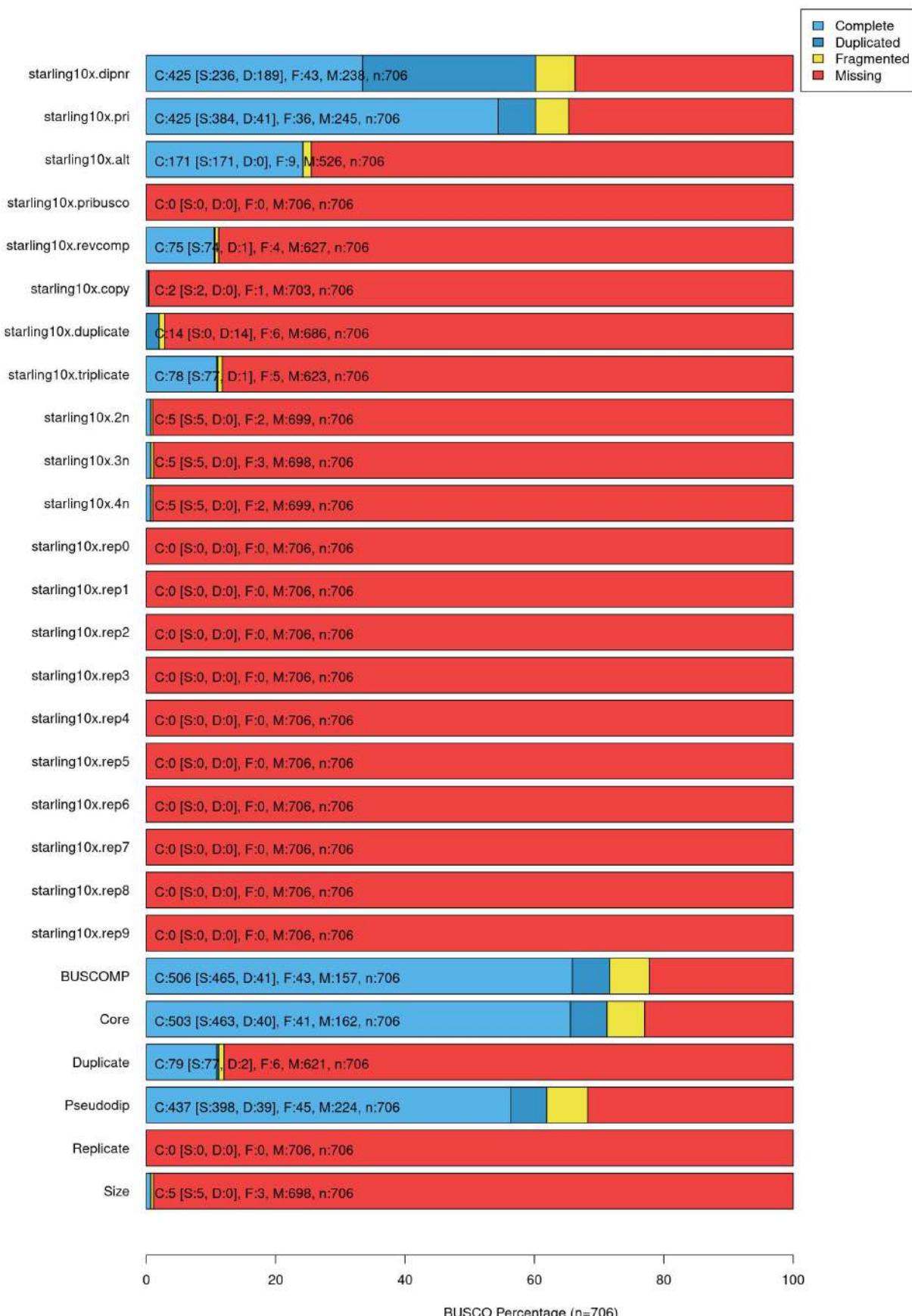
BUSCOMP ratings for **Missing** starling10x.rep5 BUSCO genes:

Missing starling10x.rep5 BUSCOs: BUSCOMP ratingsBUSCOMP ratings for **Missing** starling10x.rep5 BUSCOMP genes:

Missing starling10x.rep5 BUSCOMPs**5.28 Missing starling10x.rep6 BUSCO genes**

BUSCO ratings for Missing starling10x.rep6 BUSCO genes:

Missing starling10x.rep6 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep6 BUSCO genes:

