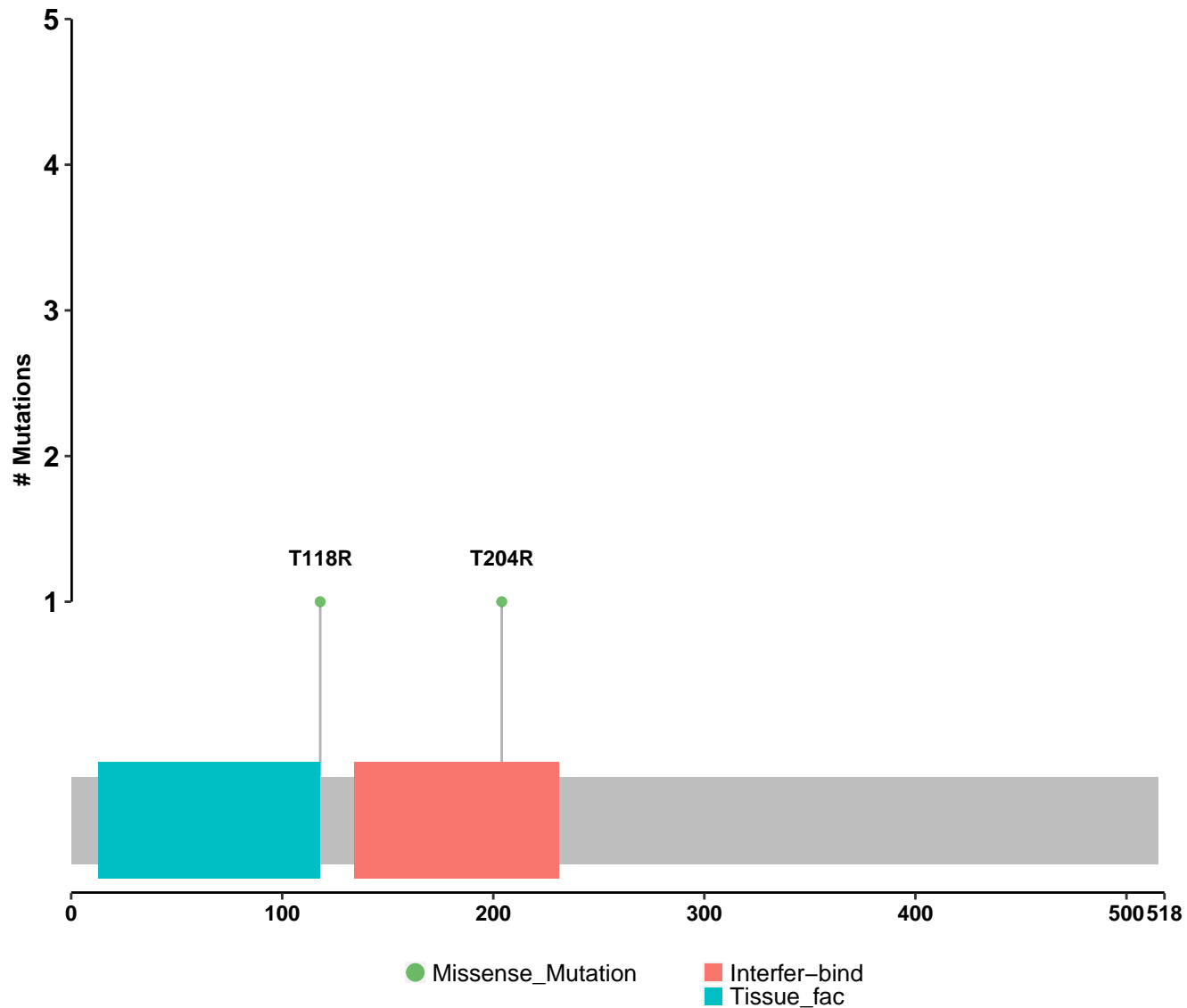


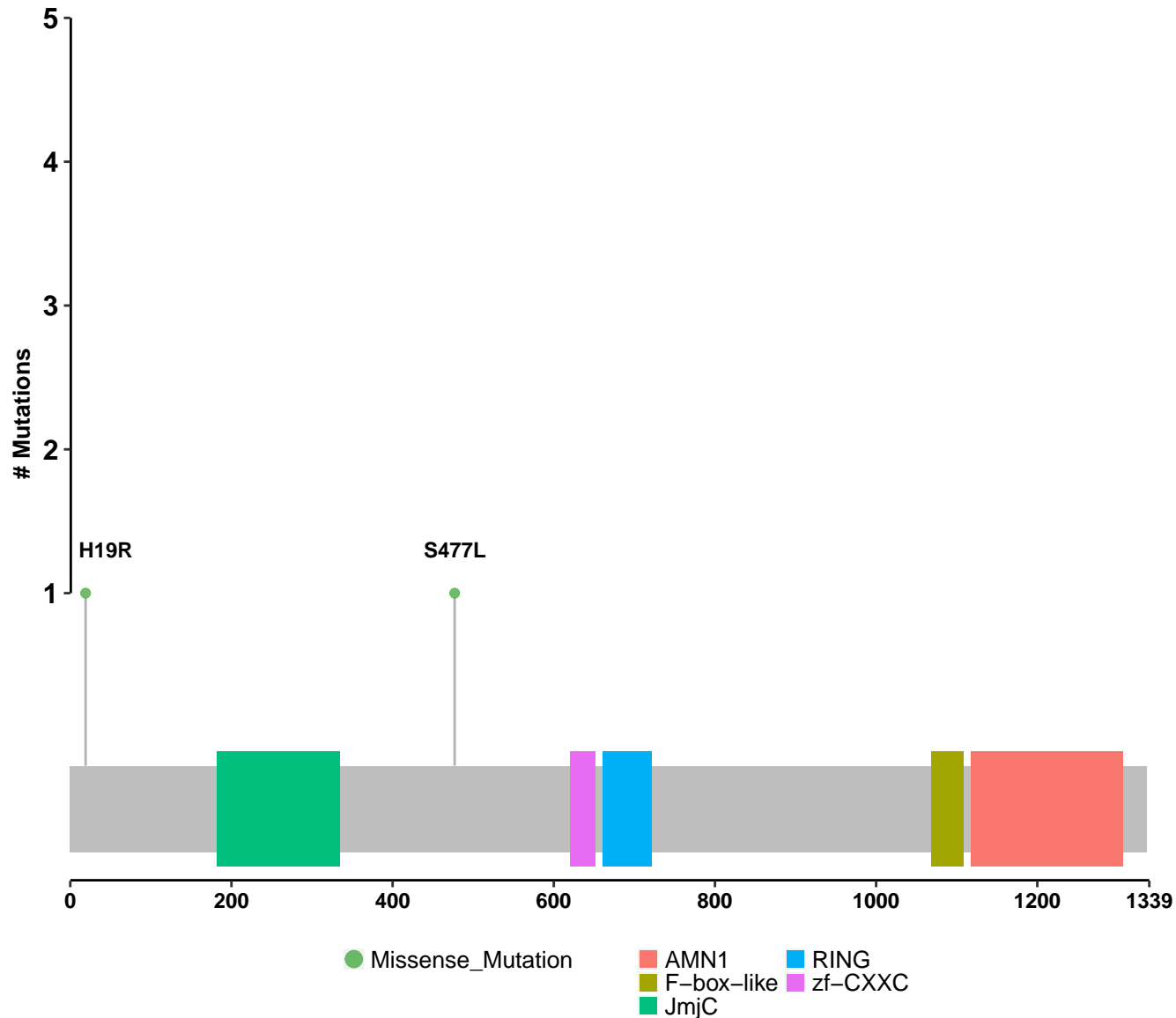
IFNAR2: [Somatic Mutation Rate: 6.06%]

NM_207585



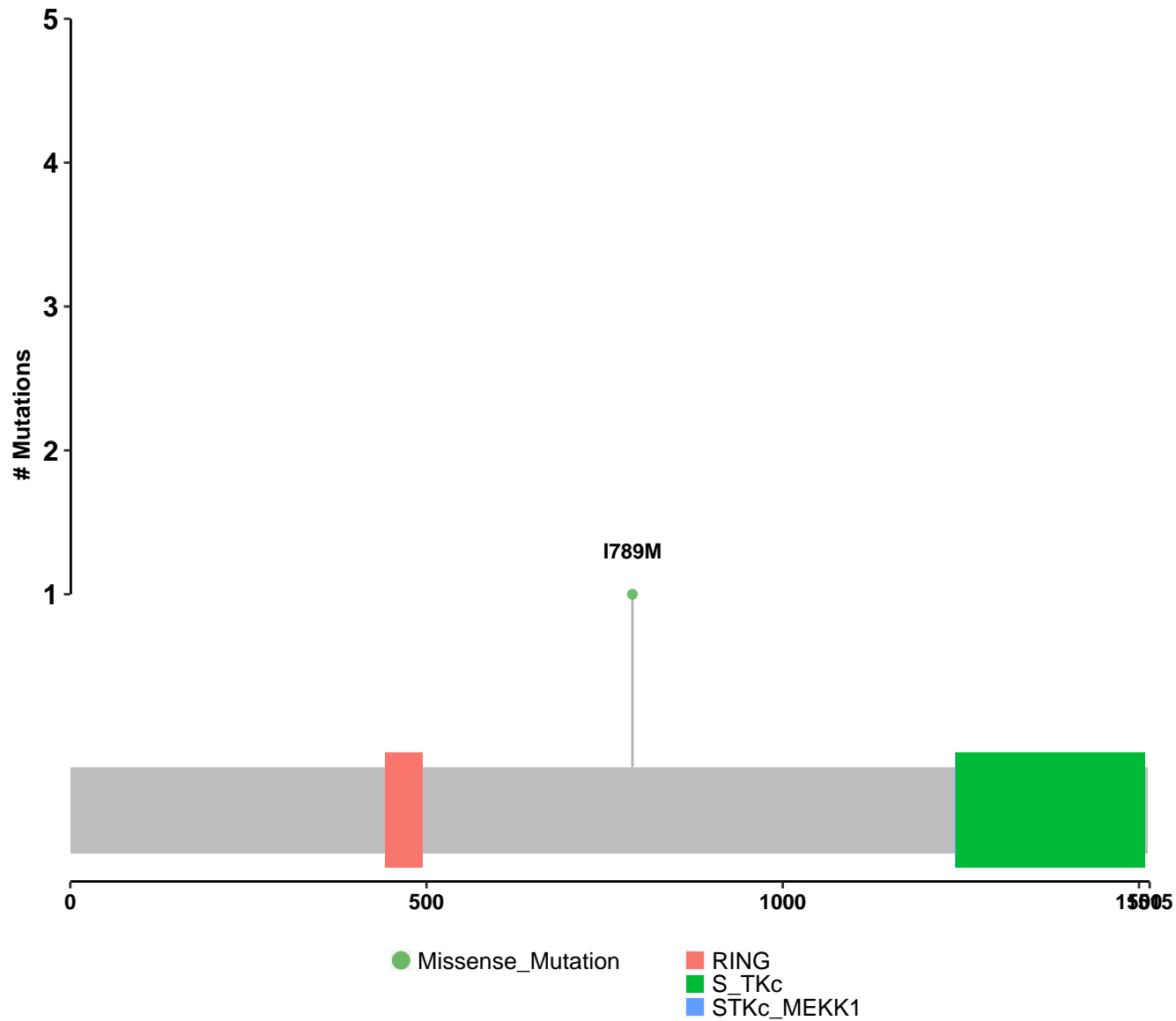
KDM2B: [Somatic Mutation Rate: 6.06%]

NM_032590



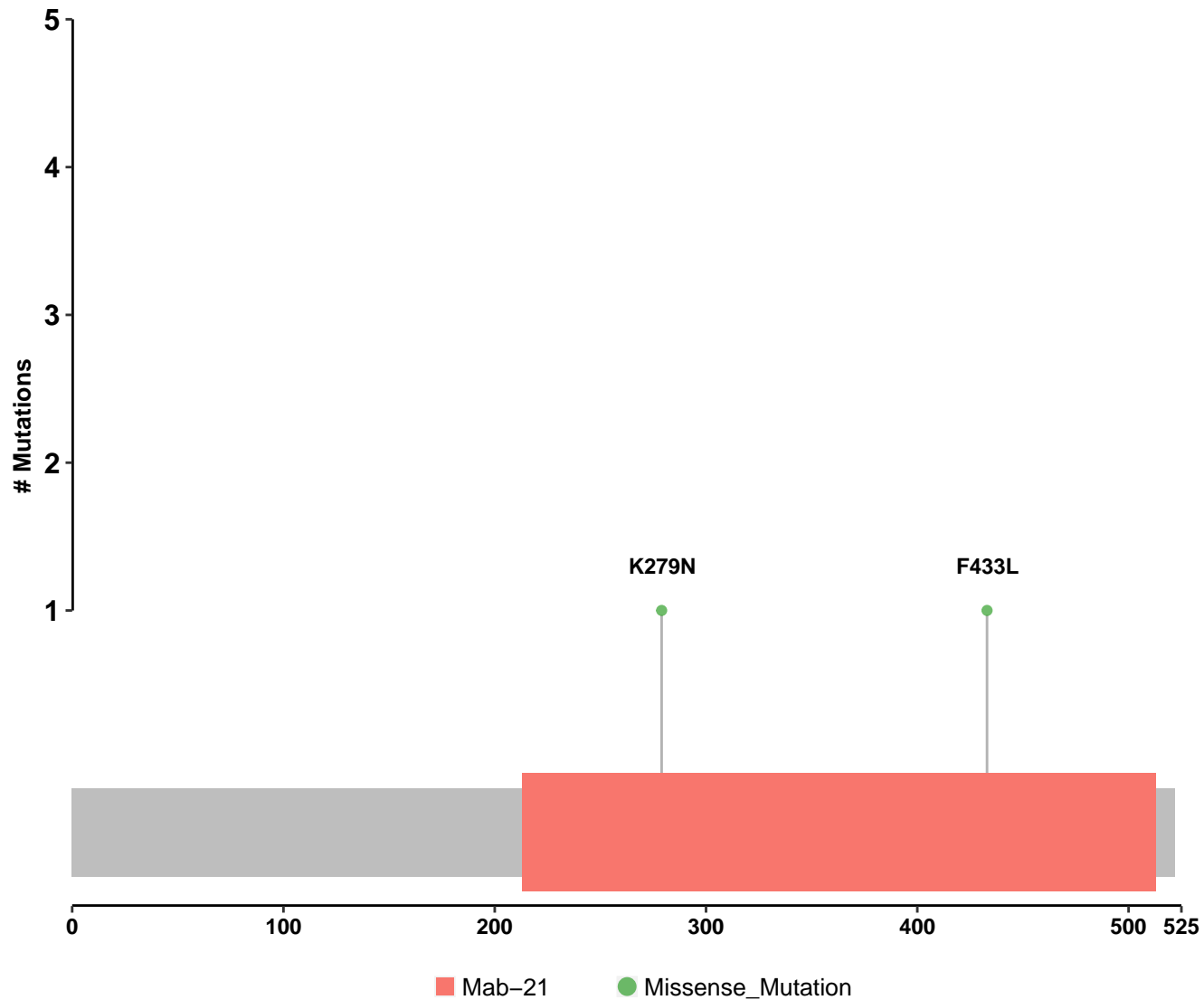
MAP3K1: [Somatic Mutation Rate: 3.03%]

NM_005921



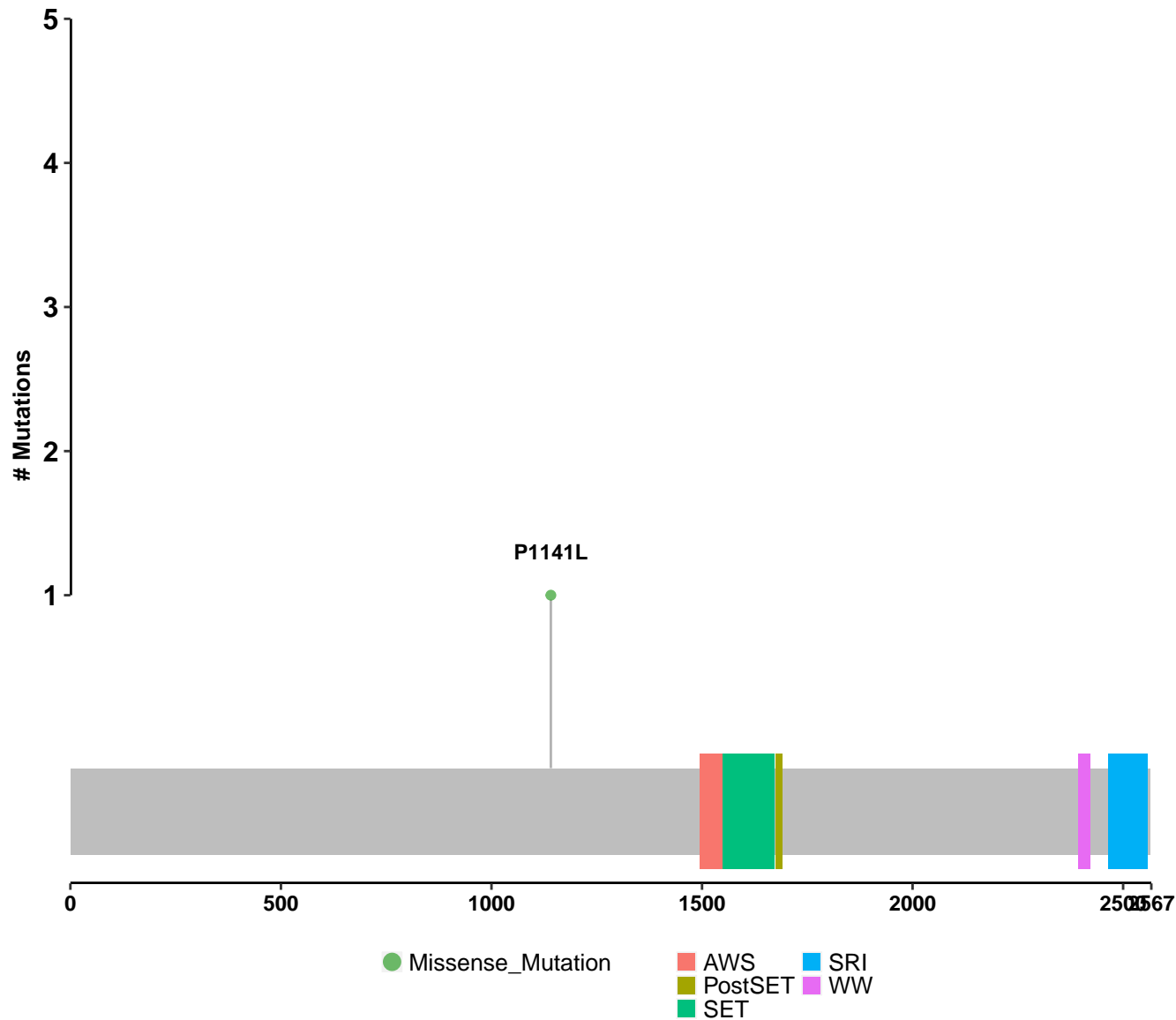
MB21D1: [Somatic Mutation Rate: 6.06%]

NM_138441



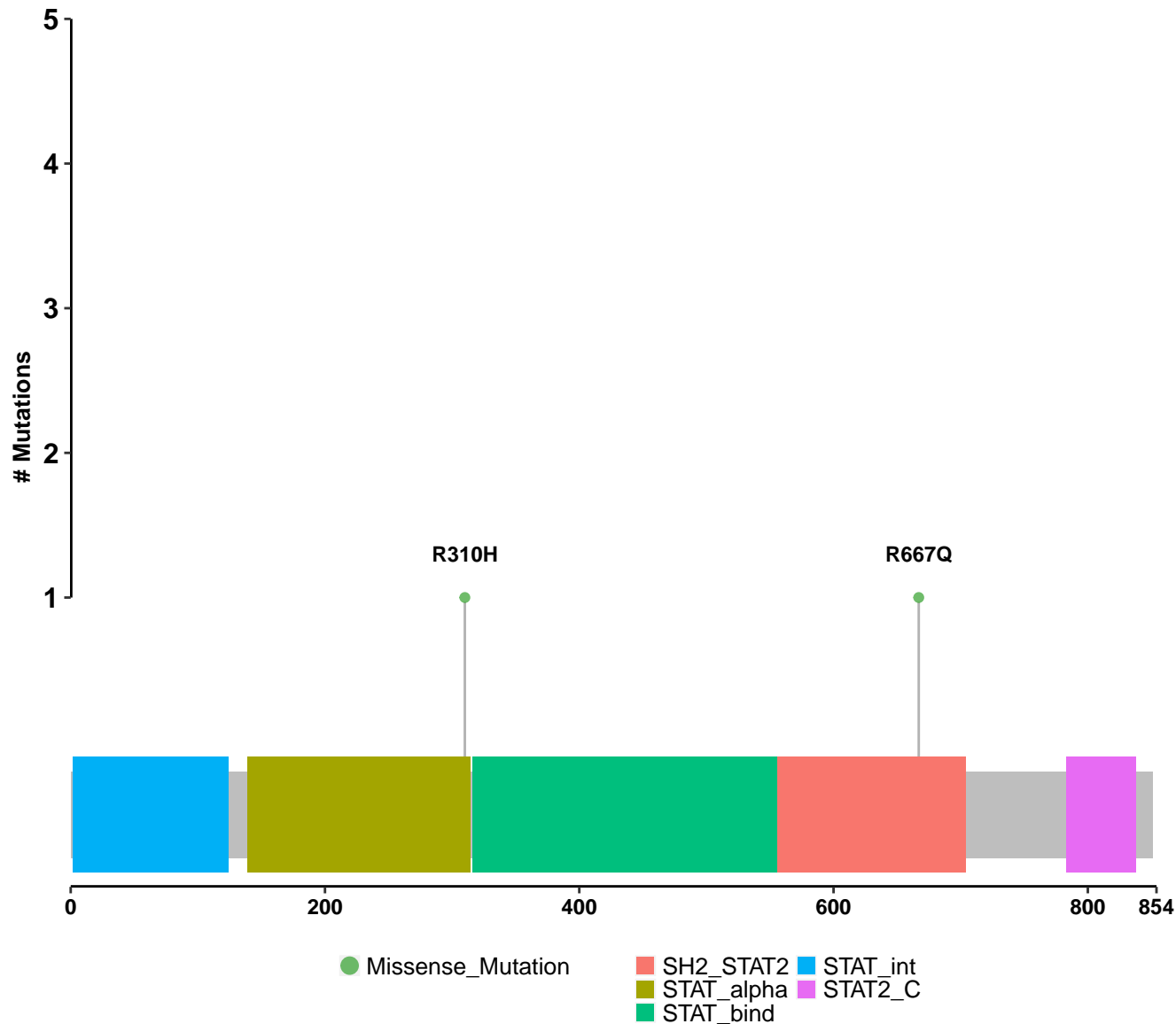
SETD2: [Somatic Mutation Rate: 3.03%]

NM_014159



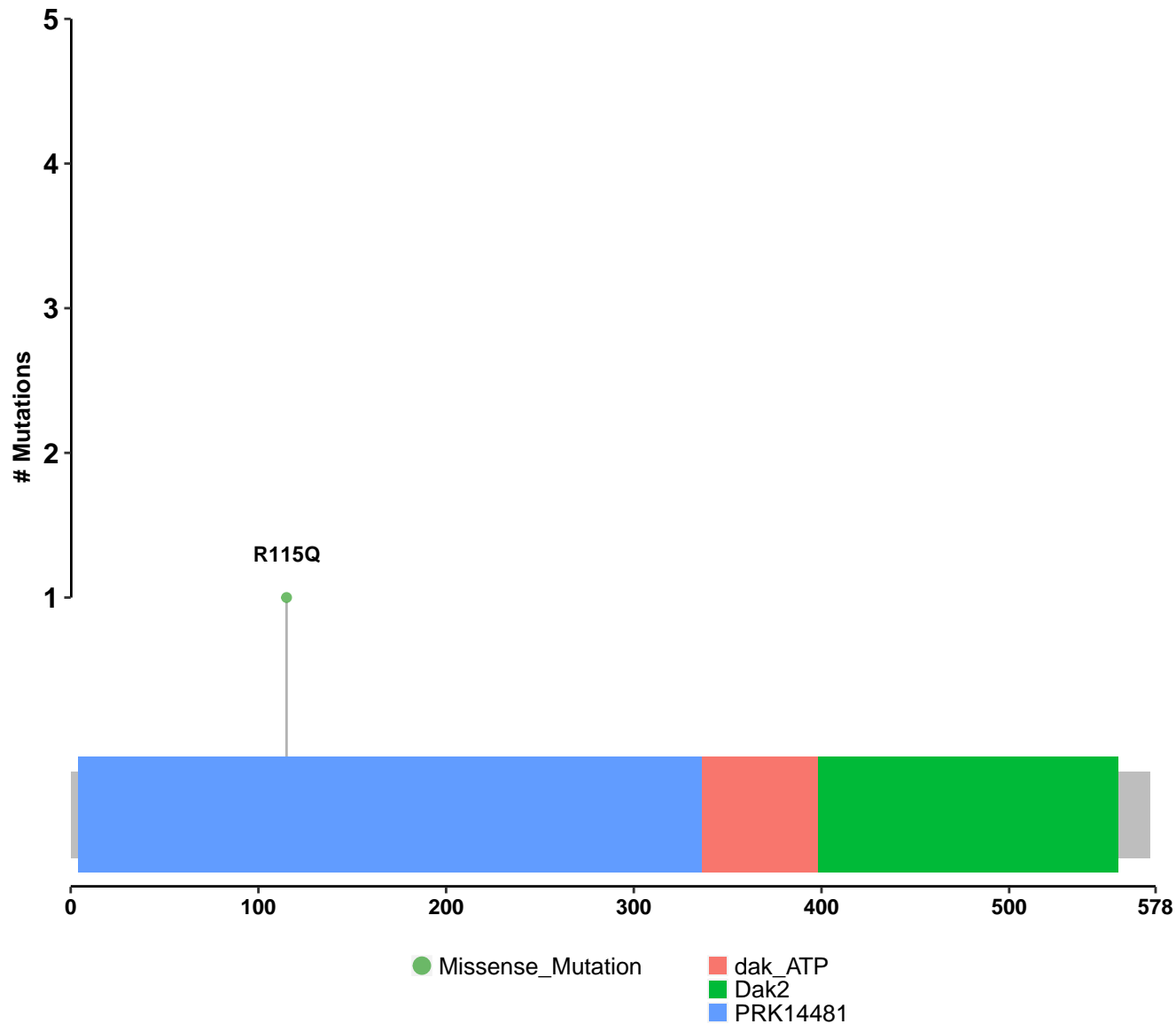
STAT2: [Somatic Mutation Rate: 6.06%]

NM_005419



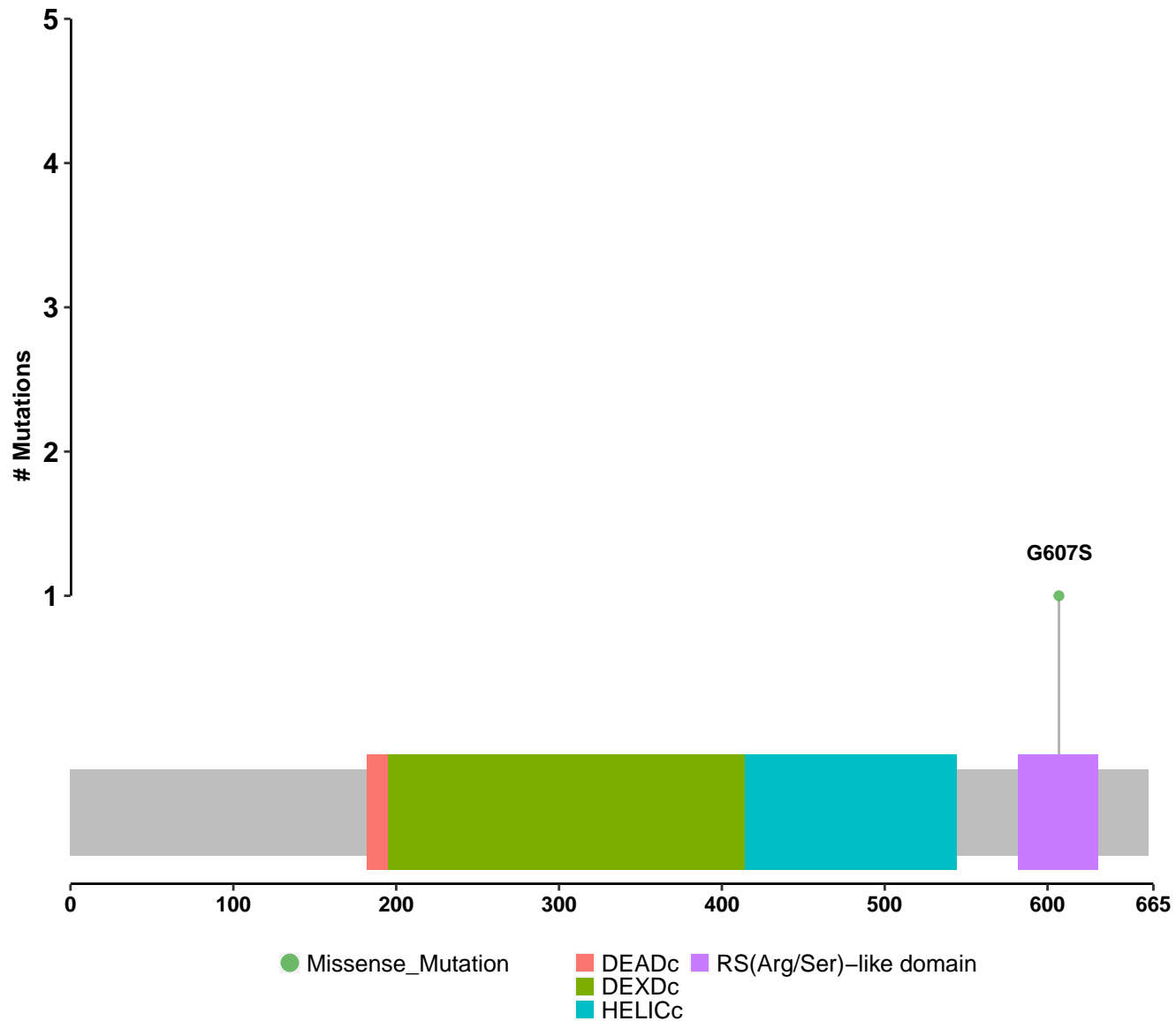
DAK: [Somatic Mutation Rate: 3.03%]

NM_015533



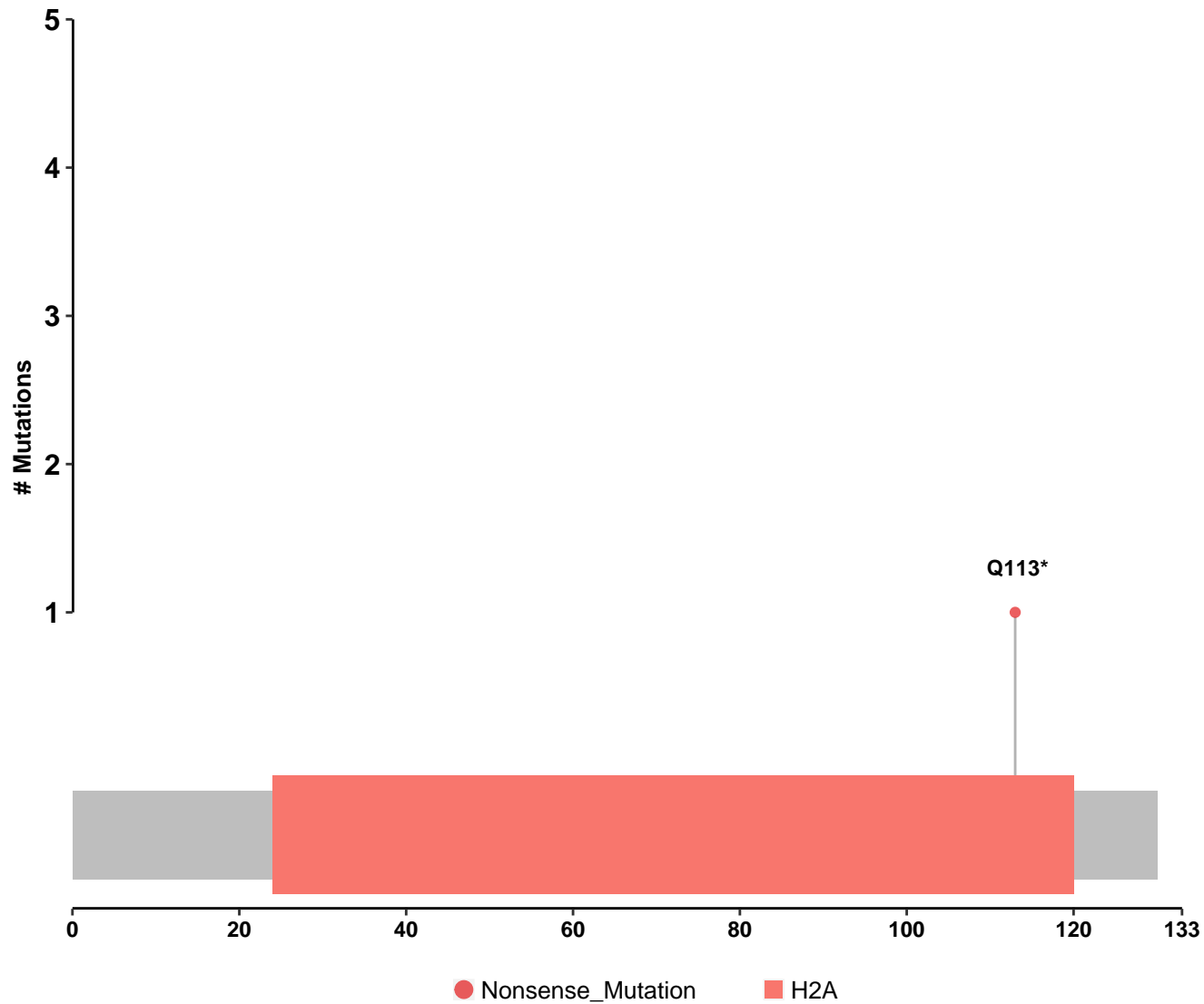
DDX3X: [Somatic Mutation Rate: 3.03%]

NM_001356



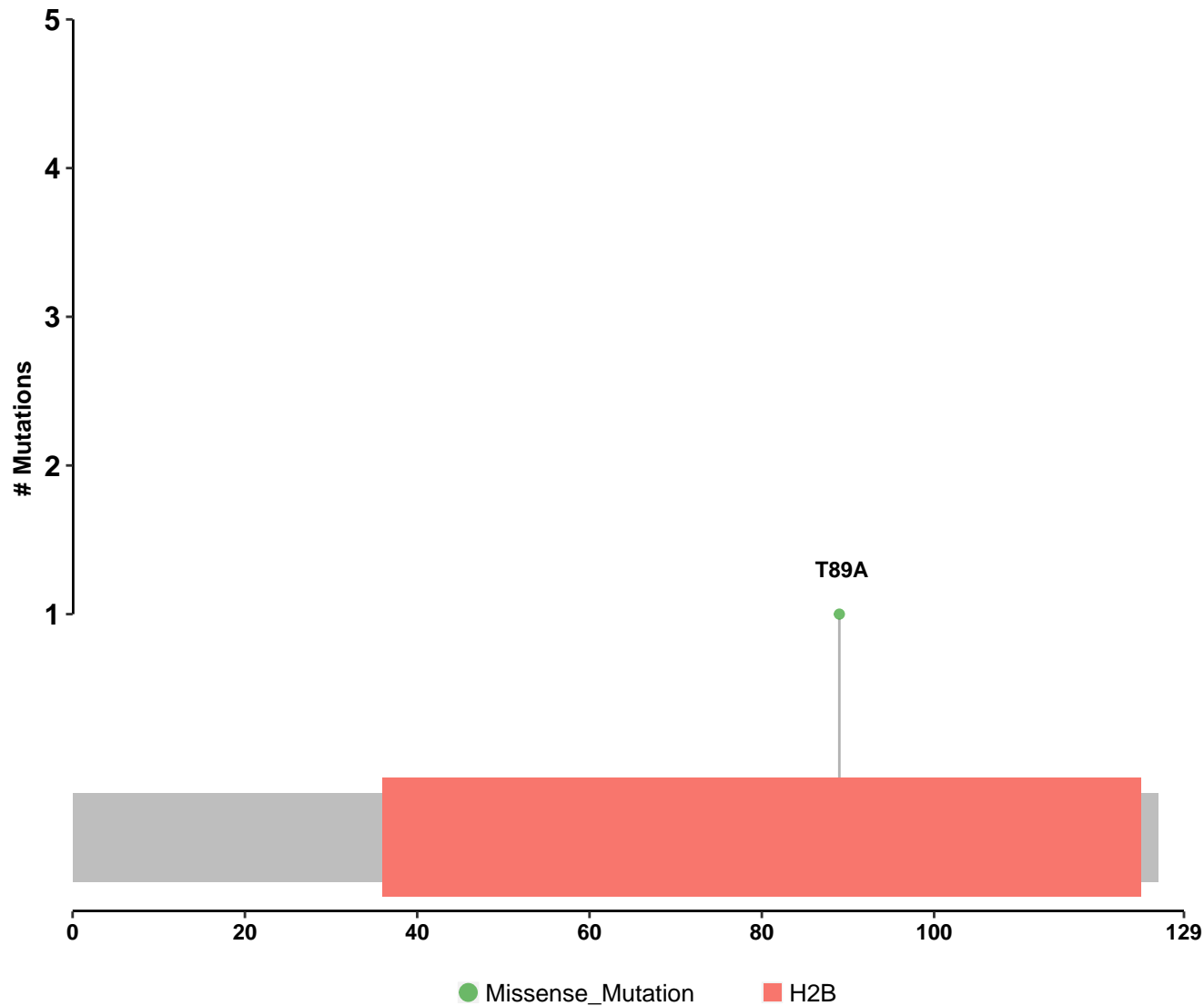
HIST1H2AM: [Somatic Mutation Rate: 3.03%]

NM_003514



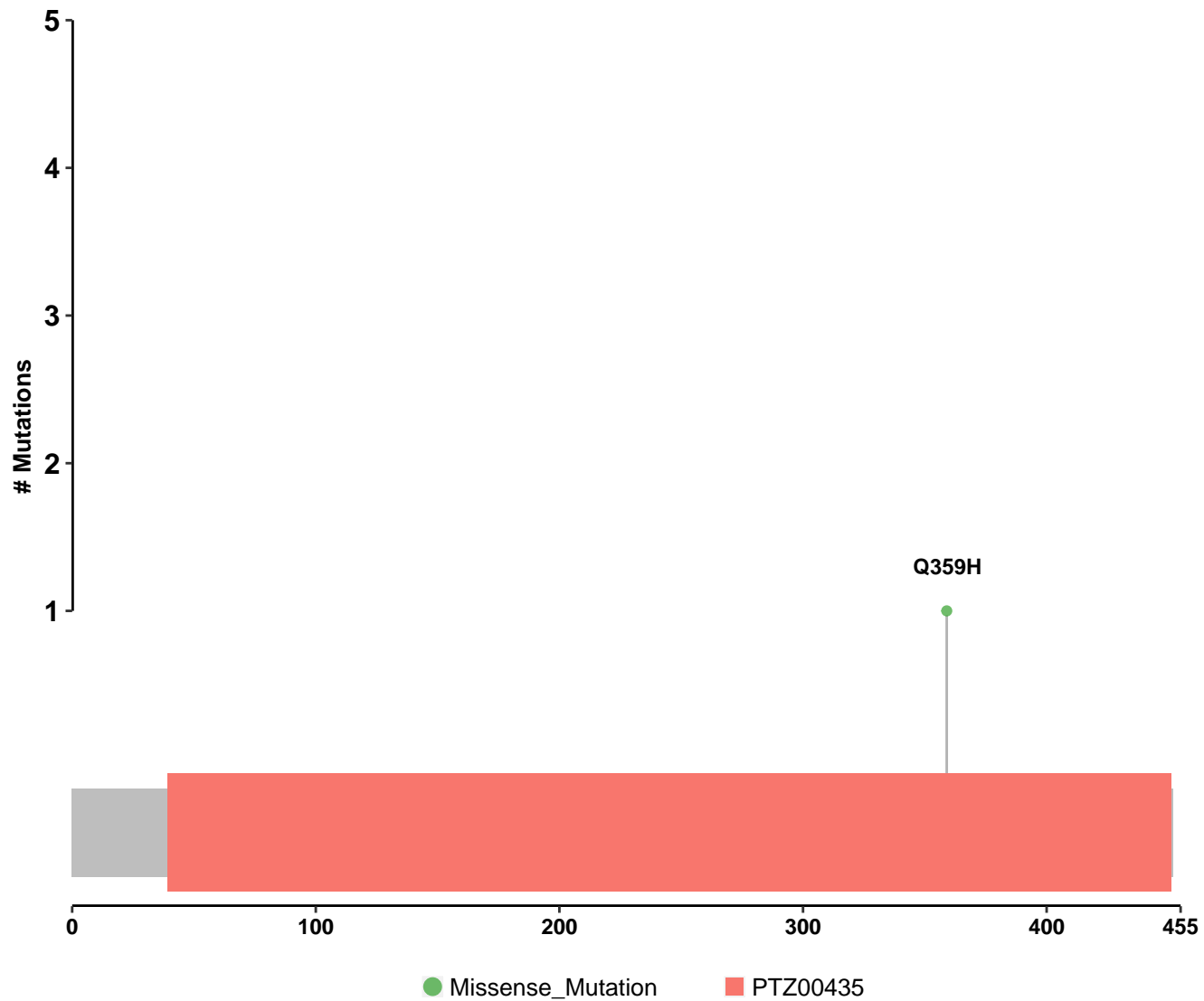
HIST1H2BK: [Somatic Mutation Rate: 3.03%]

NM_080593



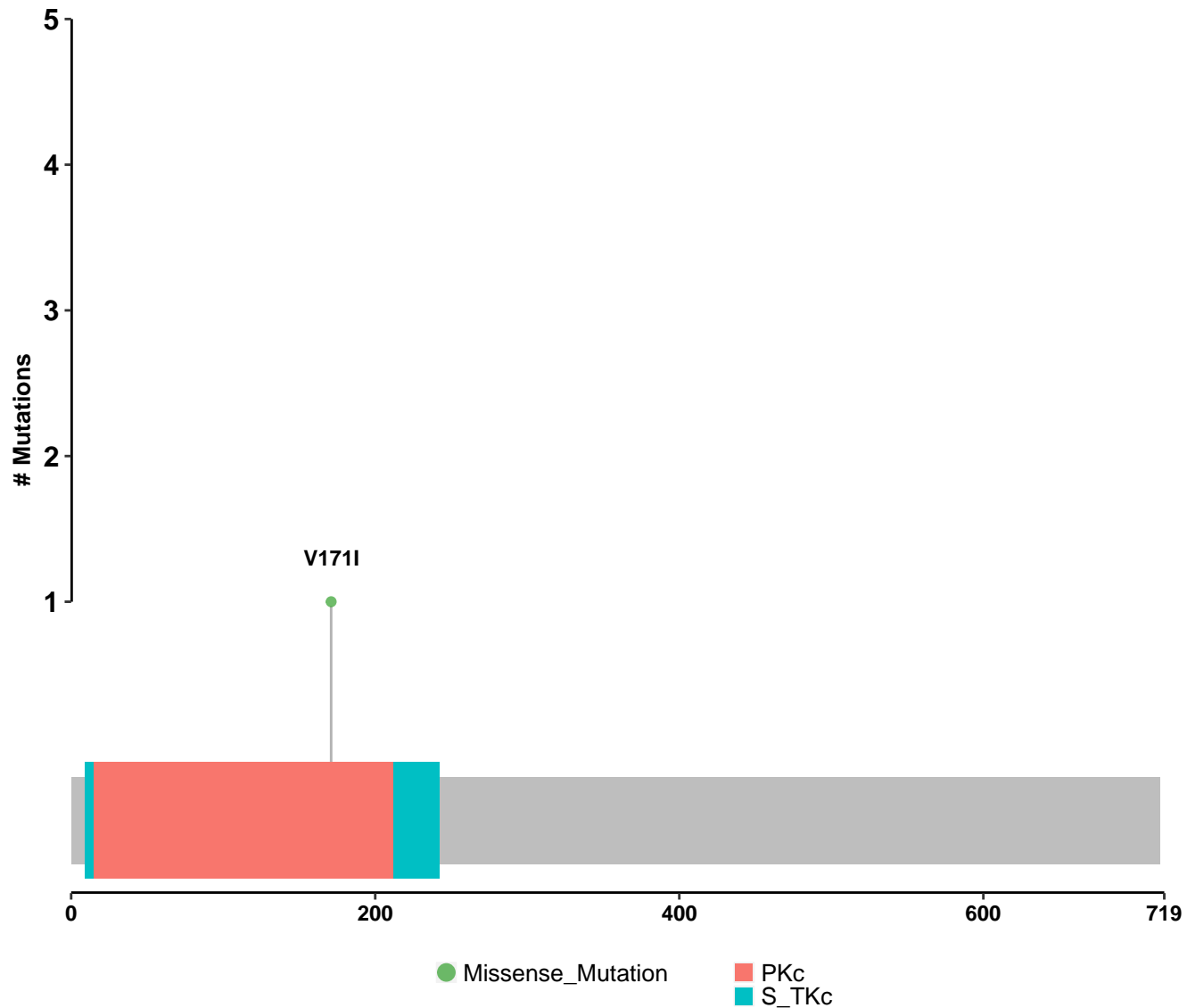
IDH2: [Somatic Mutation Rate: 3.03%]

NM_002168



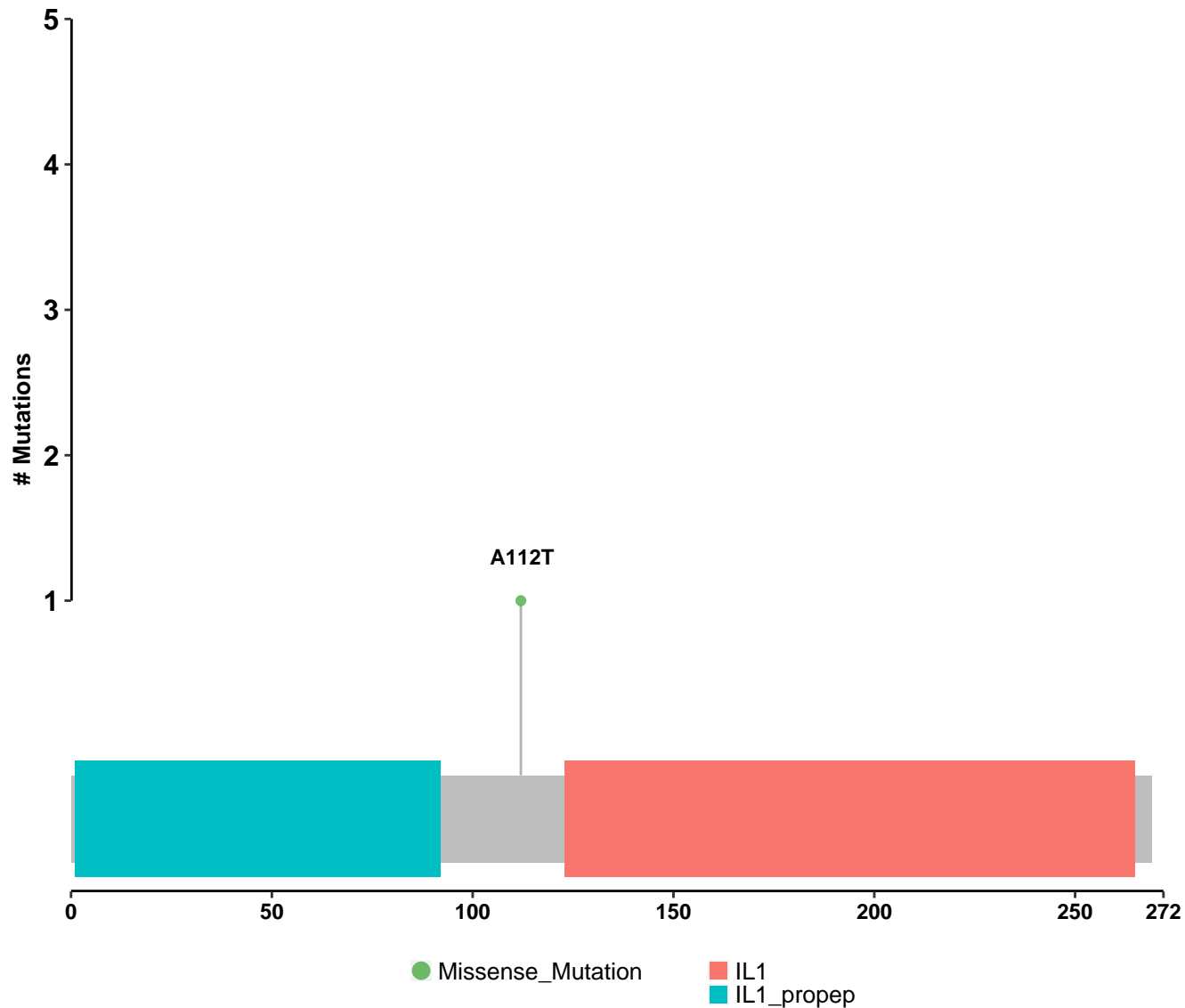
IKBKE: [Somatic Mutation Rate: 3.03%]

NM_014002



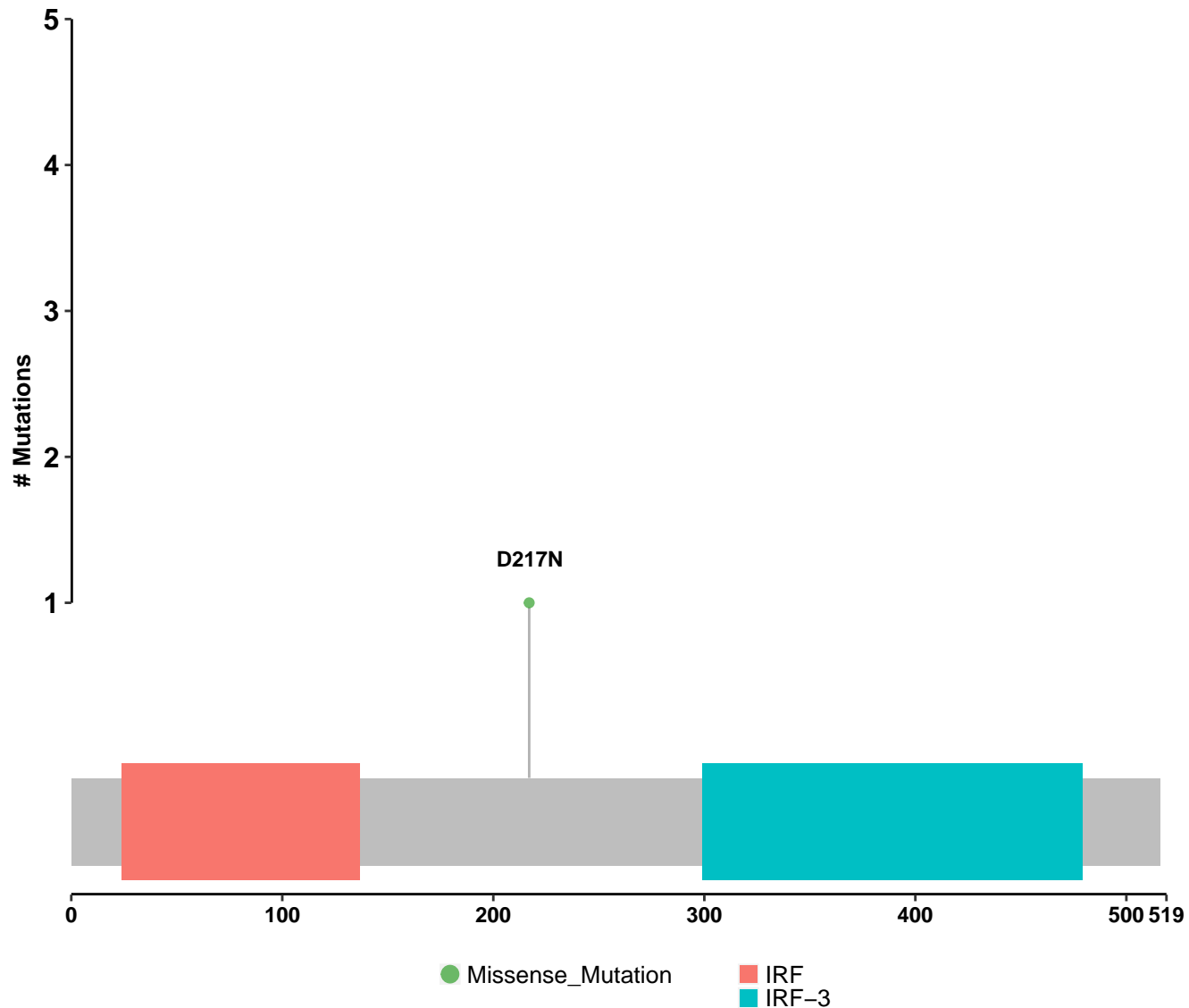
IL1B: [Somatic Mutation Rate: 3.03%]

