

Fig S1

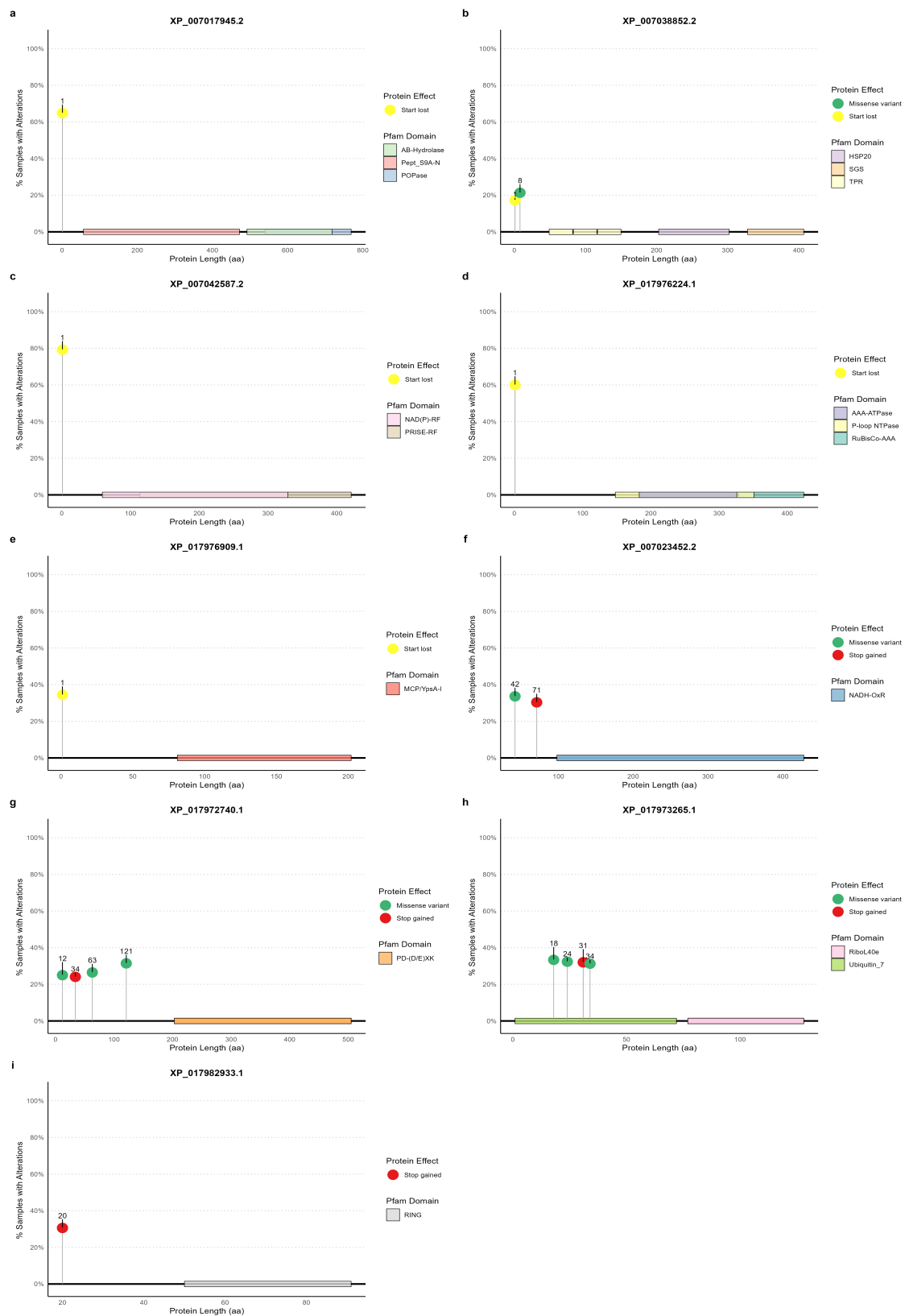


Fig S1. Lollipop plots showing of high and moderate impact variants identified in genes located in neutral windows. Each panel (a–i) represents an individual protein, with the total protein length displayed on the x-axis. Variant frequency across genotypes is shown on the y-axis. Circles along the protein sequence indicate the positions of affected amino acid residues and the type of mutation: missense variants (green), stop-gained (red), and start-lost (yellow). Colored boxes along the protein sequences represent predicted functional domains annotated using Pfam and InterProScan. Numbers above each lollipop indicate the amino acid position at where the variant occurs.