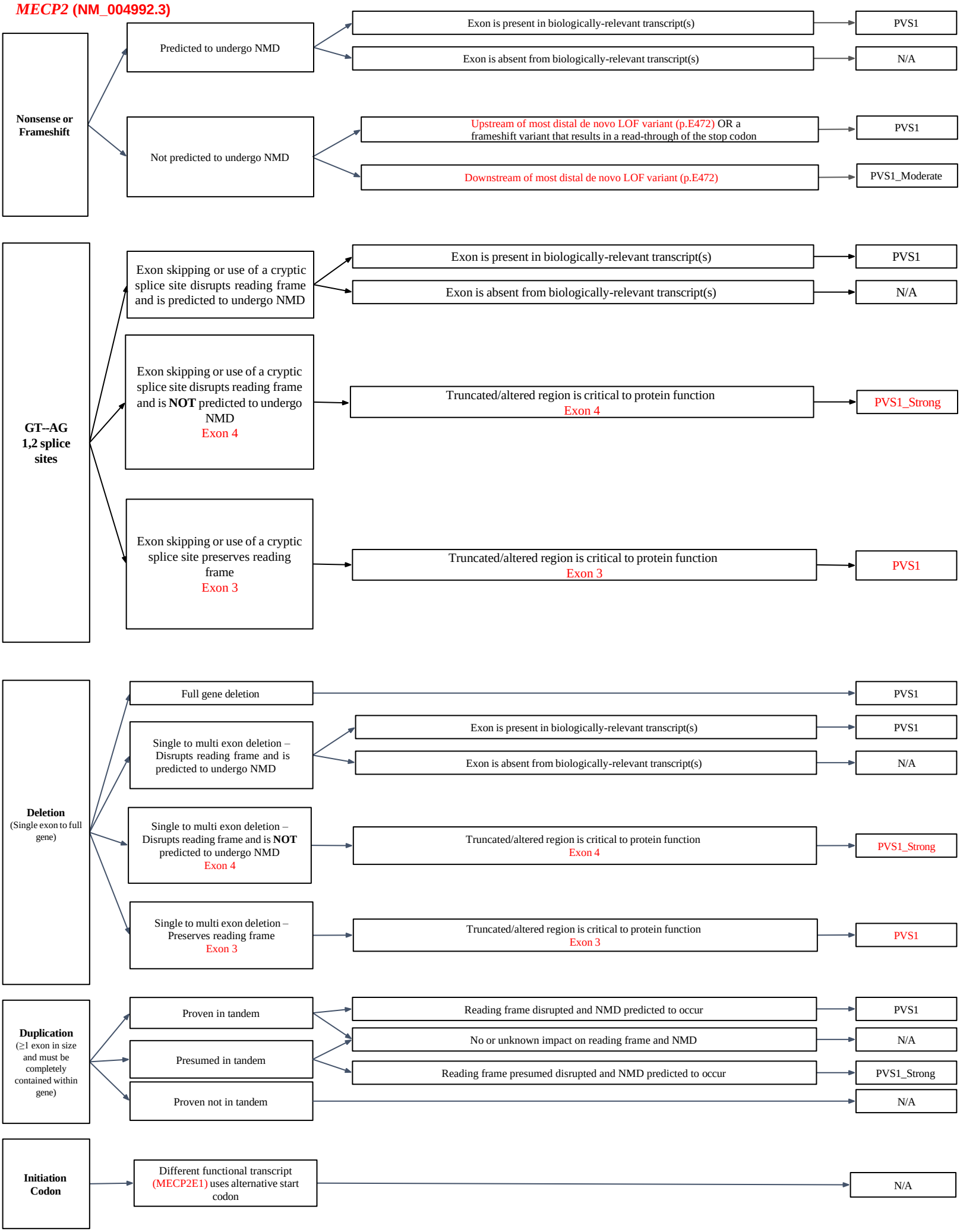
MECP2 (NM_004992.3)
Nonsense or Frameshift
Predicted to undergo NMD
Exon is present in biologically-relevant transcript(s)
PVS1
Exon is absent from biologically-relevant transcript(s)
N/A
Not predicted to undergo NMD
Upstream of most distal de novo LOF variant (p.E472) OR a frameshift variant that results in a read-through of the stop codon
PVS1
Downstream of most distal de novo LOF variant (p.E472)
PVS1_Moderate
GT–AG 1,2 splice sites
Exon skipping or use of a cryptic splice site disrupts reading frame and is predicted to undergo NMD
Exon is present in biologically-relevant transcript(s)
PVS1
Exon is absent from biologically-relevant transcript(s)
N/A
Exon skipping or use of a cryptic splice site disrupts reading frame and is NOT predicted to undergo NMD
Exon 4
Truncated/altered region is critical to protein function
Exon 4
PVS1_Strong
Exon skipping or use of a cryptic splice site preserves reading frame
Exon 3
Truncated/altered region is critical to protein function
Exon 3
PVS1
Deletion
(Single exon to full gene)
Full gene deletion
PVS1
Single to multi exon deletion – Disrupts reading frame and is predicted to undergo NMD
Exon is present in biologically-relevant transcript(s)
PVS1
Exon is absent from biologically-relevant transcript(s)
N/A
Single to multi exon deletion – Disrupts reading frame and is NOT predicted to undergo NMD
Exon 4
Truncated/altered region is critical to protein function
Exon 4
PVS1_Strong
Single to multi exon deletion – Preserves reading frame
Exon 3
Truncated/altered region is critical to protein function
Exon 3
PVS1
Duplication
(≥1 exon in size and must be completely contained within gene)
Proven in tandem
Reading frame disrupted and NMD predicted to occur
PVS1
Presumed in tandem
No or unknown impact on reading frame and NMD
N/A
Reading frame presumed disrupted and NMD predicted to occur
PVS1_Strong
Proven not in tandem
N/A
Initiation Codon
Different functional transcript (MECP2E1) uses alternative start codon
N/A