NM_000576



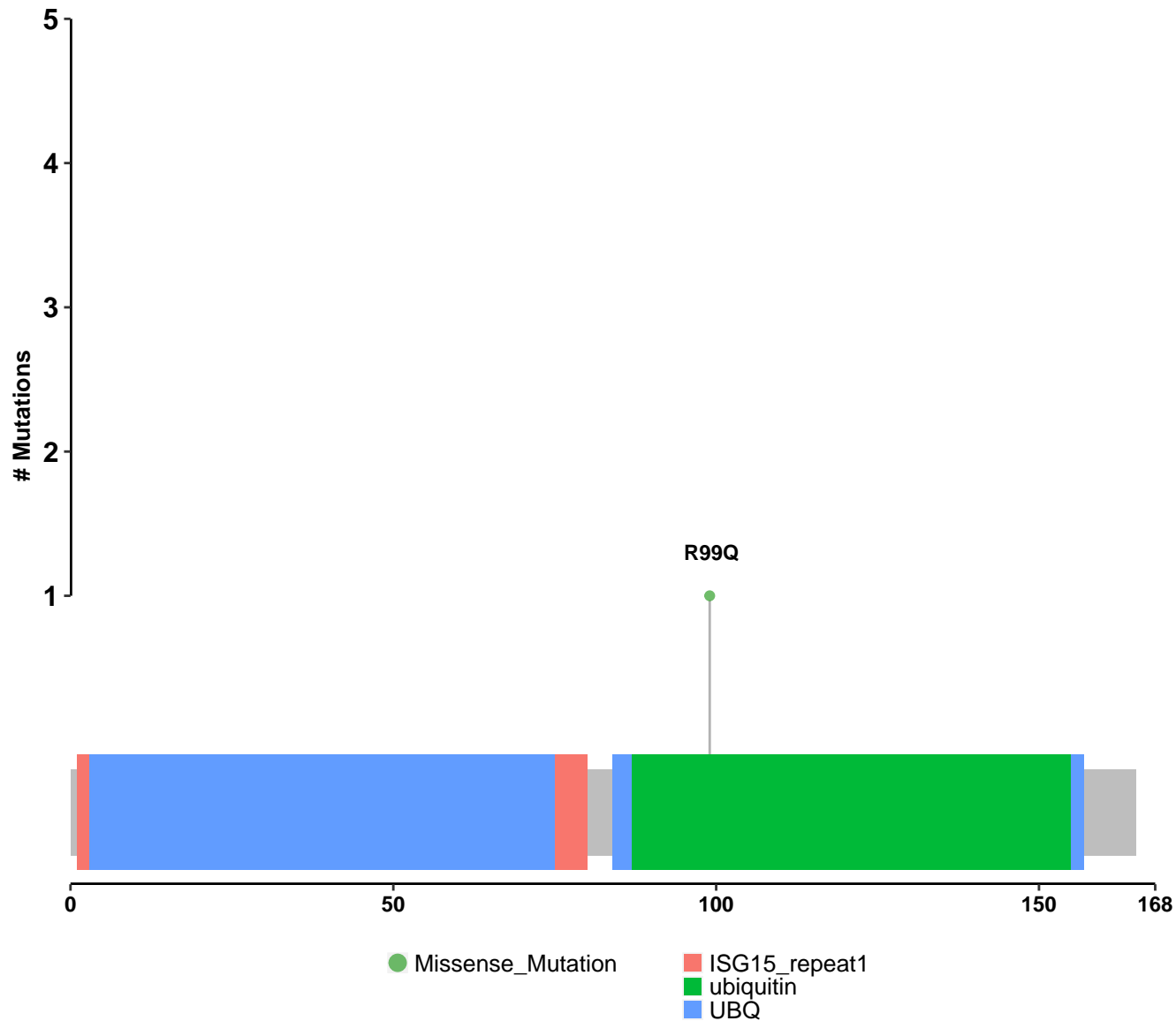
IRF7: [Somatic Mutation Rate: 3.03%]

NM_004031



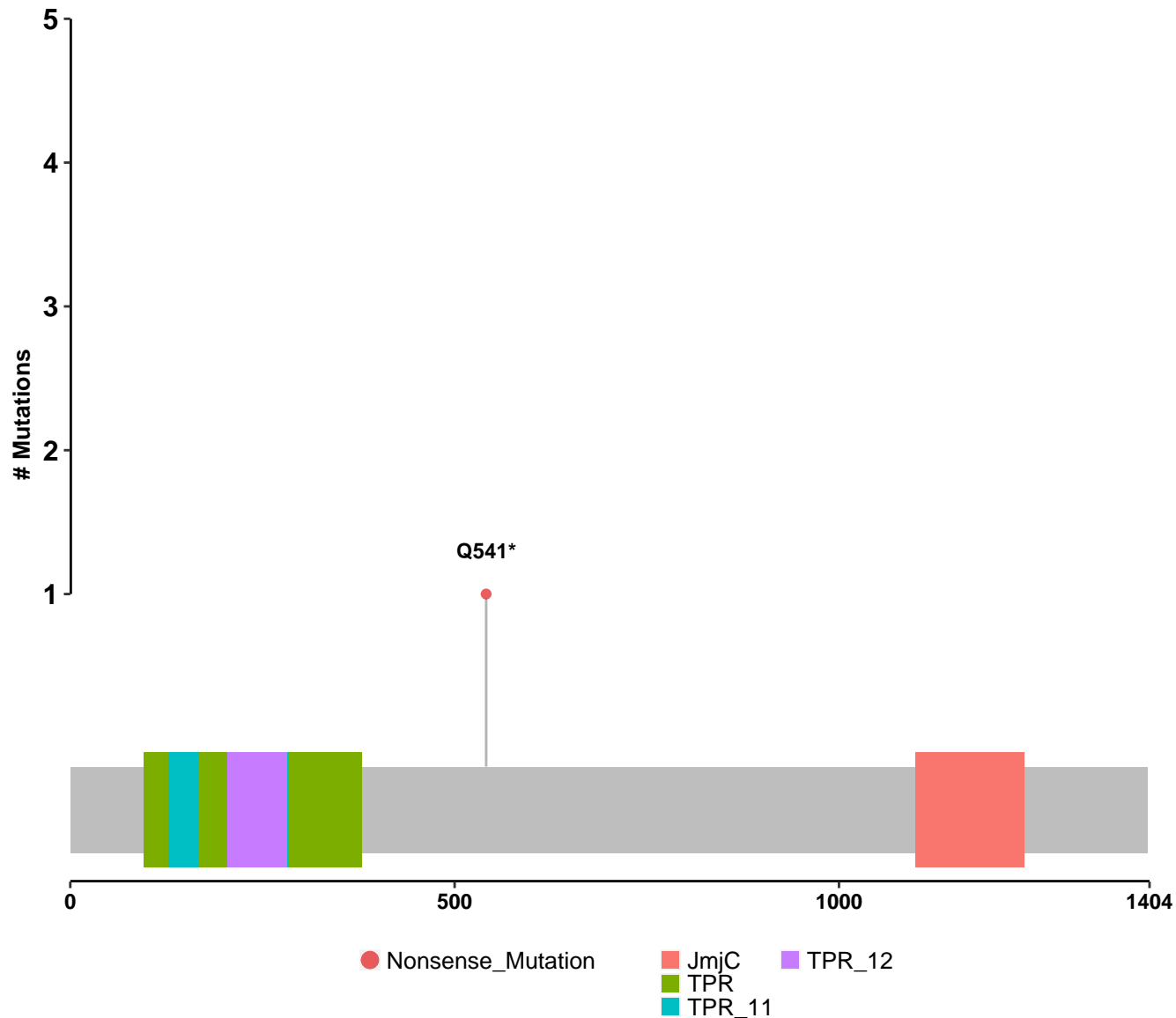
ISG15: [Somatic Mutation Rate: 3.03%]

NM_005101



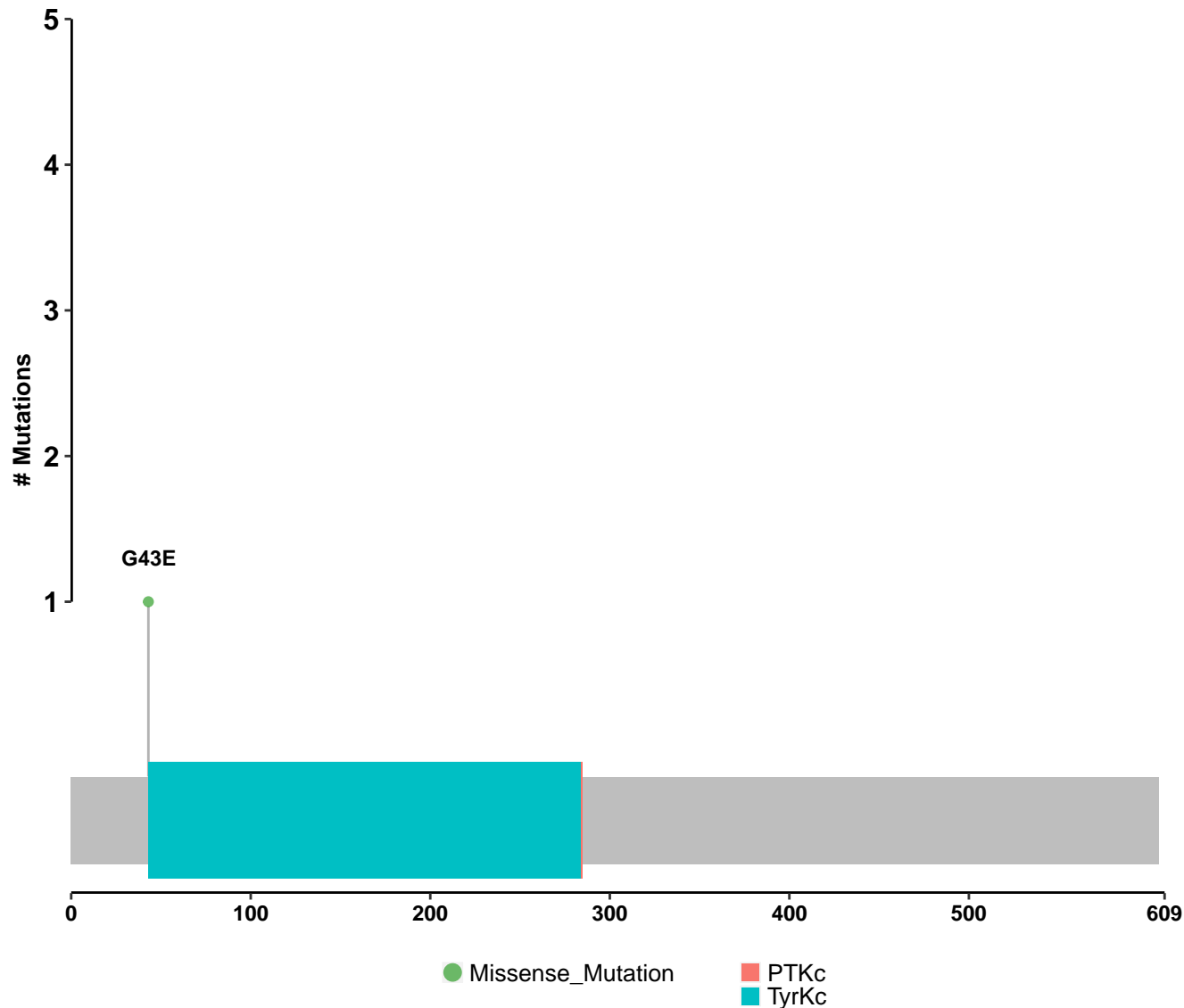
KDM6A: [Somatic Mutation Rate: 3.03%]

NM_021140



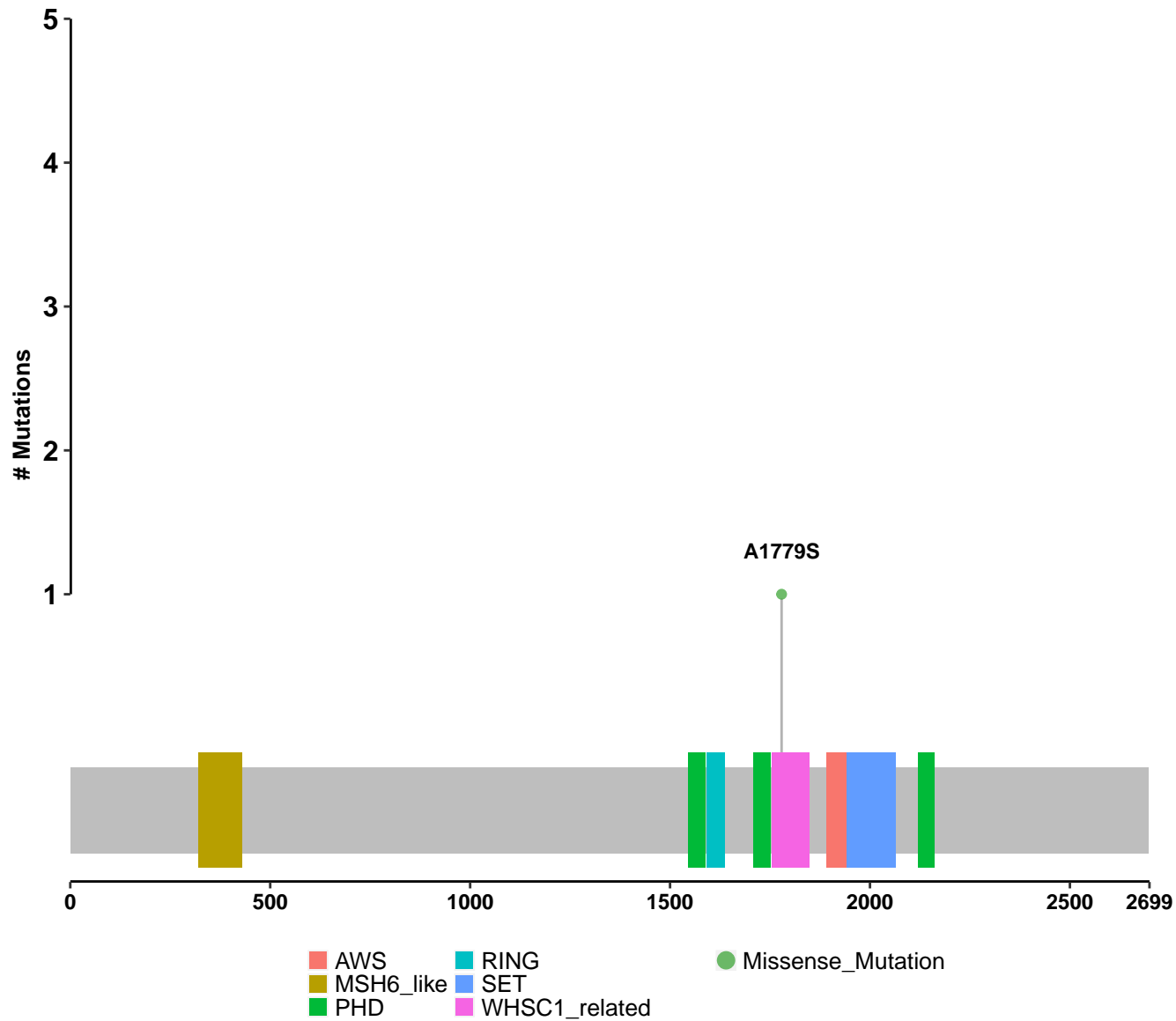
MAP3K7: [Somatic Mutation Rate: 3.03%]

NM_145331



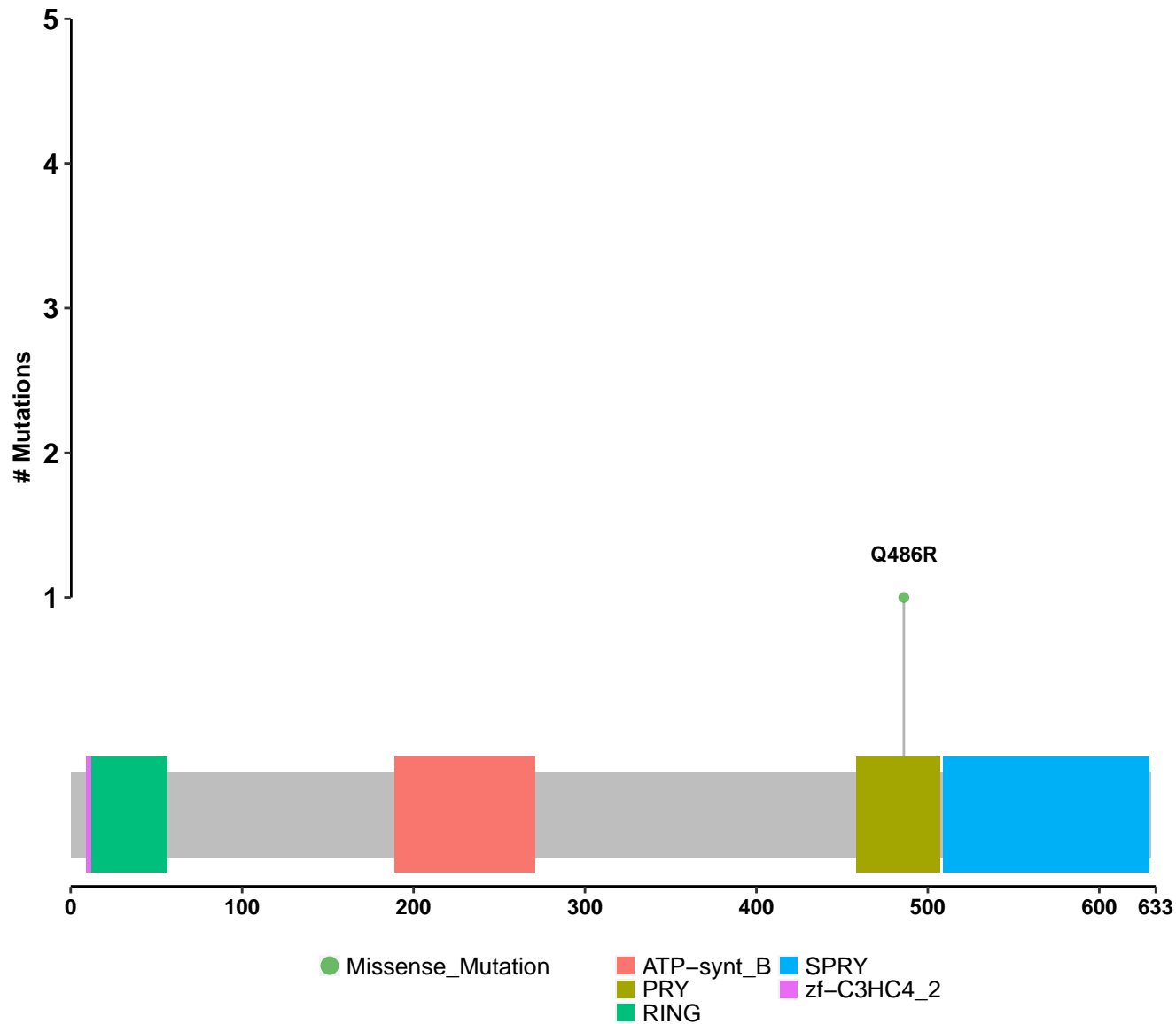
NSD1: [Somatic Mutation Rate: 3.03%]

NM_022455



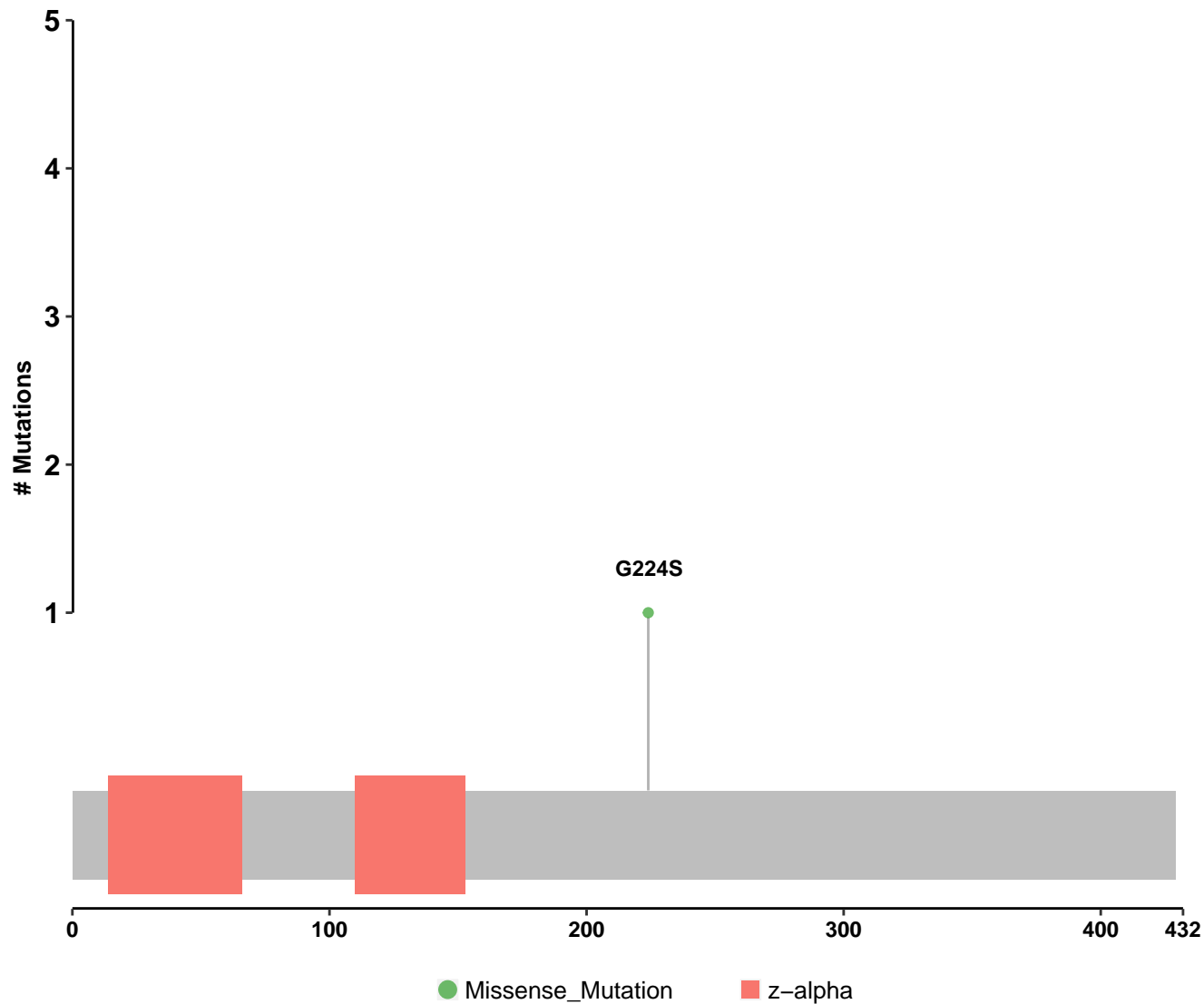
TRIM25: [Somatic Mutation Rate: 3.03%]

NM_005082



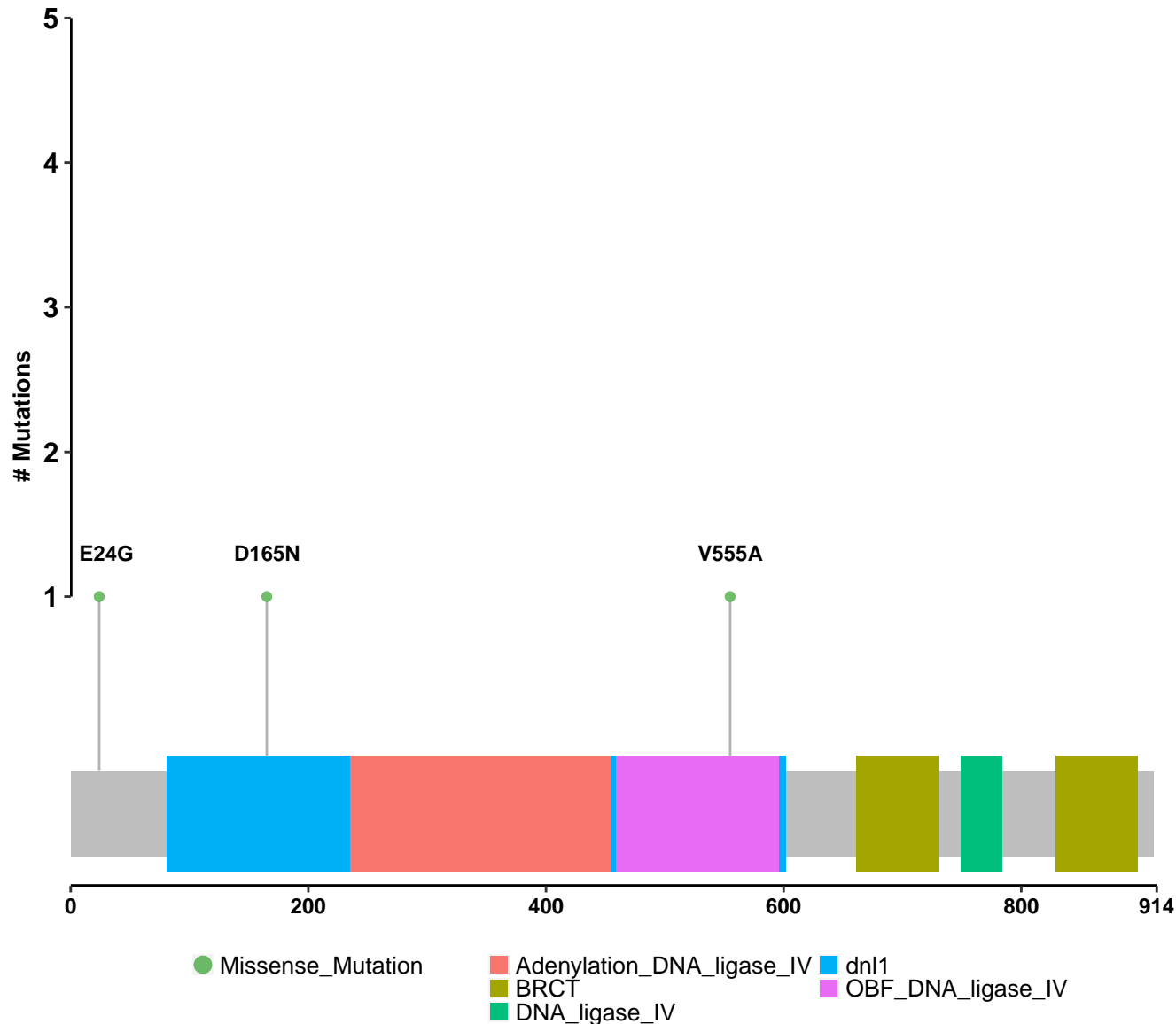
ZBP1: [Somatic Mutation Rate: 3.03%]

NM_030776



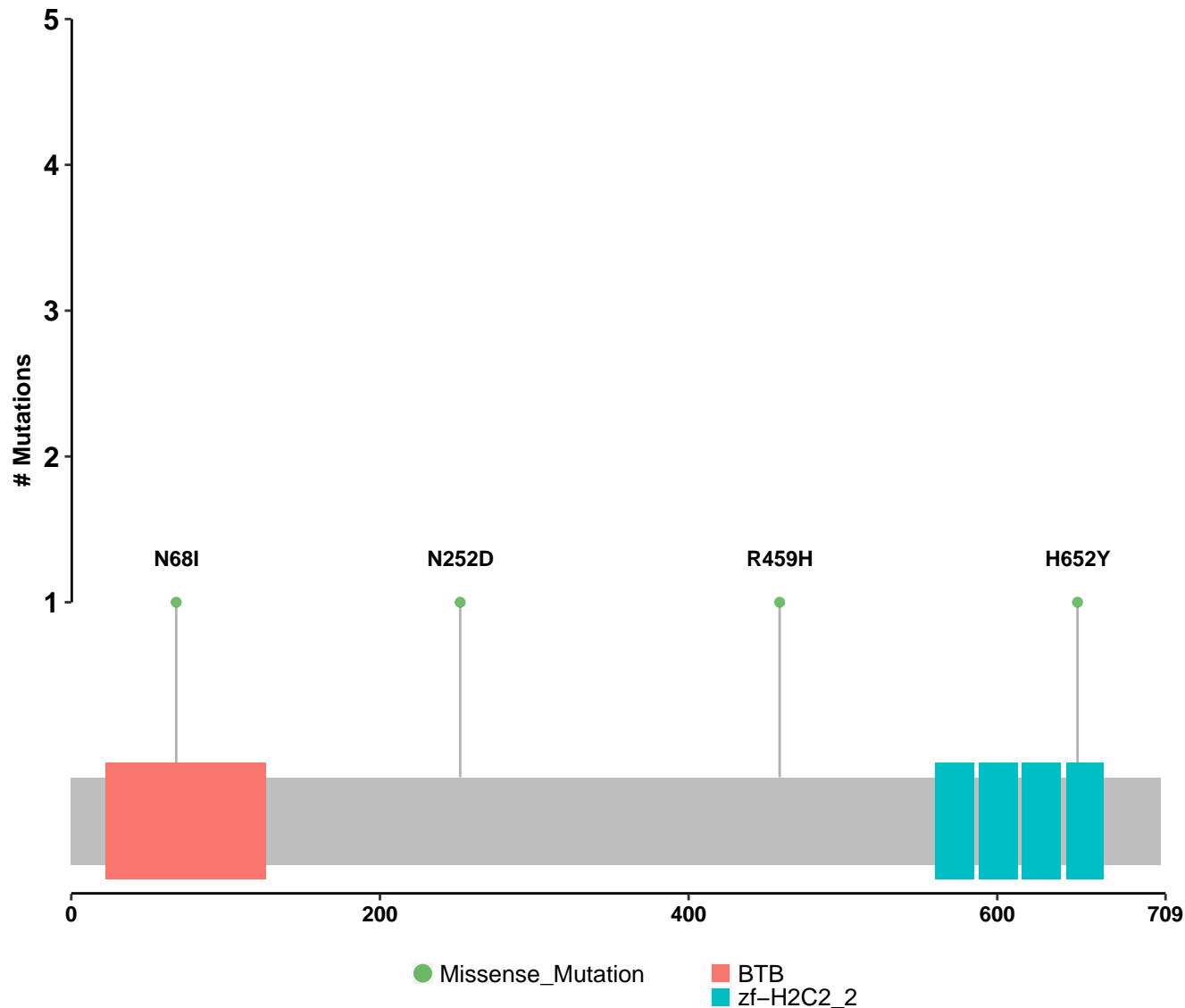
LIG4: [Somatic Mutation Rate: 9.09%]

NM_001098268



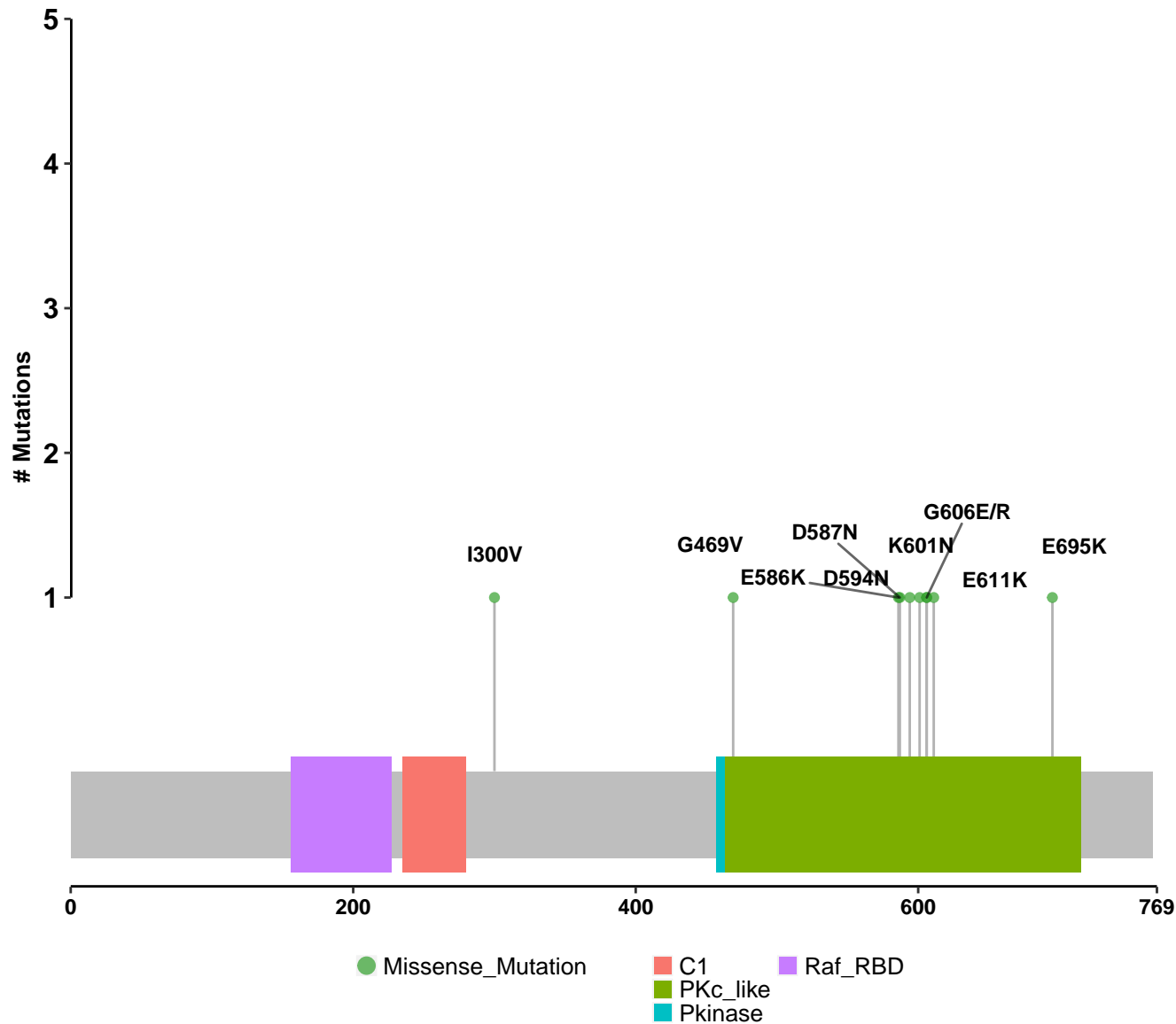
BCL6: [Somatic Mutation Rate: 12.12%]

NM_001130845



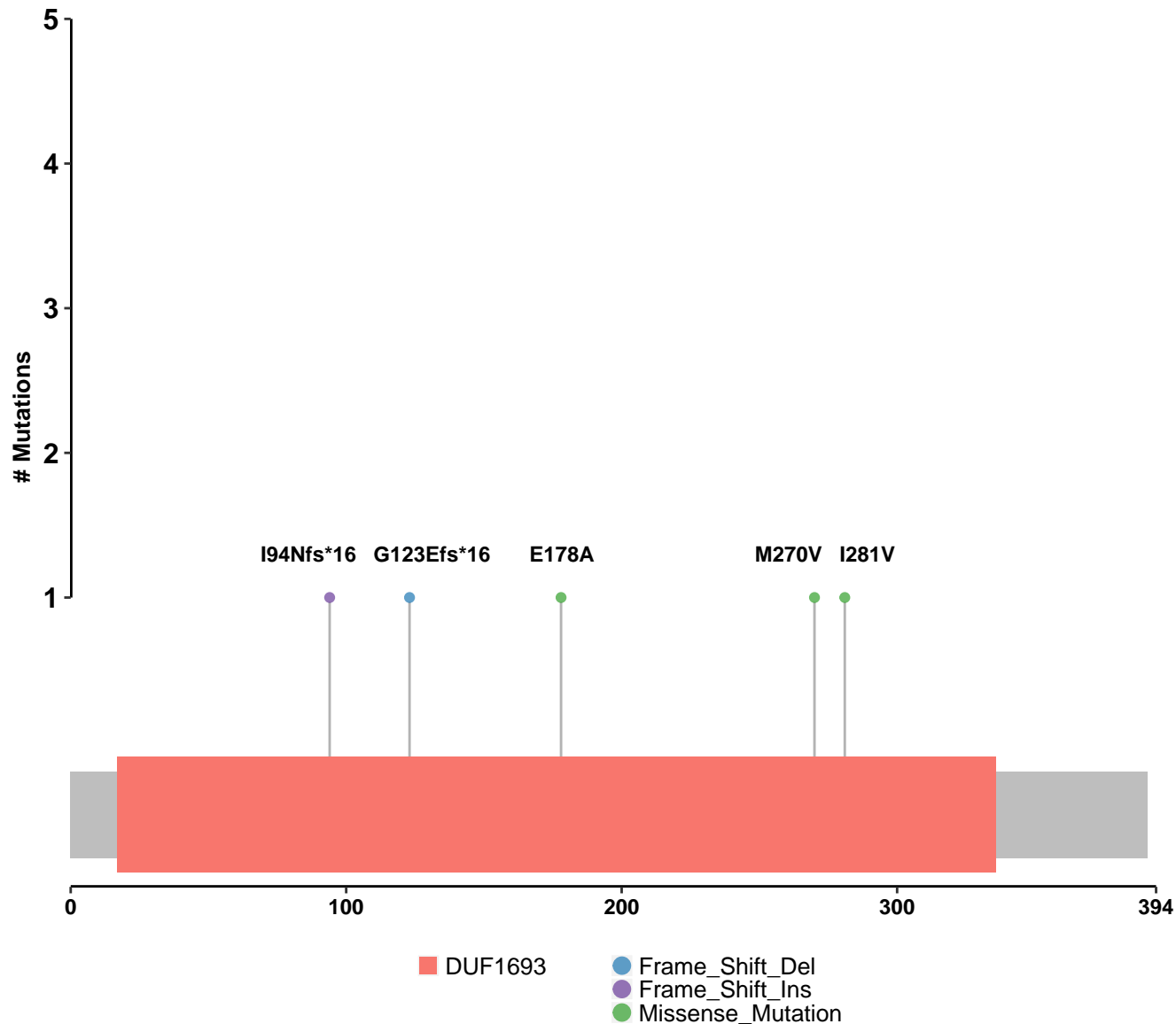
BRAF: [Somatic Mutation Rate: 15.15%]

NM_004333



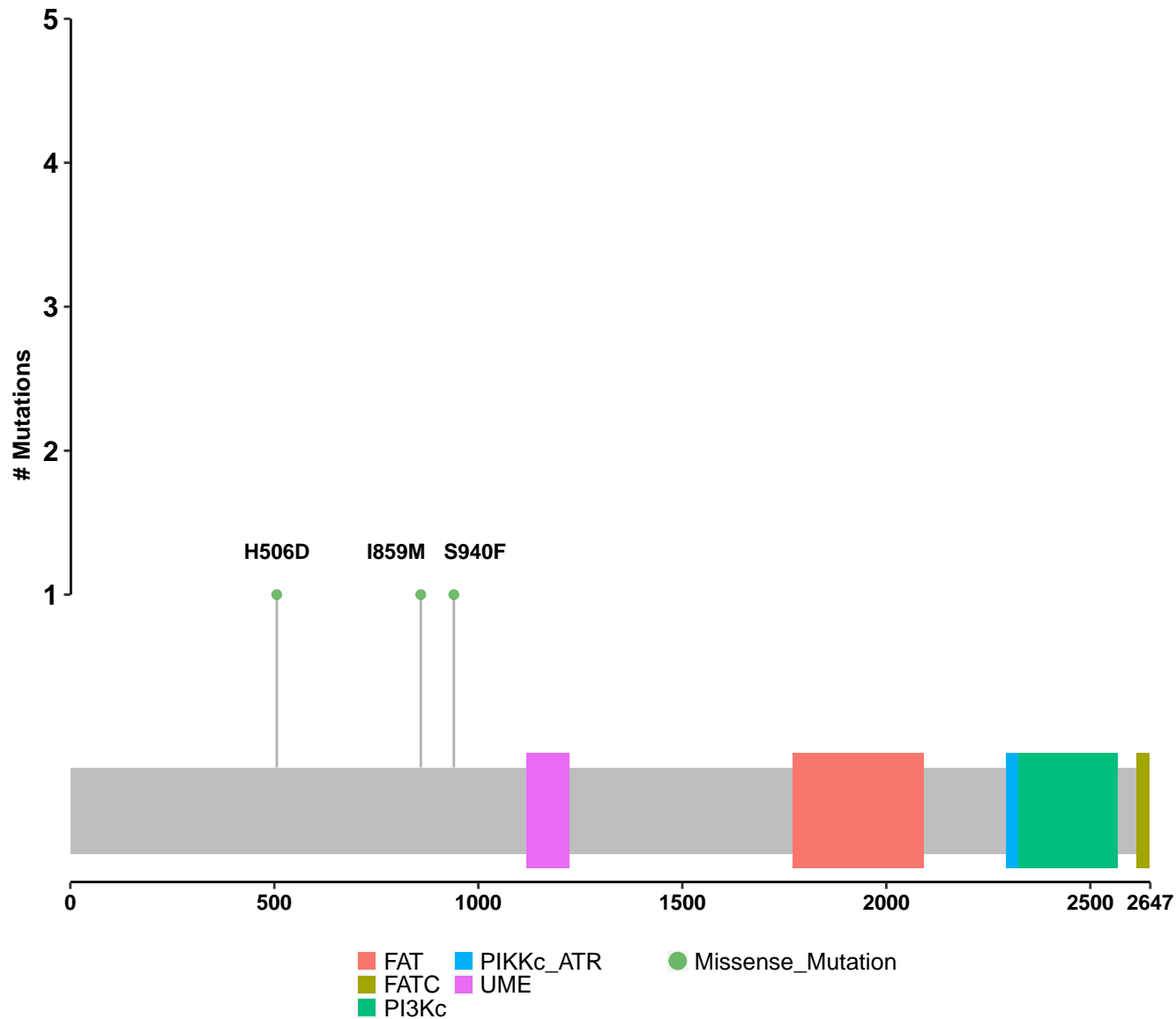
FAM46C: [Somatic Mutation Rate: 15.15%]

NM_017709



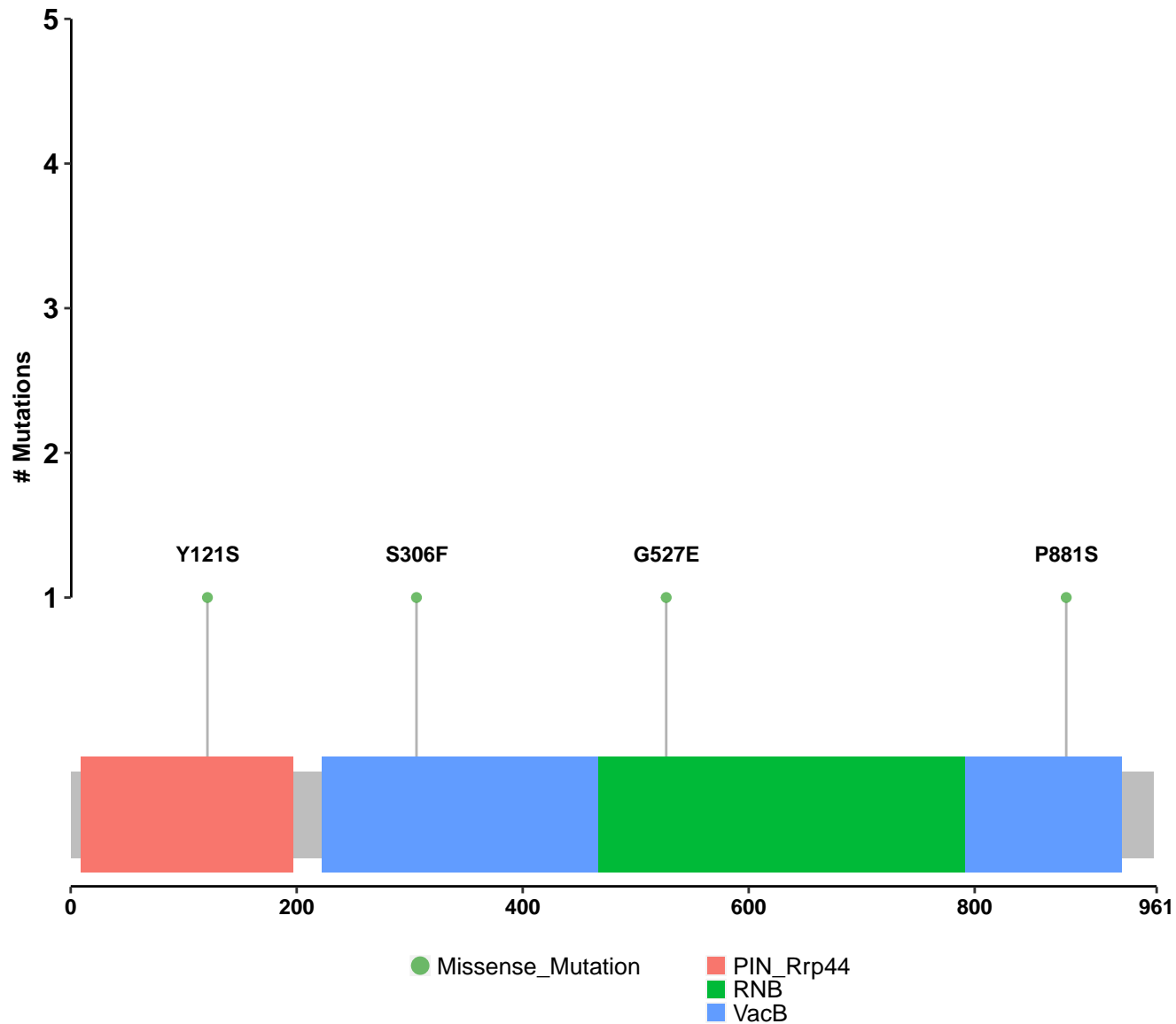
ATR: [Somatic Mutation Rate: 9.09%]

NM_001184



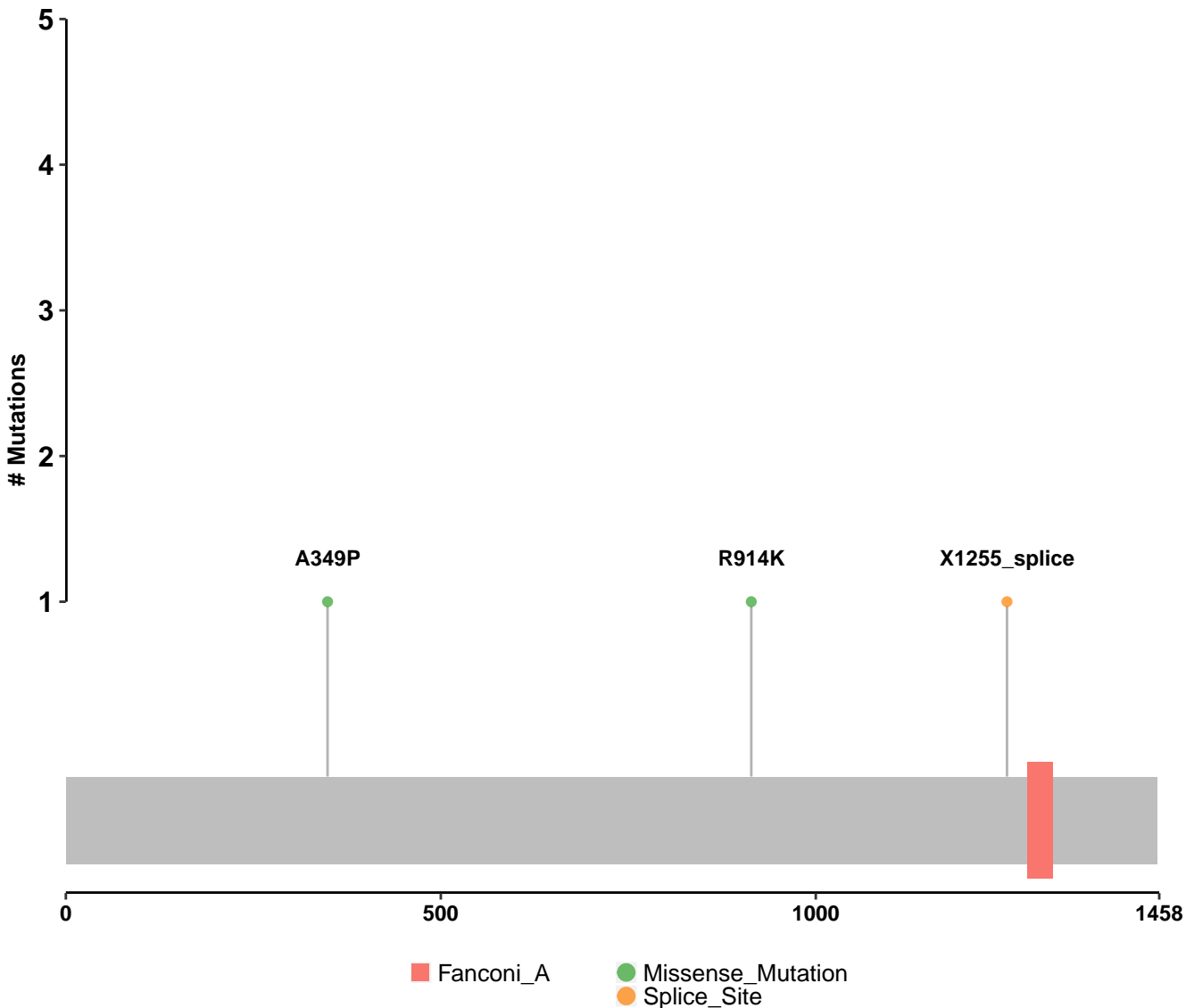
DIS3: [Somatic Mutation Rate: 12.12%]

NM_014953



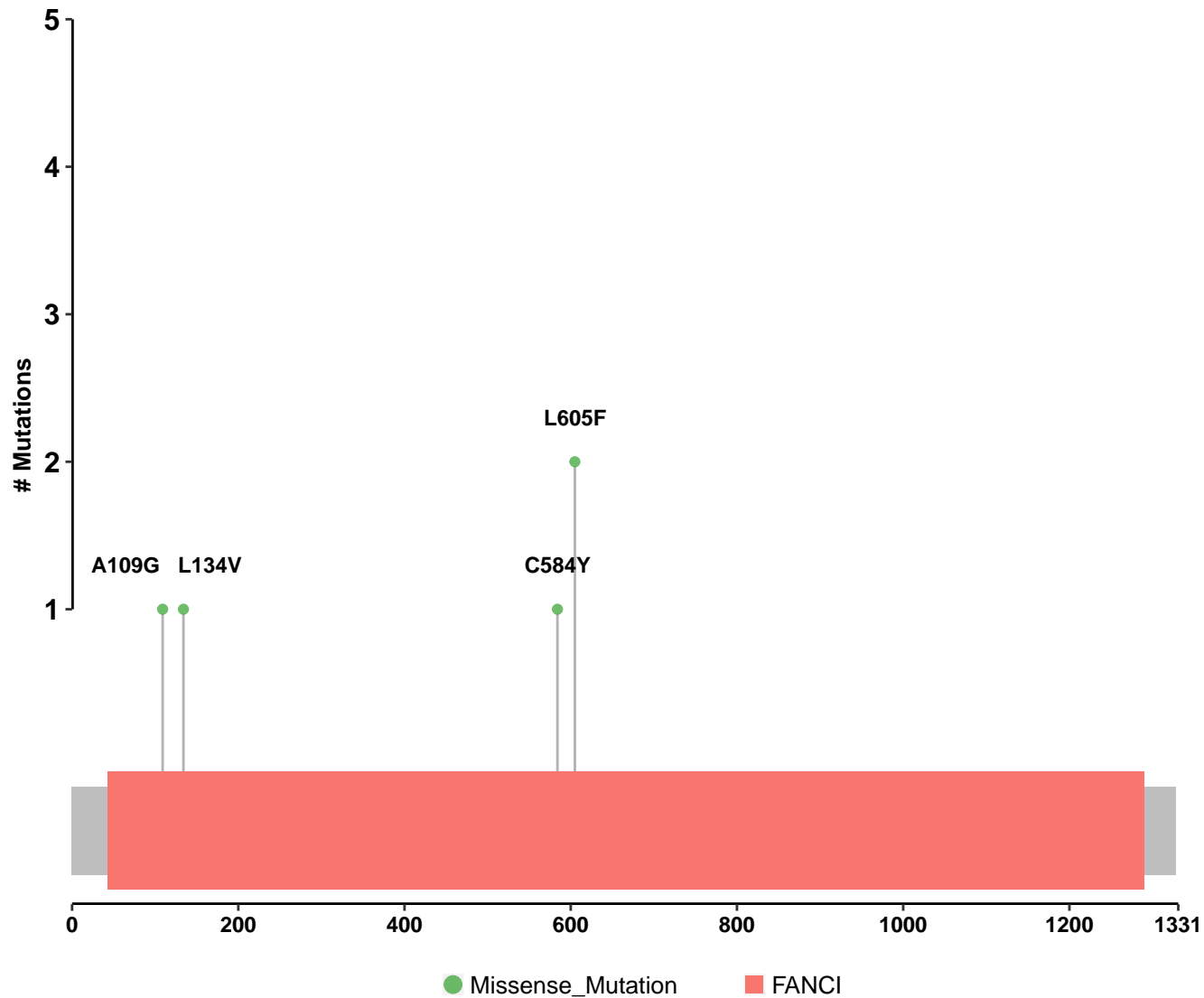
FANCA: [Somatic Mutation Rate: 9.09%]