Missing starling10x.rep6 BUSCOs: BUSCOMP ratings

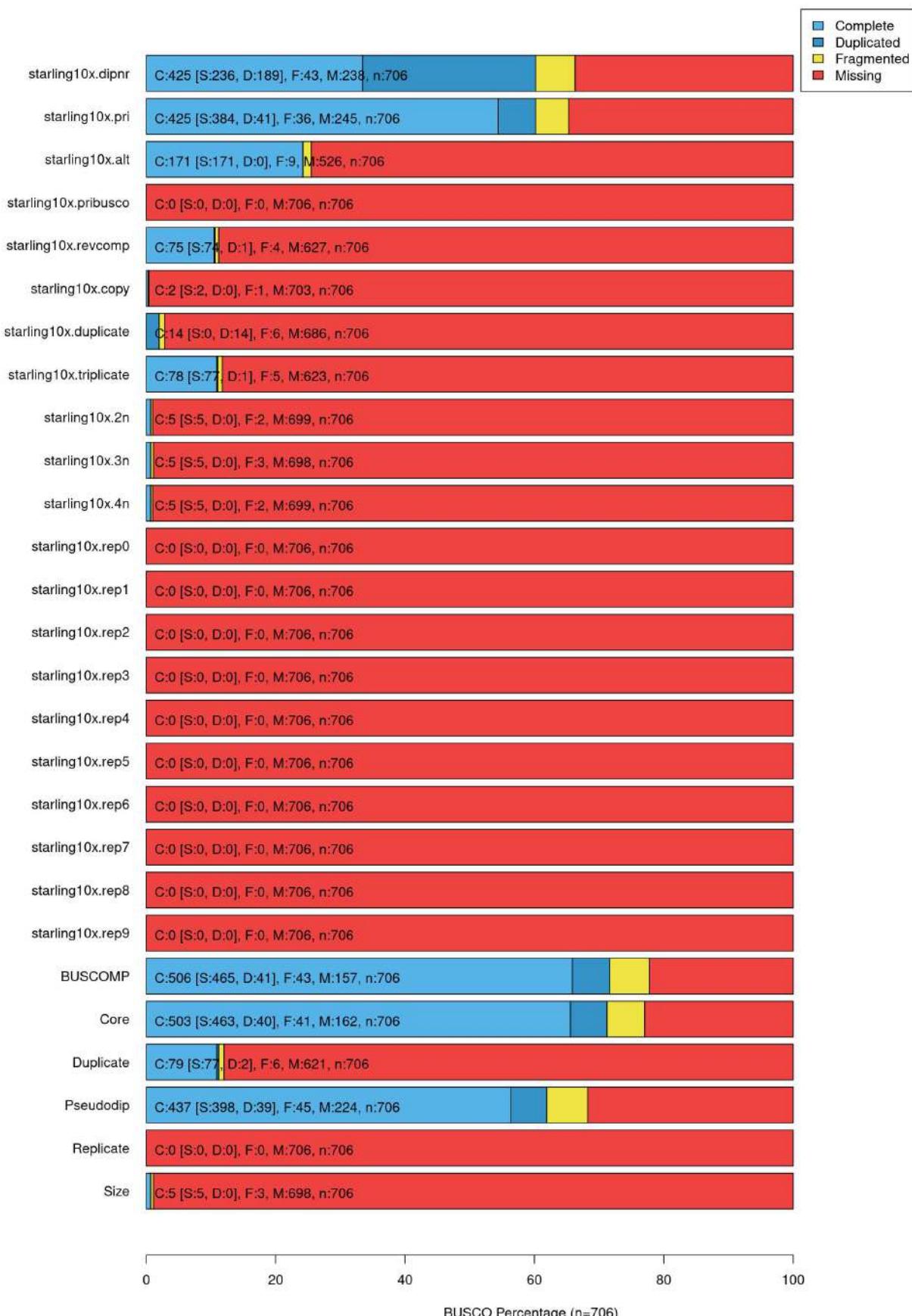


BUSCOMP ratings for [Missing] starling10x.rep6 BUSCOMP genes:

