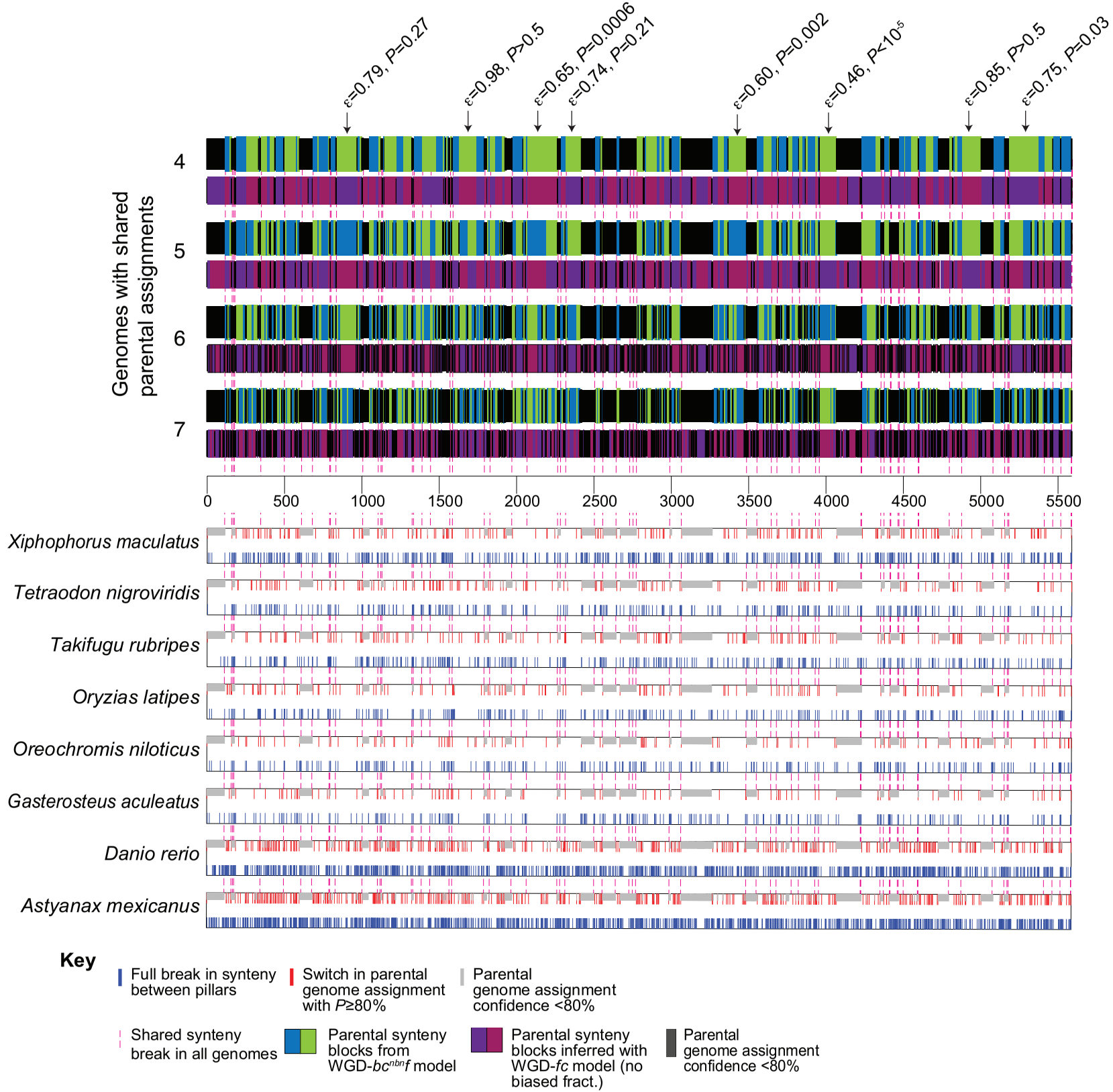
ε=0.79, P=0.27
ε=0.98, P>0.5
ε=0.65, P=0.0006
ε=0.74, P=0.21
ε=0.60, P=0.002
ε=0.46, P<10^-5
ε=0.85, P>0.5
ε=0.75, P=0.03
Genomes with shared parental assignments
4
5
6
7
0
500
1000
1500
2000
2500
3000
3500
4000
4500
5000
5500
Xiphophorus maculatus
Tetraodon nigroviridis
Takifugu rubripes
Oryzias latipes
Oreochromis niloticus
Gasterosteus aculeatus
Danio rerio
Astyanax mexicanus
Key
Full break in synteny between pillars
Switch in parental genome assignment with P≥80%
Parental genome assignment confidence <80%
Shared synteny break in all genomes
Parental synteny blocks from WGD-bc^nbnf model
Parental synteny blocks inferred with WGD-fc model (no biased fract.)
Parental genome assignment confidence <80%