NM_000135



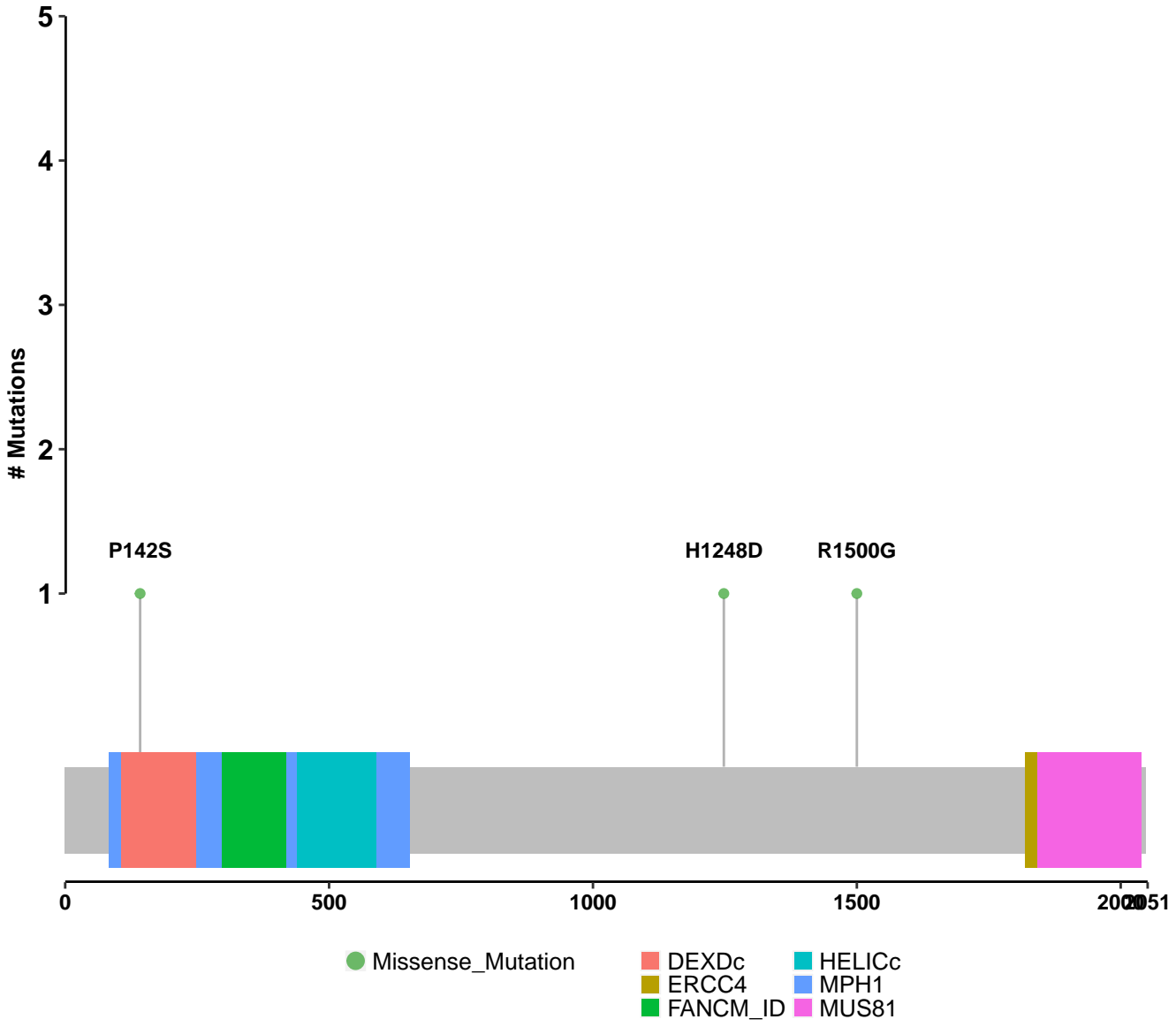
FANCI: [Somatic Mutation Rate: 12.12%]

NM_001113378



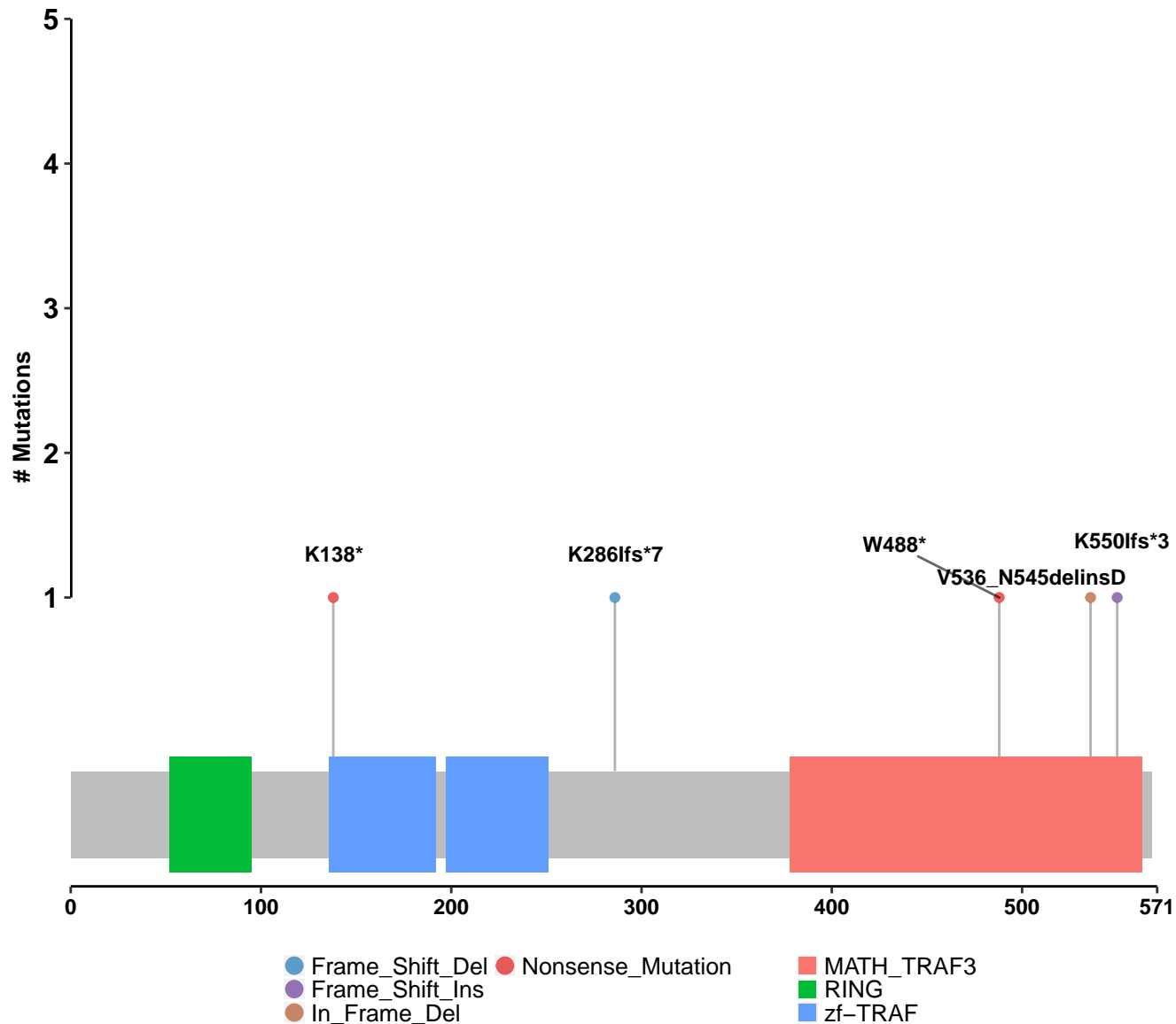
FANCM: [Somatic Mutation Rate: 9.09%]

NM_020937



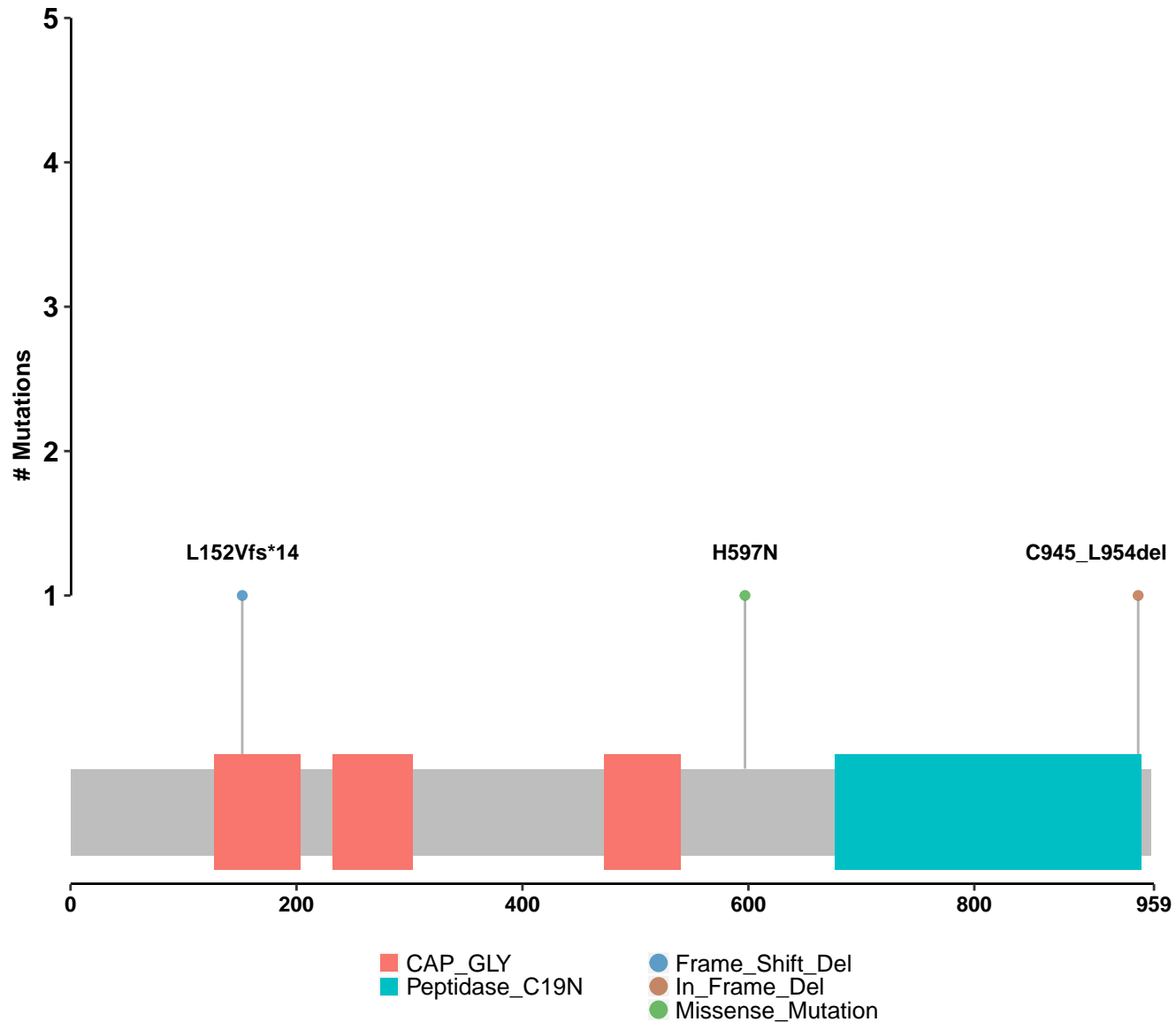
TRAF3: [Somatic Mutation Rate: 12.12%]

NM_145725



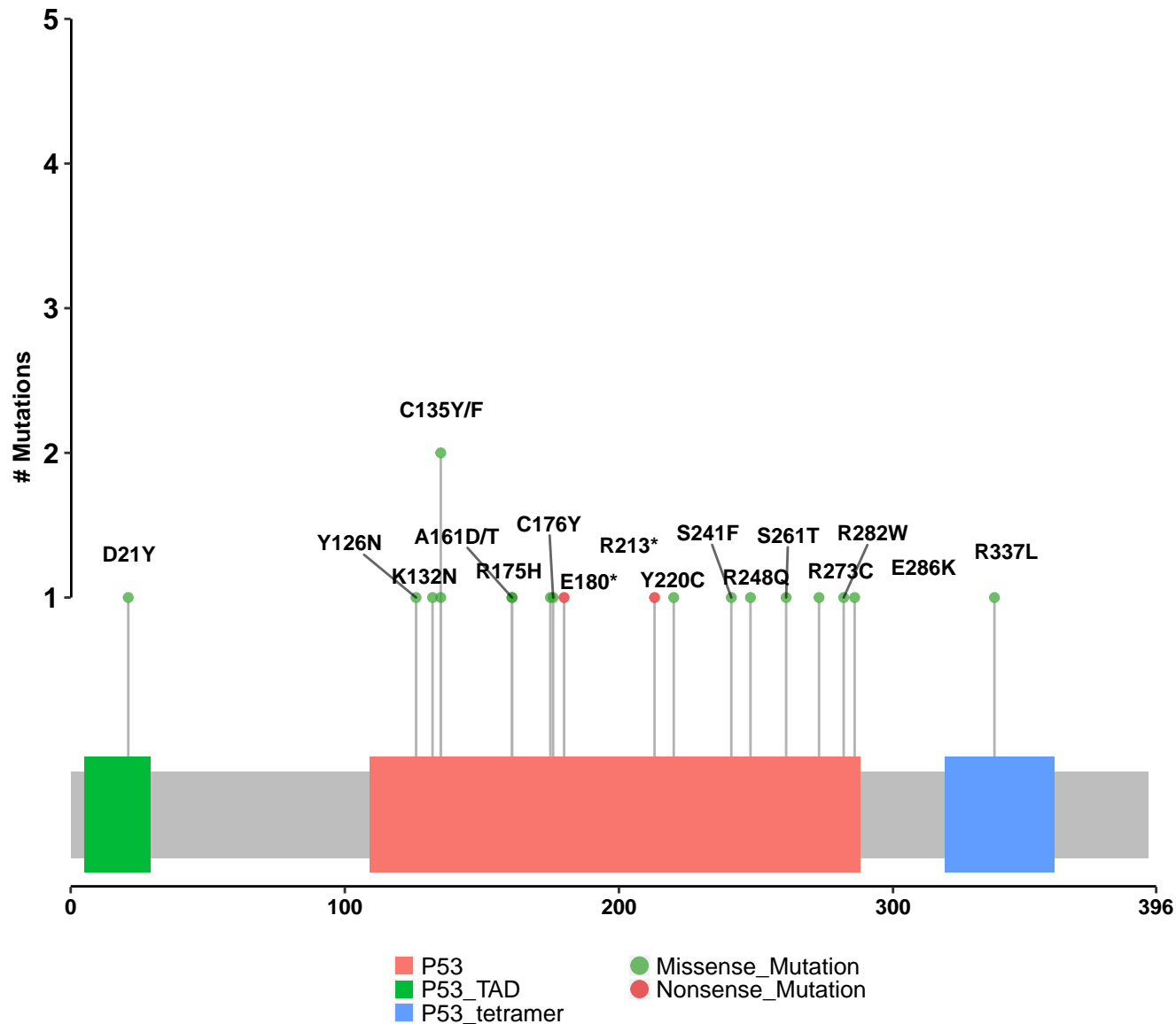
CYLD: [Somatic Mutation Rate: 9.09%]

NM_015247



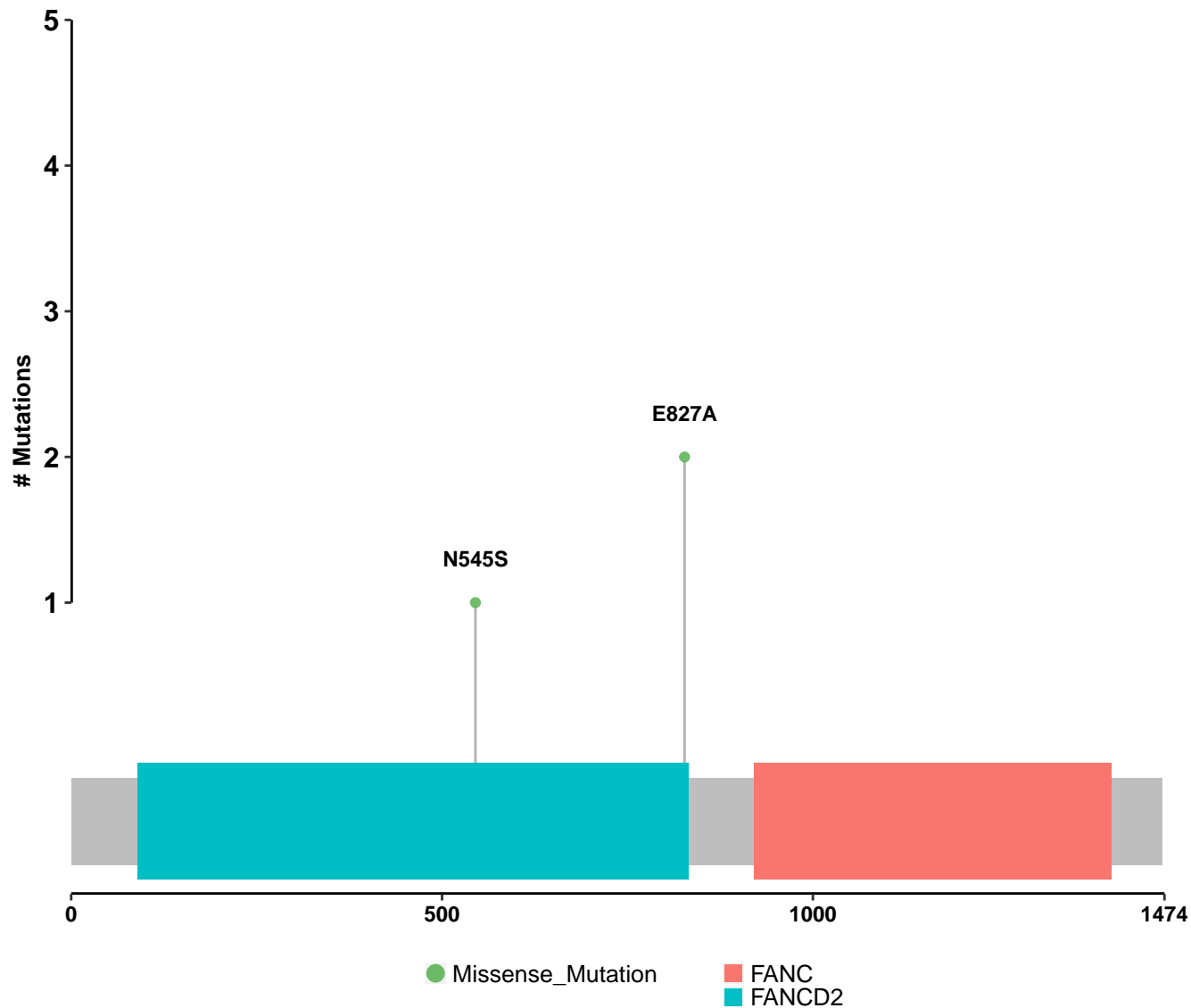
TP53: [Somatic Mutation Rate: 54.55%]

NM_000546



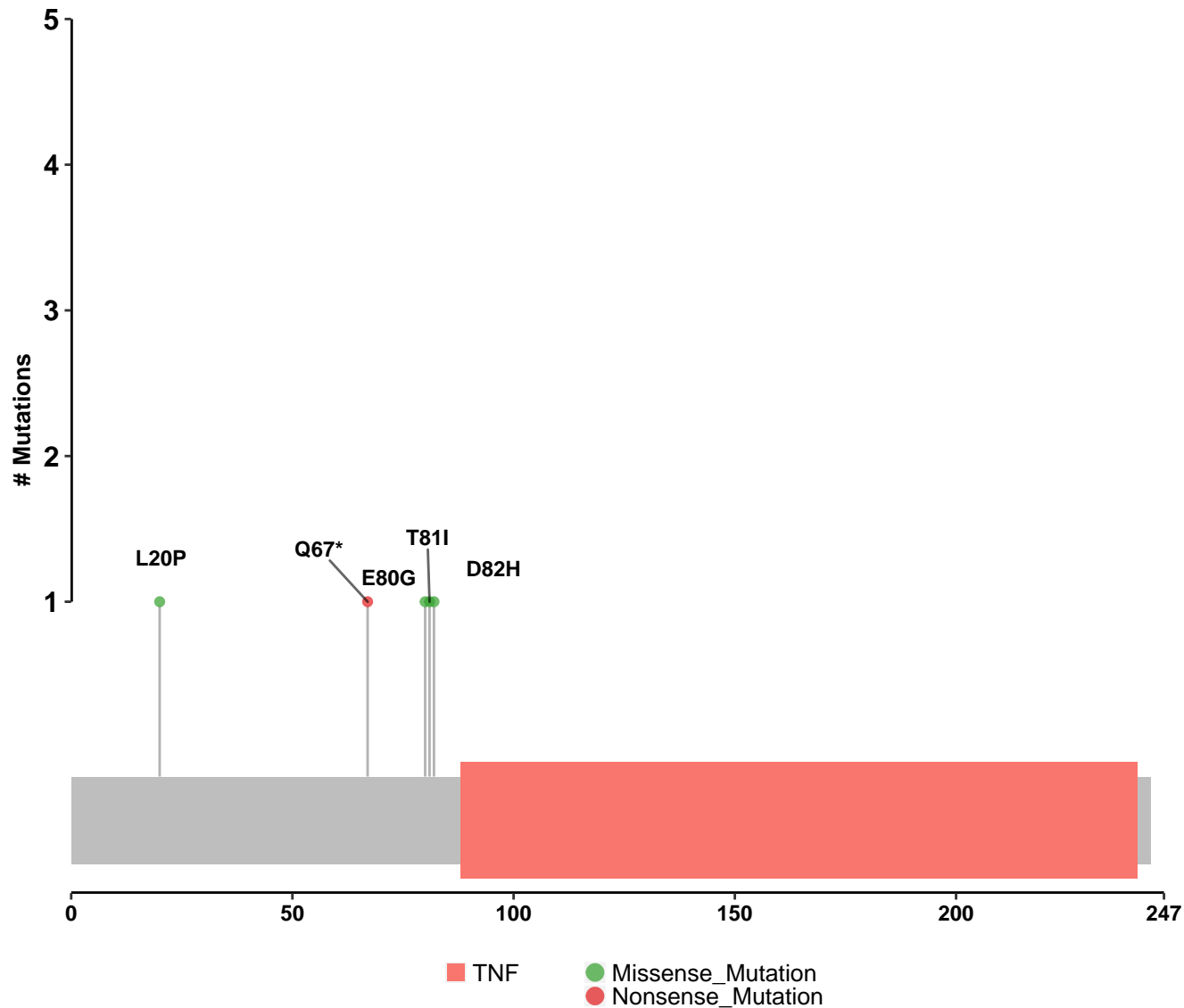
FANCD2: [Somatic Mutation Rate: 9.09%]

NM_033084



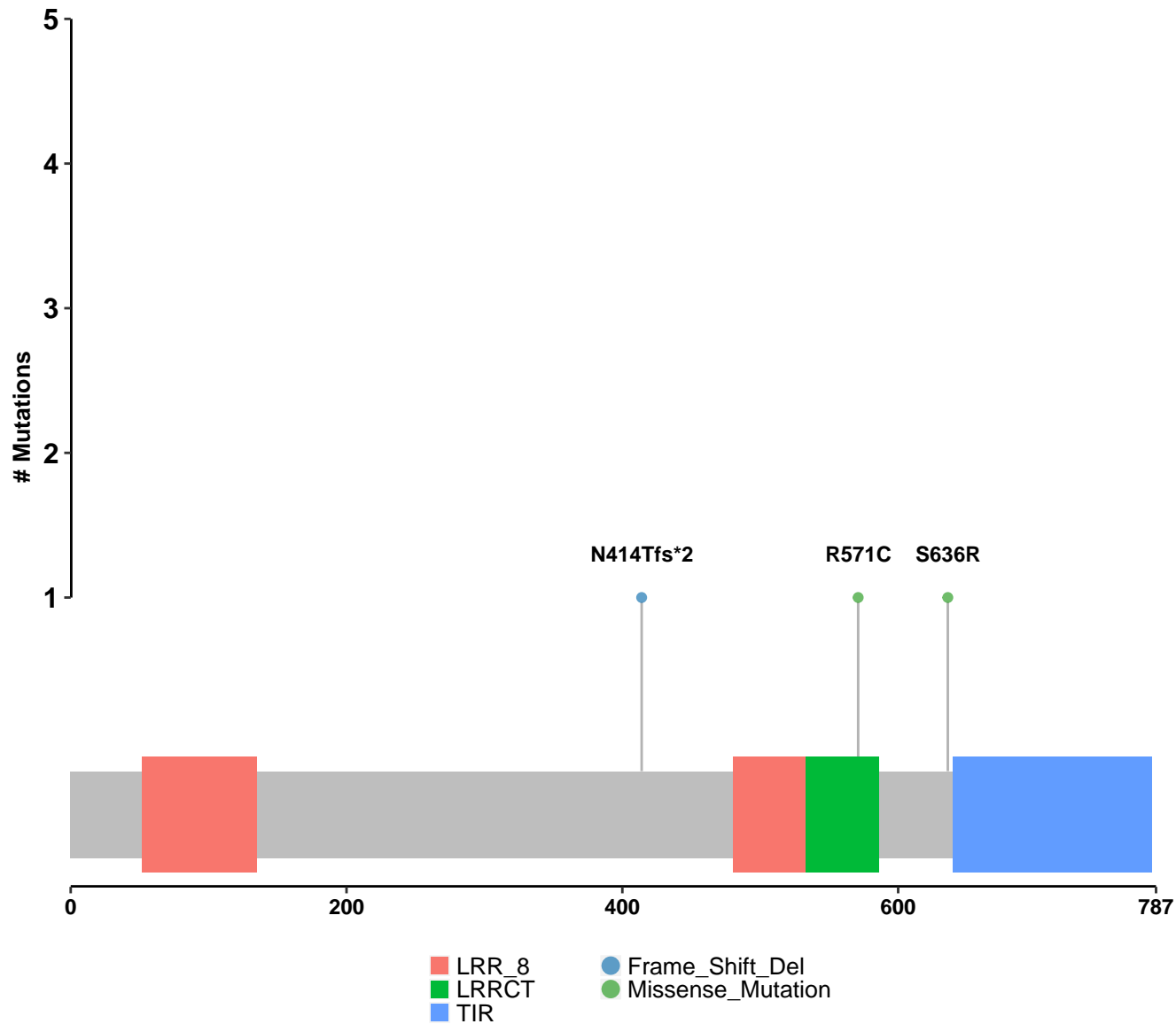
LTB: [Somatic Mutation Rate: 9.09%]

NM_002341



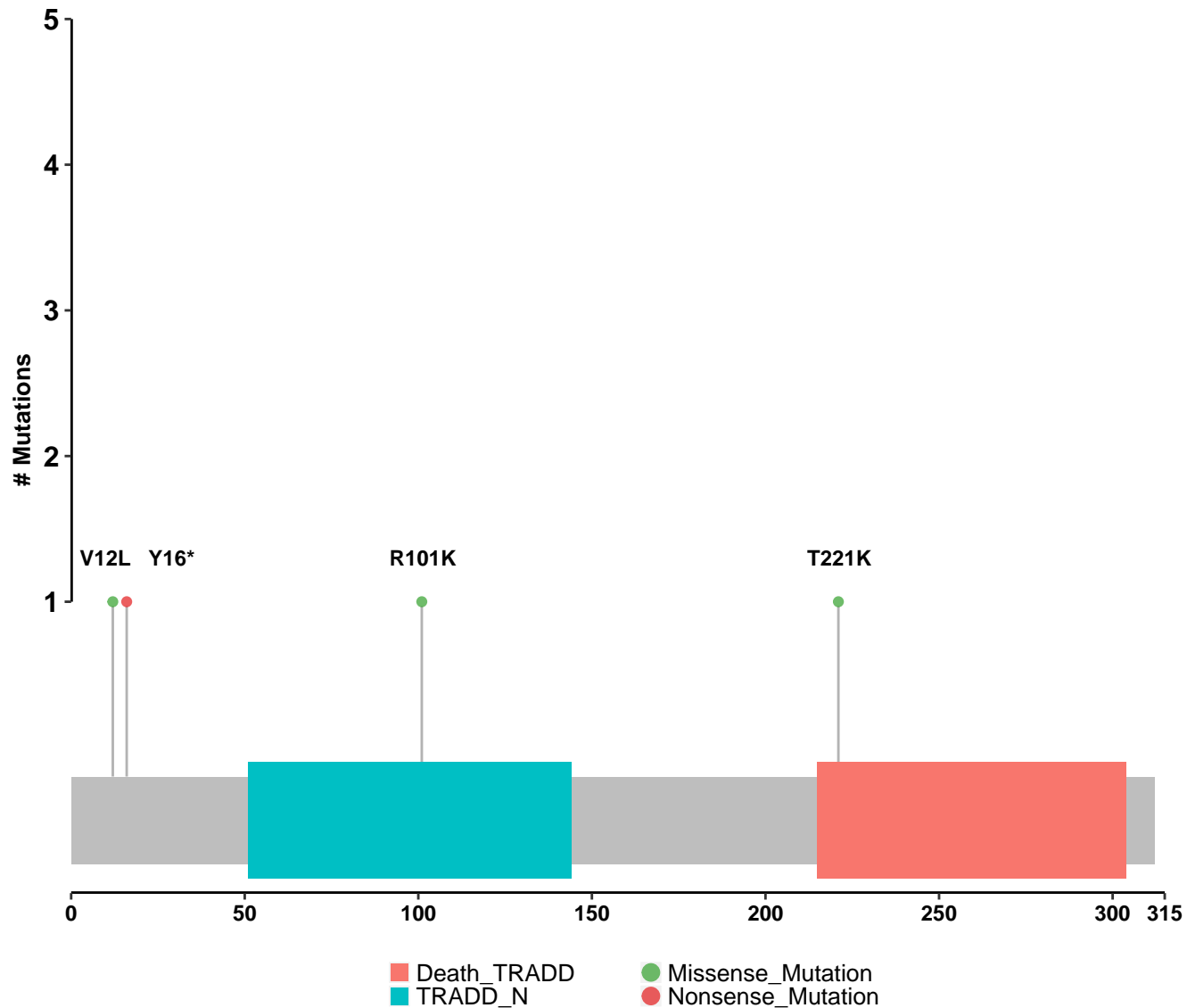
TLR2: [Somatic Mutation Rate: 9.09%]

NM_003264



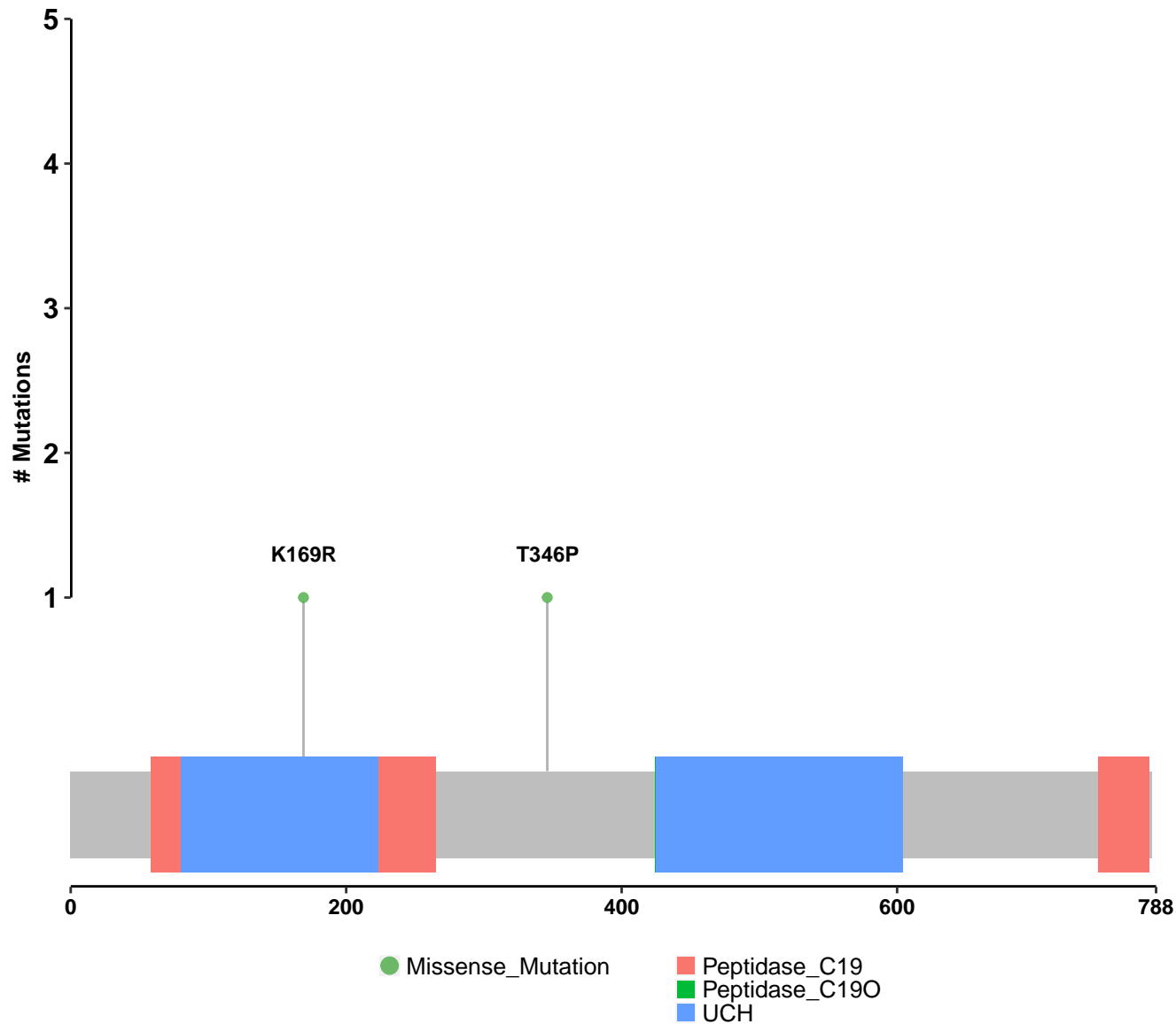
TRADD: [Somatic Mutation Rate: 9.09%]

NM_003789



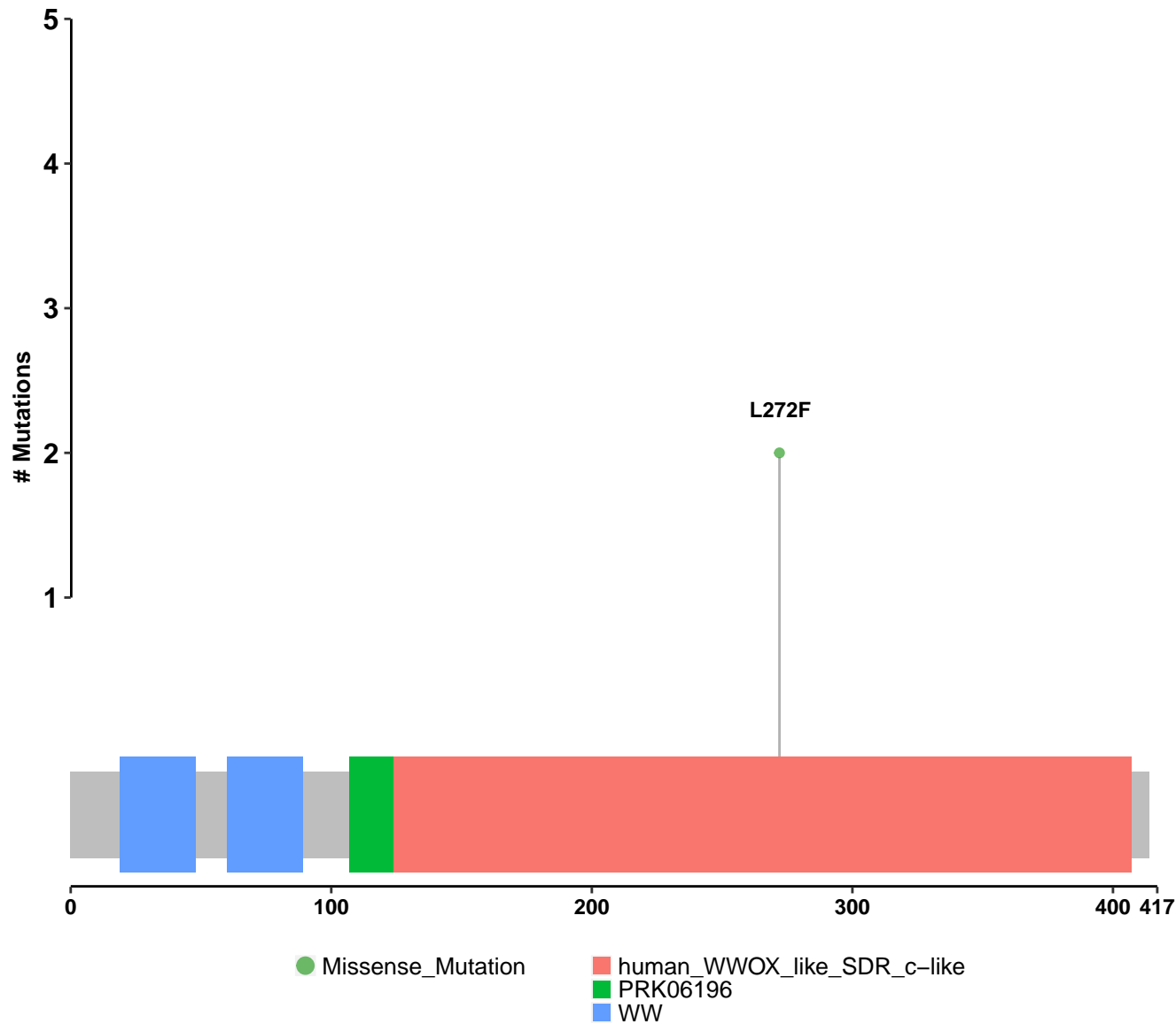
USP1: [Somatic Mutation Rate: 6.06%]

NM_003368



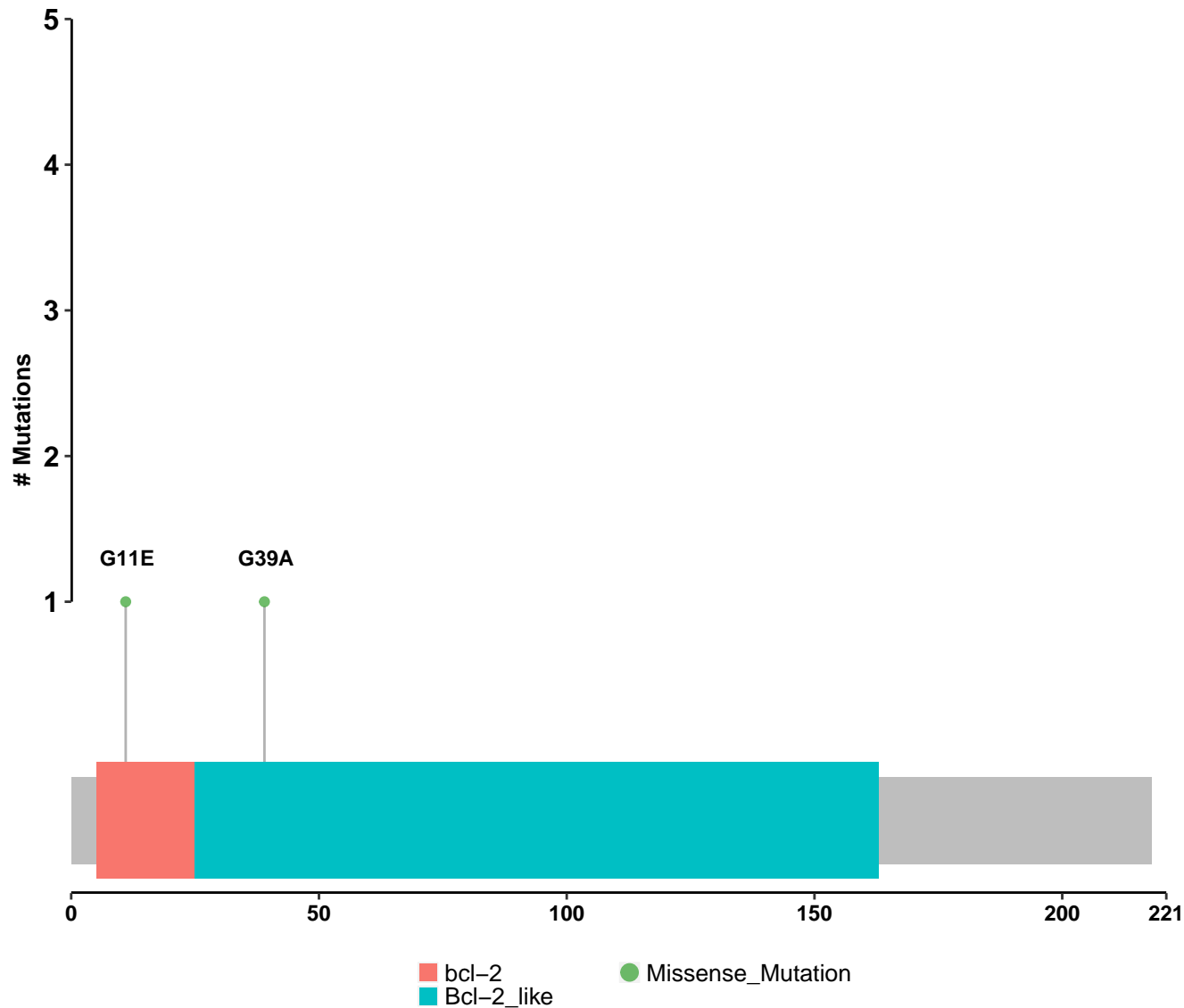
WVOX: [Somatic Mutation Rate: 6.06%]

NM_016373



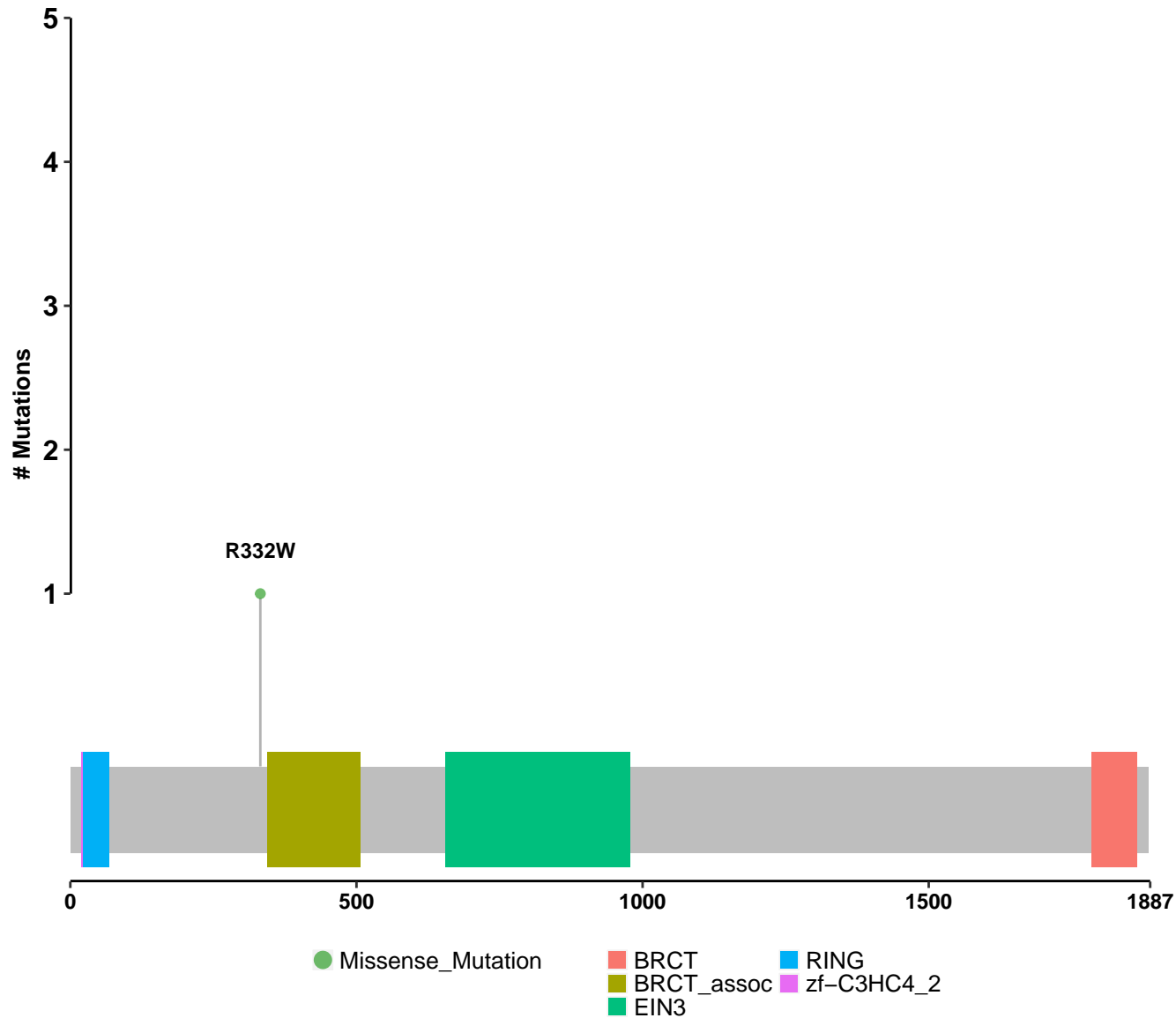
BAX: [Somatic Mutation Rate: 6.06%]

NM_004324



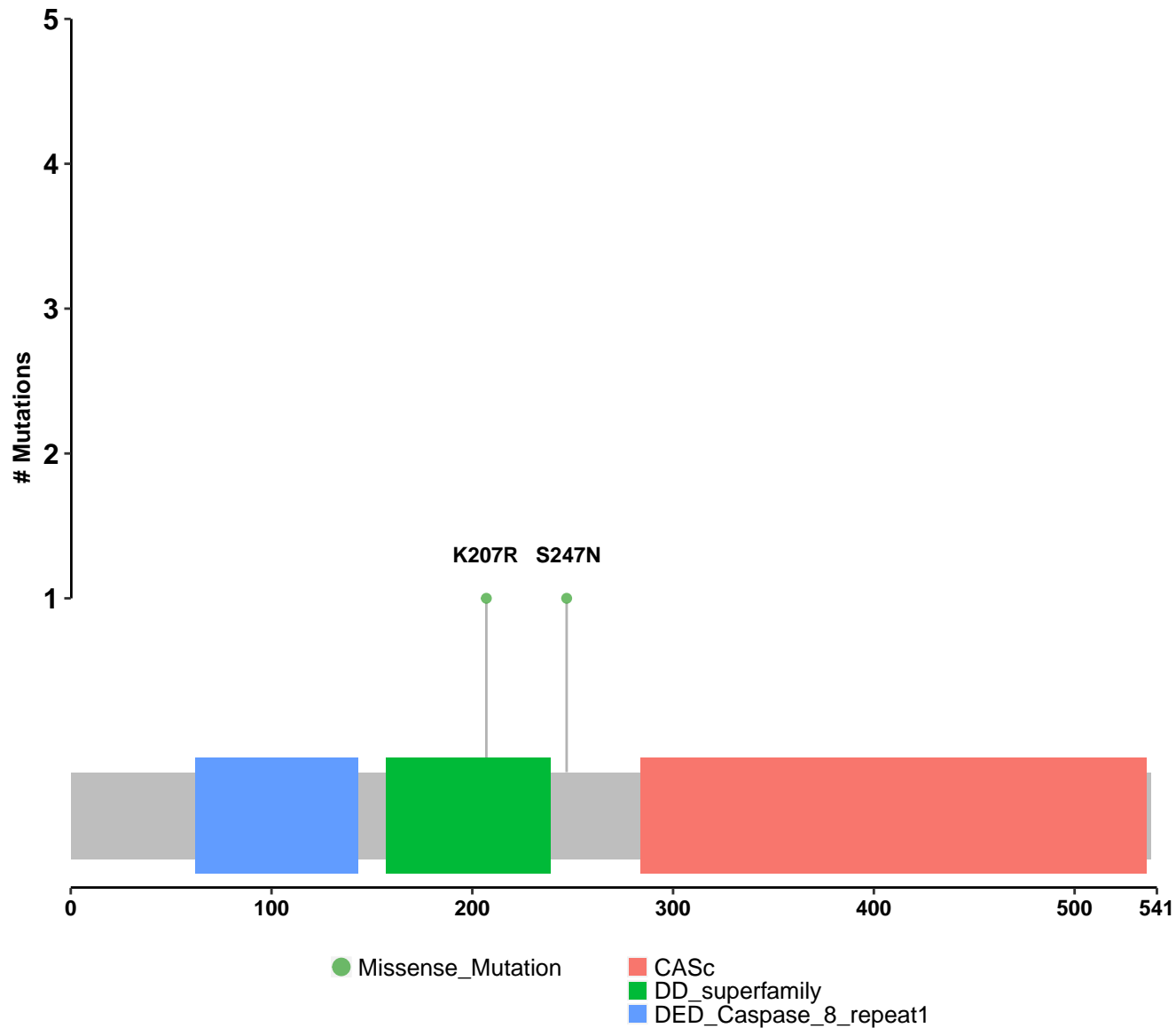
BRCA1: [Somatic Mutation Rate: 3.03%]