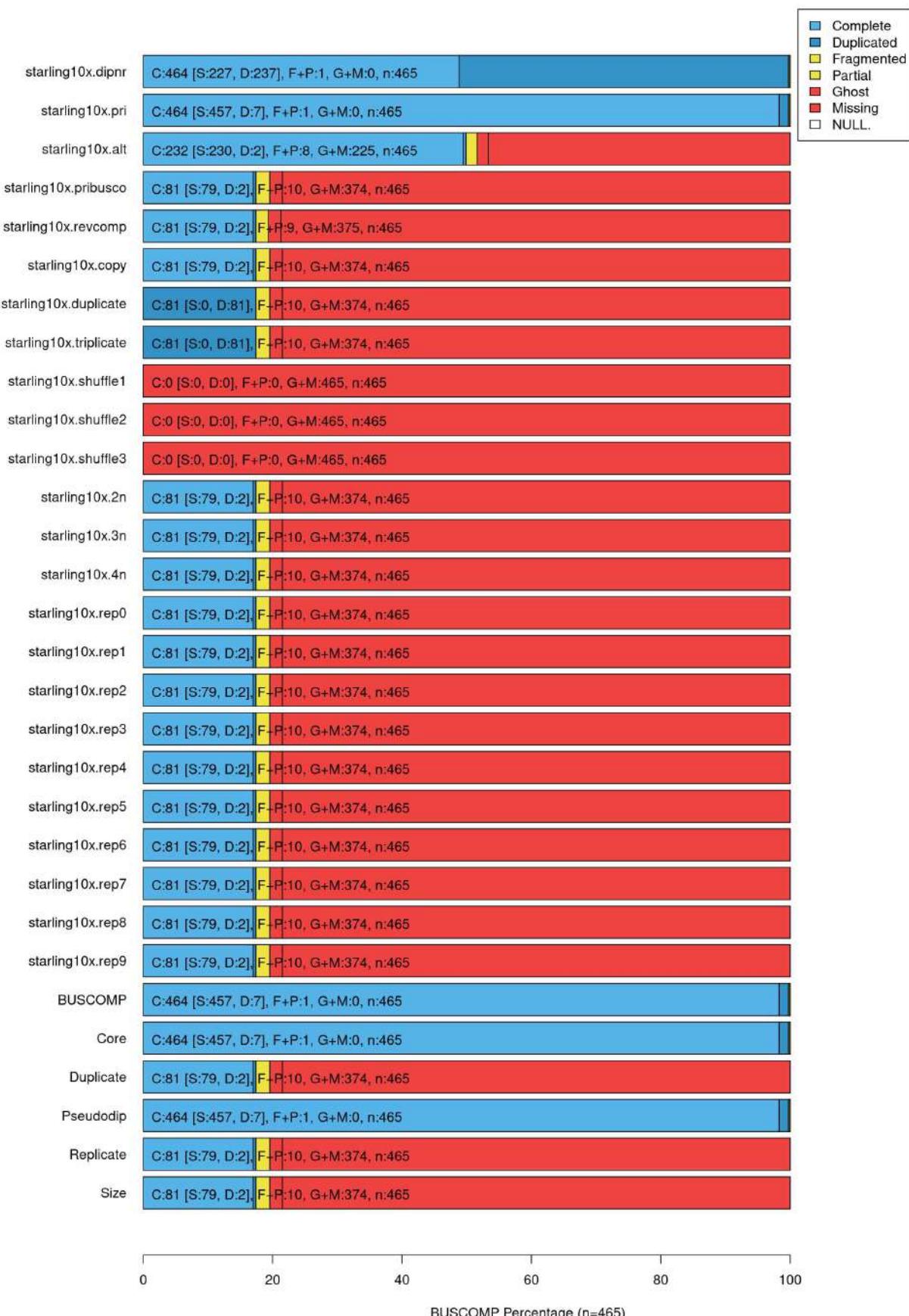
Missing starling10x.rep6 BUSCOMPs**5.29 Missing starling10x.rep7 BUSCO genes**

BUSCO ratings for Missing starling10x.rep7 BUSCO genes:

Missing starling10x.rep7 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep7 BUSCO genes:

