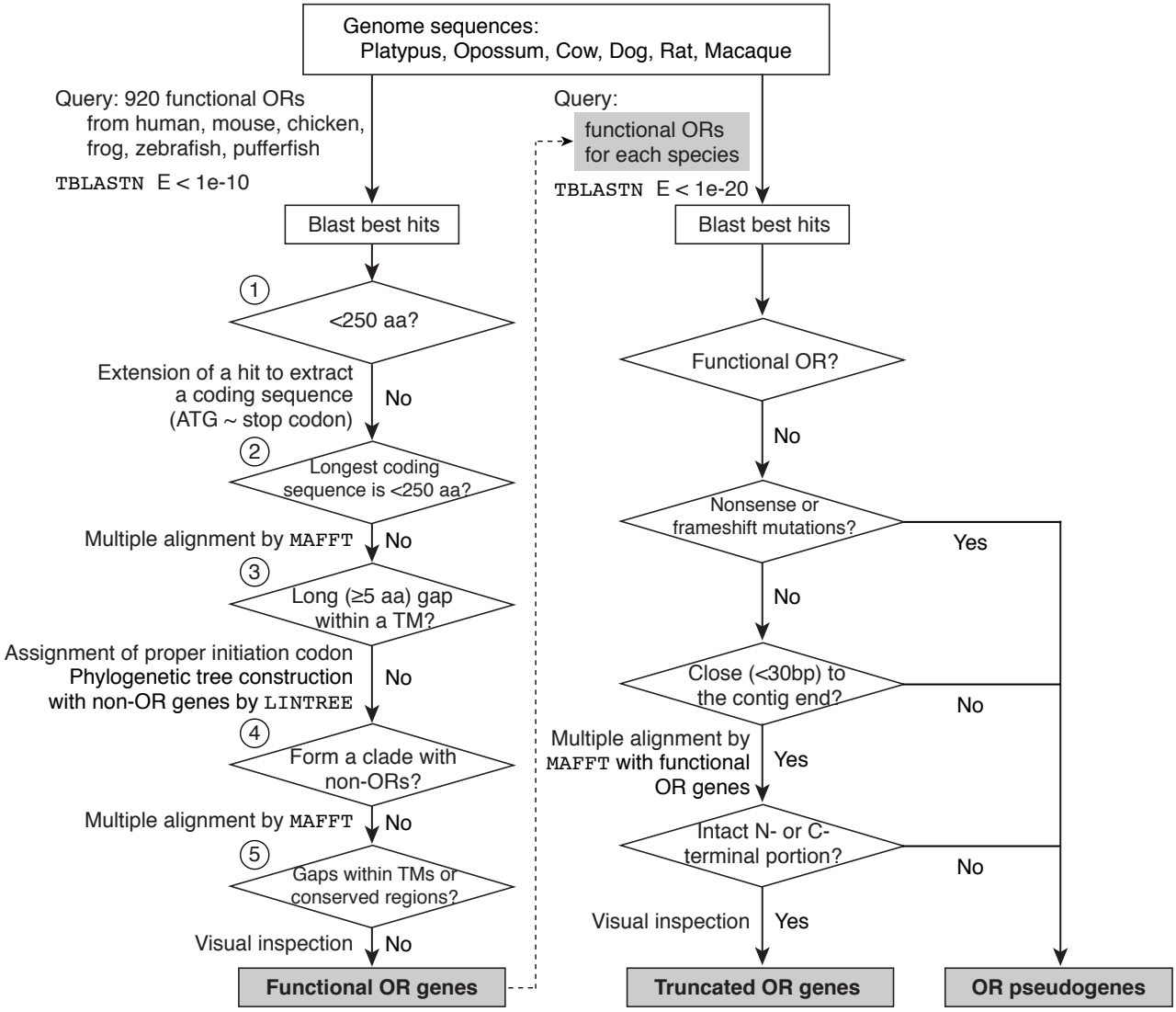
Genome sequences:
Platypus, Opossum, Cow, Dog, Rat, Macaque
Query: 920 functional ORs
from human, mouse, chicken,
frog, zebrafish, pufferfish
TBLASTN E < 1e-10
Blast best hits
1
<250 aa?
Extension of a hit to extract
a coding sequence
(ATG ~ stop codon)
No
2
Longest coding
sequence is <250 aa?
Multiple alignment by MAFFT
No
3
Long (≥5 aa) gap
within a TM?
Assignment of proper initiation codon
Phylogenetic tree construction
with non-OR genes by LINTREE
No
4
Form a clade with
non-ORs?
Multiple alignment by MAFFT
No
5
Gaps within TMs or
conserved regions?
Visual inspection
No
Functional OR genes
Query:
functional ORs
for each species
TBLASTN E < 1e-20
Blast best hits
Functional OR?
No
Nonsense or
frameshift mutations?
Yes
No
Close (<30bp) to
the contig end?
No
Multiple alignment by
MAFFT with functional
OR genes
Yes
Intact N- or C-
terminal portion?
No
Visual inspection
Yes
Truncated OR genes
OR pseudogenes

Figure S2