NM_007300



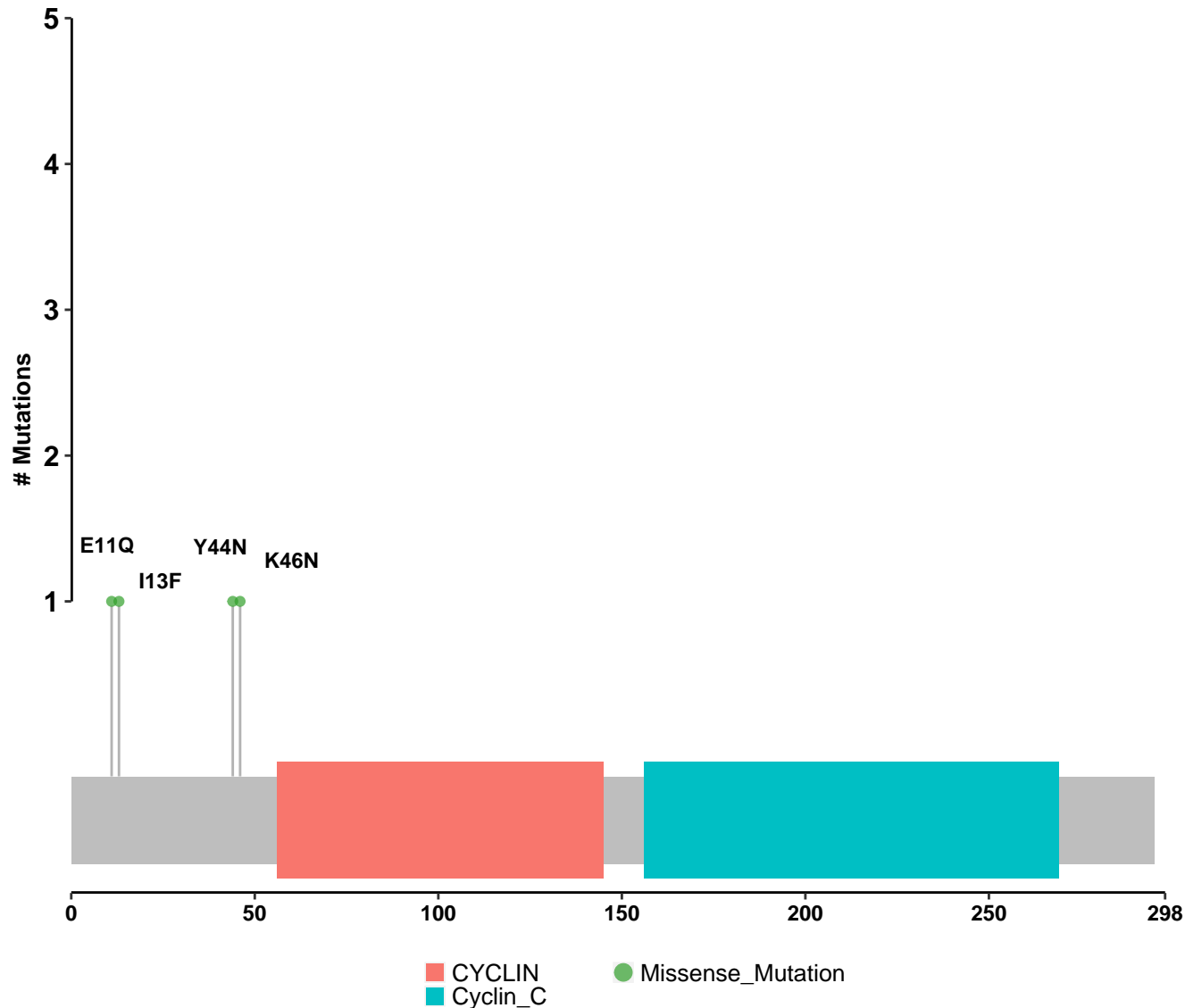
CASP8: [Somatic Mutation Rate: 6.06%]

NM_001080125



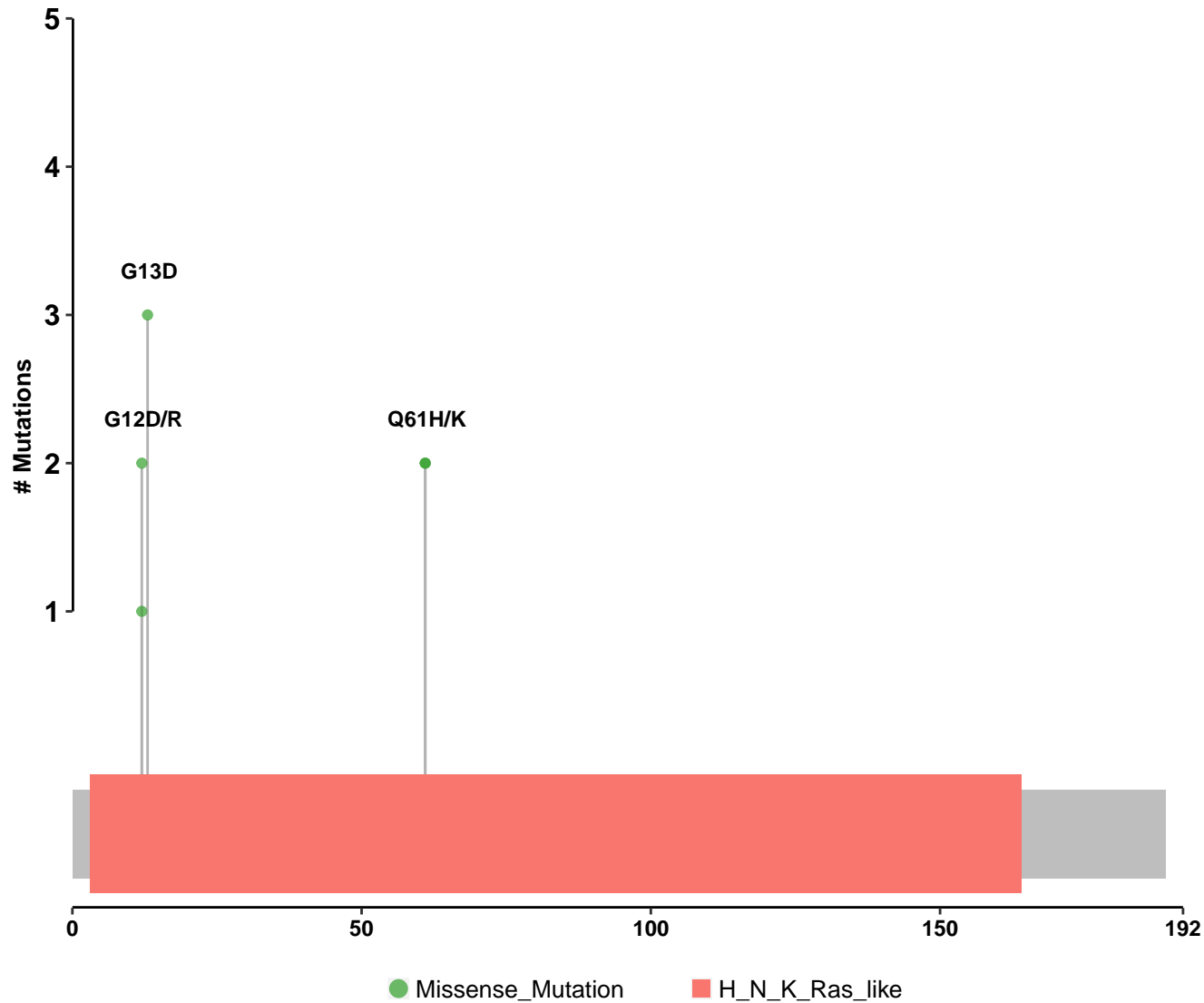
CCND1: [Somatic Mutation Rate: 3.03%]

NM_053056



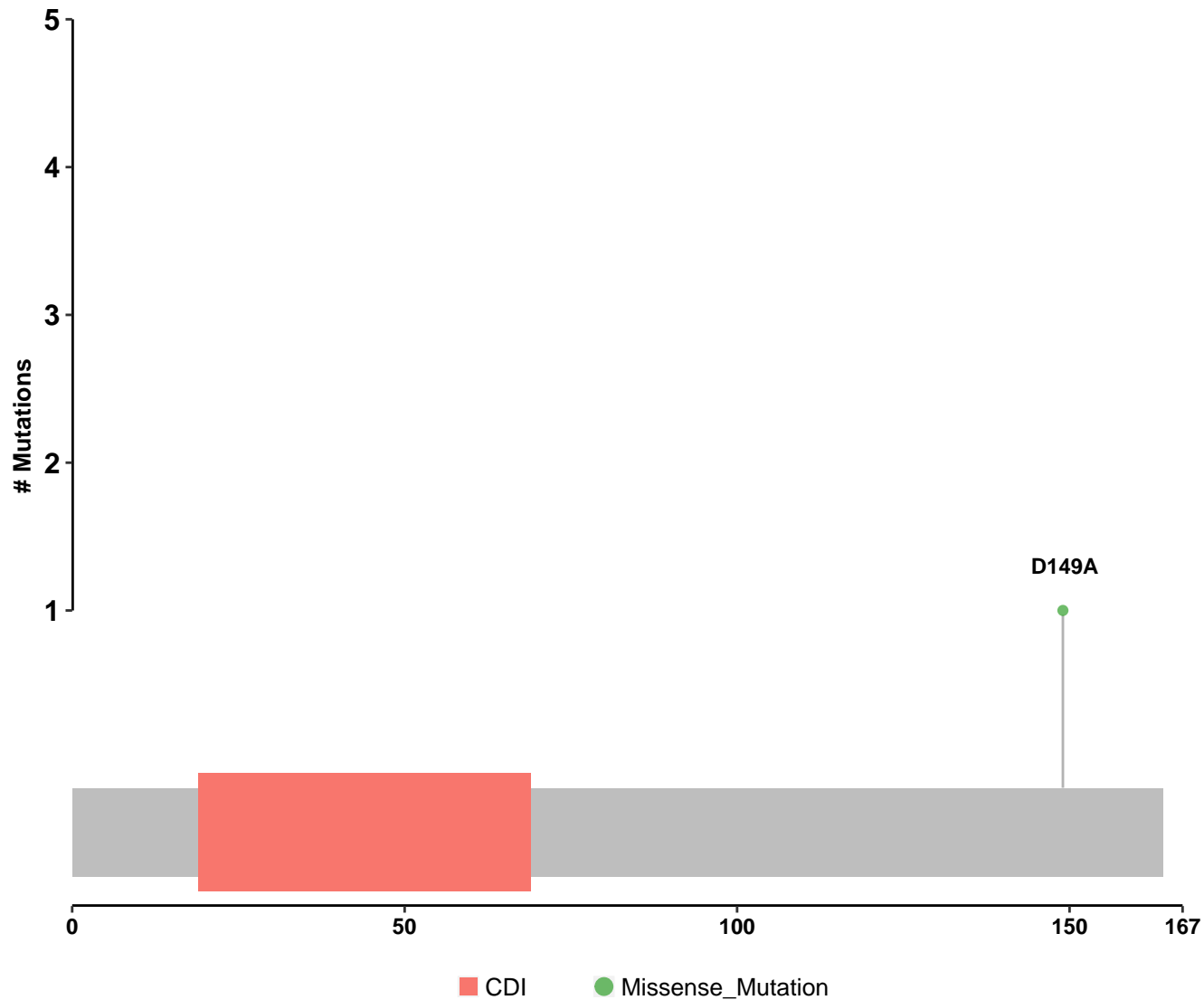
NRAS: [Somatic Mutation Rate: 30.3%]

NM_002524



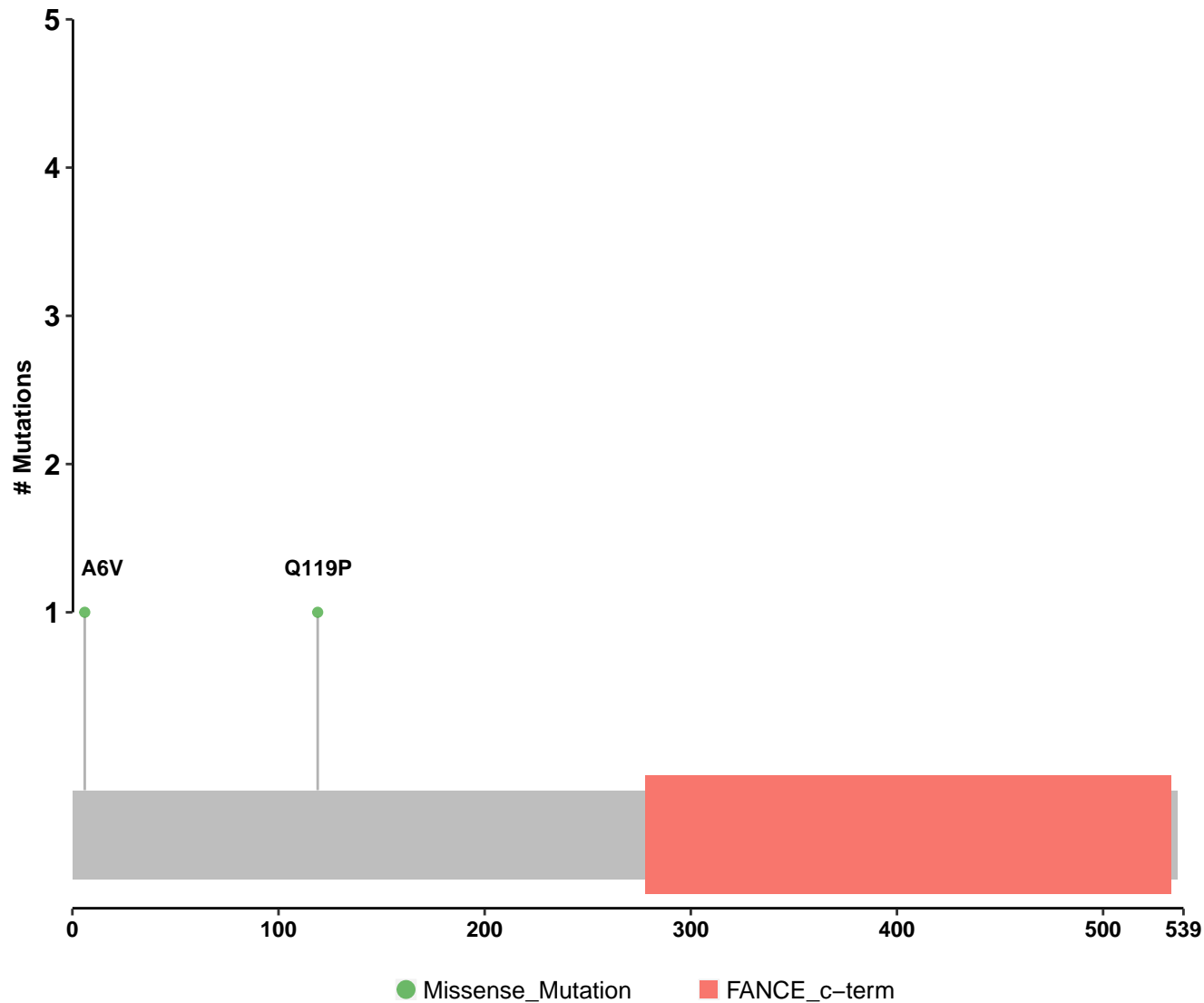
CDKN1A: [Somatic Mutation Rate: 3.03%]

NM_000389



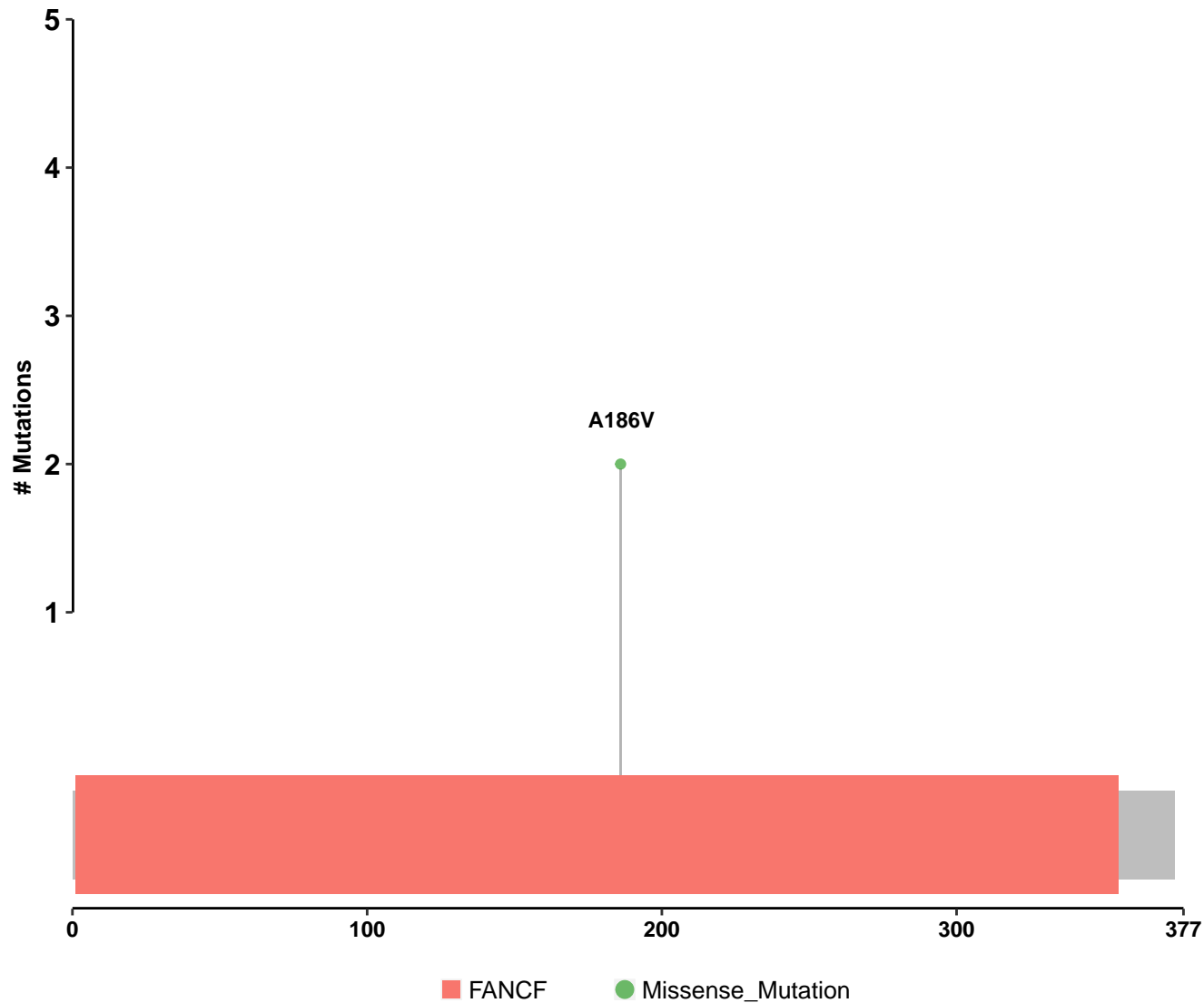
FANCE: [Somatic Mutation Rate: 6.06%]

NM_021922



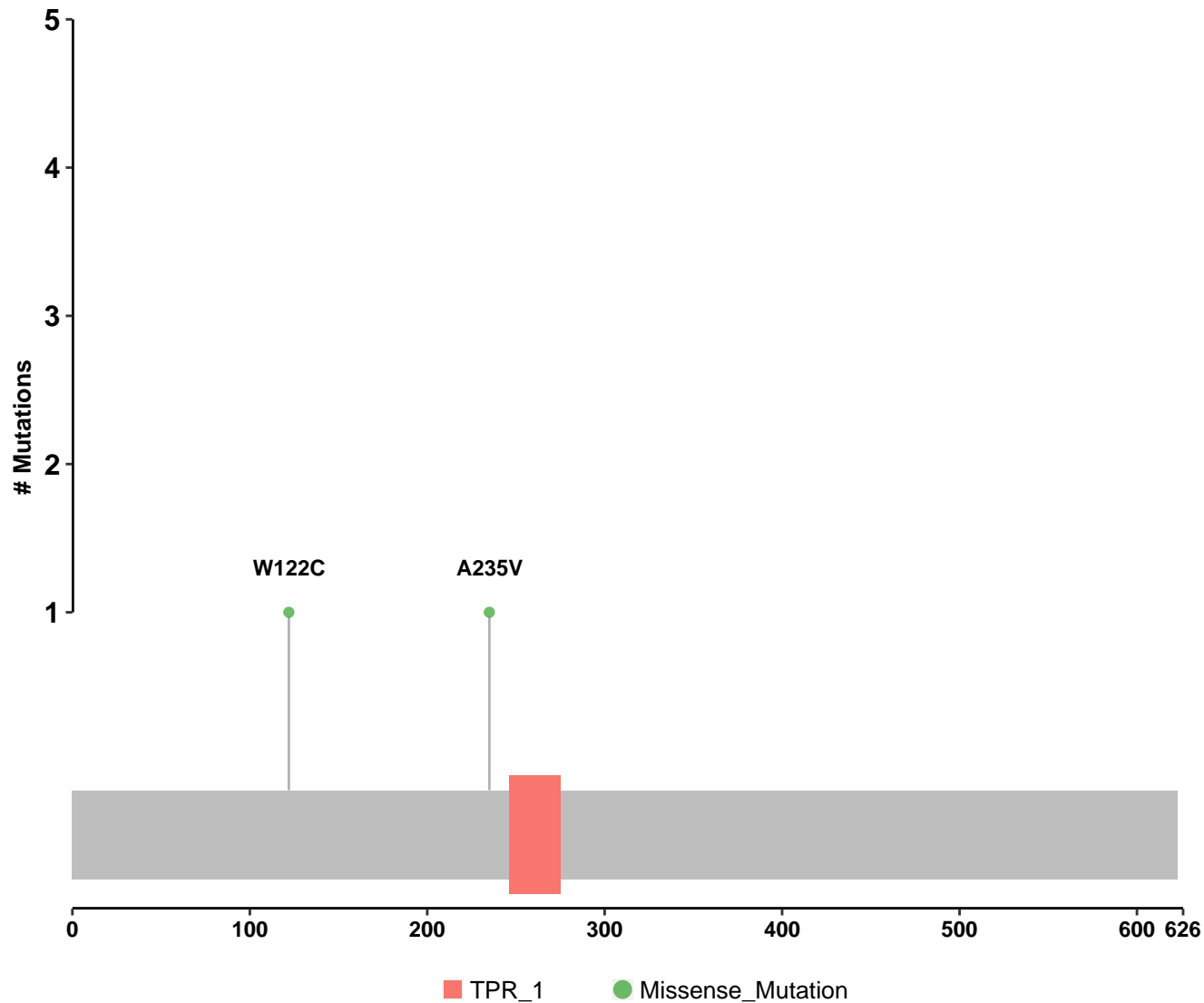
FANCF: [Somatic Mutation Rate: 6.06%]

NM_022725



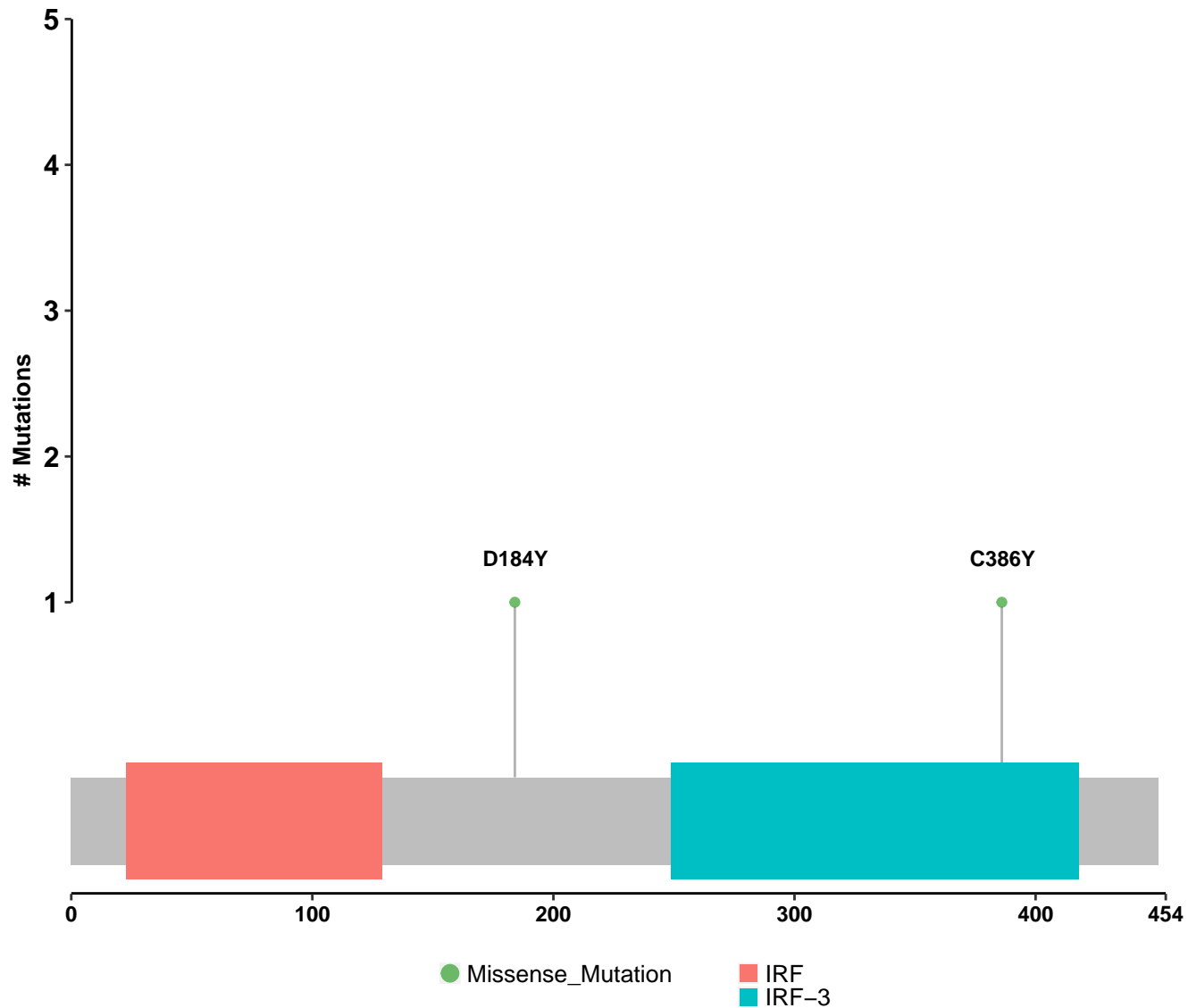
FANCG: [Somatic Mutation Rate: 6.06%]

NM_004629



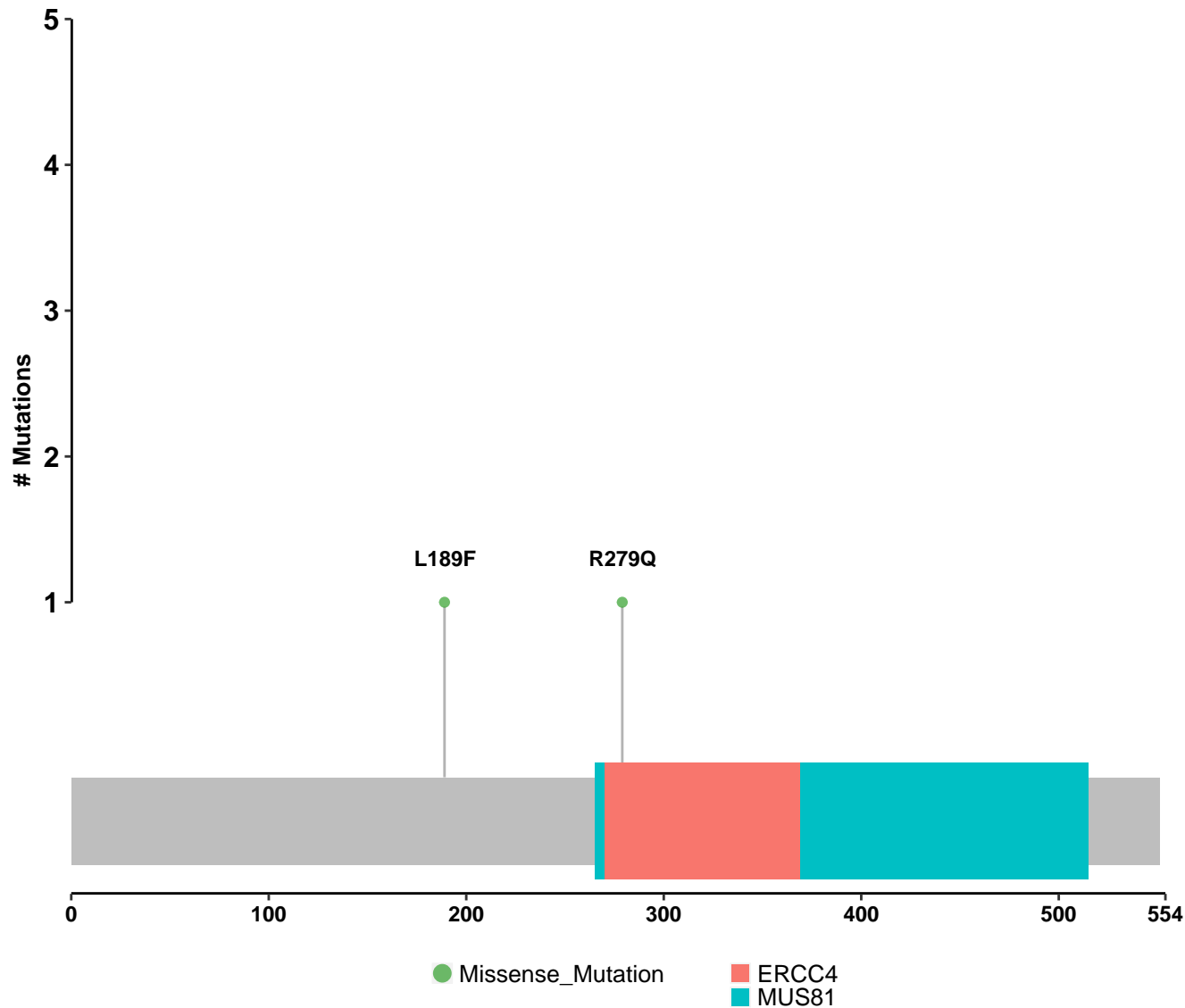
IRF4: [Somatic Mutation Rate: 6.06%]

NM_002460



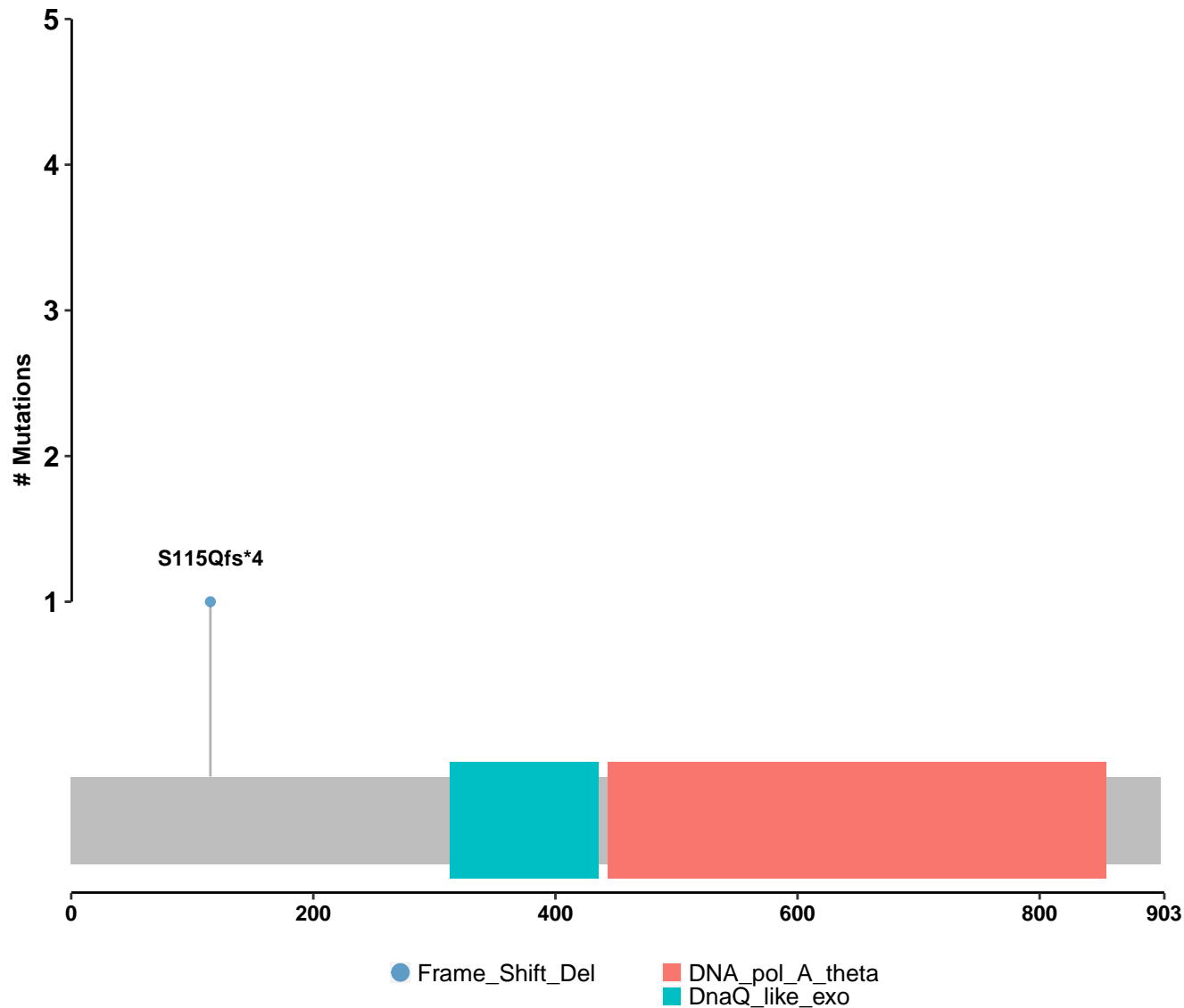
MUS81: [Somatic Mutation Rate: 6.06%]

NM_025128



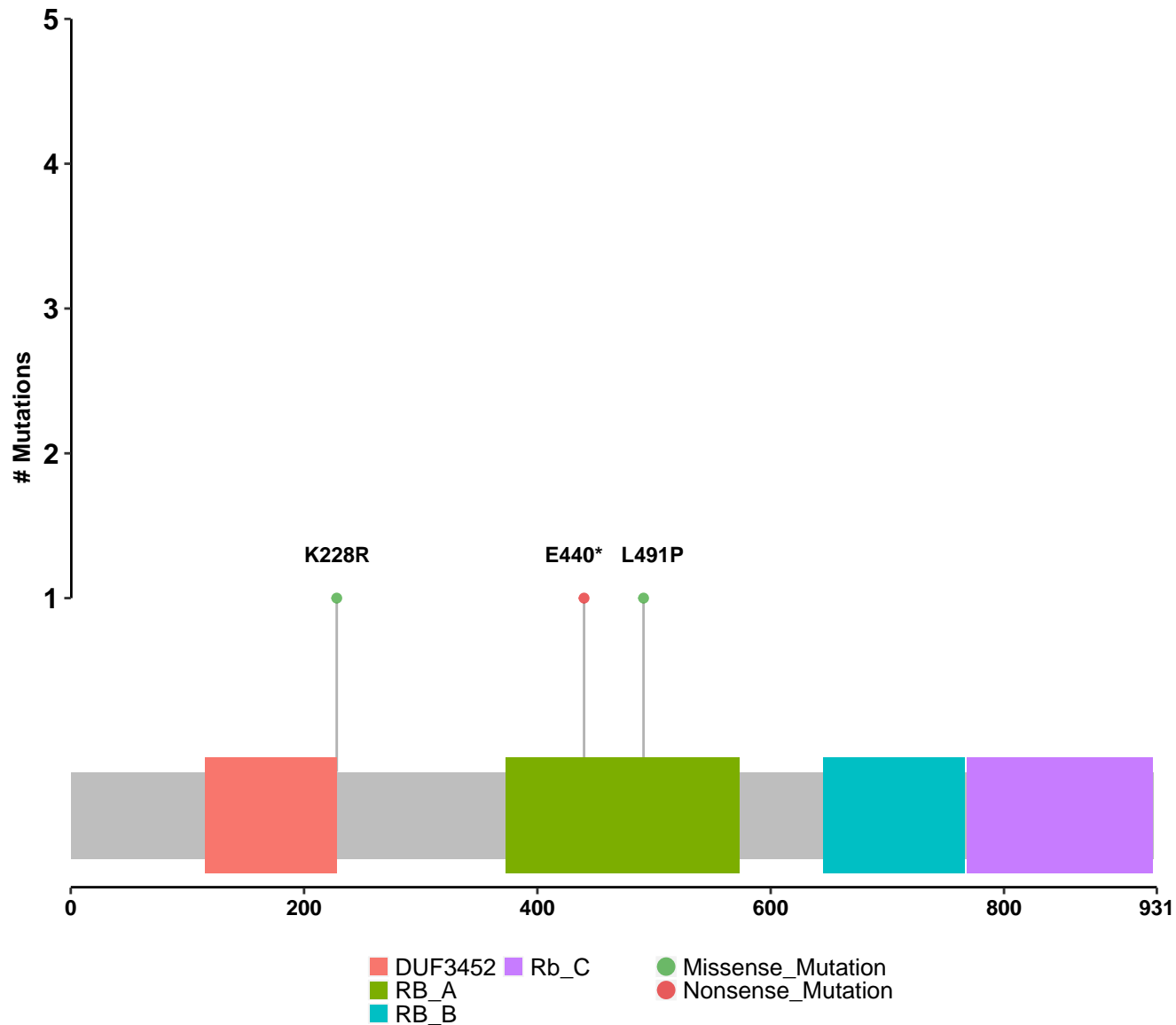
POLN: [Somatic Mutation Rate: 3.03%]

NM_181808



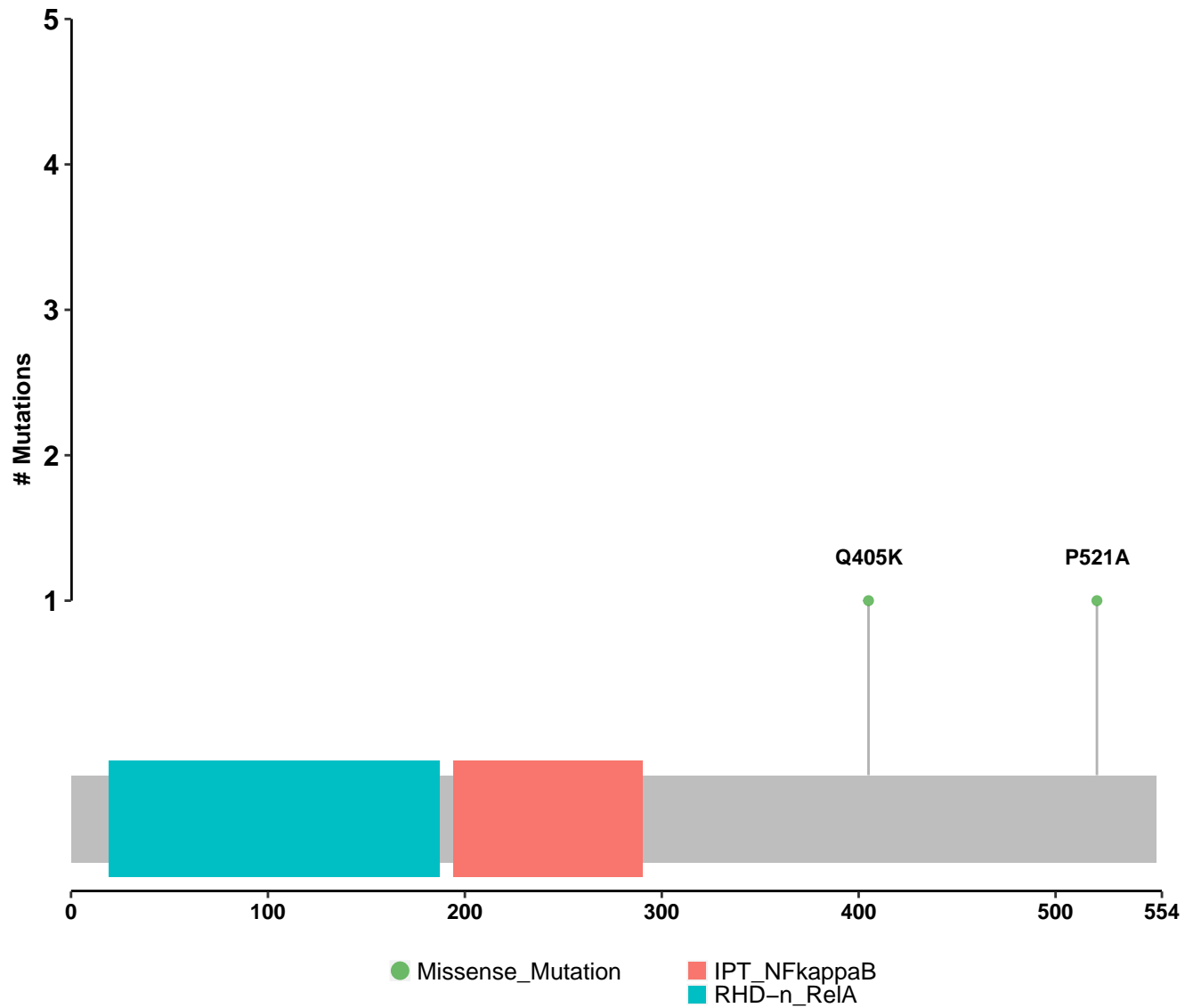
RB1: [Somatic Mutation Rate: 6.06%]

NM_000321



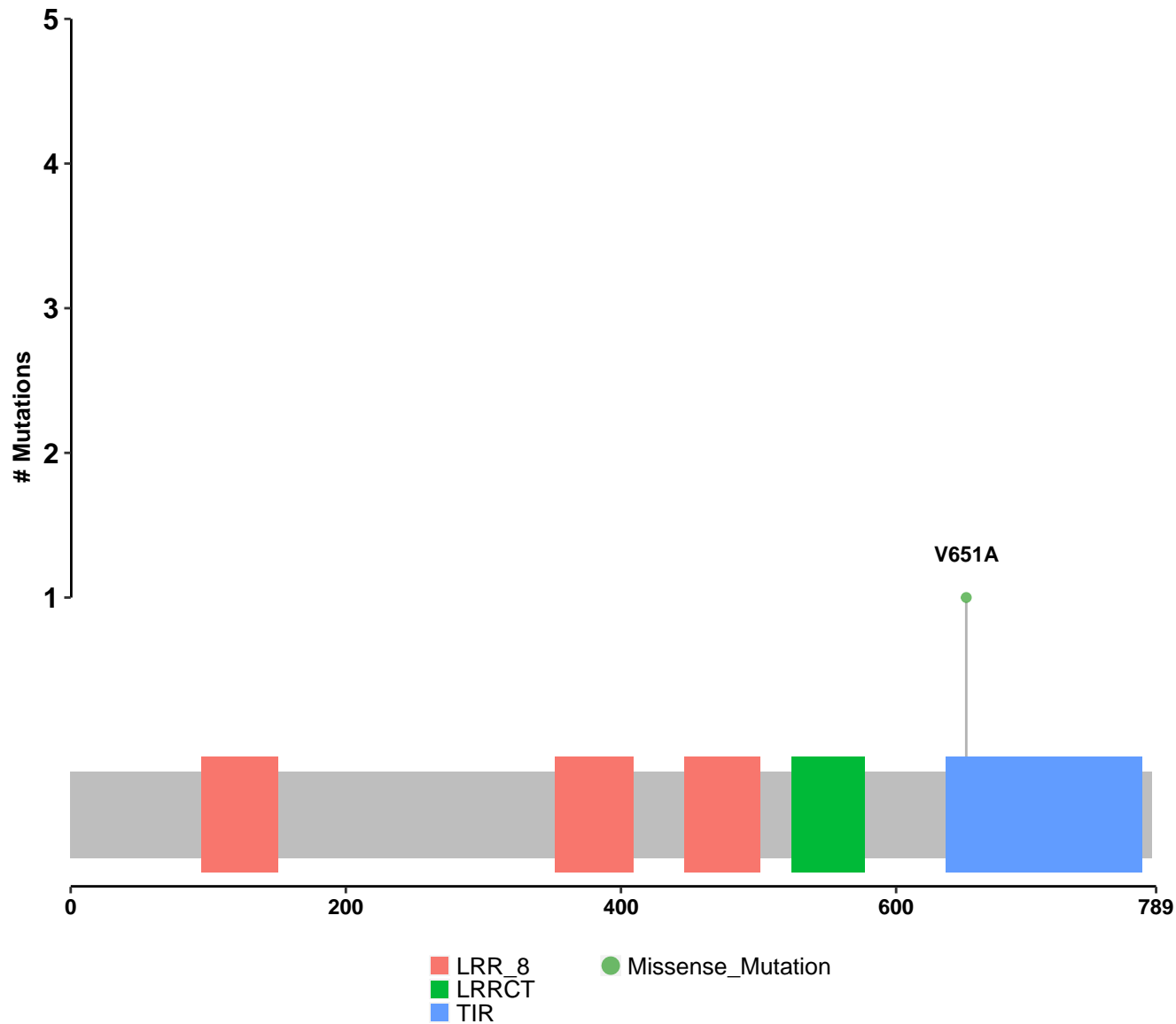
RELA: [Somatic Mutation Rate: 6.06%]

NM_021975



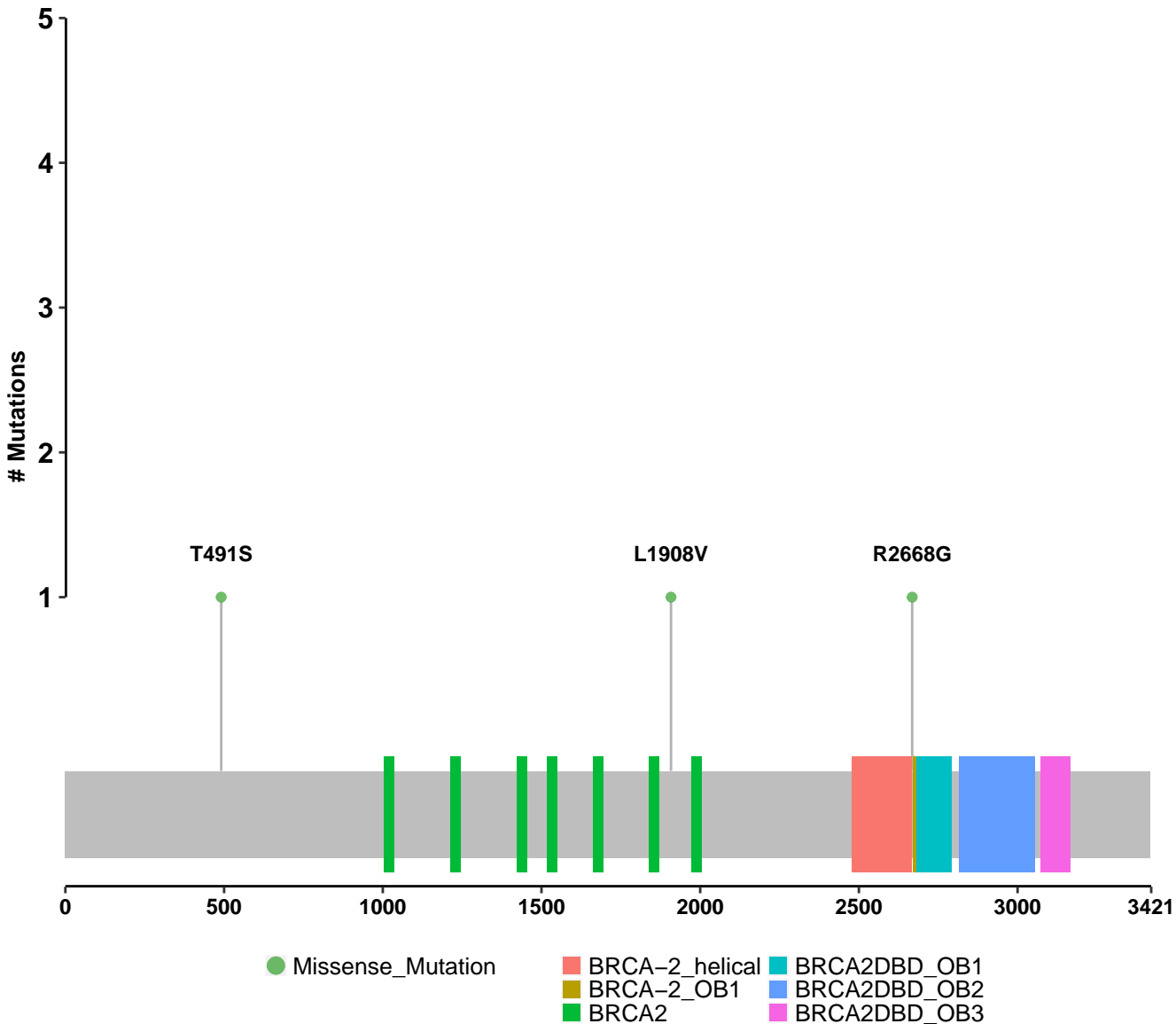
TLR1: [Somatic Mutation Rate: 3.03%]

NM_003263



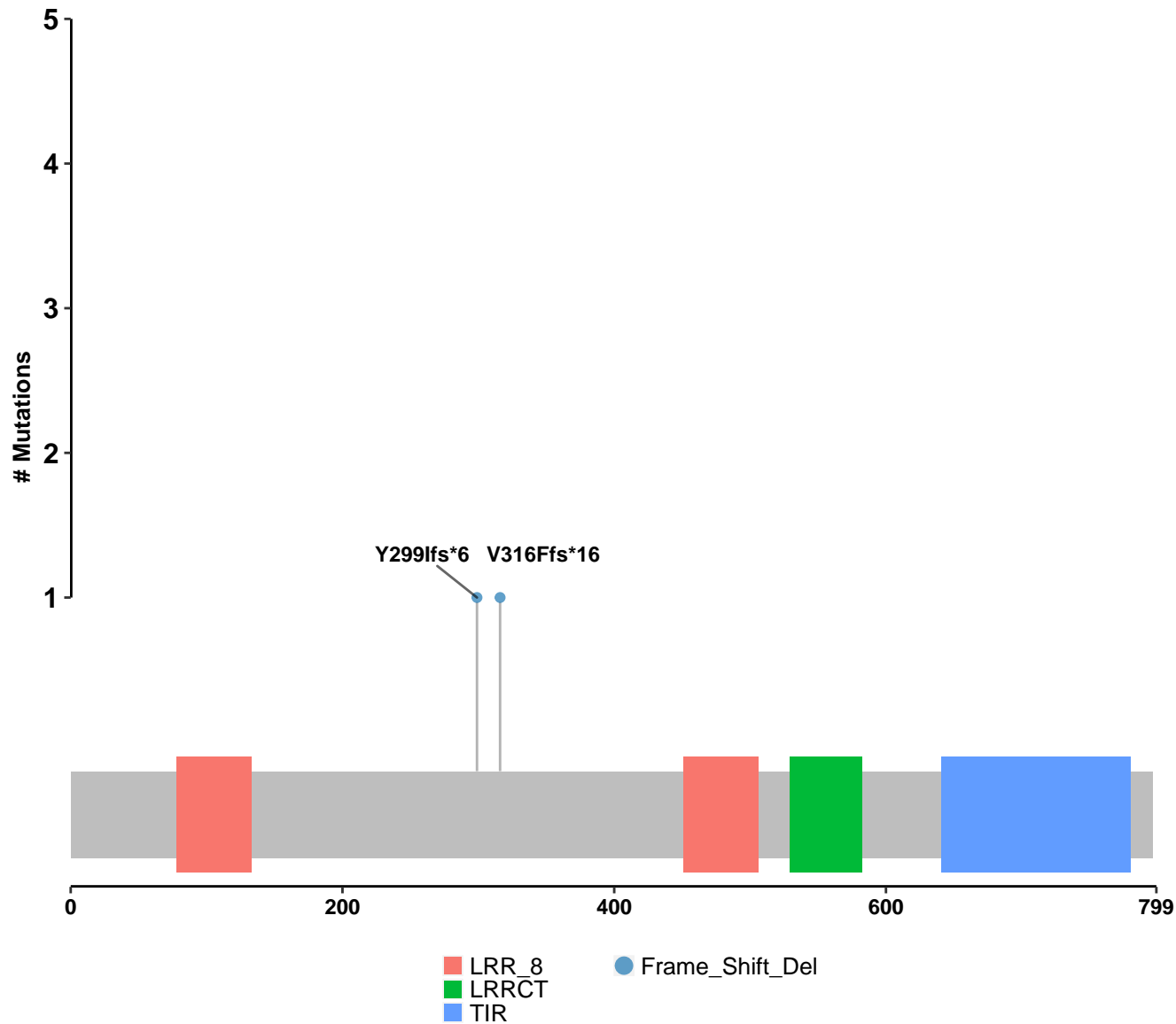
BRCA2: [Somatic Mutation Rate: 9.09%]