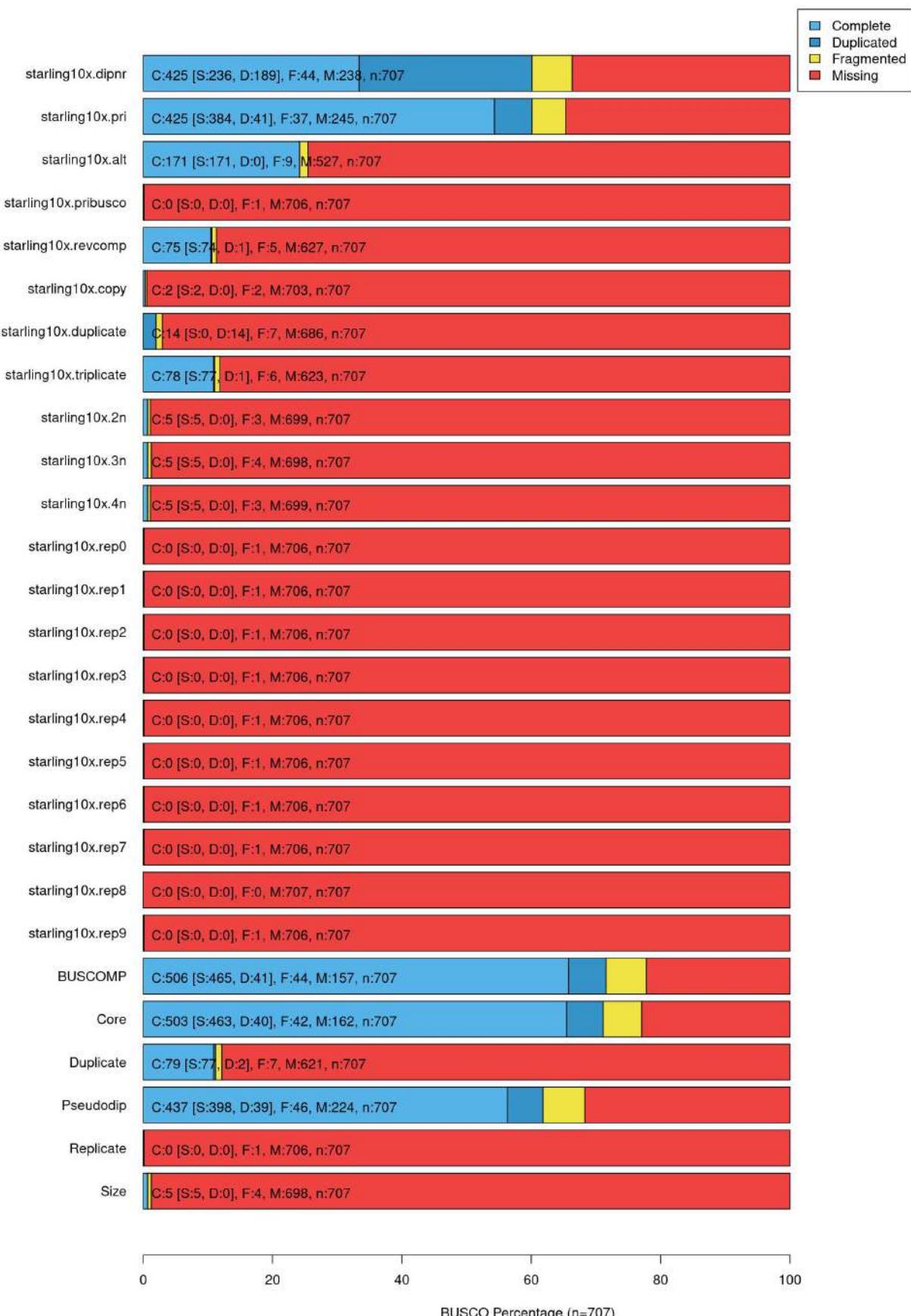
Missing starling10x.rep7 BUSCOs: BUSCOMP ratings



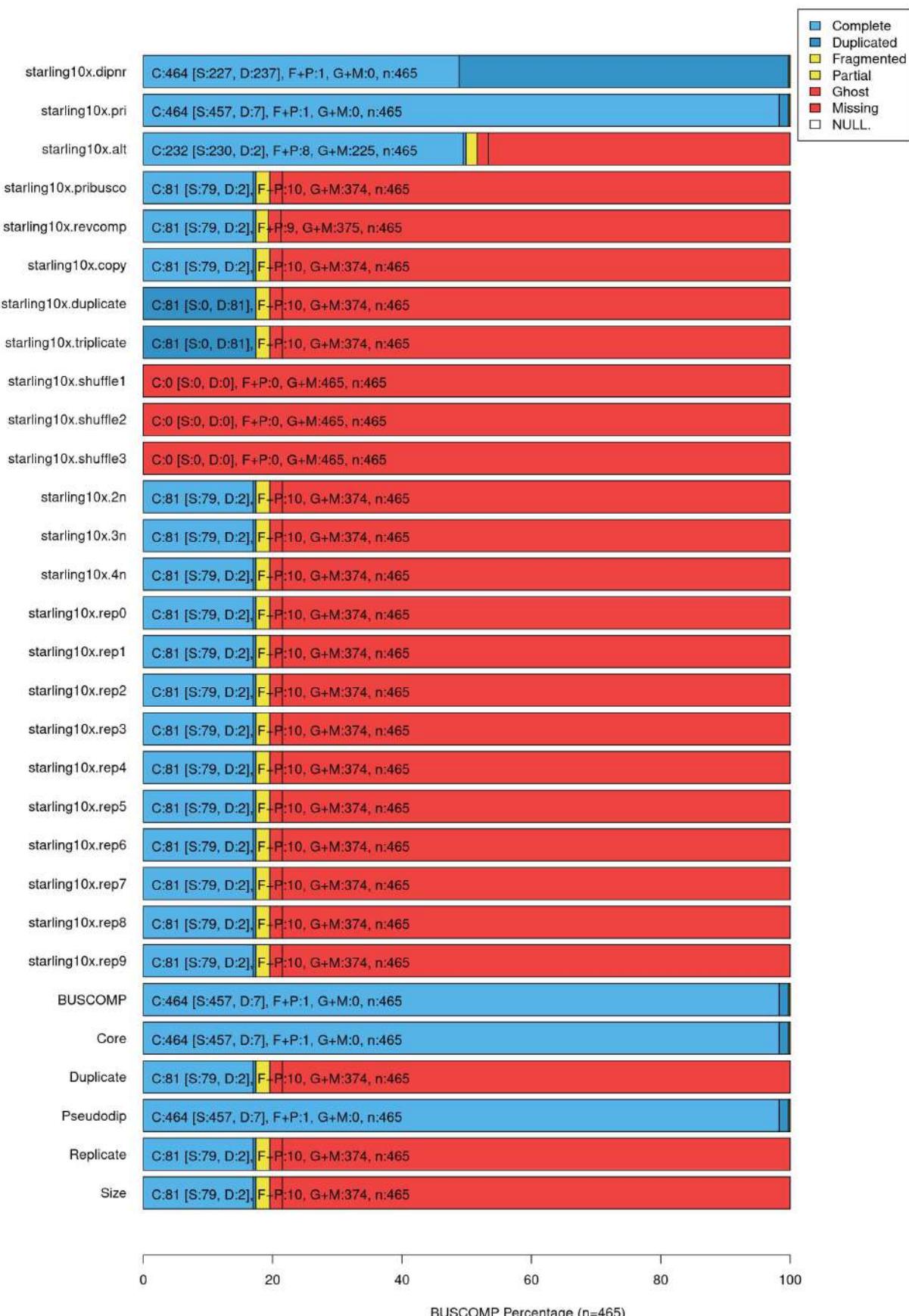
BUSCOMP ratings for [Missing] starling10x.rep7 BUSCOMP genes:

Missing starling10x.rep7 BUSCOMPs**5.30 Missing starling10x.rep8 BUSCO genes**BUSCO ratings for Missing starling10x.rep8 BUSCO genes:

Missing starling10x.rep8 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep8 BUSCO genes:

Missing starling10x.rep8 BUSCOs: BUSCOMP ratings

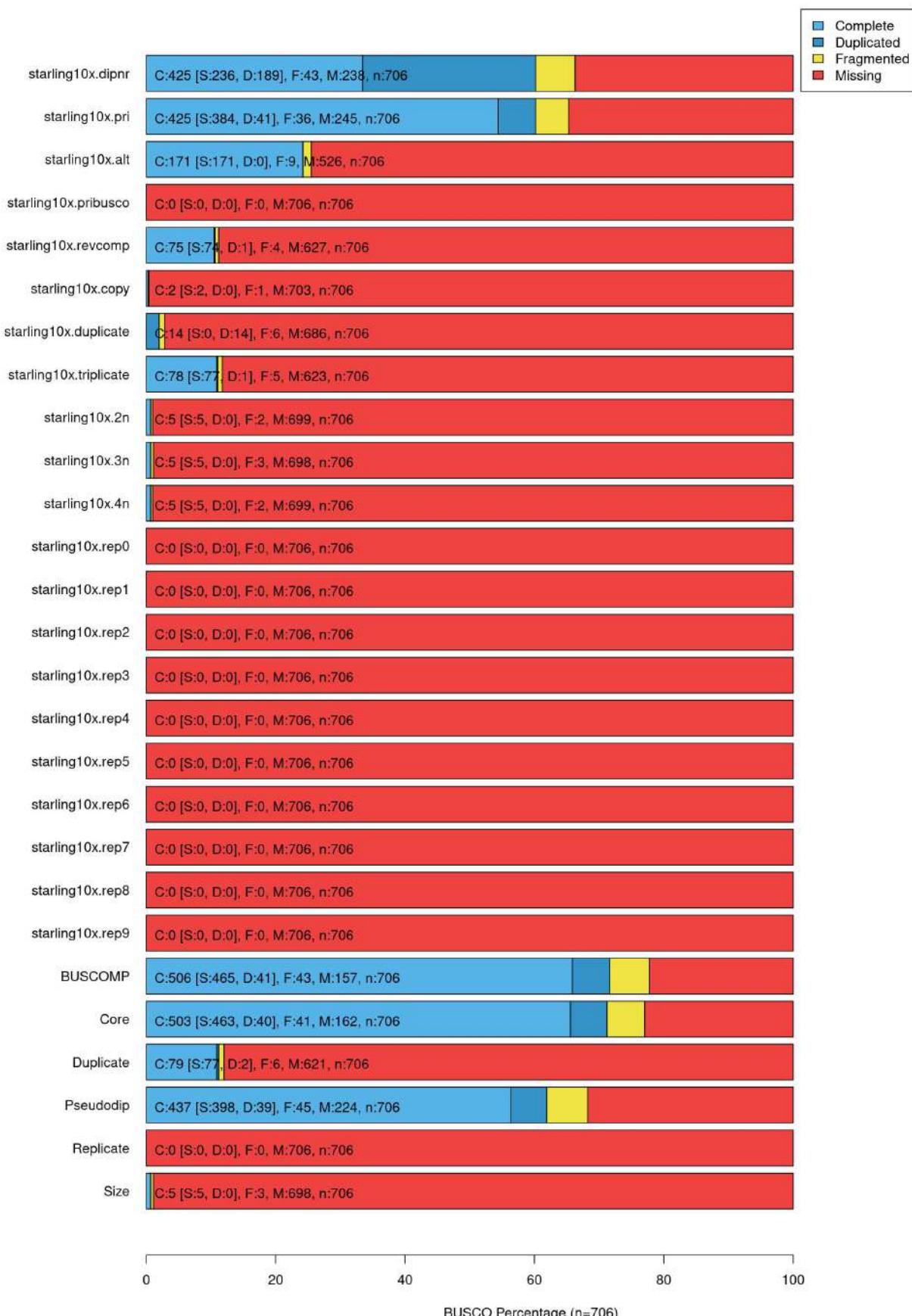


BUSCOMP ratings for [Missing] starling10x.rep8 BUSCOMP genes:

Missing starling10x.rep8 BUSCOMPs**5.31 Missing starling10x.rep9 BUSCO genes**

BUSCO ratings for Missing starling10x.rep9 BUSCO genes:

Missing starling10x.rep9 BUSCOs

BUSCOMP ratings for **Missing** starling10x.rep9 BUSCO genes:

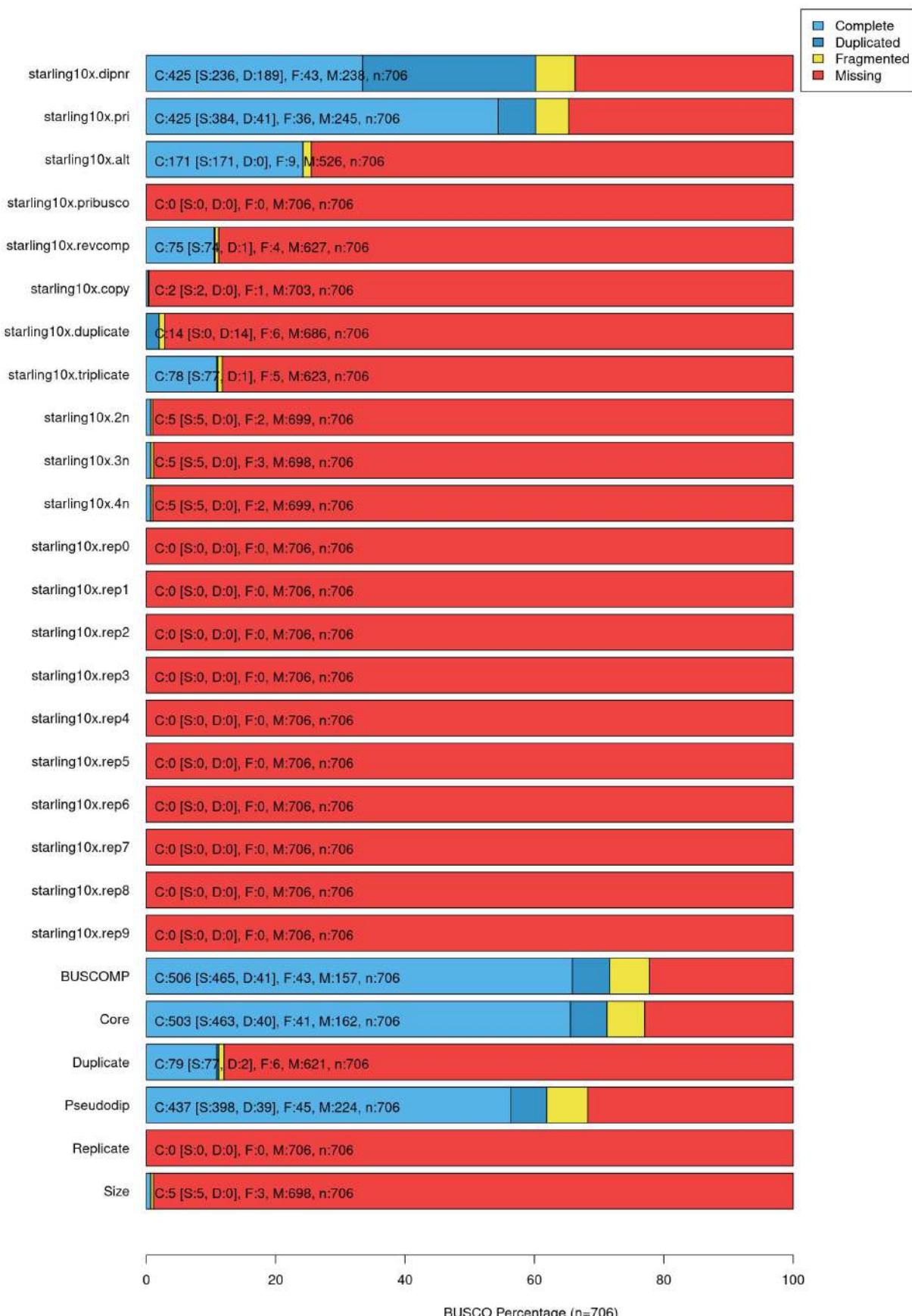
Missing starling10x.rep9 BUSCOs: BUSCOMP ratings