NM_000059



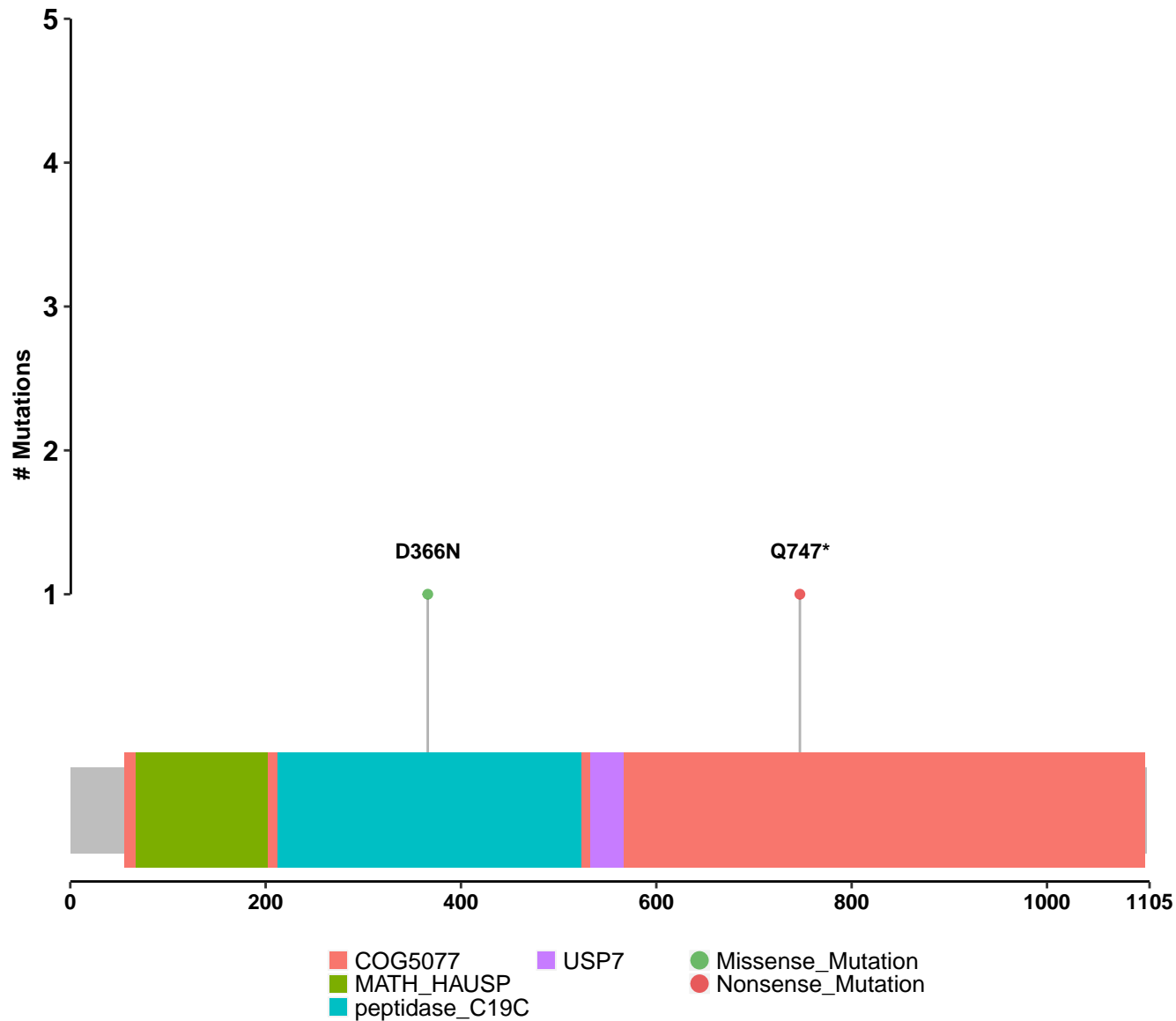
TLR6: [Somatic Mutation Rate: 6.06%]

NM_006068



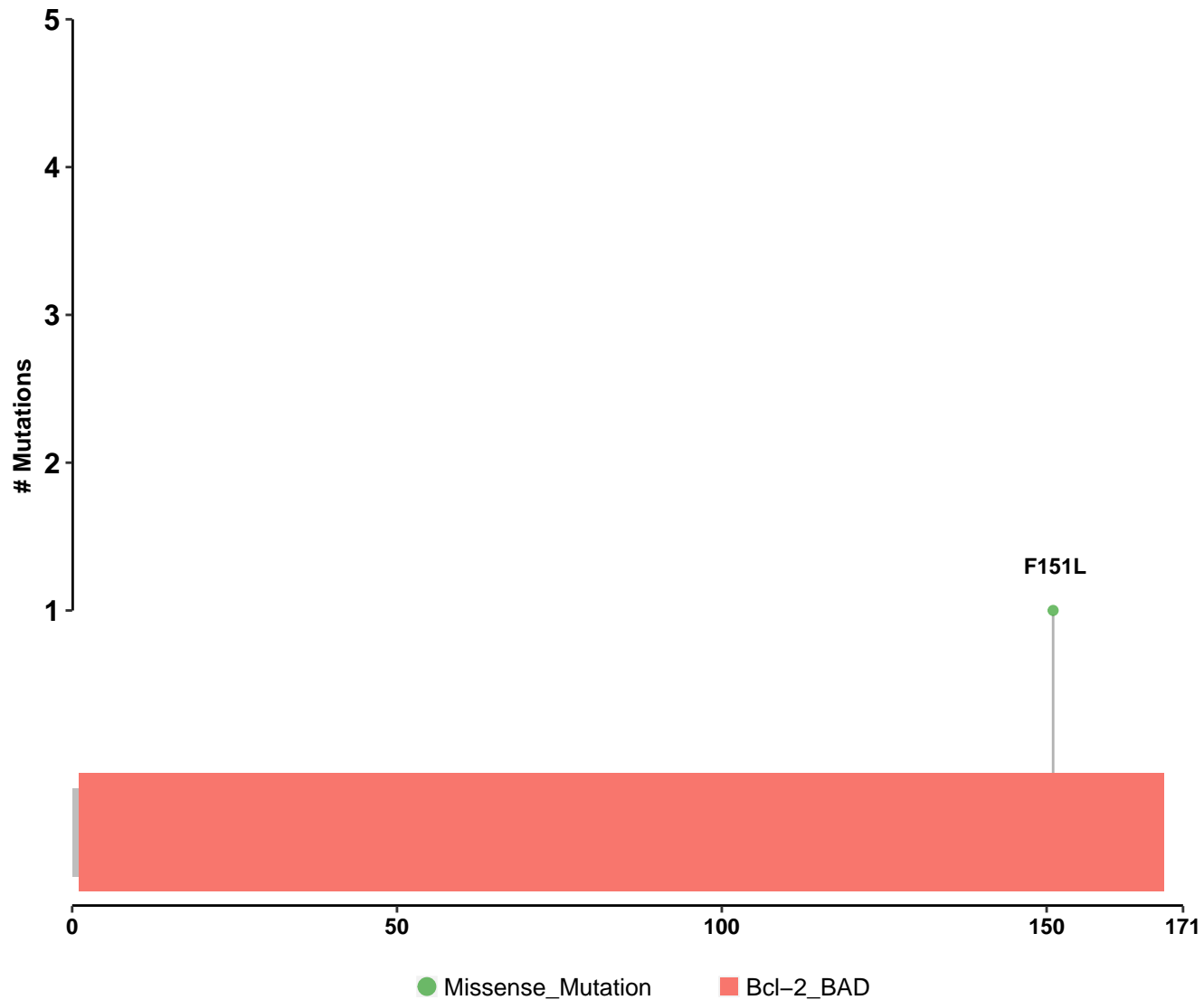
USP7: [Somatic Mutation Rate: 6.06%]

NM_003470



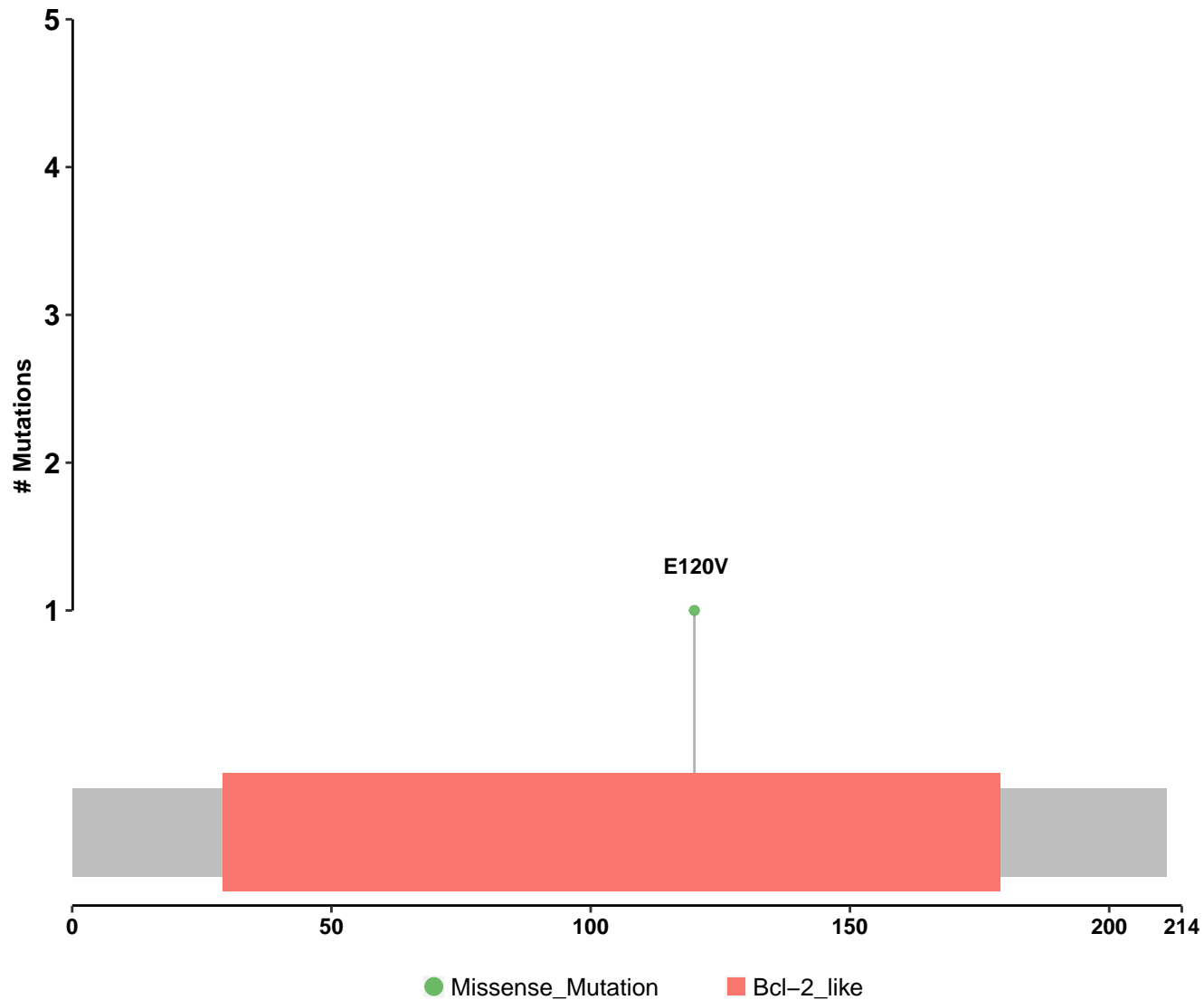
BAD: [Somatic Mutation Rate: 3.03%]

NM_004322



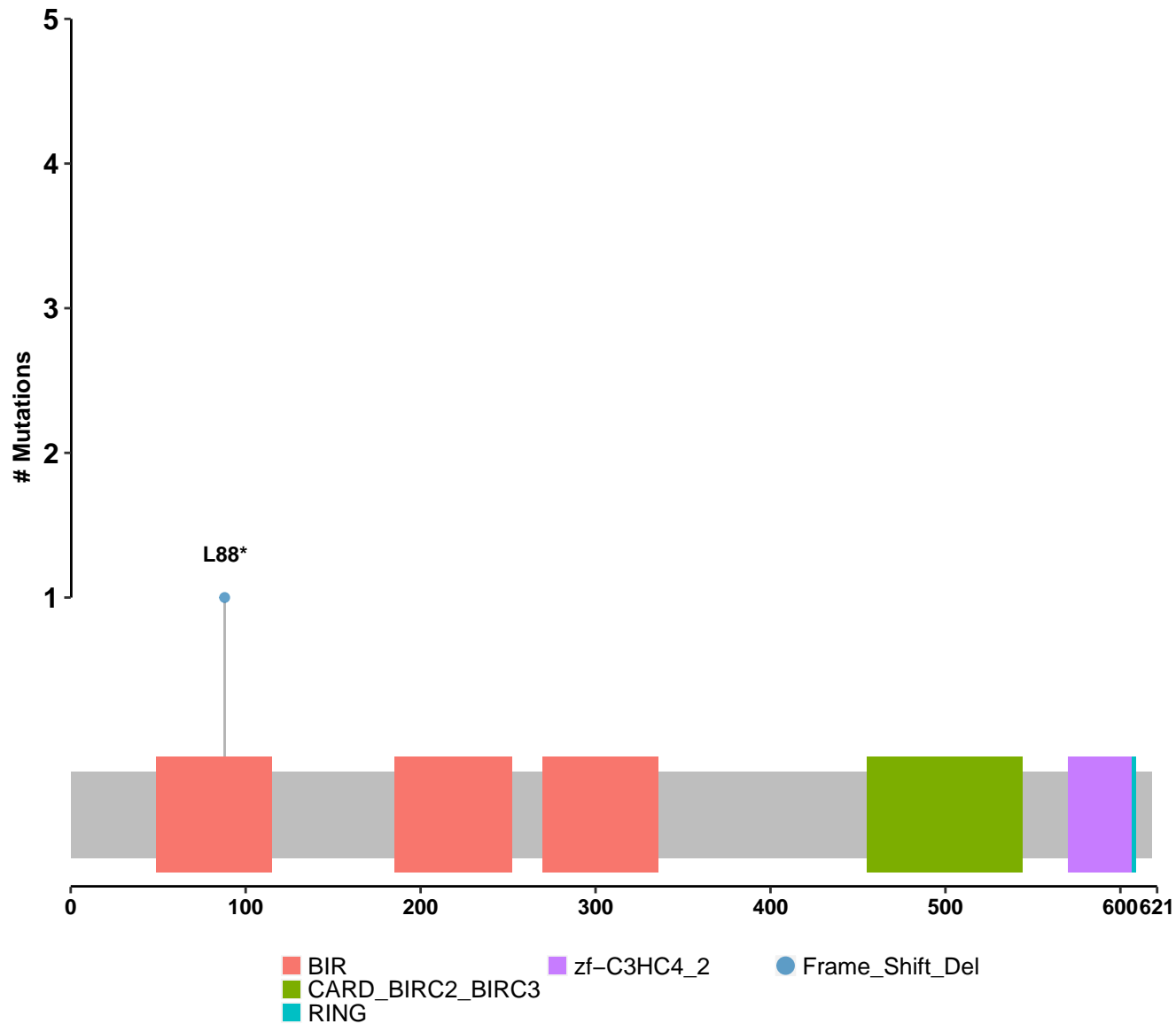
BAK1: [Somatic Mutation Rate: 3.03%]

NM_001188



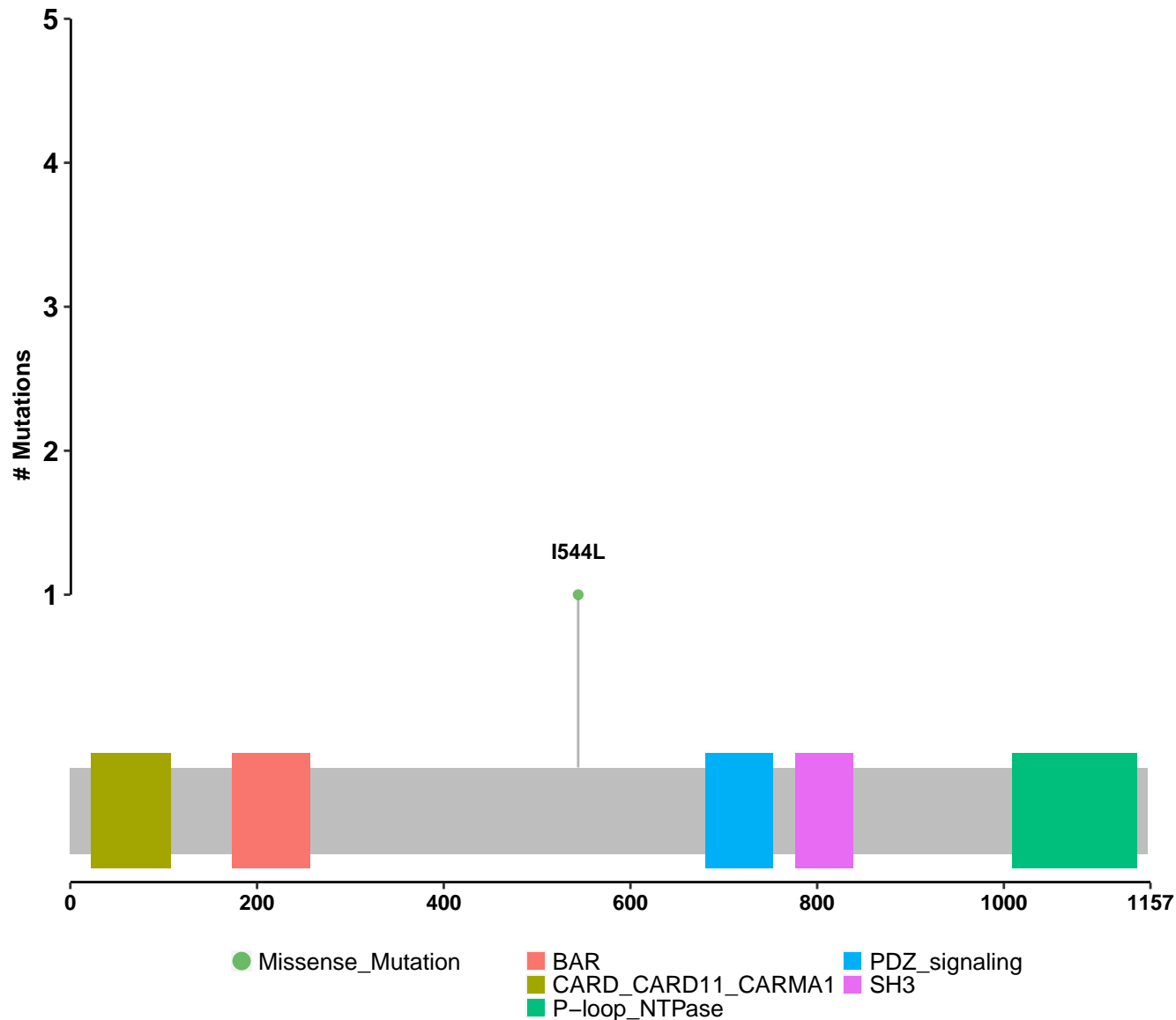
BIRC2: [Somatic Mutation Rate: 3.03%]

NM_001166



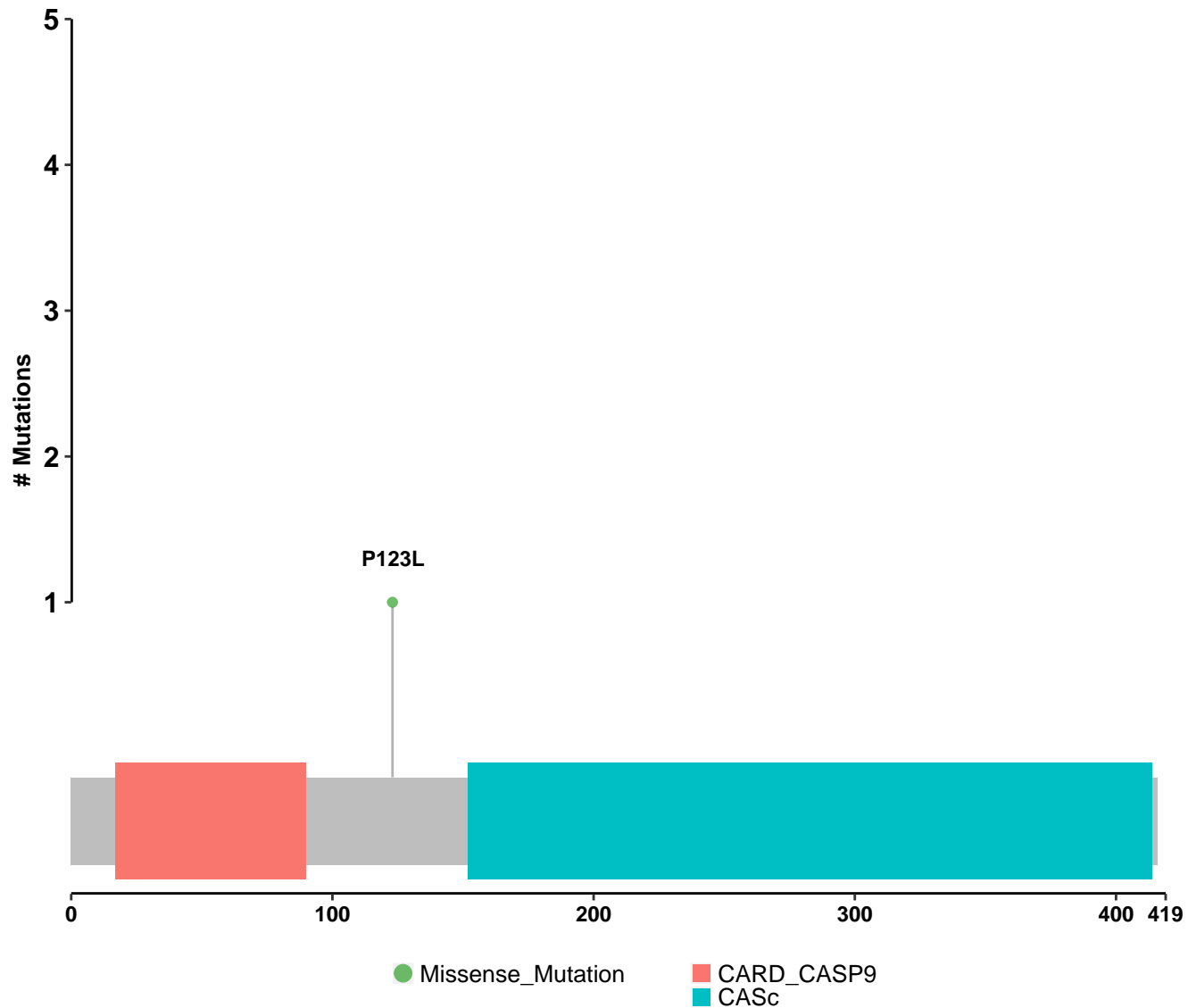
CARD11: [Somatic Mutation Rate: 3.03%]

NM_032415



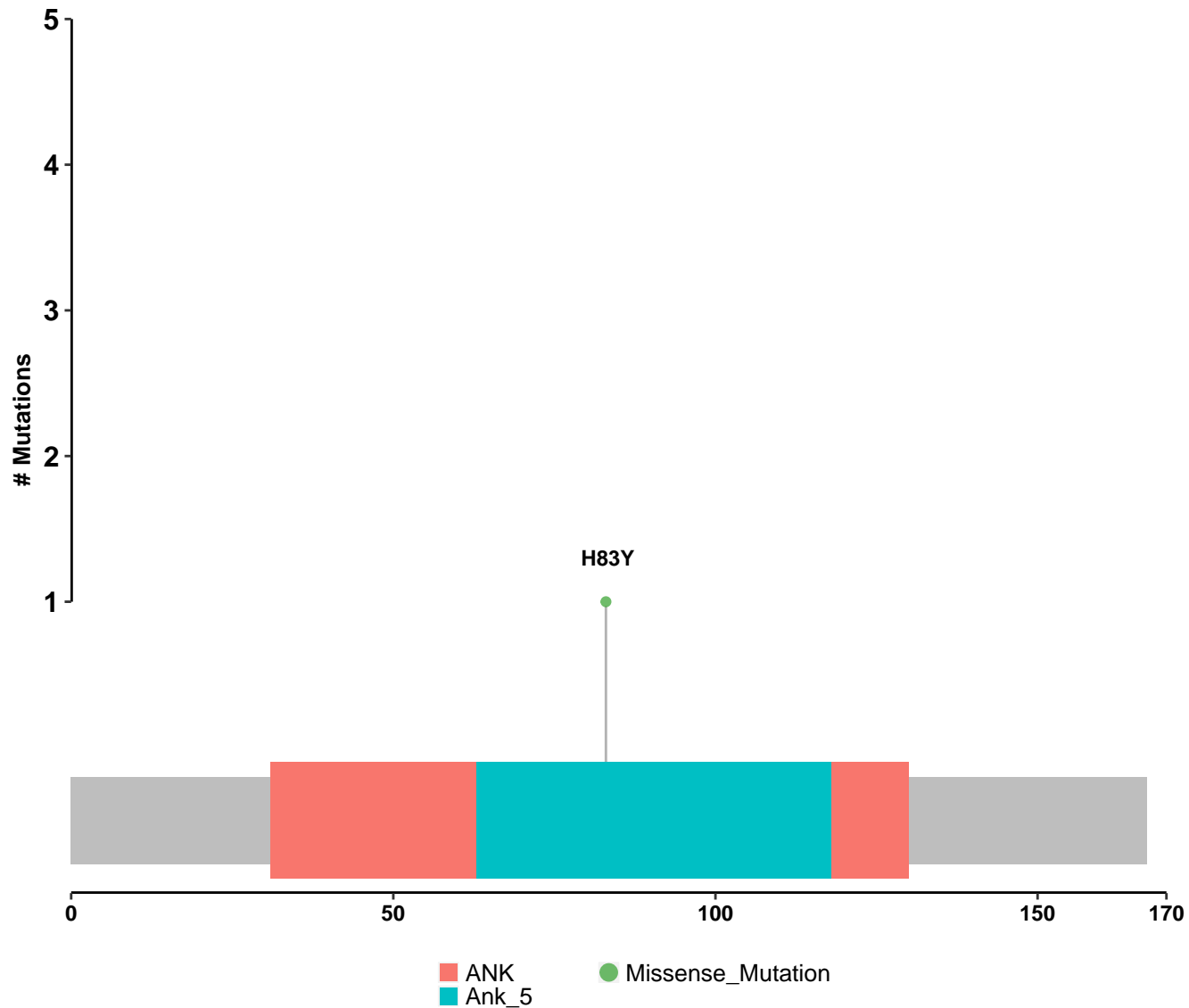
CASP9: [Somatic Mutation Rate: 3.03%]

NM_001229



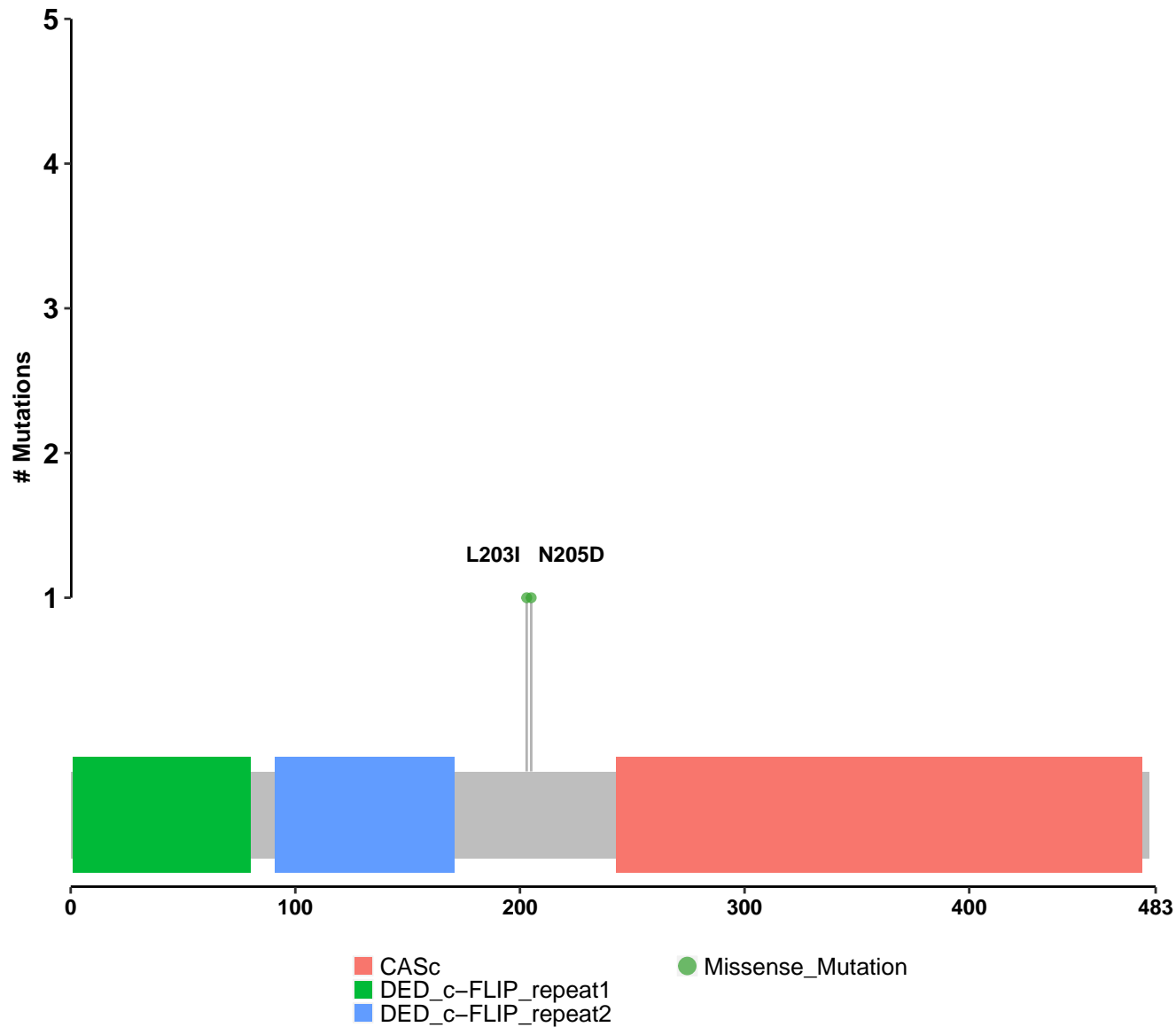
CDKN2A: [Somatic Mutation Rate: 3.03%]

NM_001195132



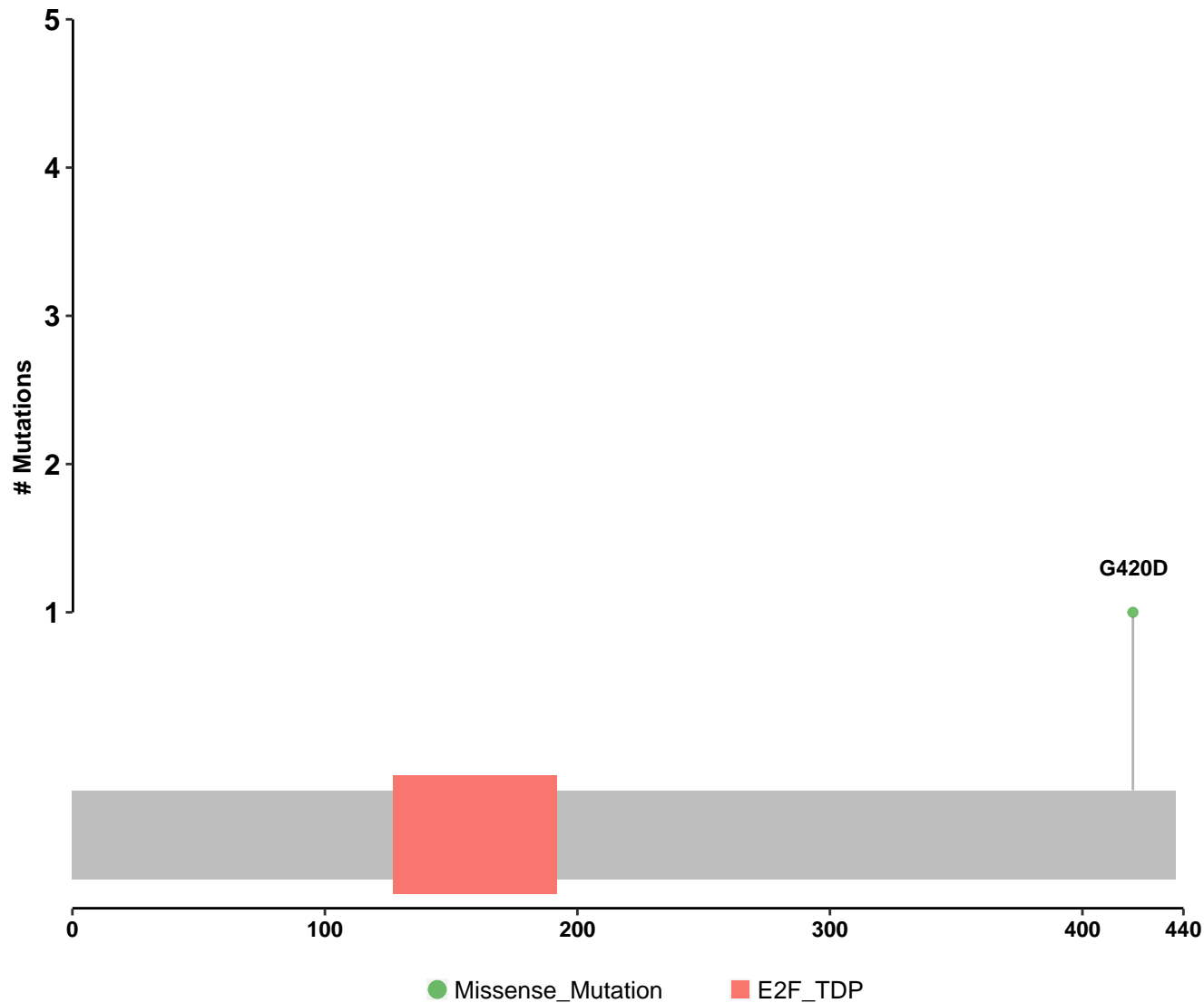
CFLAR: [Somatic Mutation Rate: 3.03%]

NM_003879



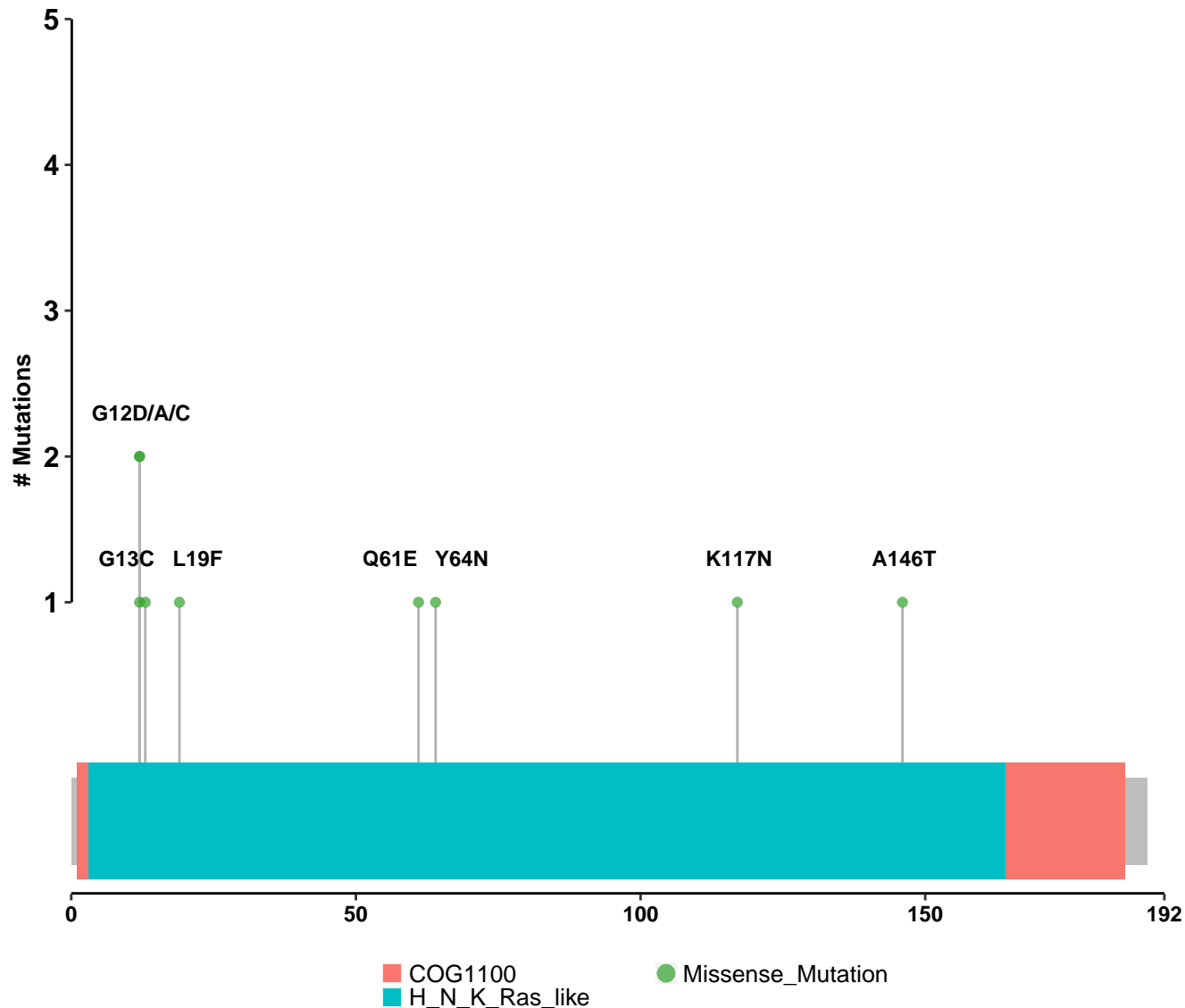
E2F1: [Somatic Mutation Rate: 3.03%]

NM_005225



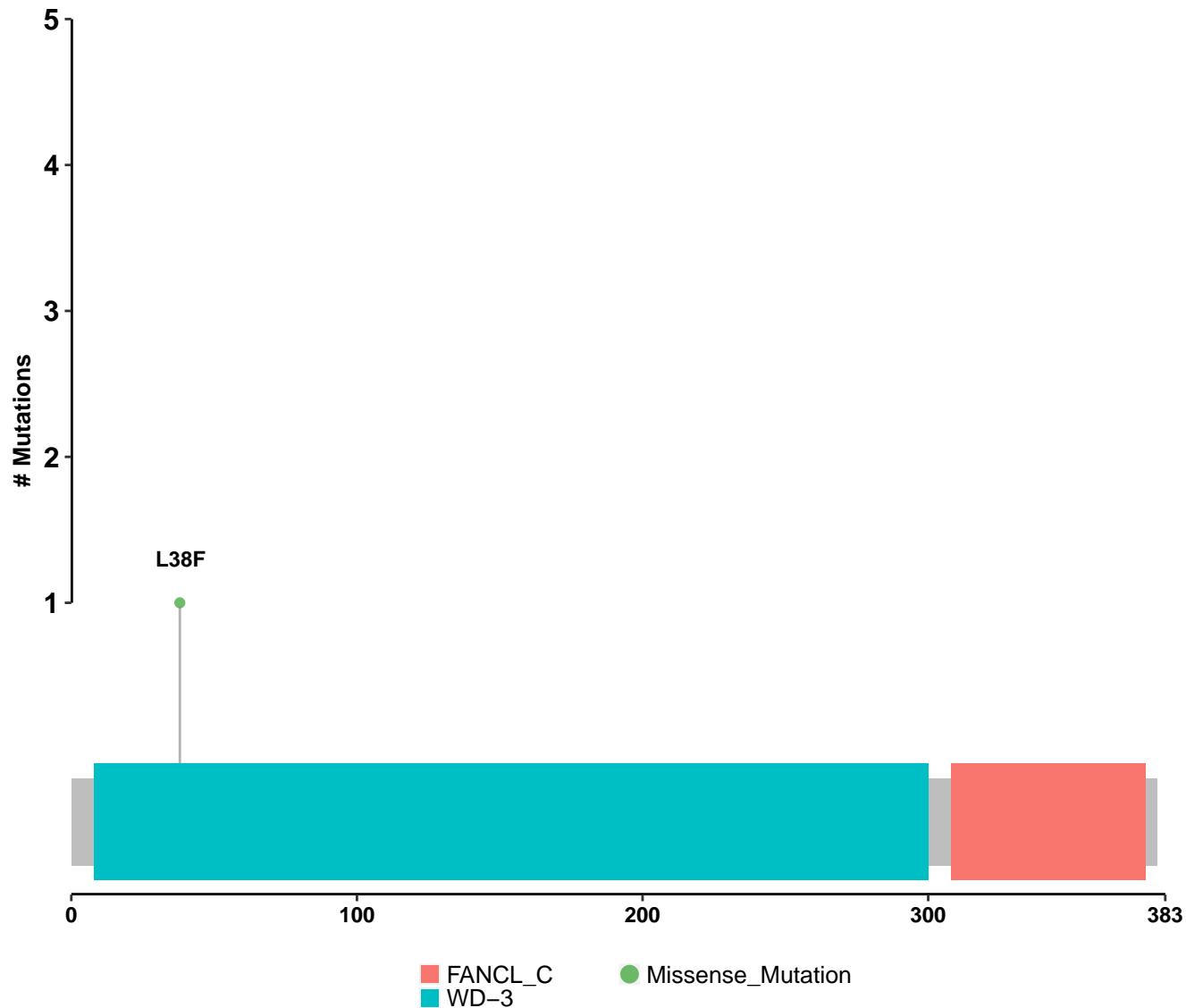
KRAS: [Somatic Mutation Rate: 27.27%]

NM_033360



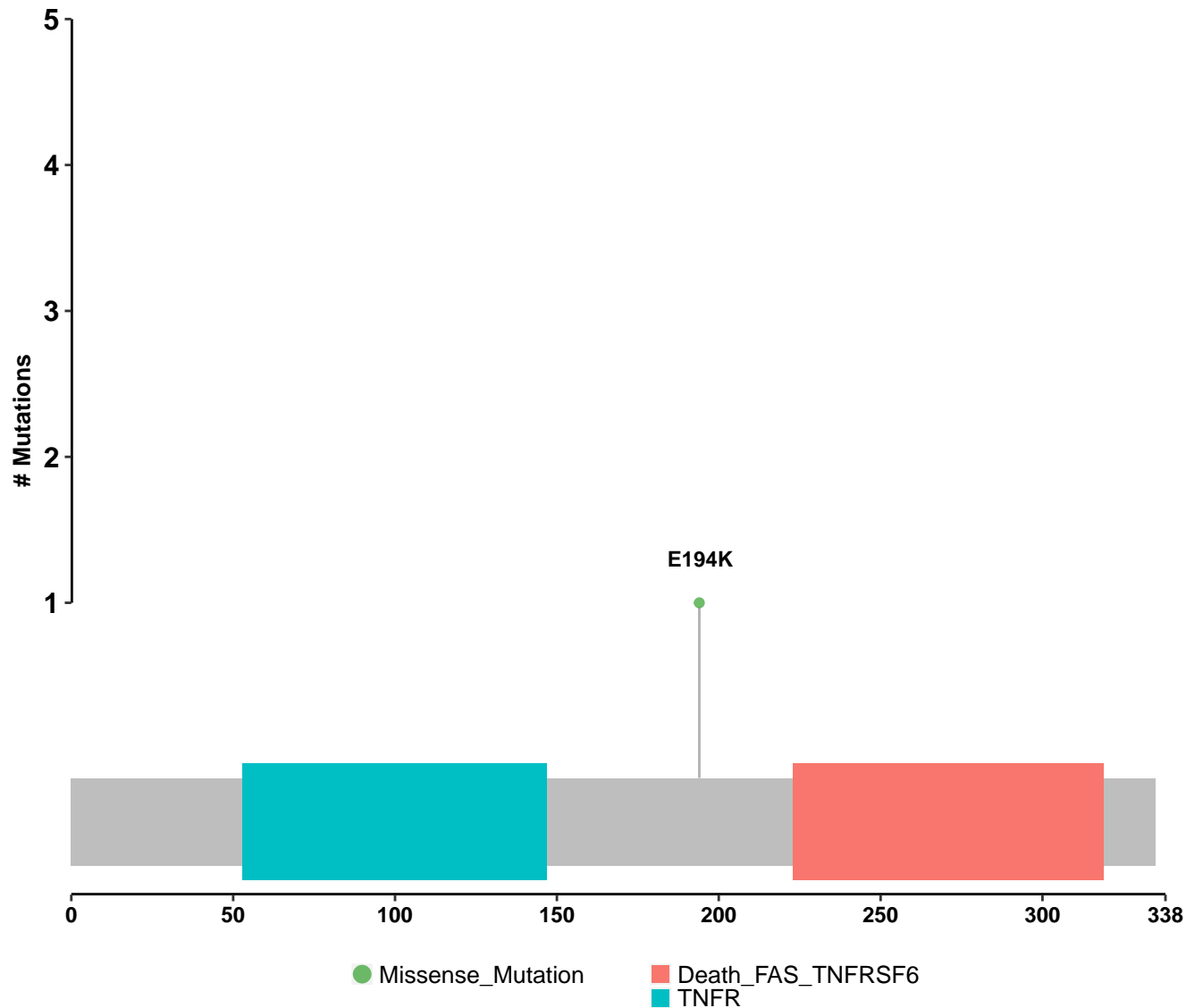
FANCL: [Somatic Mutation Rate: 3.03%]

NM_001114636



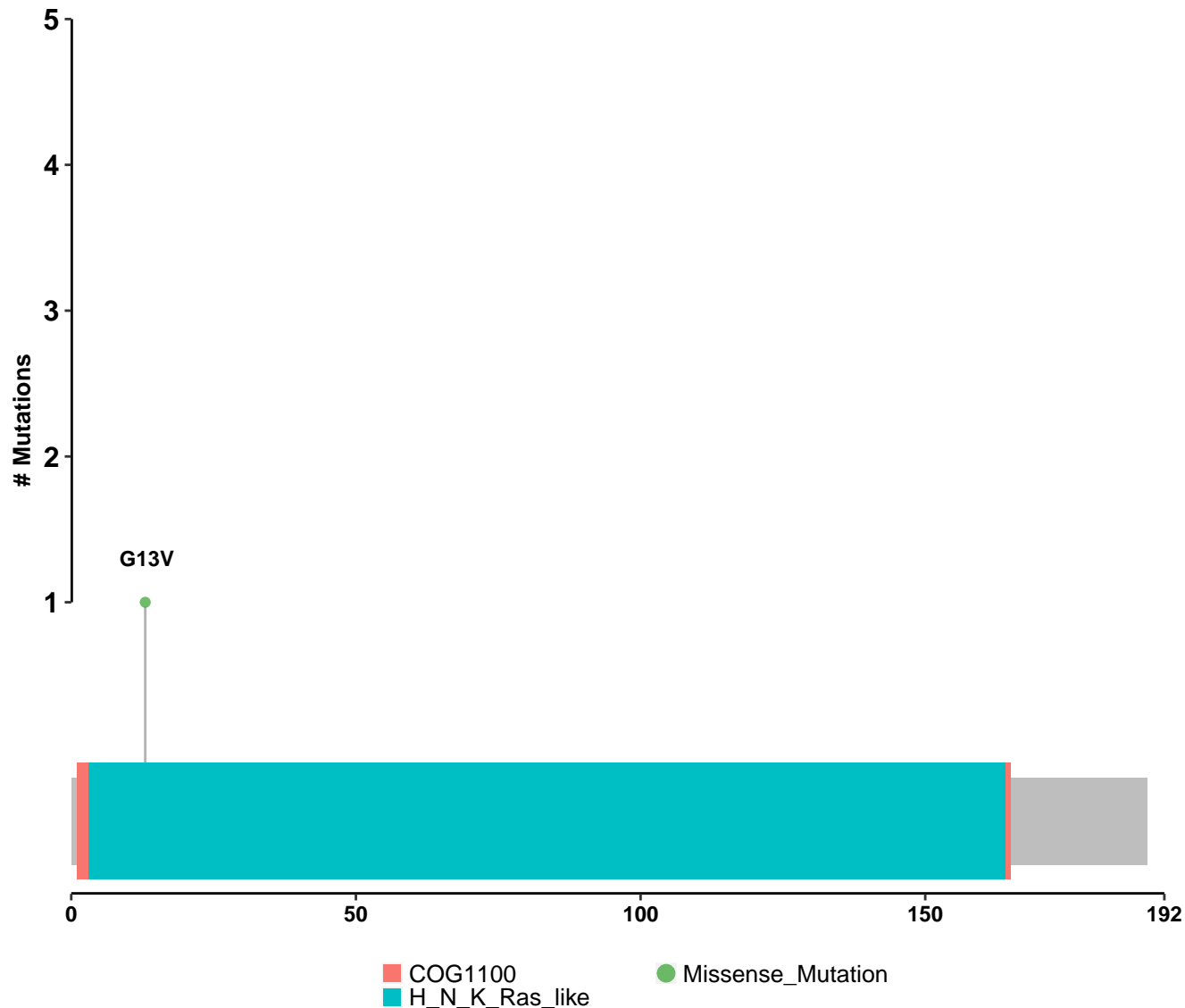
FAS: [Somatic Mutation Rate: 3.03%]

NM_000043



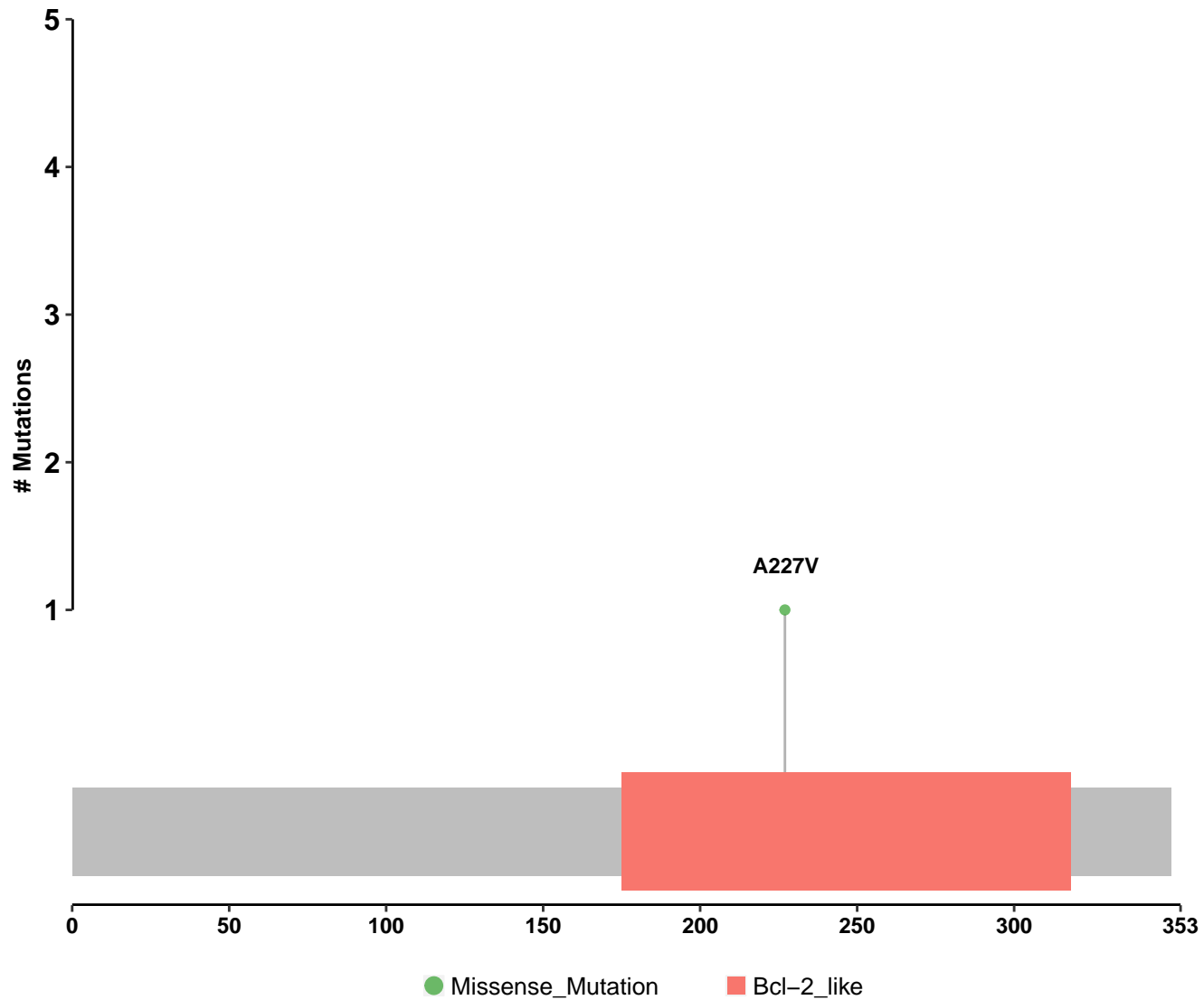
HRAS: [Somatic Mutation Rate: 3.03%]