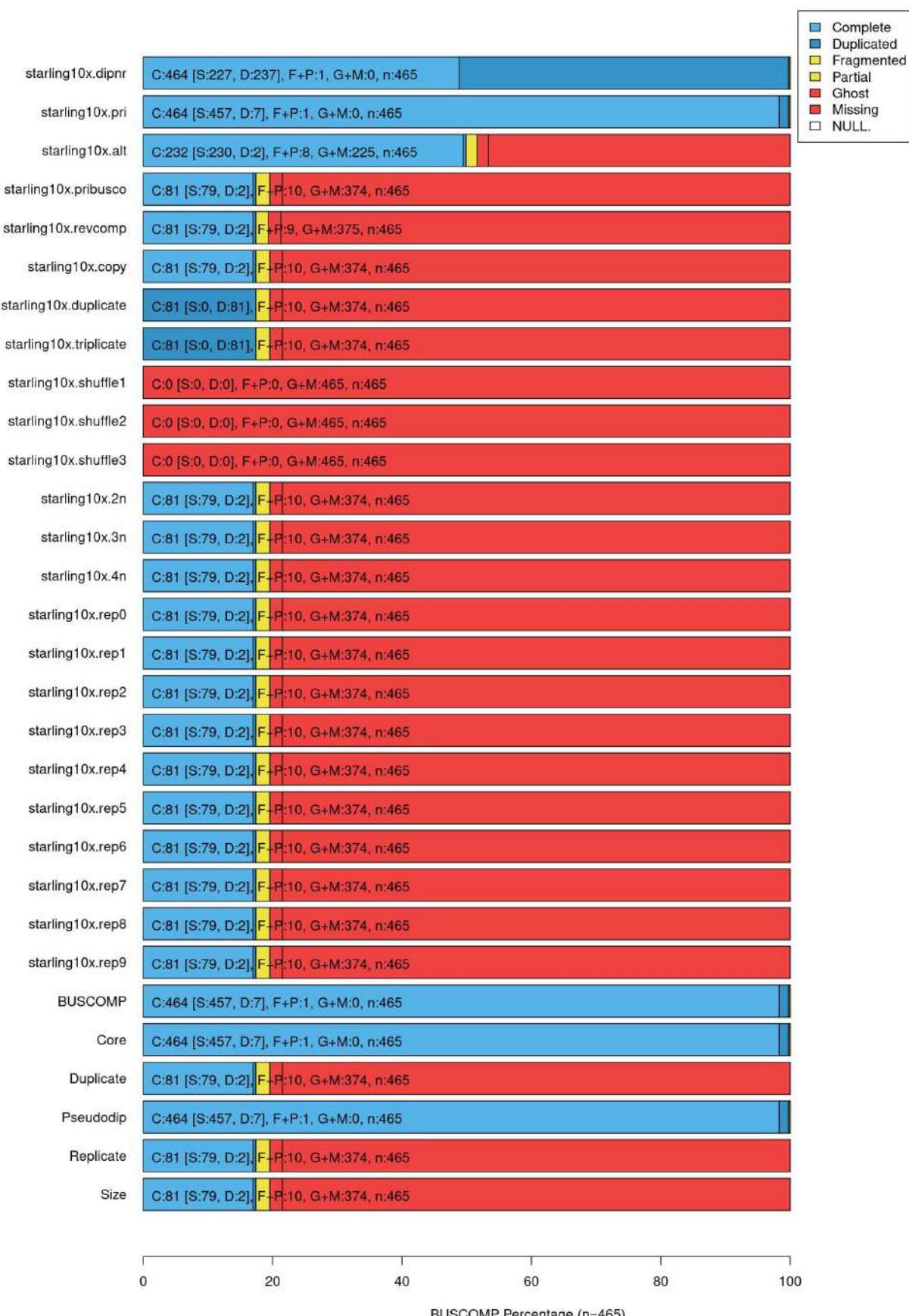
BUSCOMP ratings for [Missing] starling10x.rep9 BUSCO genes:

Missing starling10x.rep9 BUSCOMPs**5.32 Missing Replicate BUSCO genes**BUSCO ratings for Missing Replicate BUSCO genes:

Missing Replicate BUSCOs

BUSCOMP ratings for **[Missing]** Replicate BUSCO genes:

Missing Replicate BUSCOs: BUSCOMP ratings



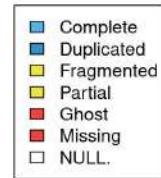
BUSCOMP ratings for [Missing] Replicate BUSCOMP genes:

Missing Replicate BUSCOMPs**5.33 Missing BUSCOMP BUSCO genes**BUSCO ratings for Missing BUSCOMP BUSCO genes:

Missing BUSCOMP BUSCOsBUSCOMP ratings for **Missing** BUSCOMP BUSCO genes:

Missing BUSCOMP BUSCOs: BUSCOMP ratings

starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0



BUSCOMP ratings for **Missing** BUSCOMP BUSCO genes:

Missing BUSCOMP BUSCOMPs

starling10x.dipnr	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pri	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.alt	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.pribusco	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.revcomp	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.copy	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.triplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.shuffle3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.2n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.3n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.4n	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep0	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep1	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep2	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep3	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep4	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep5	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep6	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep7	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep8	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
starling10x.rep9	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
BUSCOMP	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Core	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Duplicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Pseudodip	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Replicate	C:0 [S:0, D:0], F+P:0, G+M:0, n:0
Size	C:0 [S:0, D:0], F+P:0, G+M:0, n:0

**6 Appendix: BUSCOMP run details**

```
BUSCOMP V0.11.0: run Thu Mar  4 16:10:40 2021
```

This analysis was run in:

```
/scratch/tmp/z3452659/projects/BUSCOMP-Jan19/analysis/2021-03-03.10xStarling/buscompV5
```

- Log file: /scratch/tmp/z3452659/projects/BUSCOMP-Jan19/analysis/2021-03-03.10xStarling/buscompV5/starling10xV5.log
(/scratch/tmp/z3452659/projects/BUSCOMP-Jan19/analysis/2021-03-03.10xStarling/buscompV5/starling10xV5.log)
- Commandline arguments: runs=../busco5/run_* fastadir=../fasta/ ratefas=../fasta/*.fasta genomesize=1.1e9
basefile=starling10xV5 forks=24
- Full Command List: mafft=mafft clustalo=clustalo clustalw=clustalw2 blast+path= iupath=/home/z3452659/bioware/iupred/iupred
iuchdir=T minregion=5 iicut=0.2 rpath=R modpurge=T runs=../busco5/run_* fastadir=../fasta/ ratefas=../fasta/*.fasta
genomesize=1.1e9 basefile=starling10xV5 forks=24

6.1 BUSCOMP errors

BUSCOMP returned no runtime errors.

6.2 BUSCOMP warnings

See run log for further details:

```
#WARN 00:32:40 116 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 00:32:40 71 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 00:43:06 74 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 00:43:06 51 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 00:49:04 37 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 00:49:04 26 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 00:53:45 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 00:53:45 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:01:44 58 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:01:44 32 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:09:08 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:09:08 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:15:14 96 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:15:14 75 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:26:39 155 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:26:39 110 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:48:26 47 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:48:26 33 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 01:55:35 48 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 01:55:35 33 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:03:24 48 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:03:24 37 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:08:31 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:08:31 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:13:47 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:13:47 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:19:04 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:19:04 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:24:21 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:24:21 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:29:50 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:29:50 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:34:59 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:34:59 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:40:18 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:40:18 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:45:41 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:45:41 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:50:53 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:50:53 38 Identity mismatches from PAF file (PAF identity ignores Ns).
#WARN 02:56:19 49 Length/AlnLen mismatches from PAF file. (May be disparity with N treatment.)
#WARN 02:56:19 38 Identity mismatches from PAF file (PAF identity ignores Ns).
```

Report contents:

- Run summary
- BUSCOMP summary
- Genome summary
- BUSCO Ratings
- BUSCO full results compilation
- BUSCOMP Sequence details and rating
- BUSCOMP re-rating of genomes
- BUSCOMP re-rating full results
- Unique BUSCO and BUSCOMP Complete genes
- Ratings for Missing BUSCO genes
- Appendix: BUSCOMP run details