NM_001130442



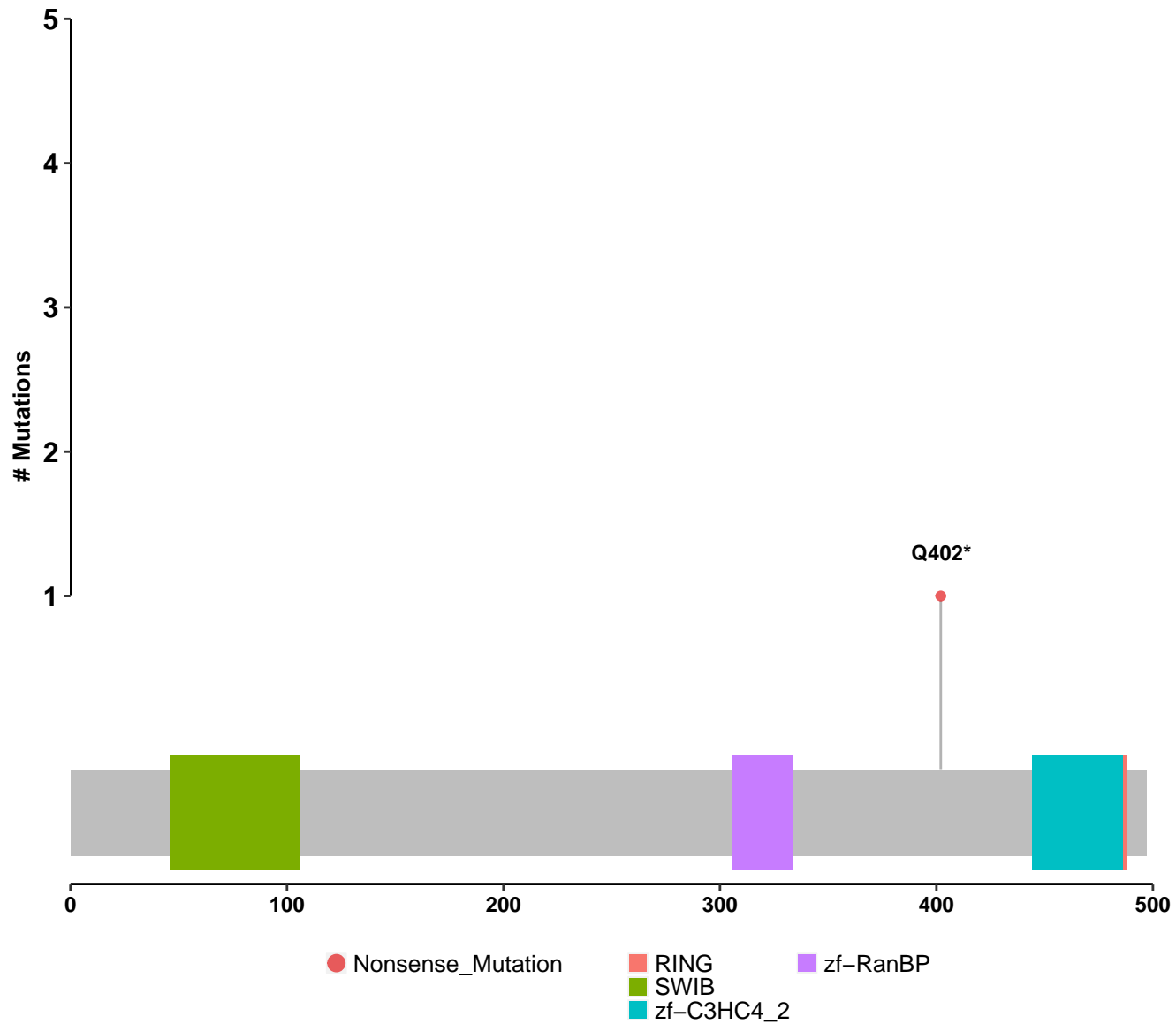
MCL1: [Somatic Mutation Rate: 3.03%]

NM_021960



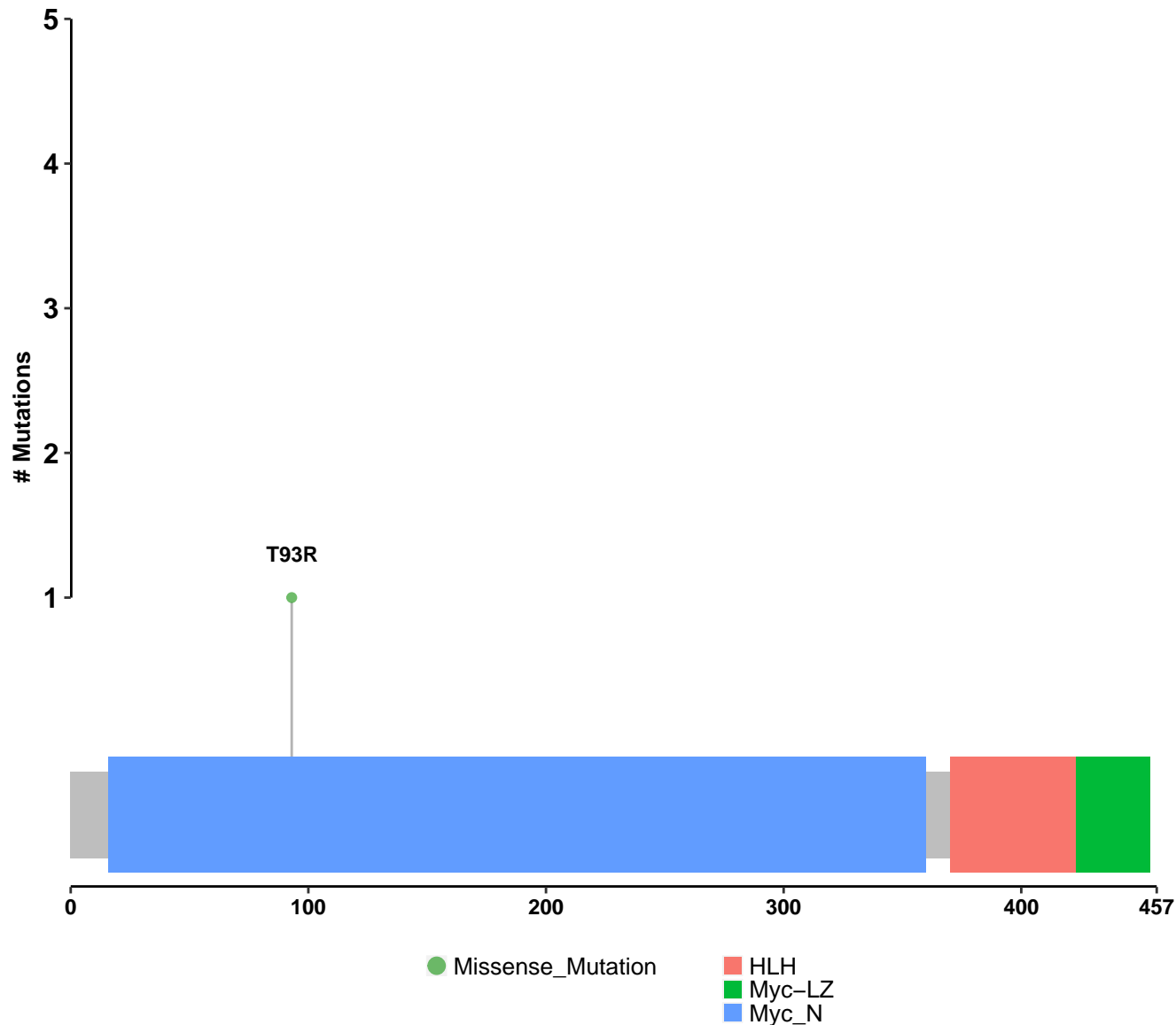
MDM2: [Somatic Mutation Rate: 3.03%]

NM_002392



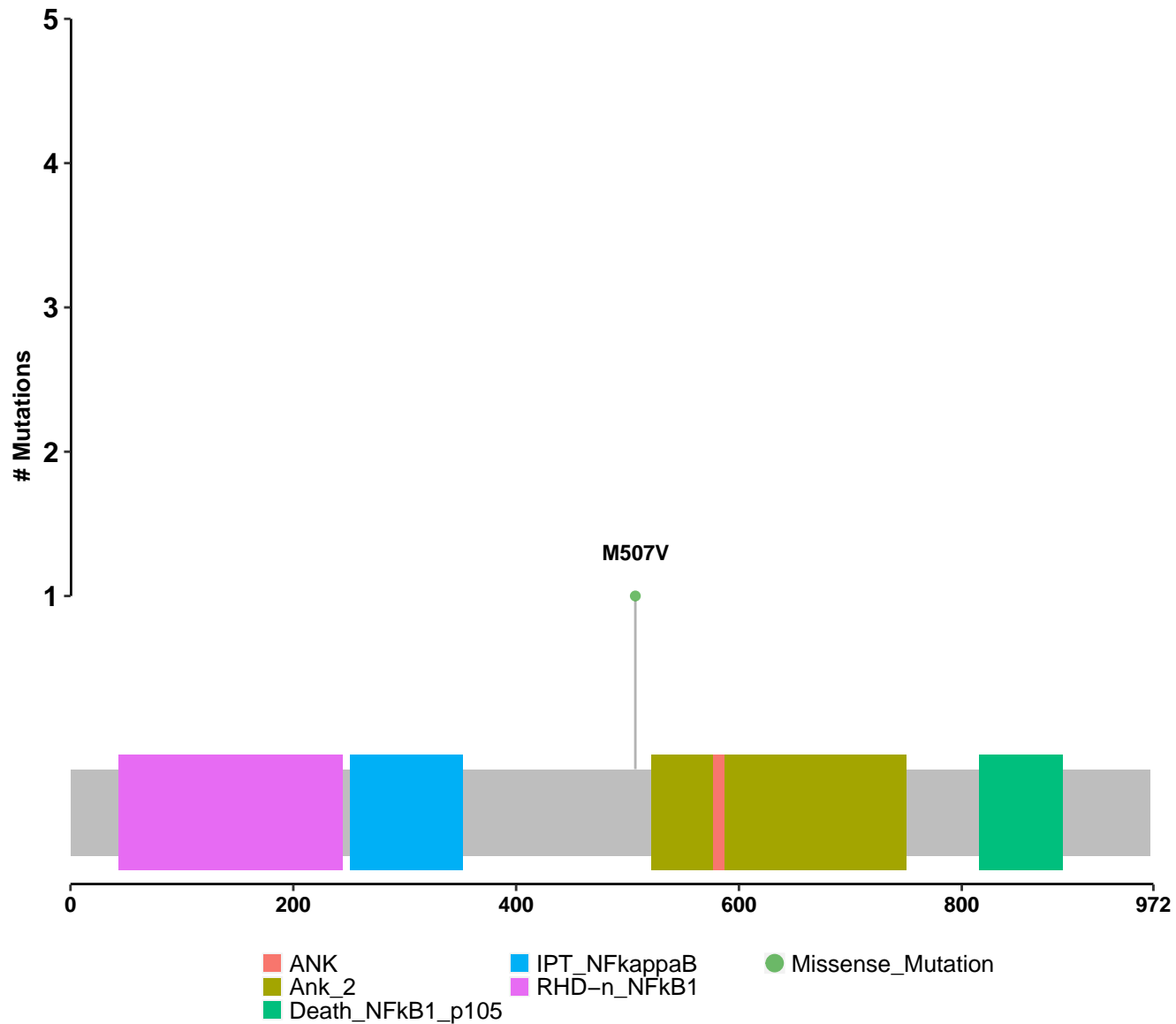
MYC: [Somatic Mutation Rate: 3.03%]

NM_002467



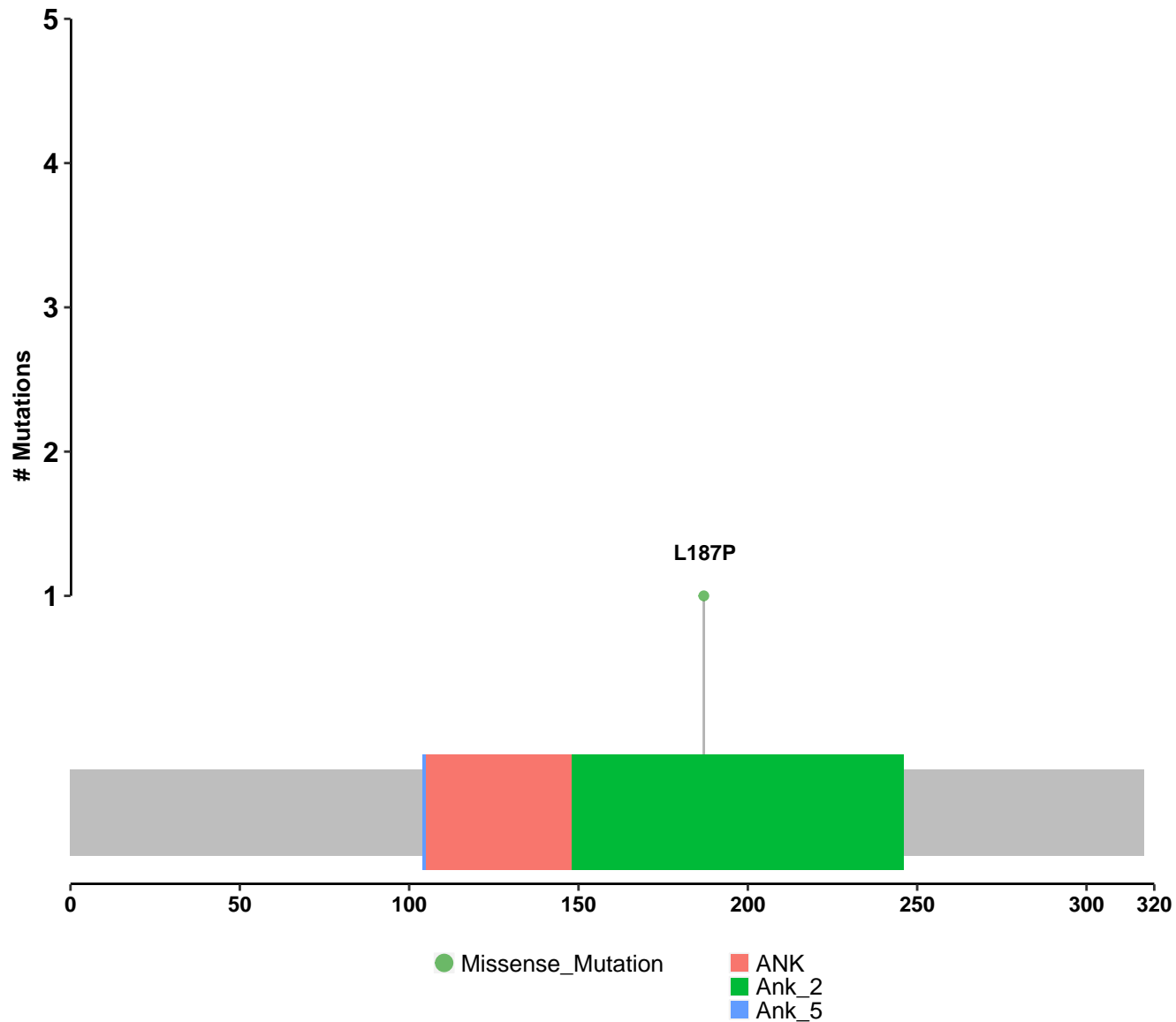
NFKB1: [Somatic Mutation Rate: 3.03%]

NM_003998



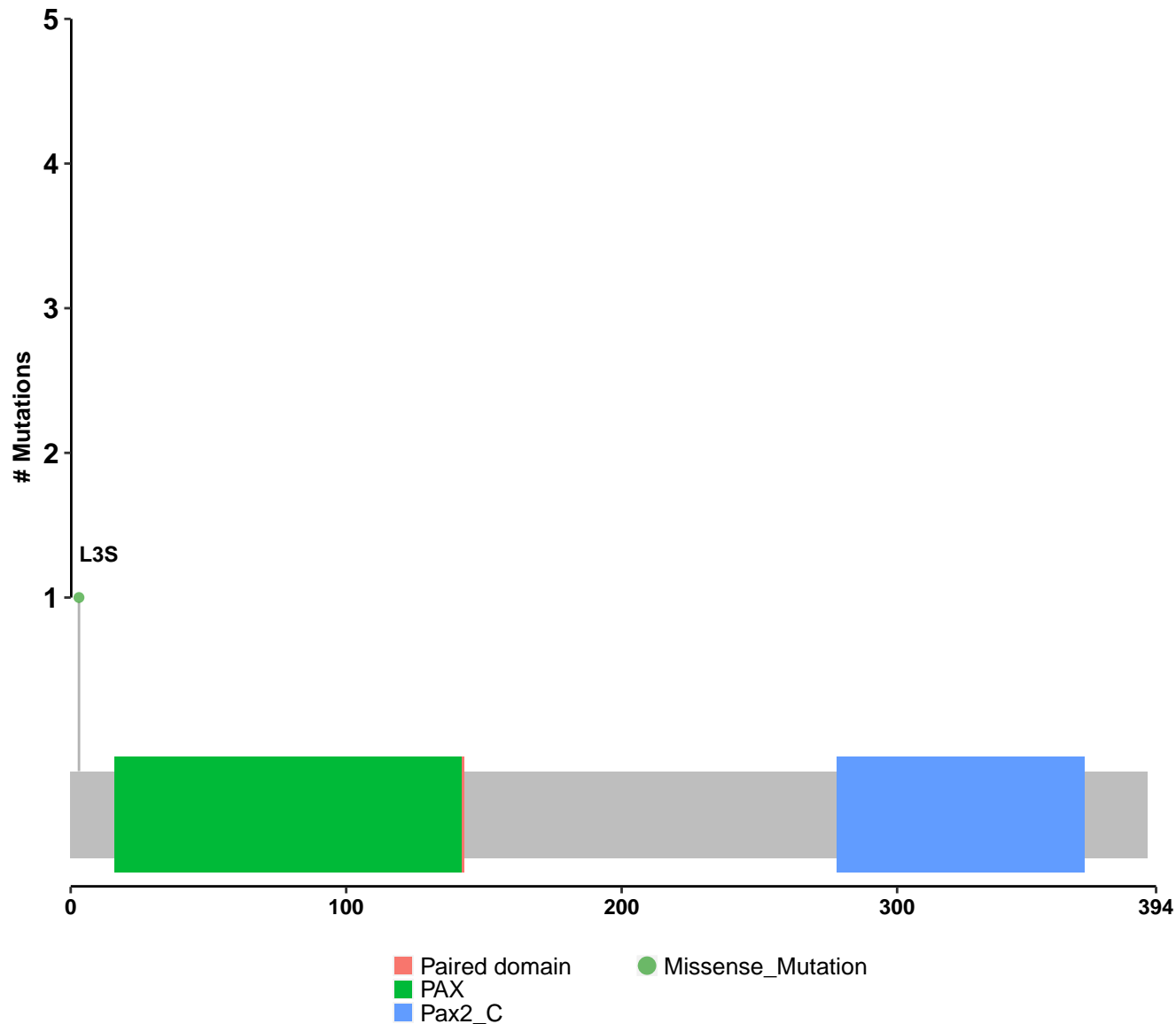
NFKBIA: [Somatic Mutation Rate: 3.03%]

NM_020529



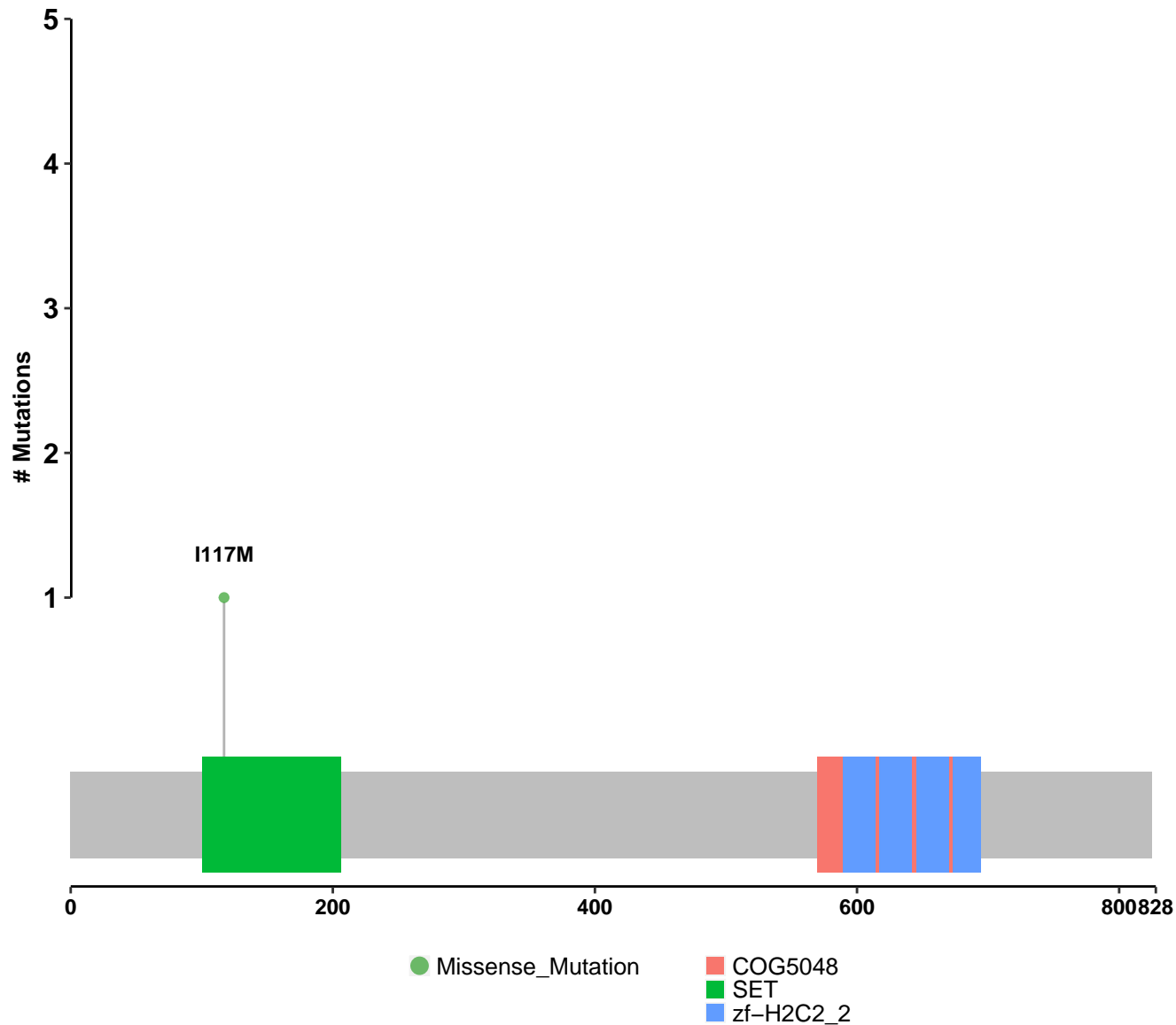
PAX5: [Somatic Mutation Rate: 3.03%]

NM_016734



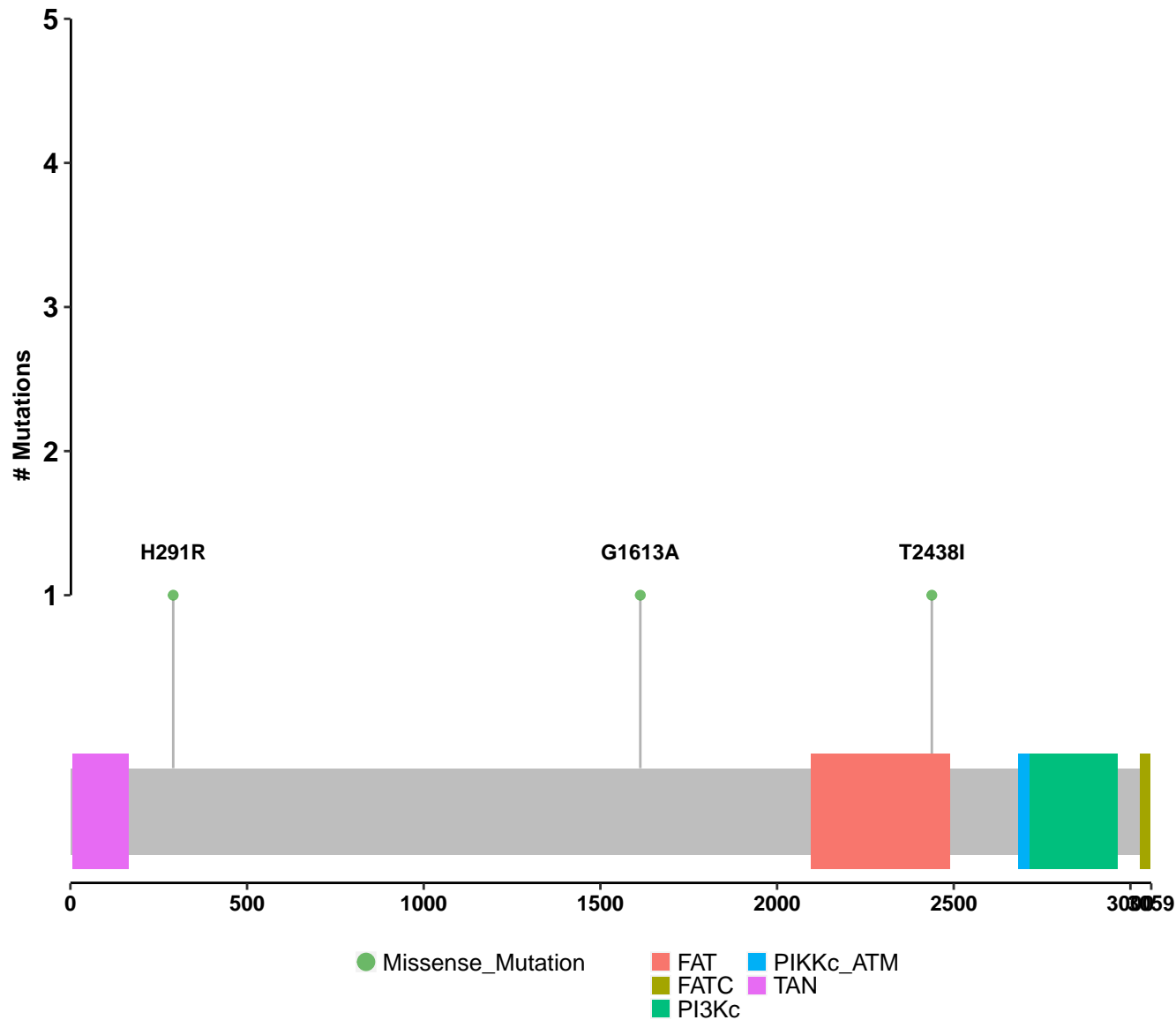
PRDM1: [Somatic Mutation Rate: 3.03%]

NM_001198



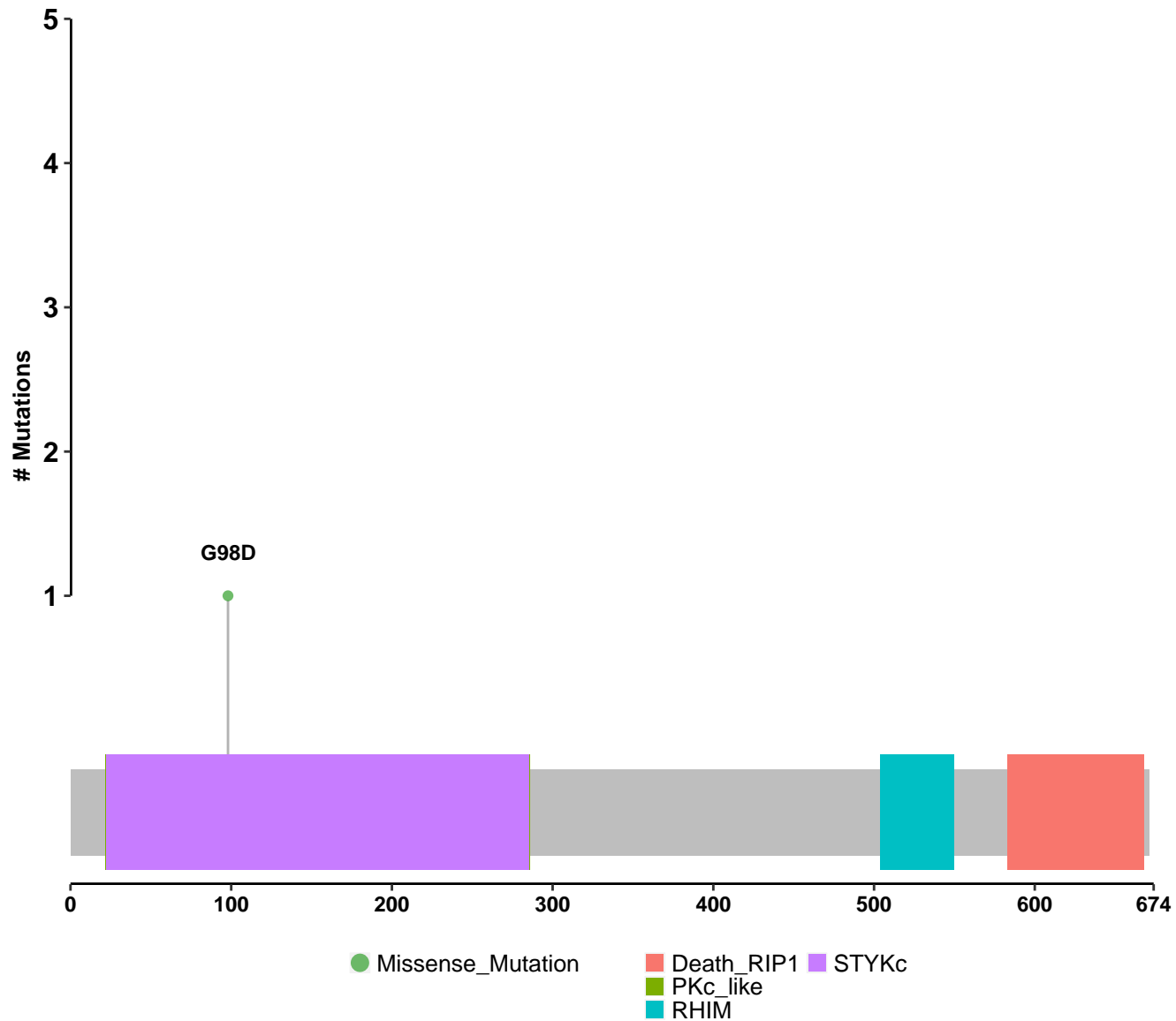
ATM: [Somatic Mutation Rate: 9.09%]

NM_000051



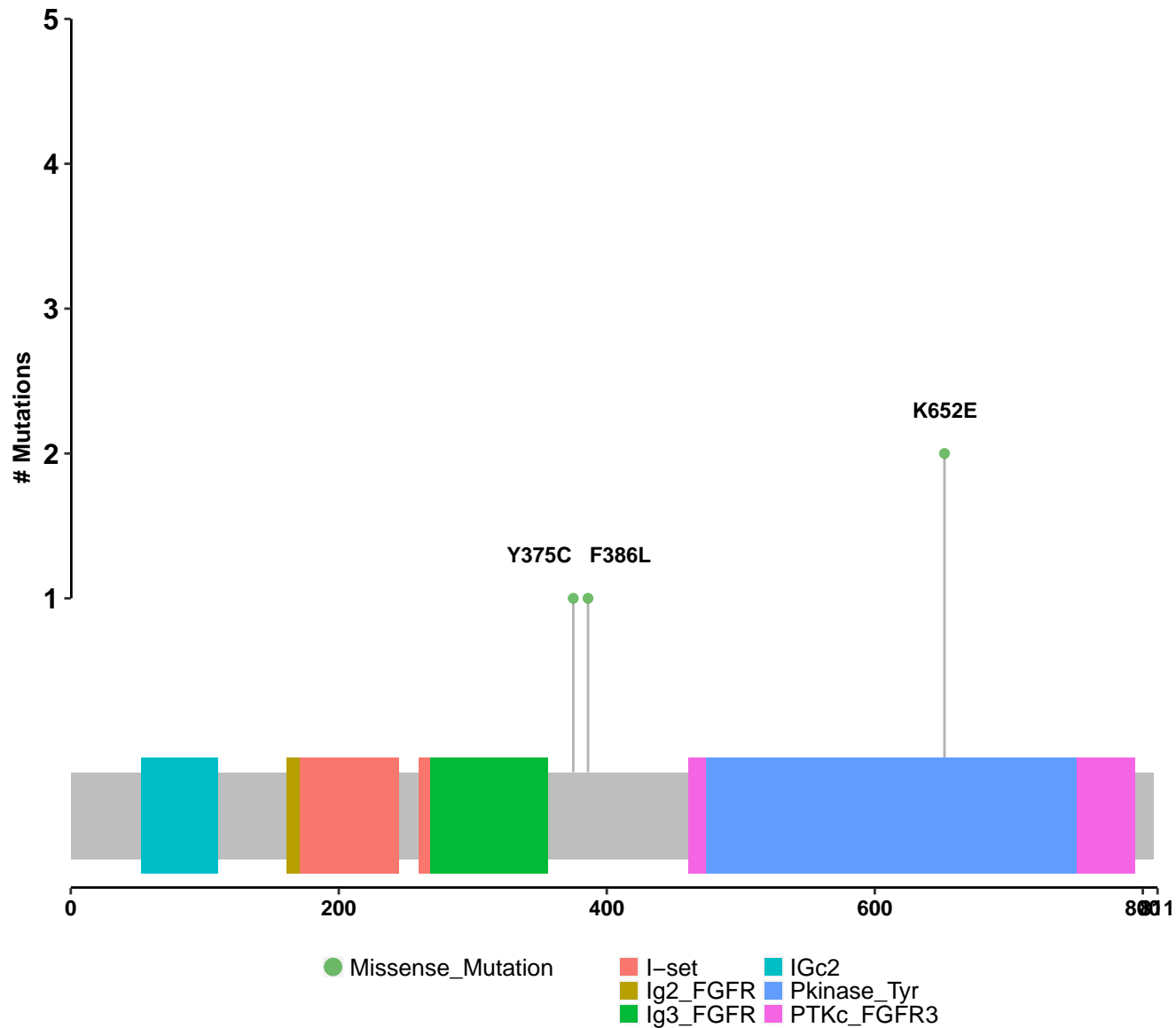
RIPK1: [Somatic Mutation Rate: 3.03%]

NM_003804



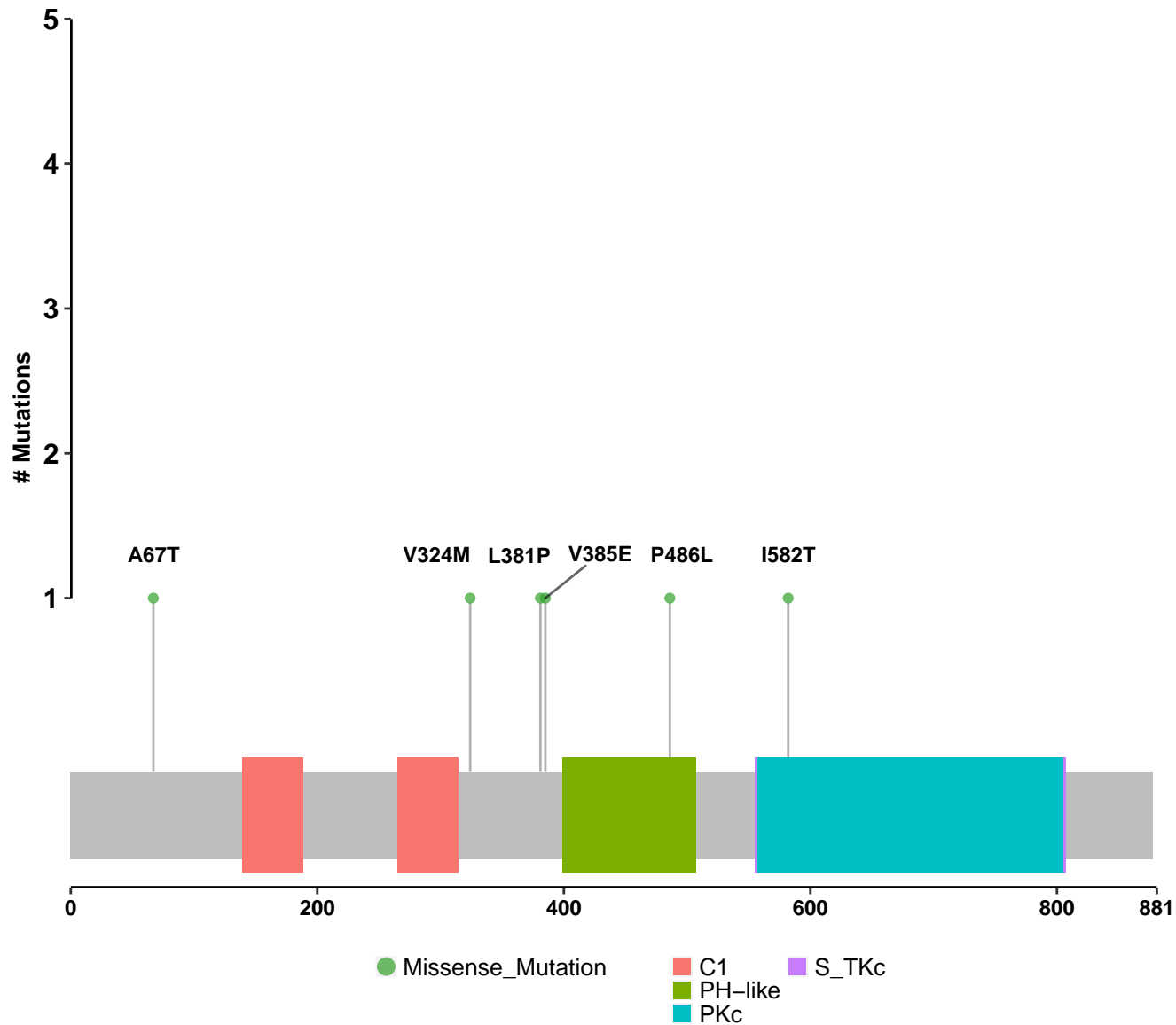
FGFR3: [Somatic Mutation Rate: 12.12%]

NM_001163213



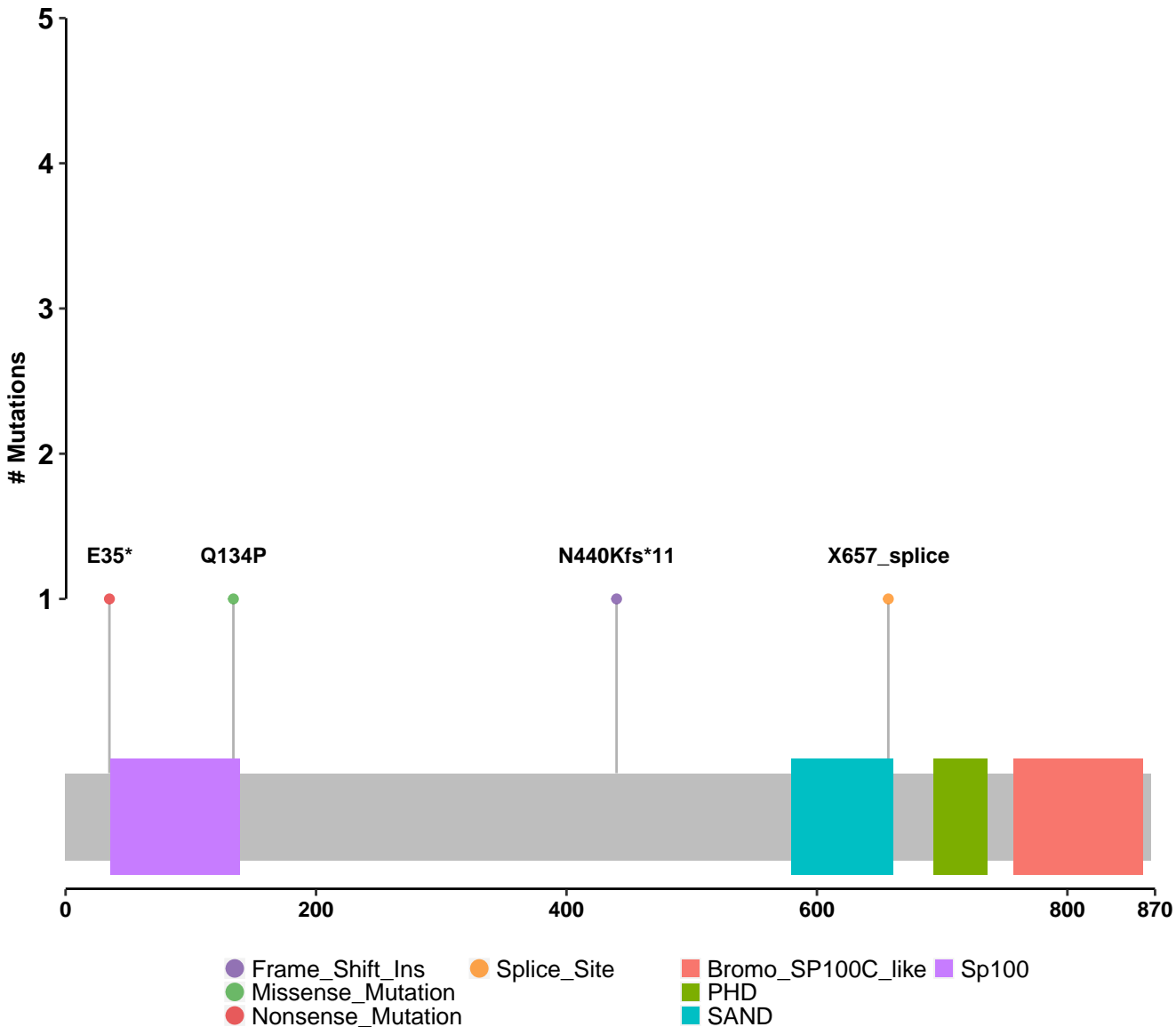
PRKD2: [Somatic Mutation Rate: 18.18%]

NM_001079880



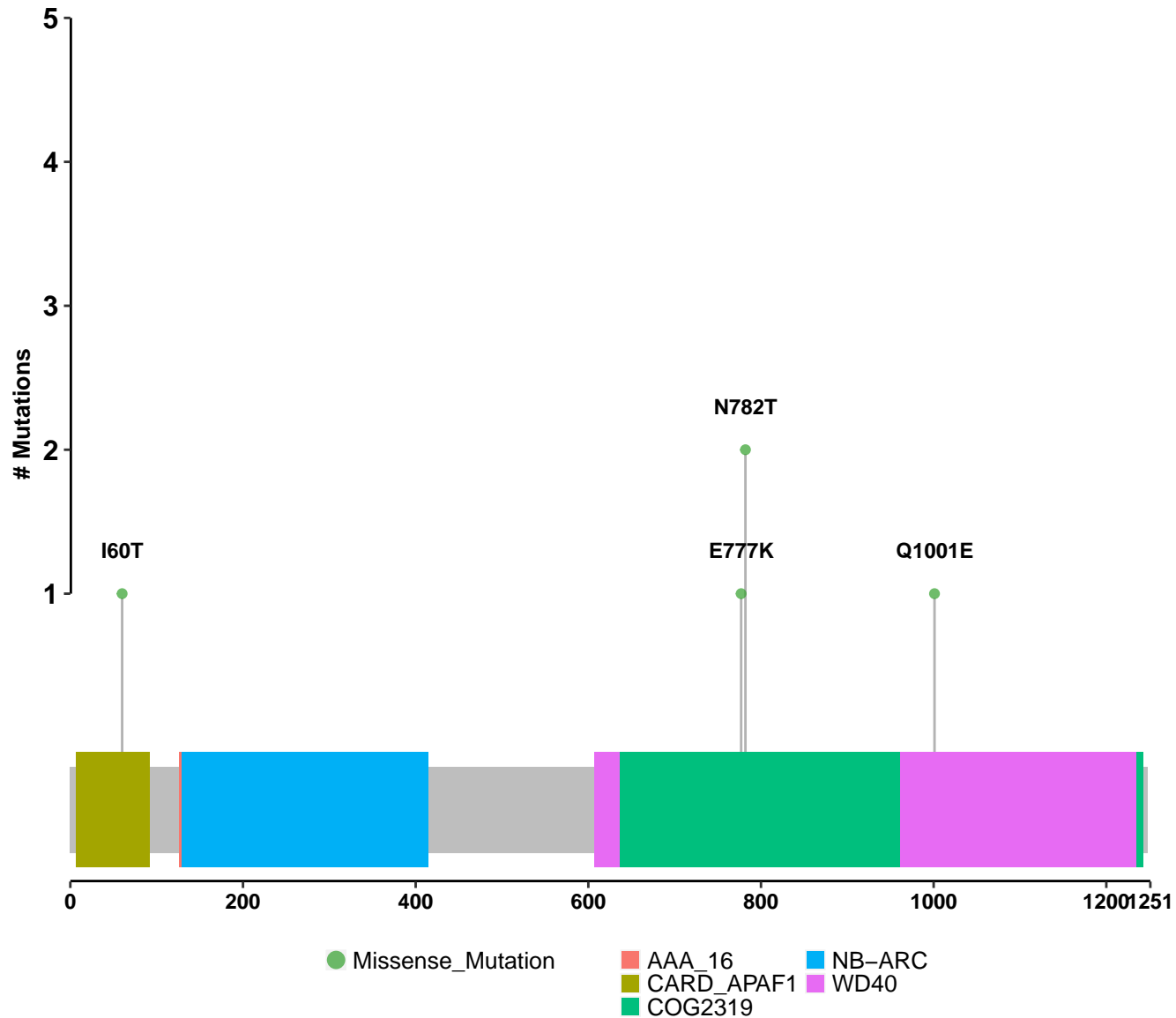
SP140: [Somatic Mutation Rate: 12.12%]

NM_007237



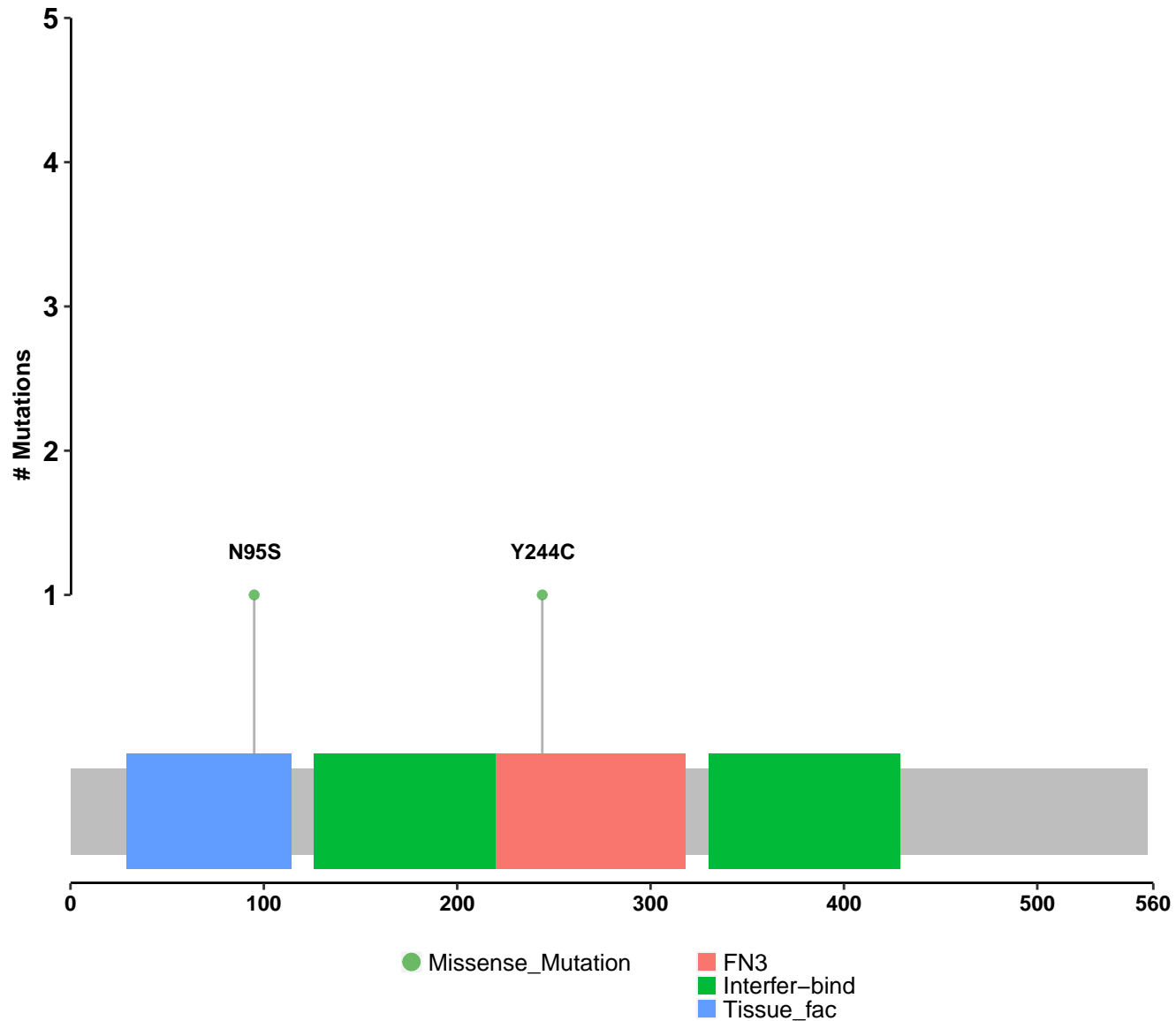
APAF1: [Somatic Mutation Rate: 15.15%]

NM_181861



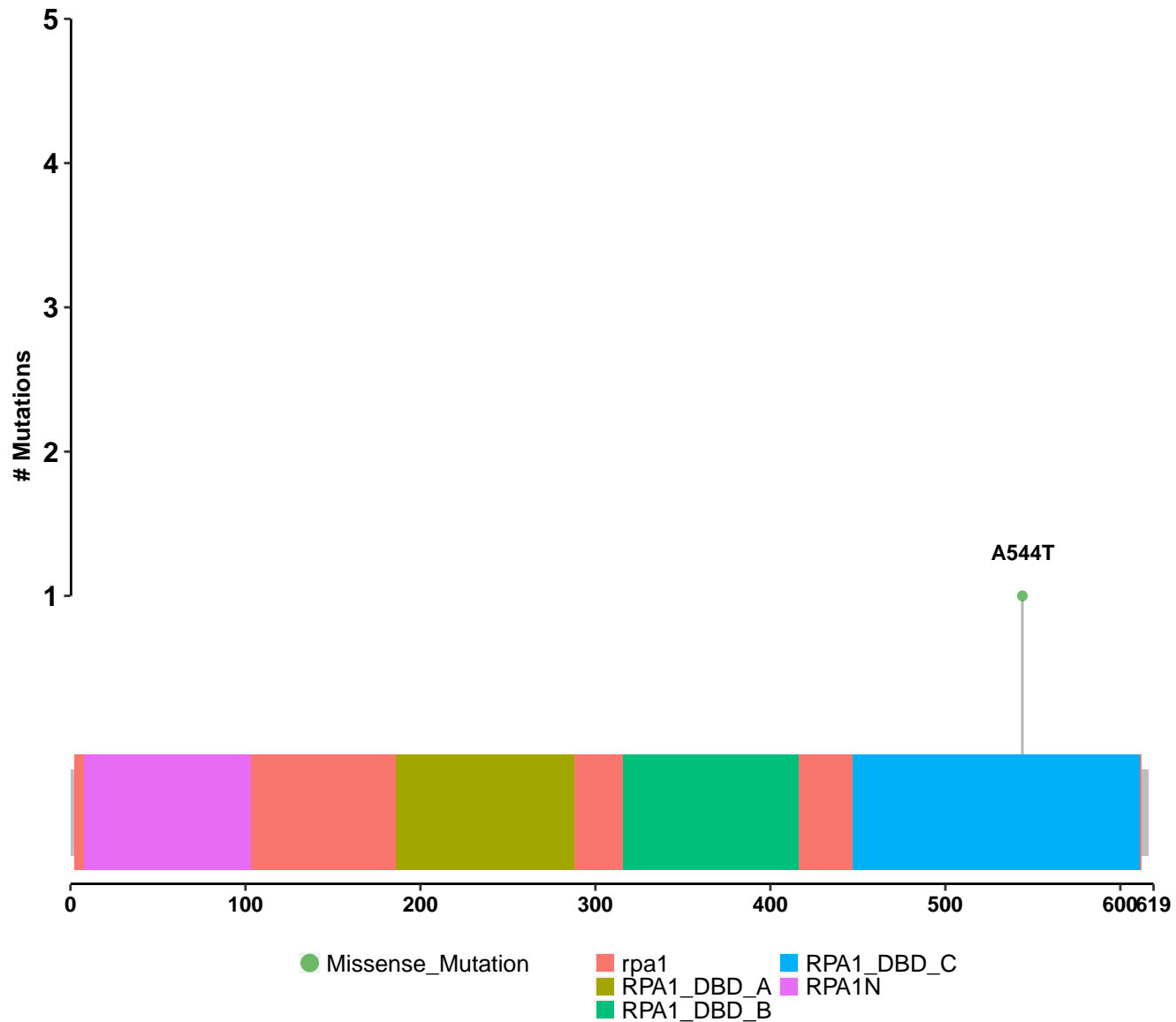
IFNAR1: [Somatic Mutation Rate: 6.06%]

NM_000629



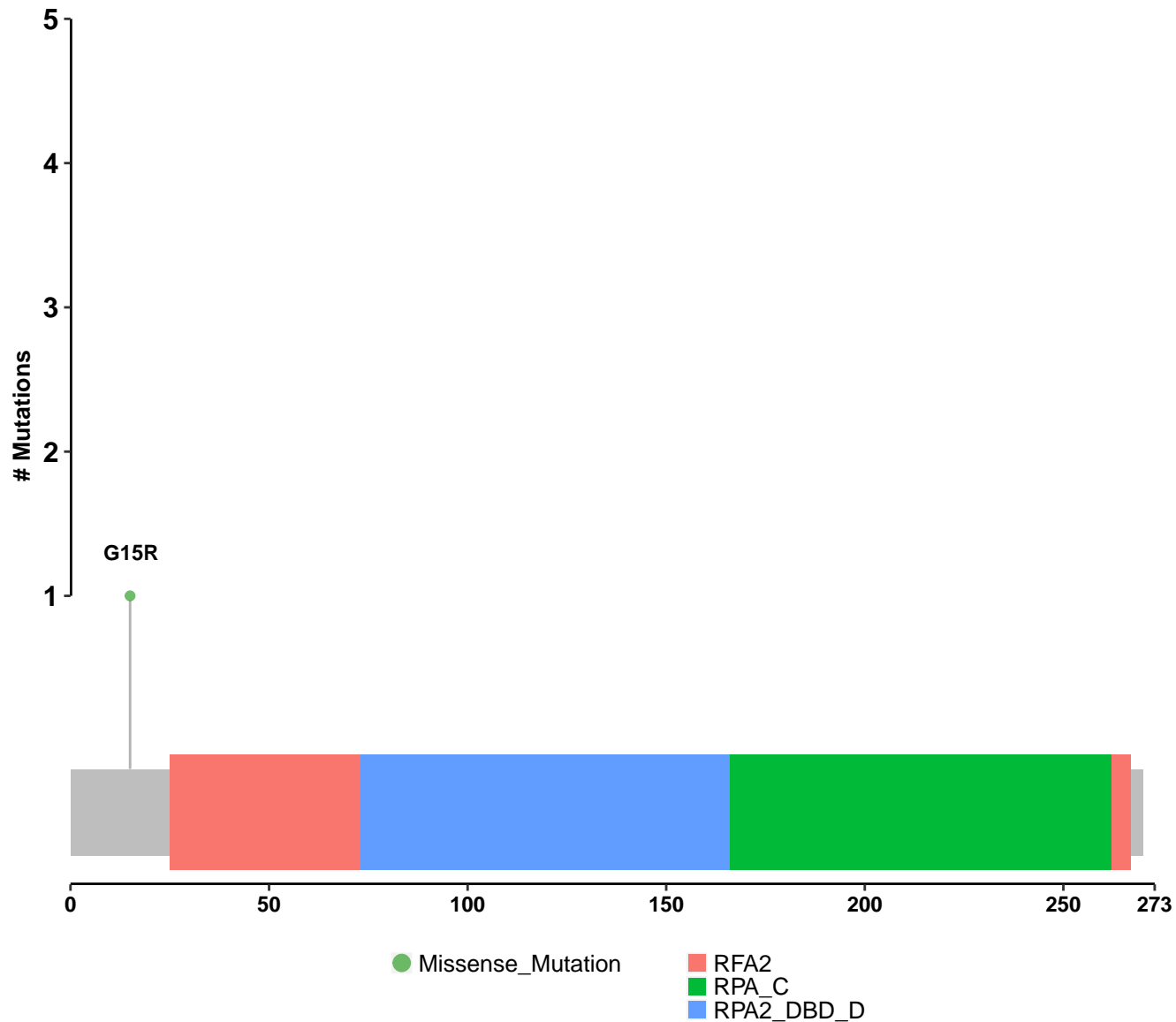
RPA1: [Somatic Mutation Rate: 3.03%]

NM_002945



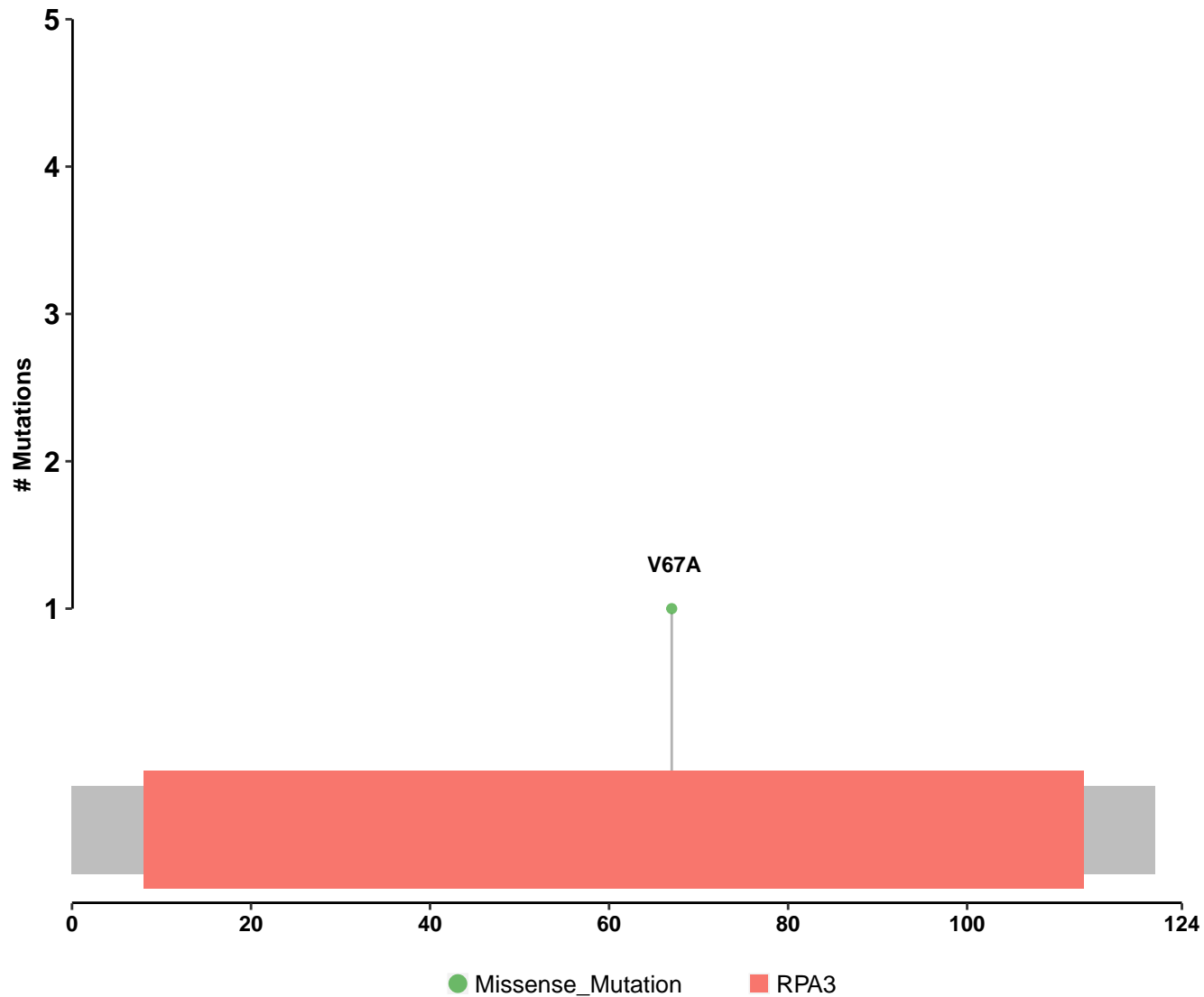
RPA2: [Somatic Mutation Rate: 3.03%]

NM_002946



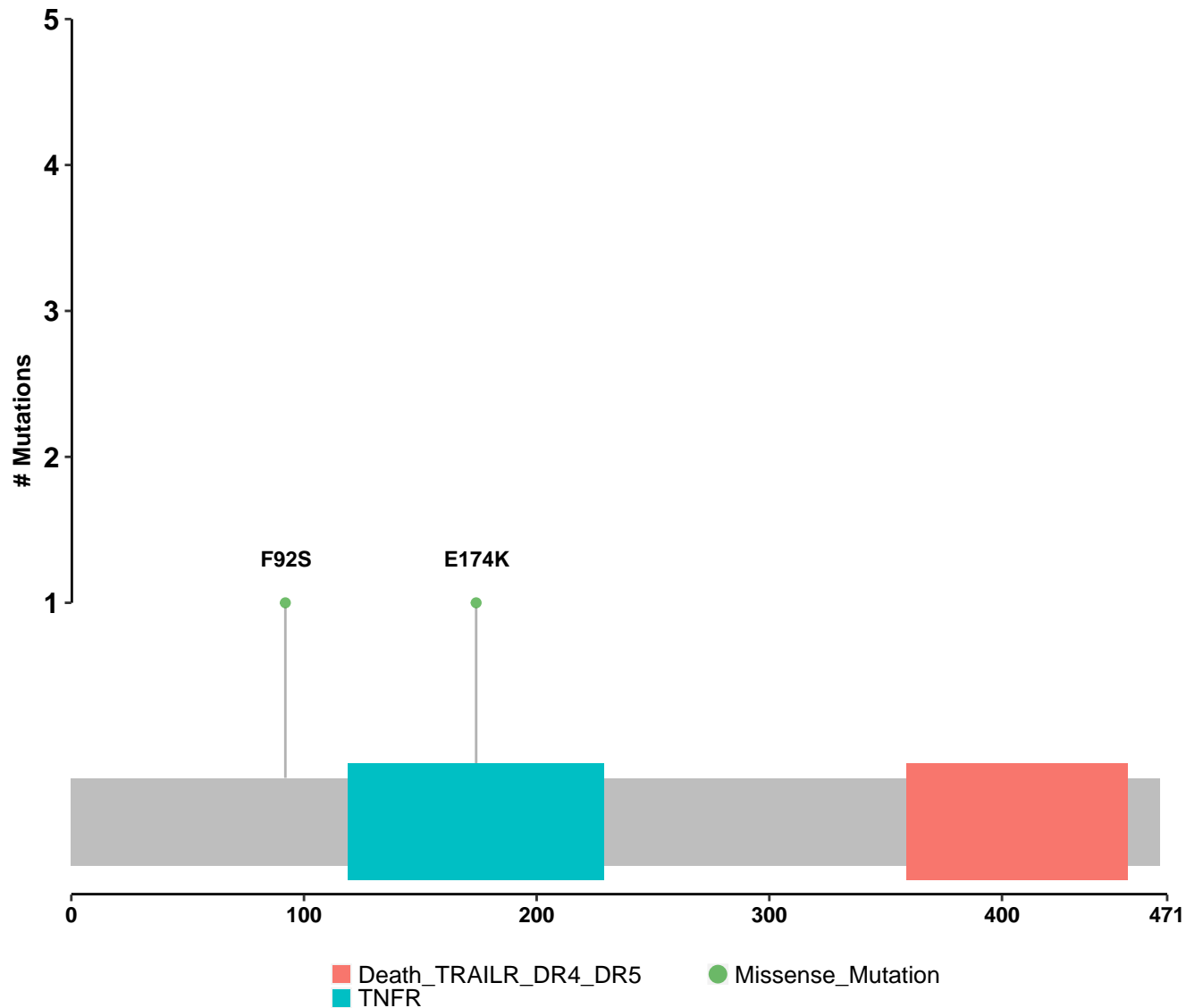
RPA3: [Somatic Mutation Rate: 3.03%]

NM_002947



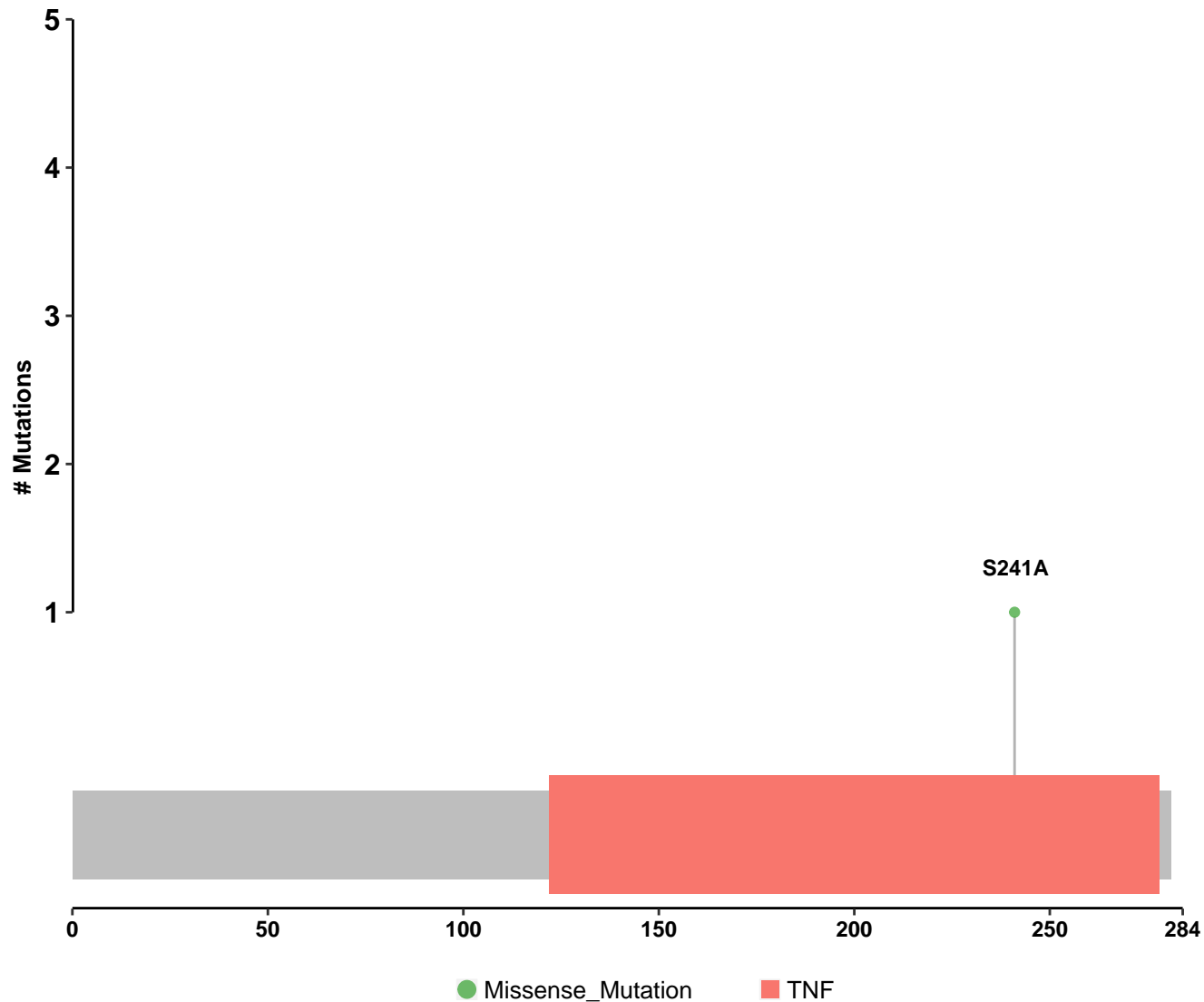
TNFRSF10A: [Somatic Mutation Rate: 3.03%]

NM_003844



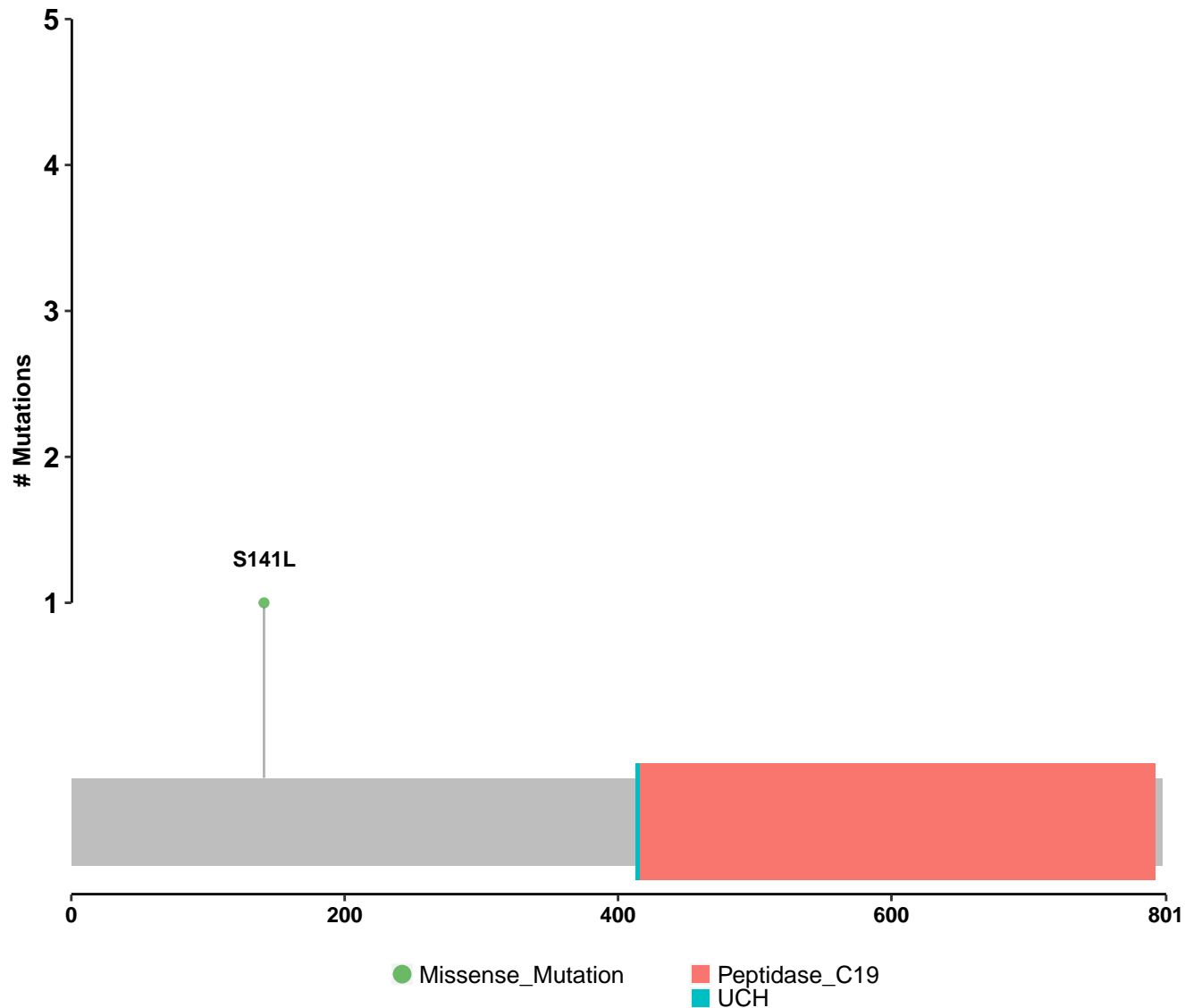
TNFSF10: [Somatic Mutation Rate: 3.03%]

NM_003810



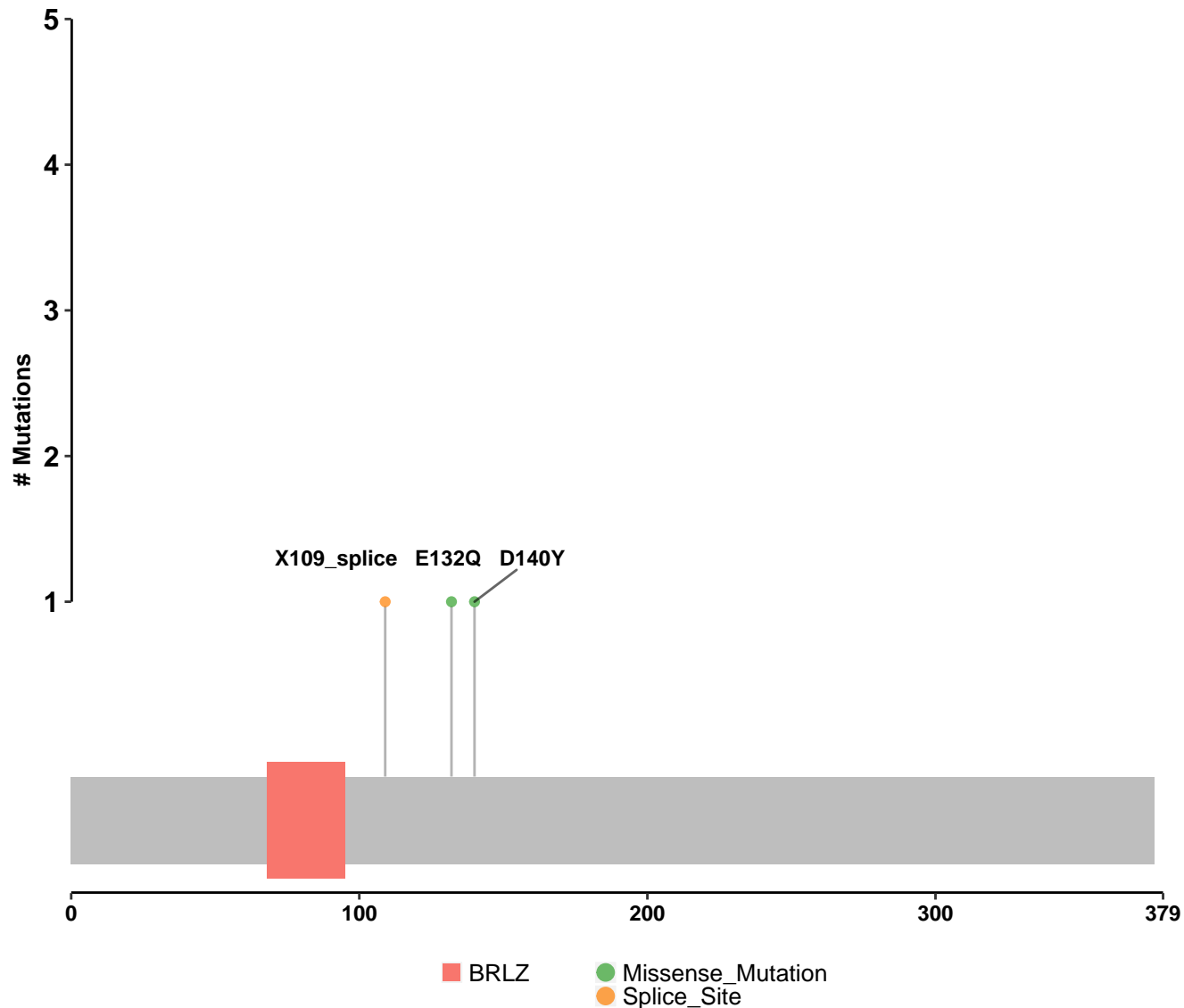
USP10: [Somatic Mutation Rate: 3.03%]

NM_005153



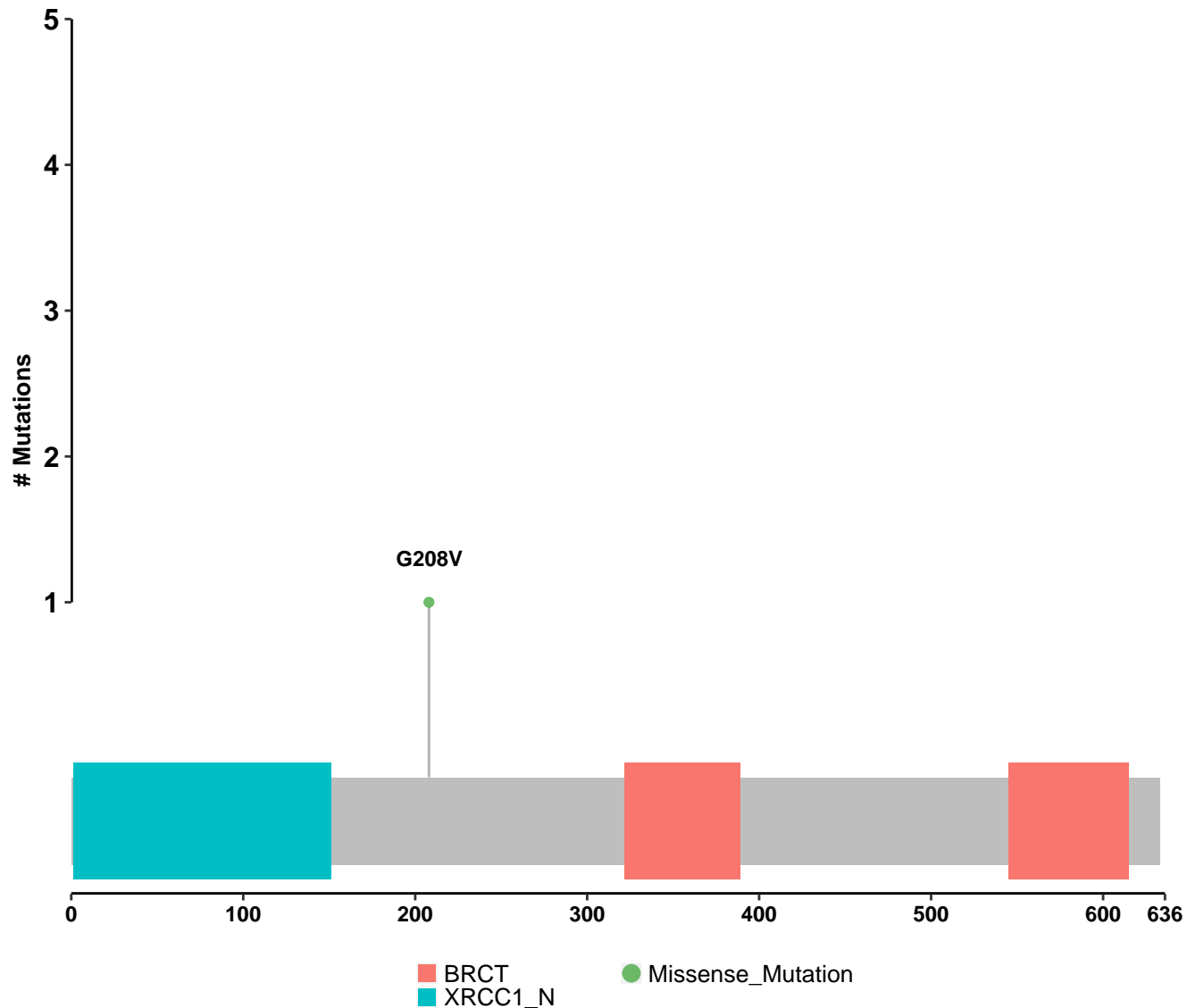
XBP1: [Somatic Mutation Rate: 3.03%]

NM_001079539



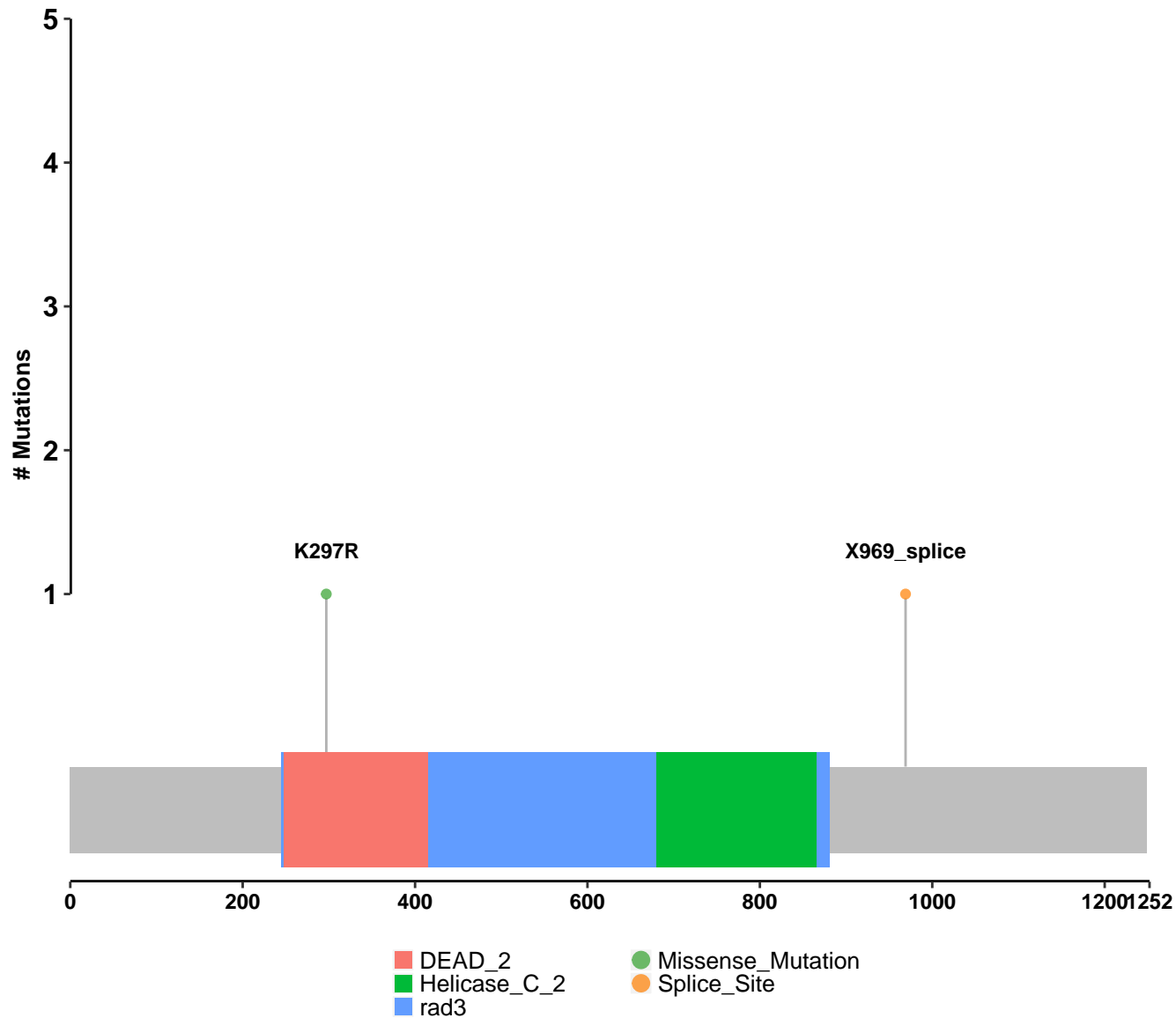
XRCC1: [Somatic Mutation Rate: 3.03%]

NM_006297



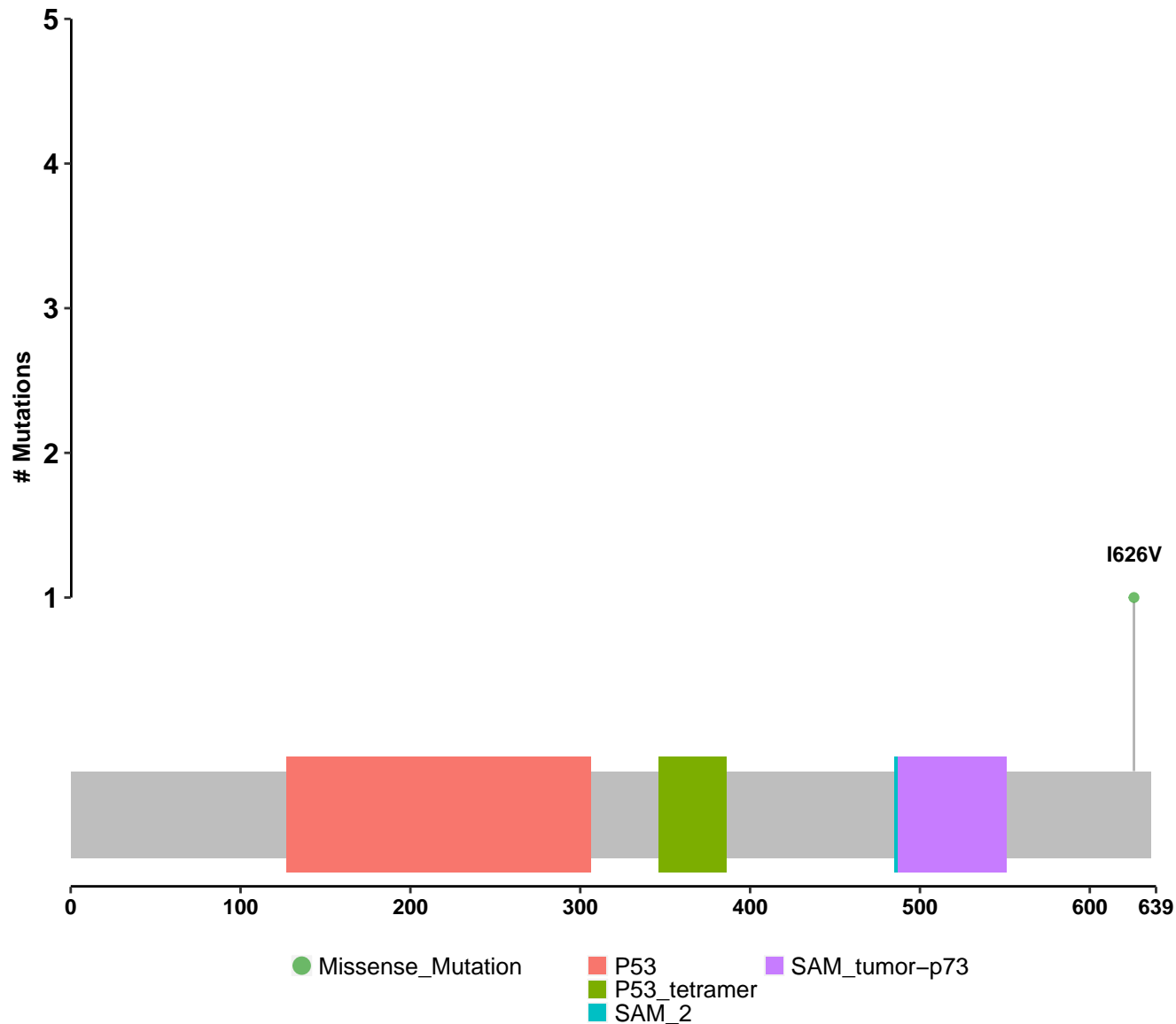
BRIP1: [Somatic Mutation Rate: 6.06%]

NM_032043



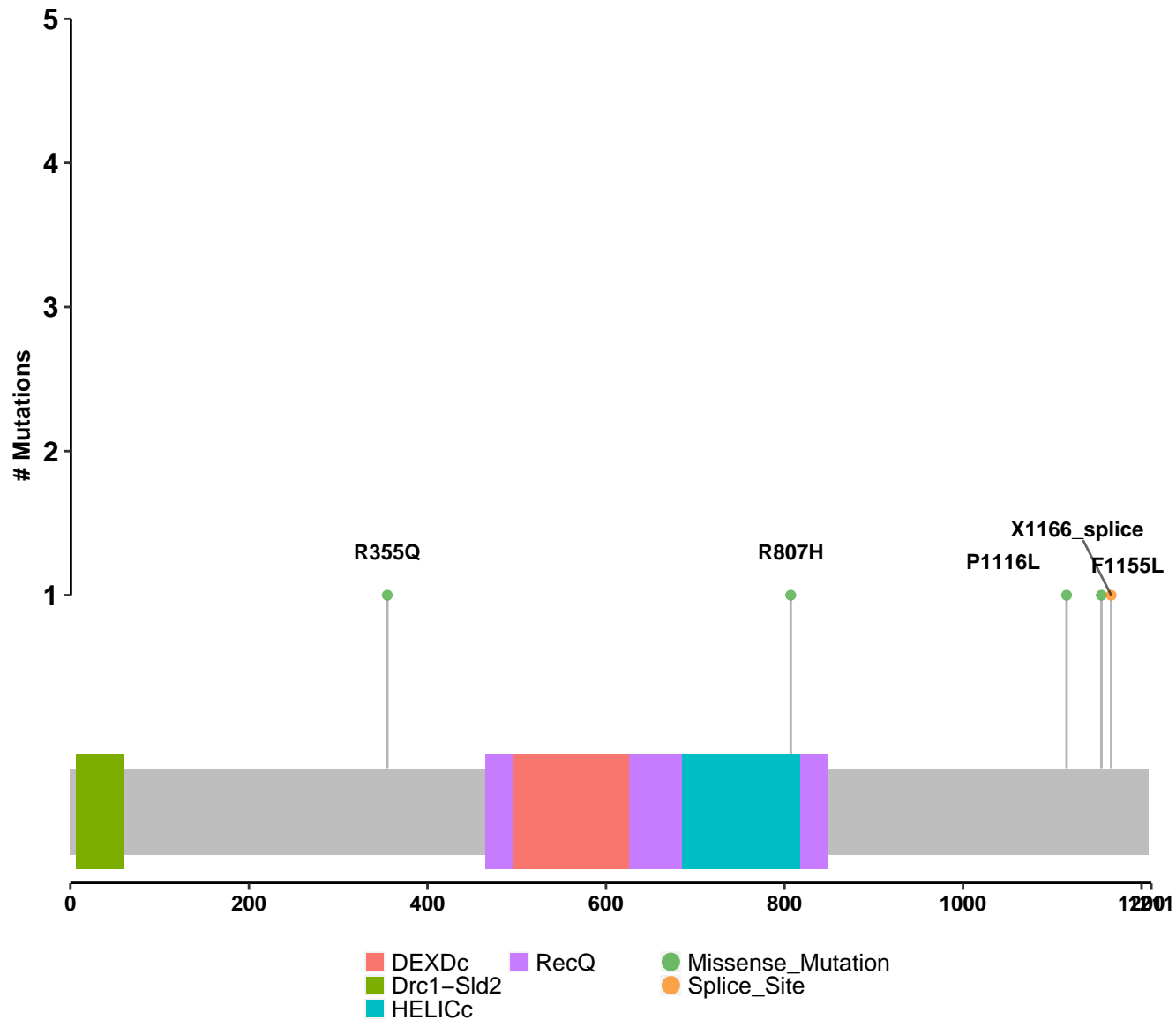
TP73: [Somatic Mutation Rate: 3.03%]

NM_005427



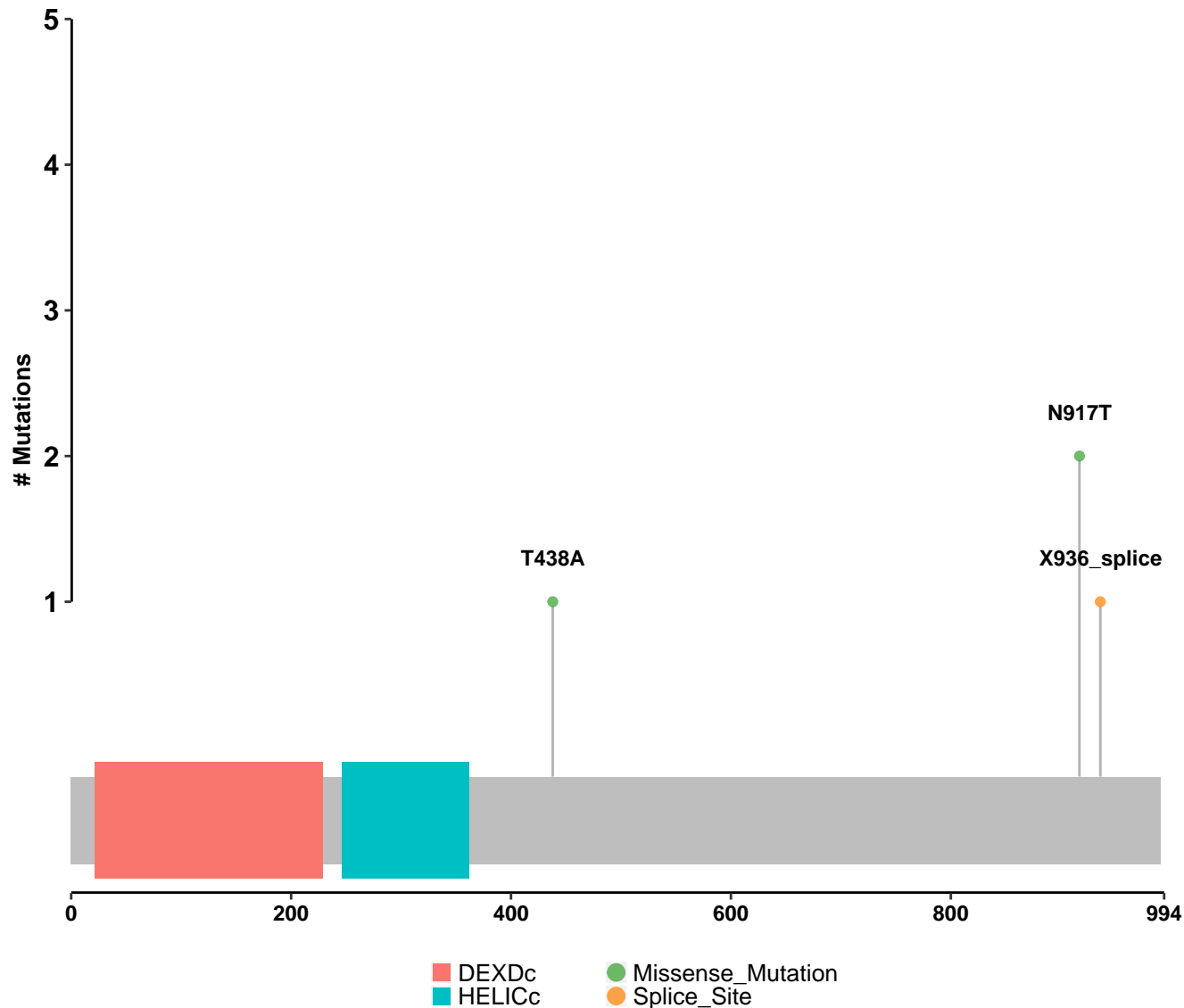
RECQL4: [Somatic Mutation Rate: 15.15%]

NM_004260



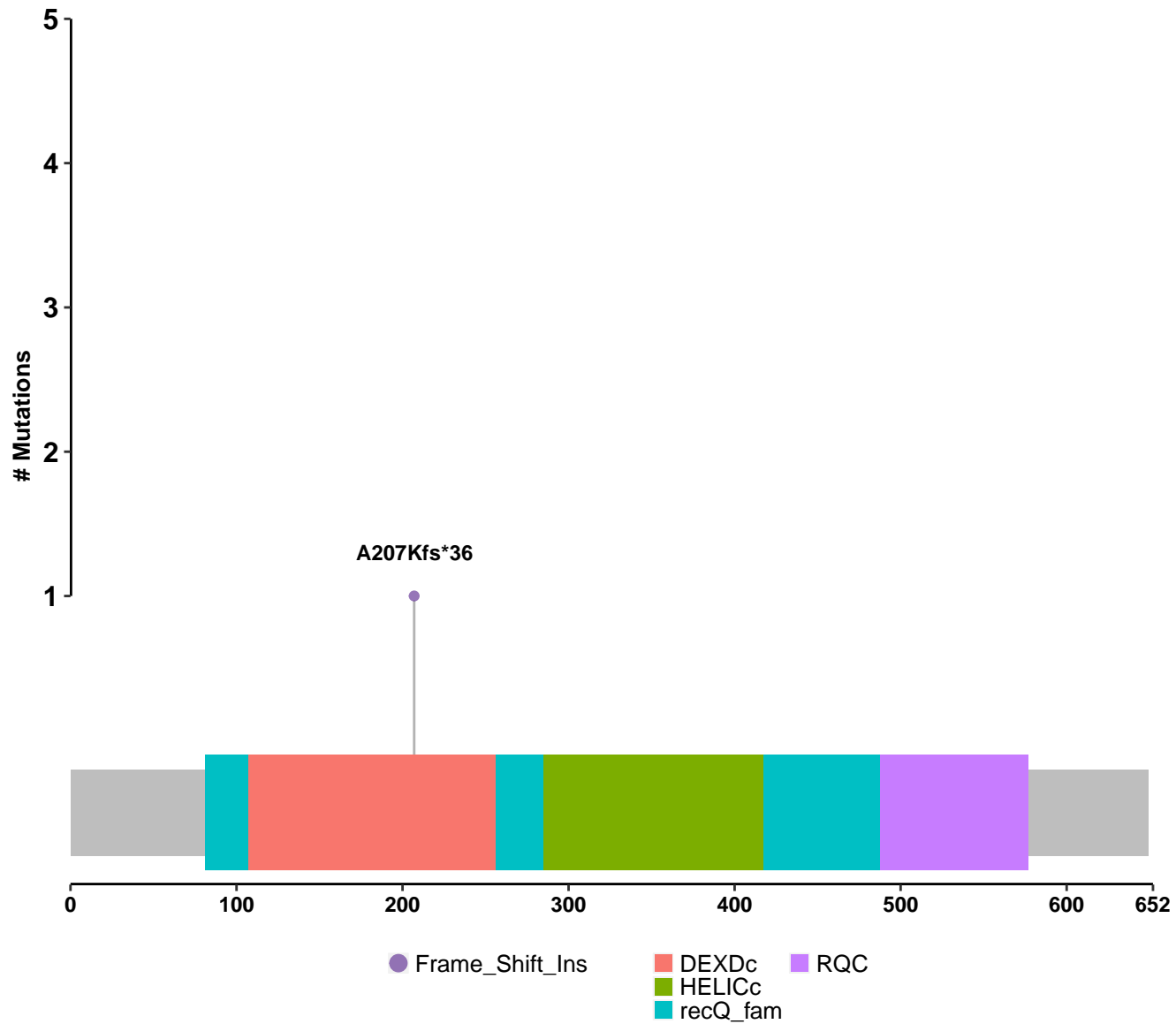
RECQL5: [Somatic Mutation Rate: 12.12%]

NM_004259



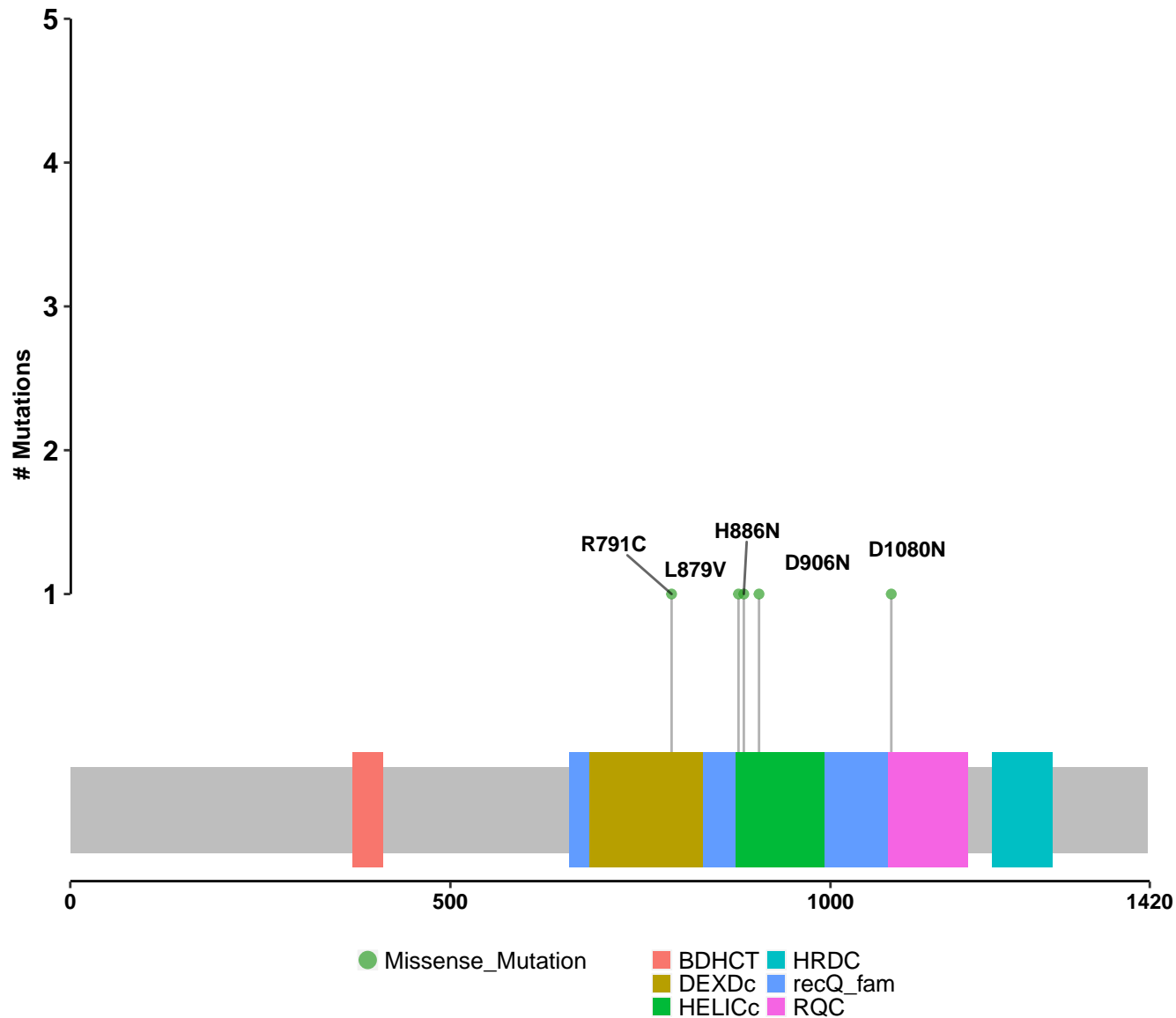
RECQL: [Somatic Mutation Rate: 3.03%]

NM_002907



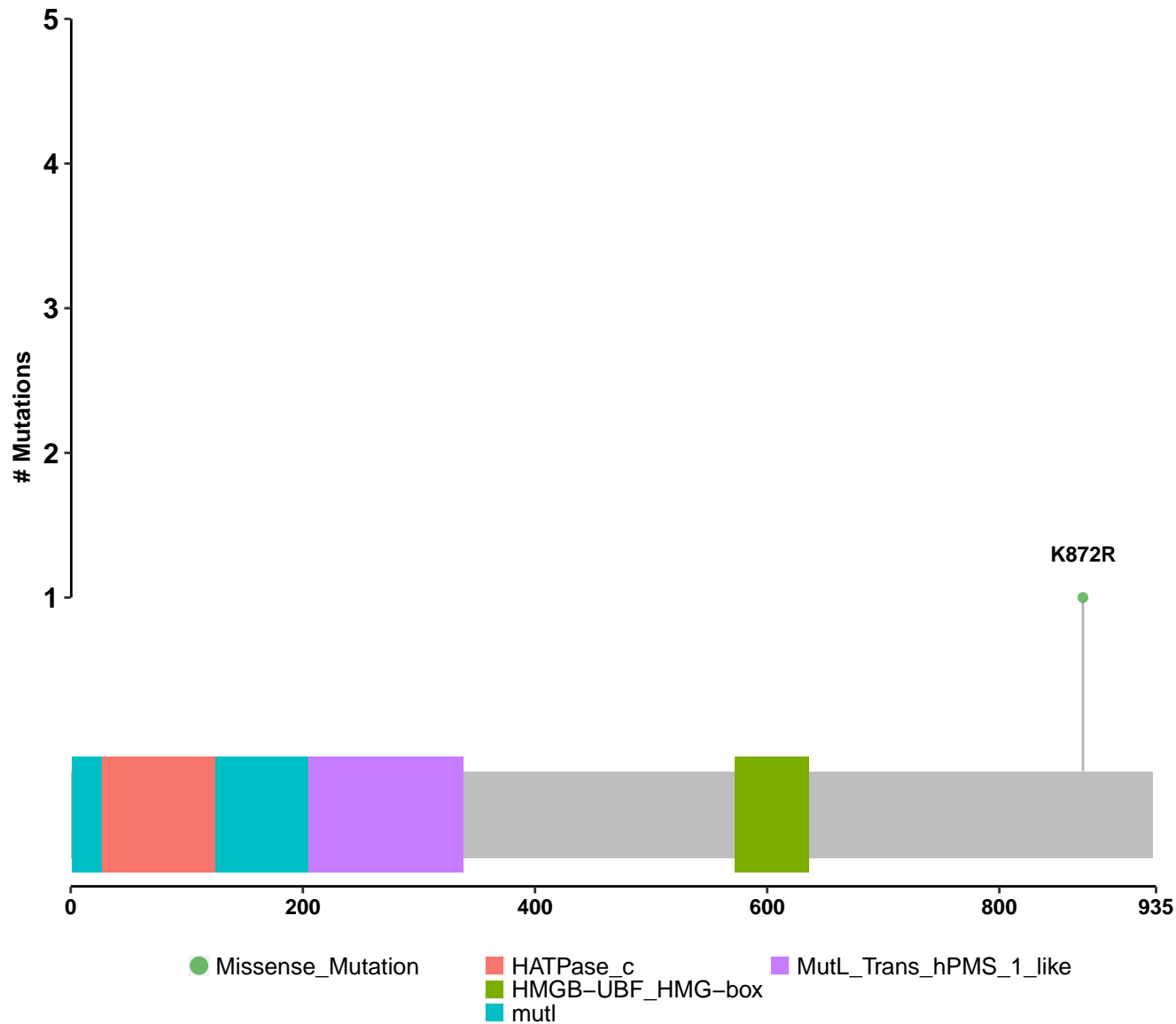
BLM: [Somatic Mutation Rate: 15.15%]

NM_000057



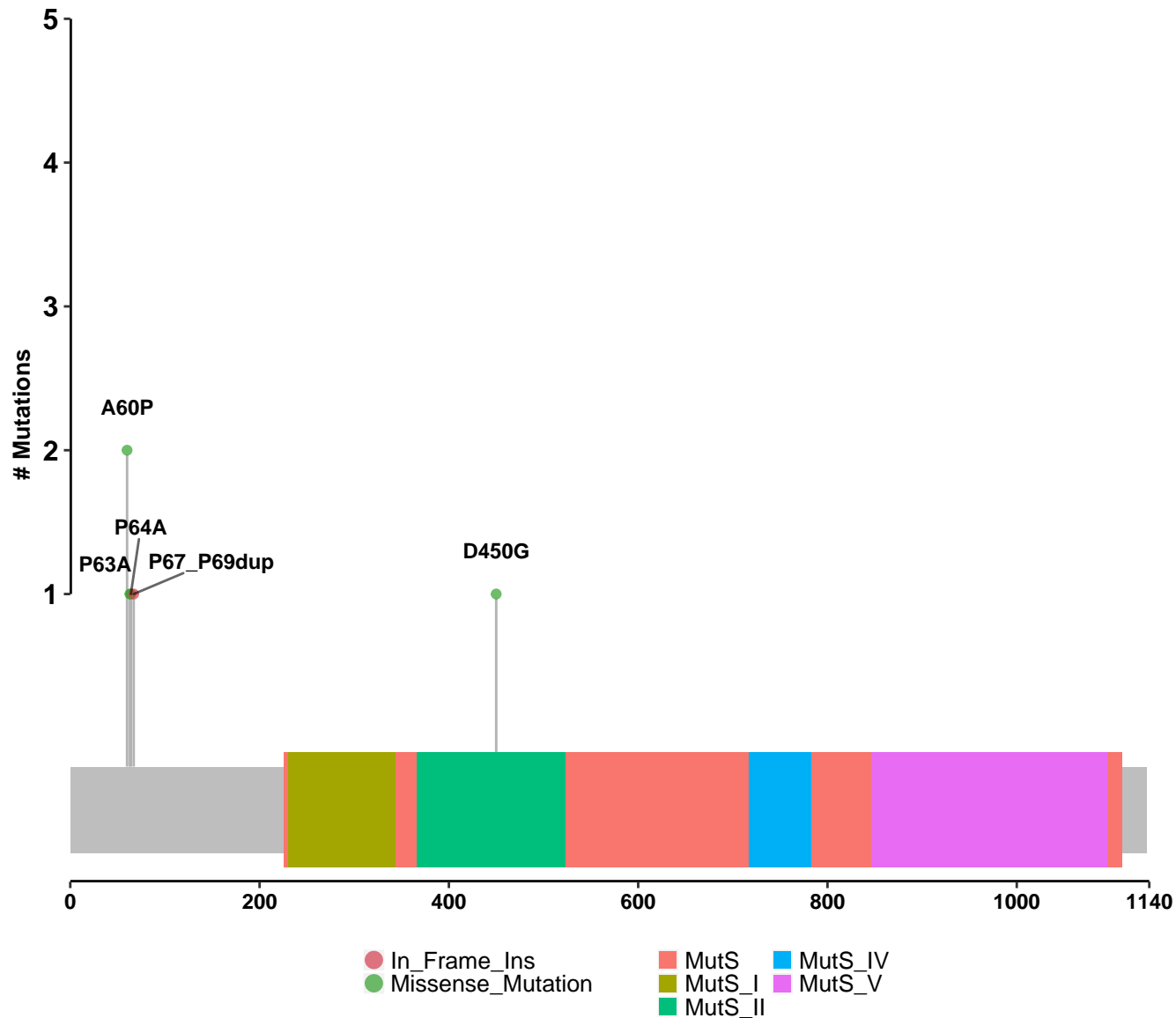
PMS1: [Somatic Mutation Rate: 3.03%]

NM_000534



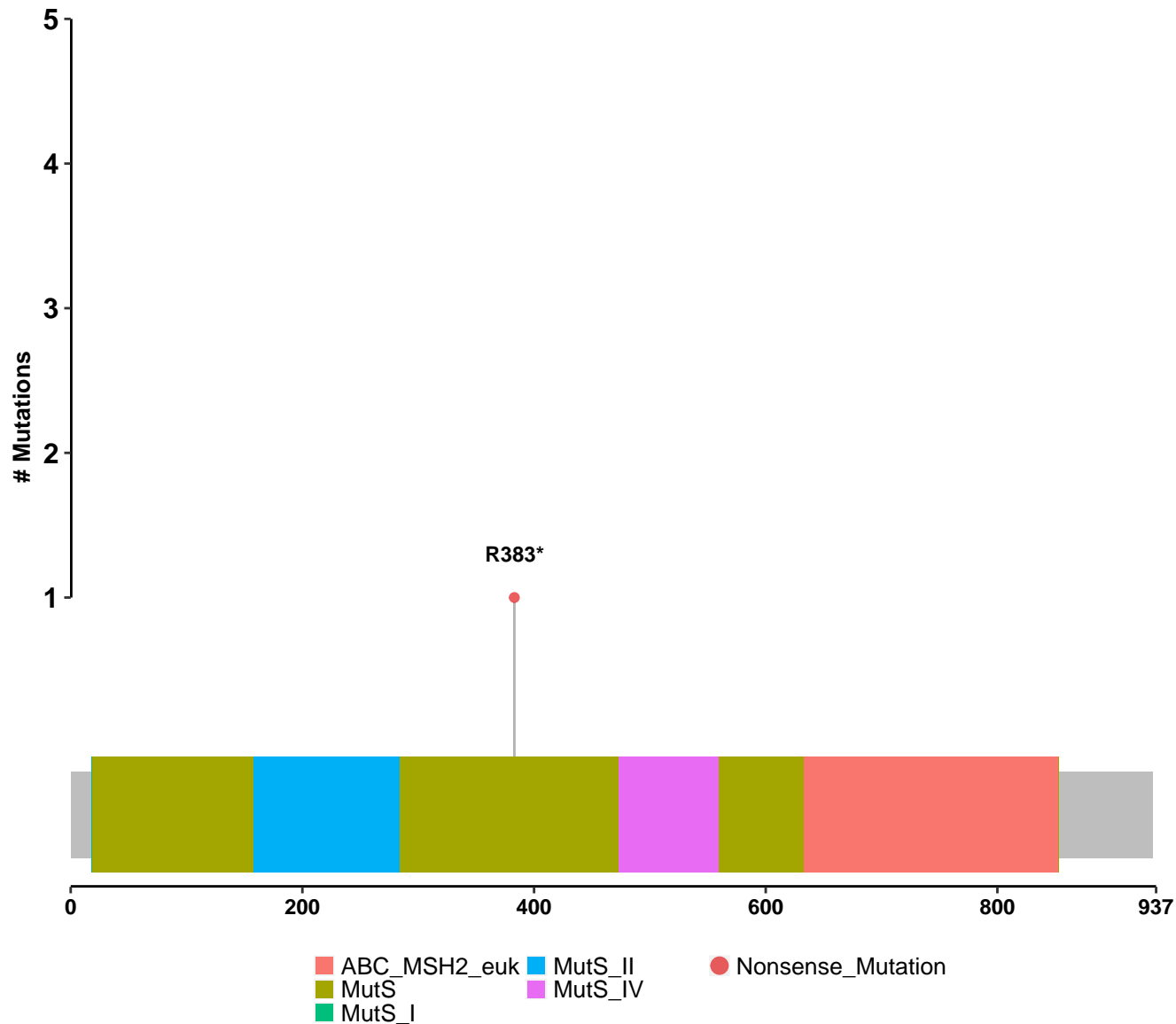
MSH3: [Somatic Mutation Rate: 12.12%]

NM_002439



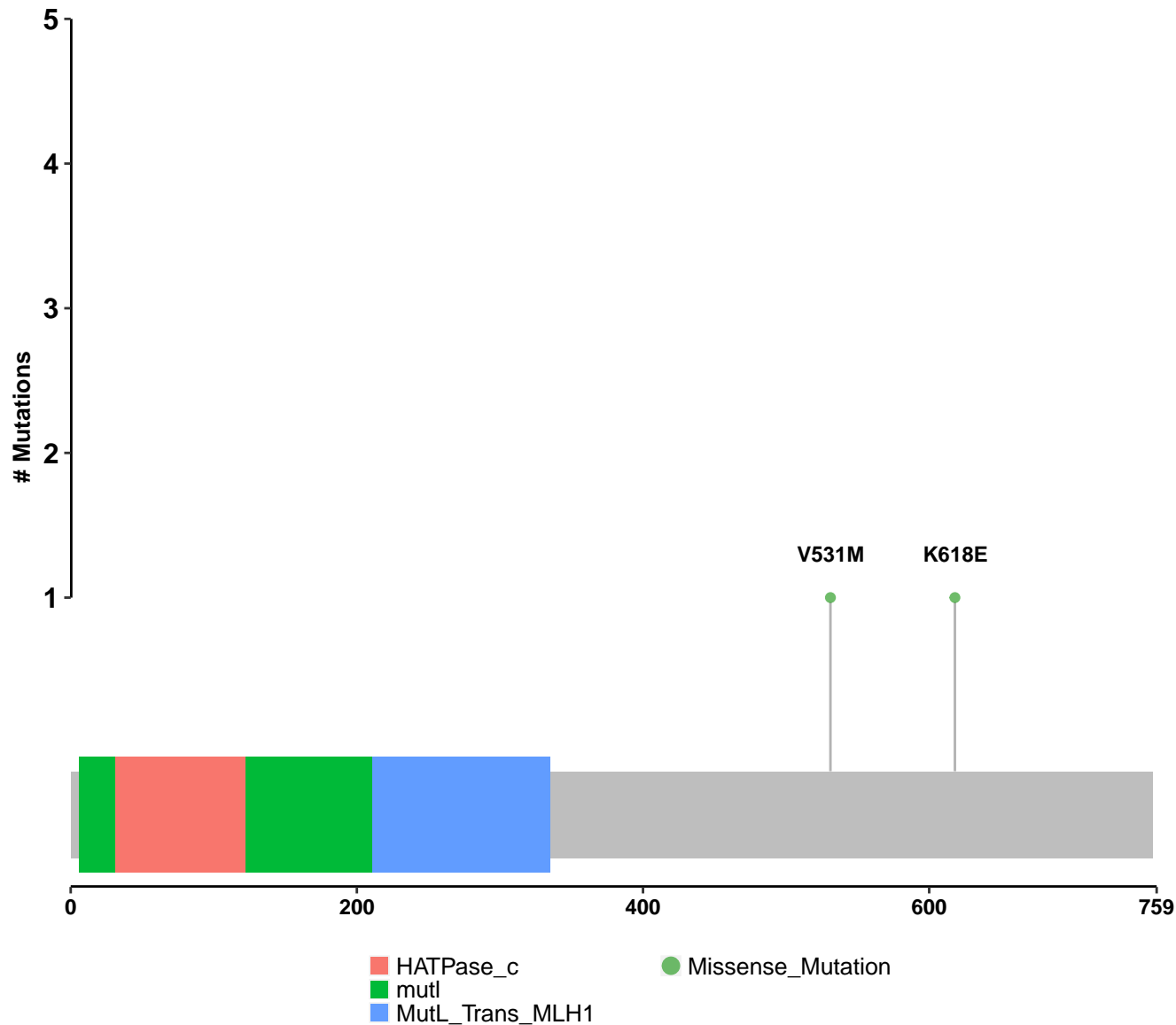
MSH2: [Somatic Mutation Rate: 3.03%]

NM_000251



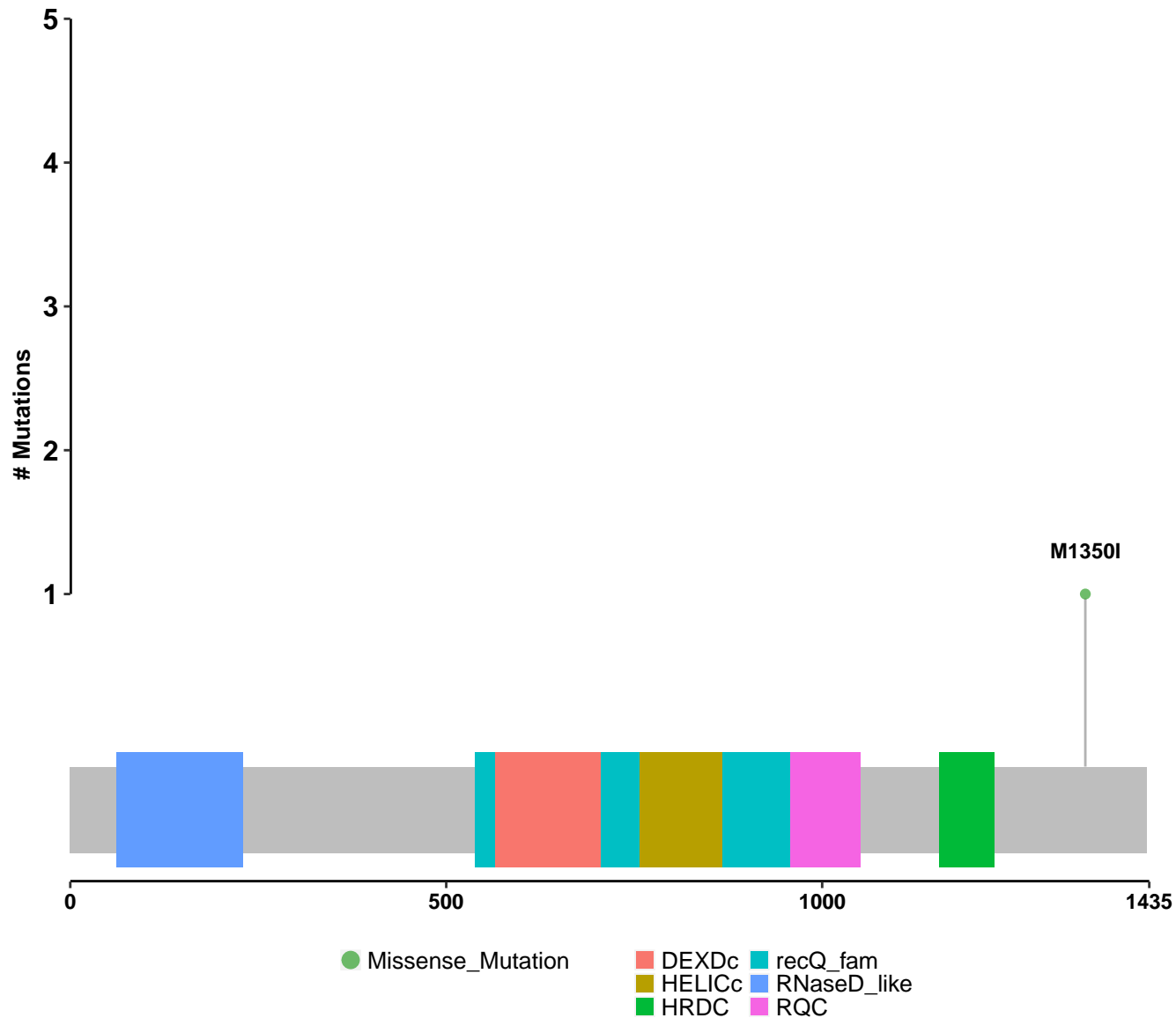
MLH1: [Somatic Mutation Rate: 6.06%]

NM_000249



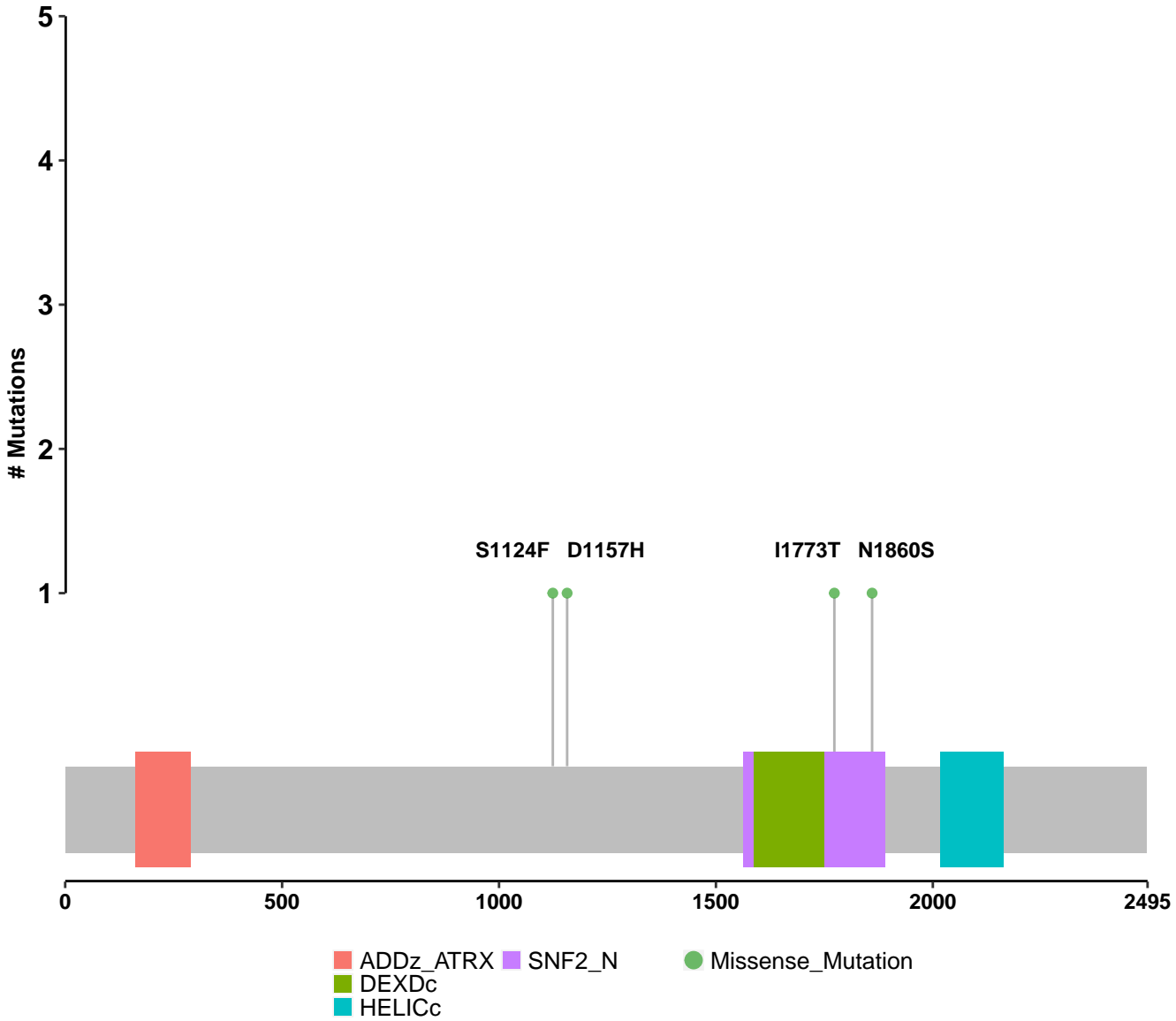
WRN: [Somatic Mutation Rate: 3.03%]

NM_000553



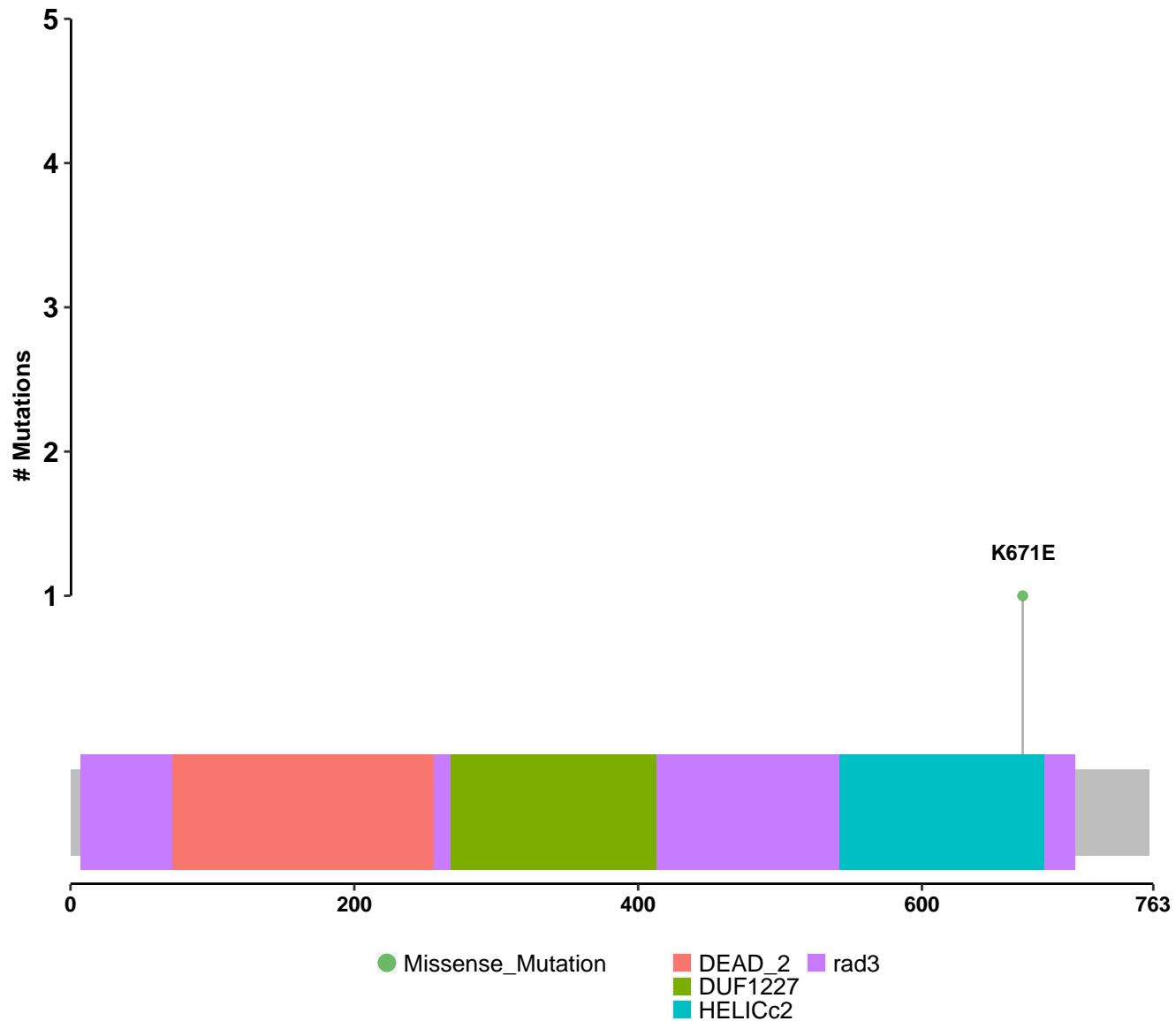
ATRX: [Somatic Mutation Rate: 12.12%]

NM_000489



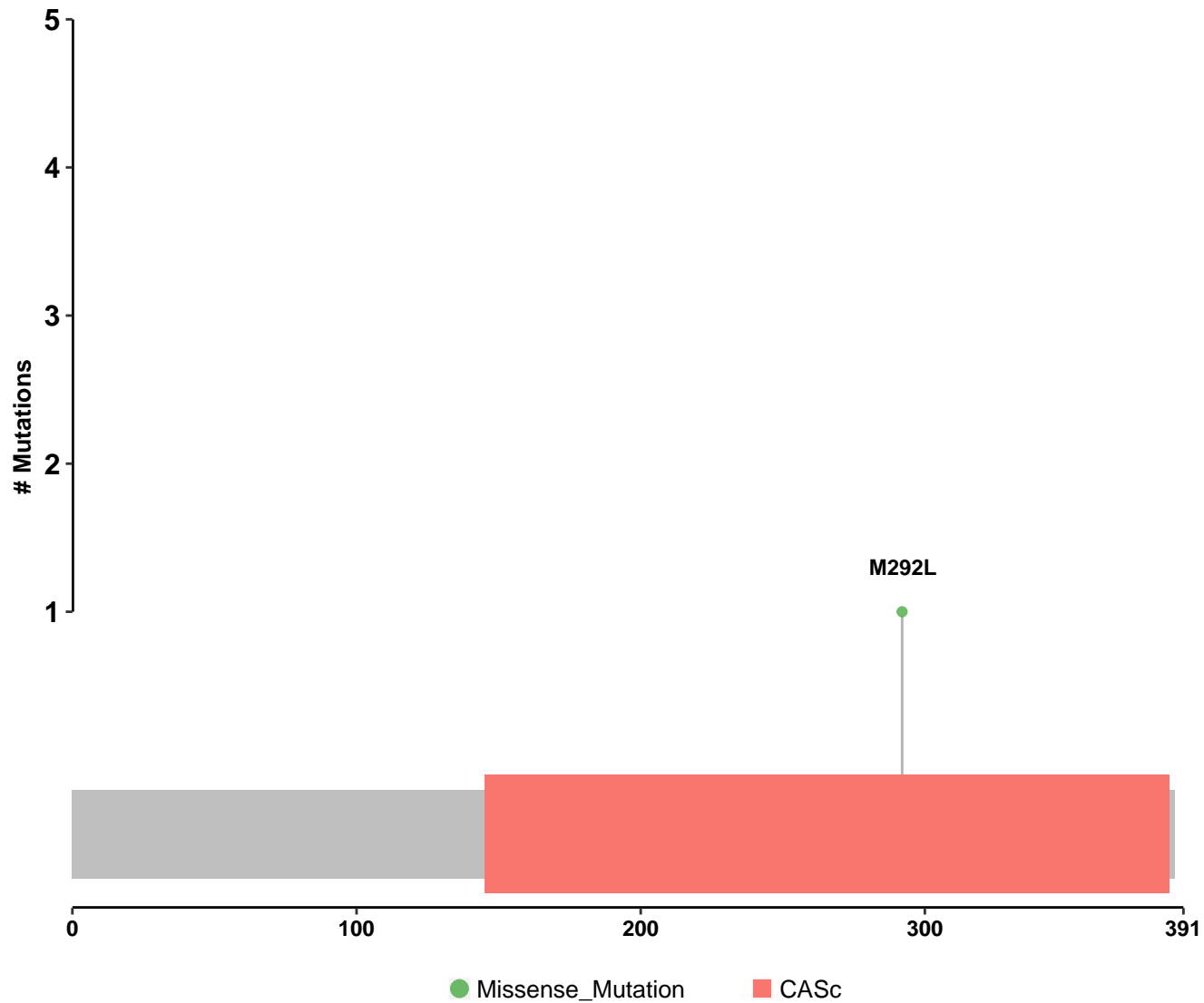
ERCC2: [Somatic Mutation Rate: 3.03%]

NM_000400



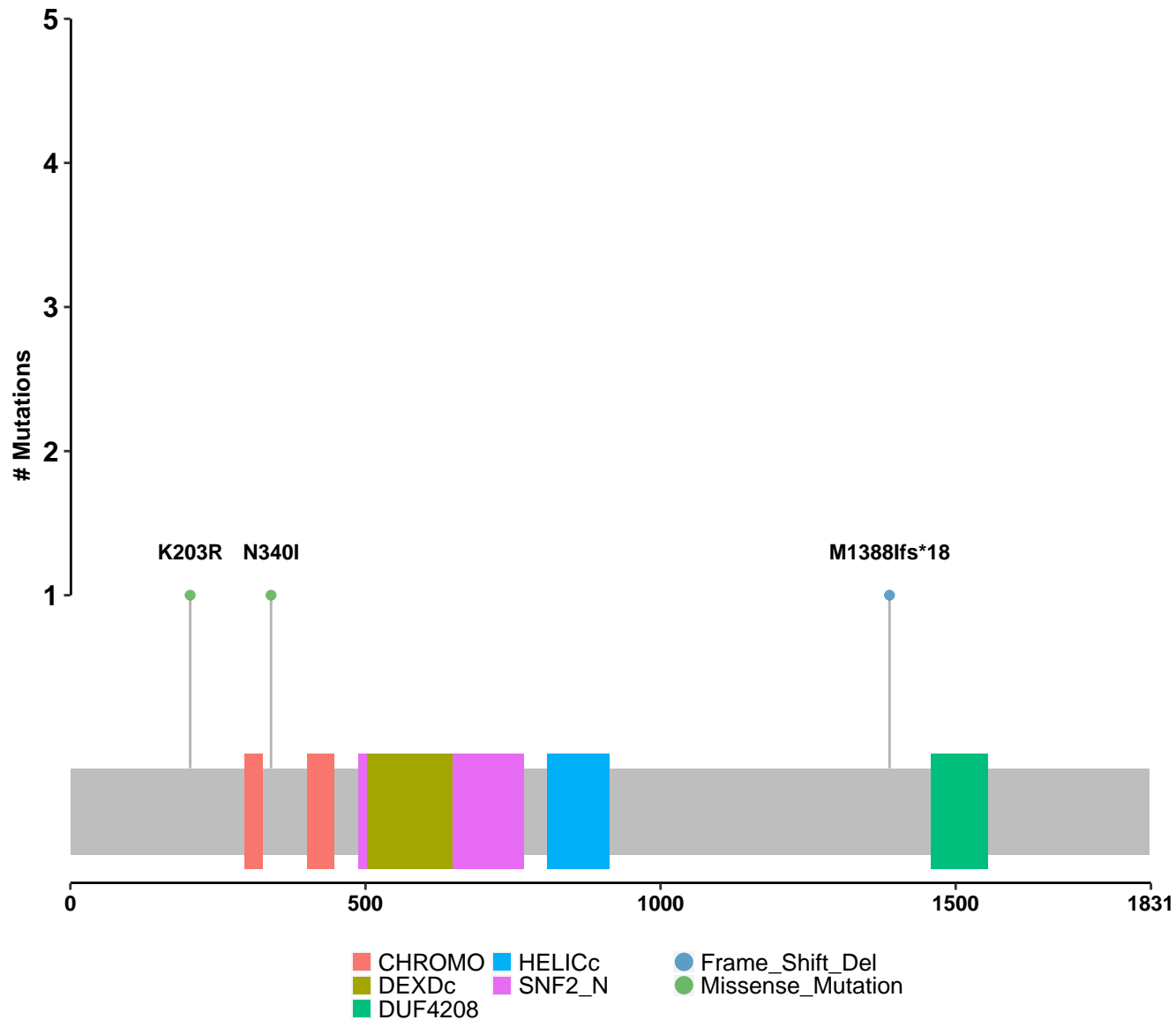
CASP7: [Somatic Mutation Rate: 3.03%]

NM_001267057



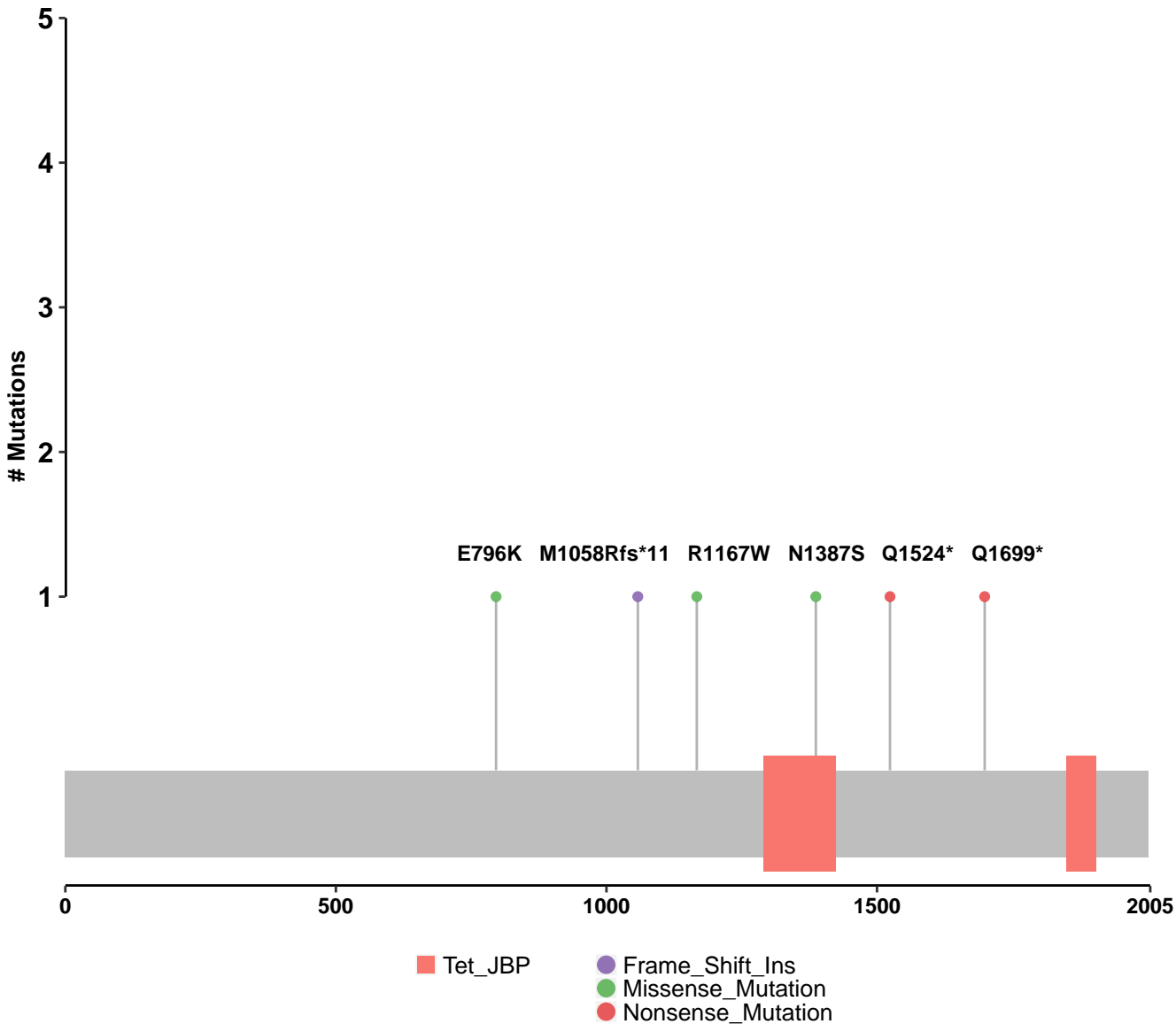
CHD2: [Somatic Mutation Rate: 9.09%]

NM_001271



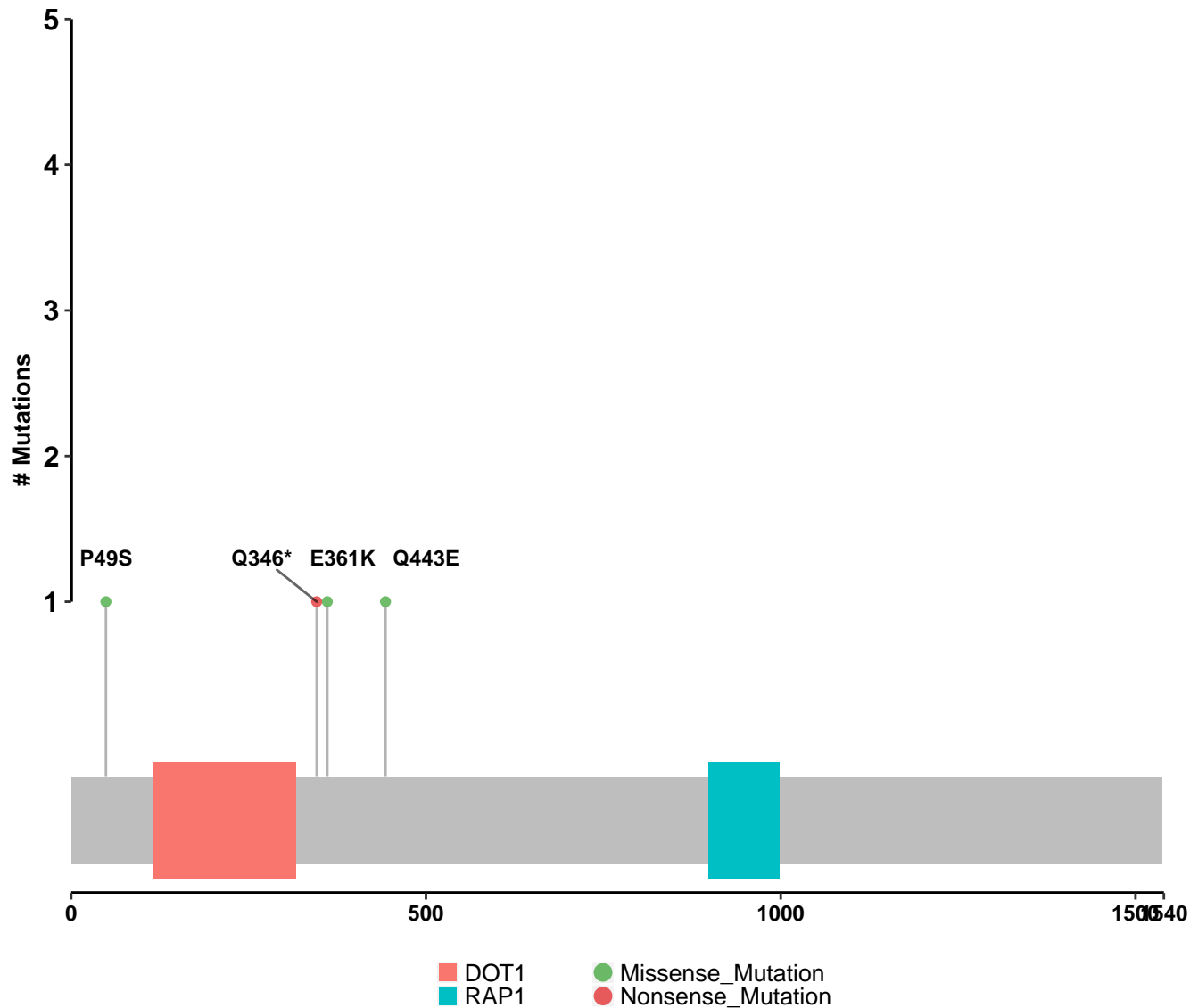
TET2: [Somatic Mutation Rate: 12.12%]

NM_001127208



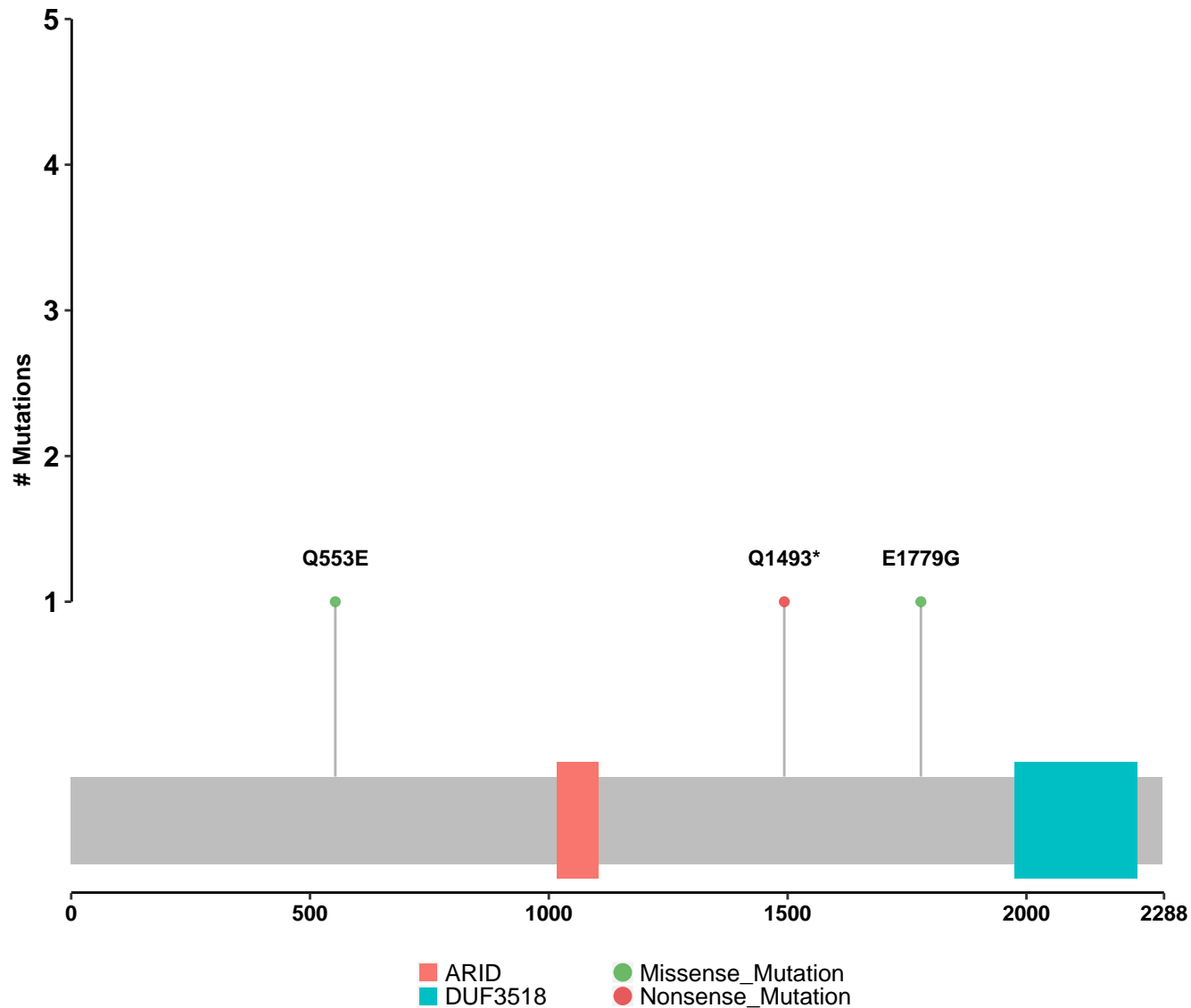
DOT1L: [Somatic Mutation Rate: 12.12%]

NM_032482



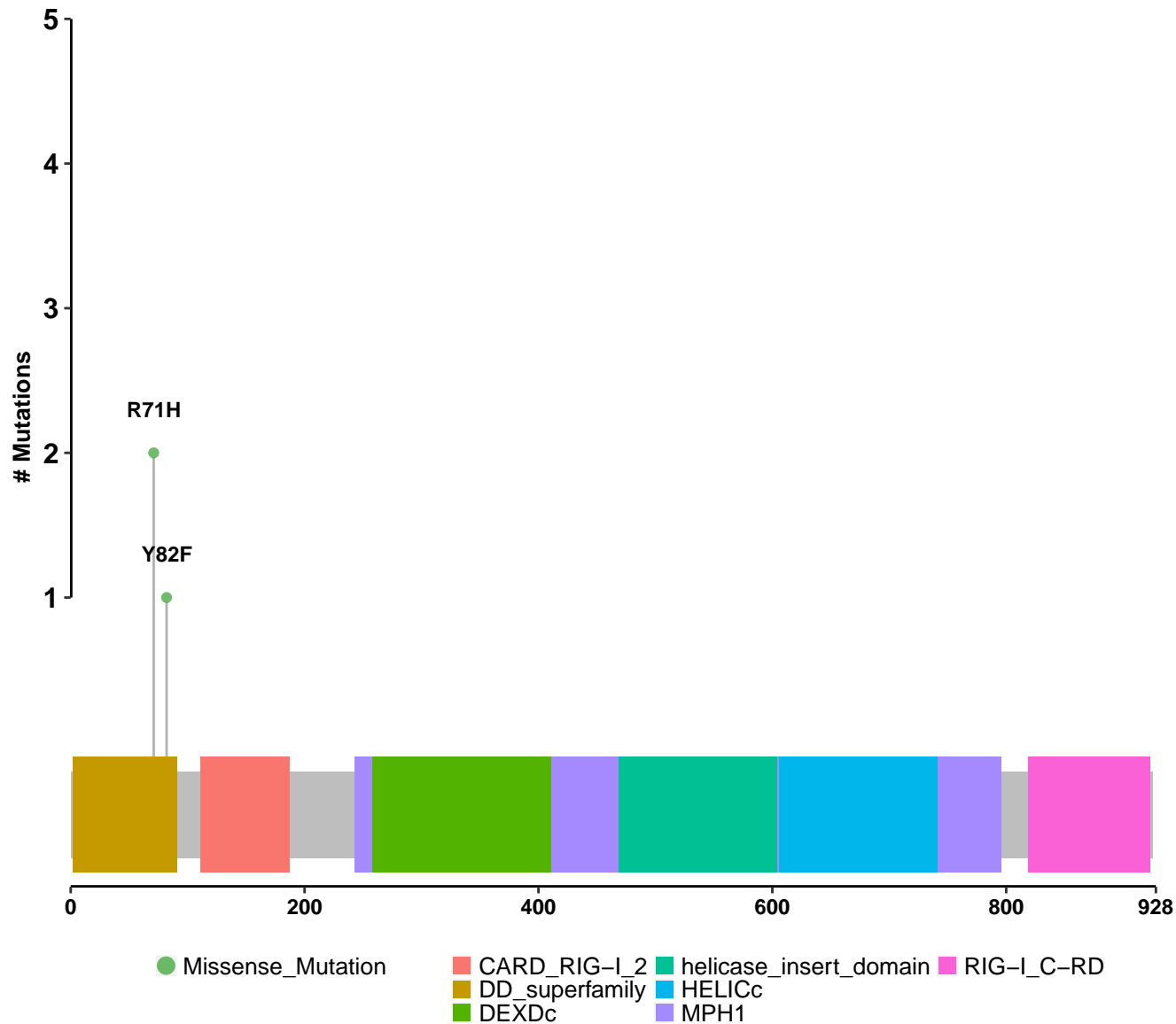
ARID1A: [Somatic Mutation Rate: 9.09%]

NM_006015



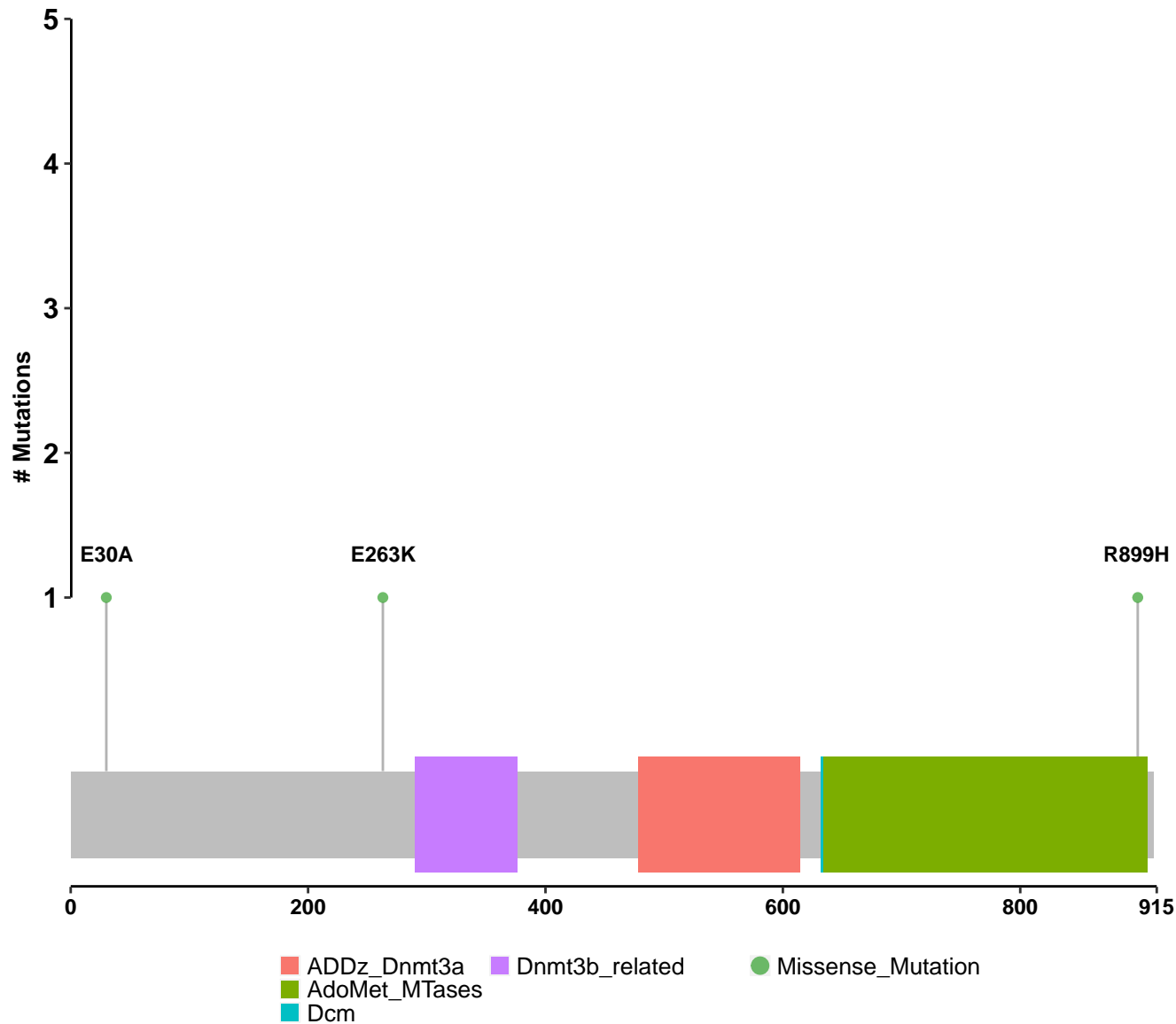
DDX58: [Somatic Mutation Rate: 9.09%]

NM_014314



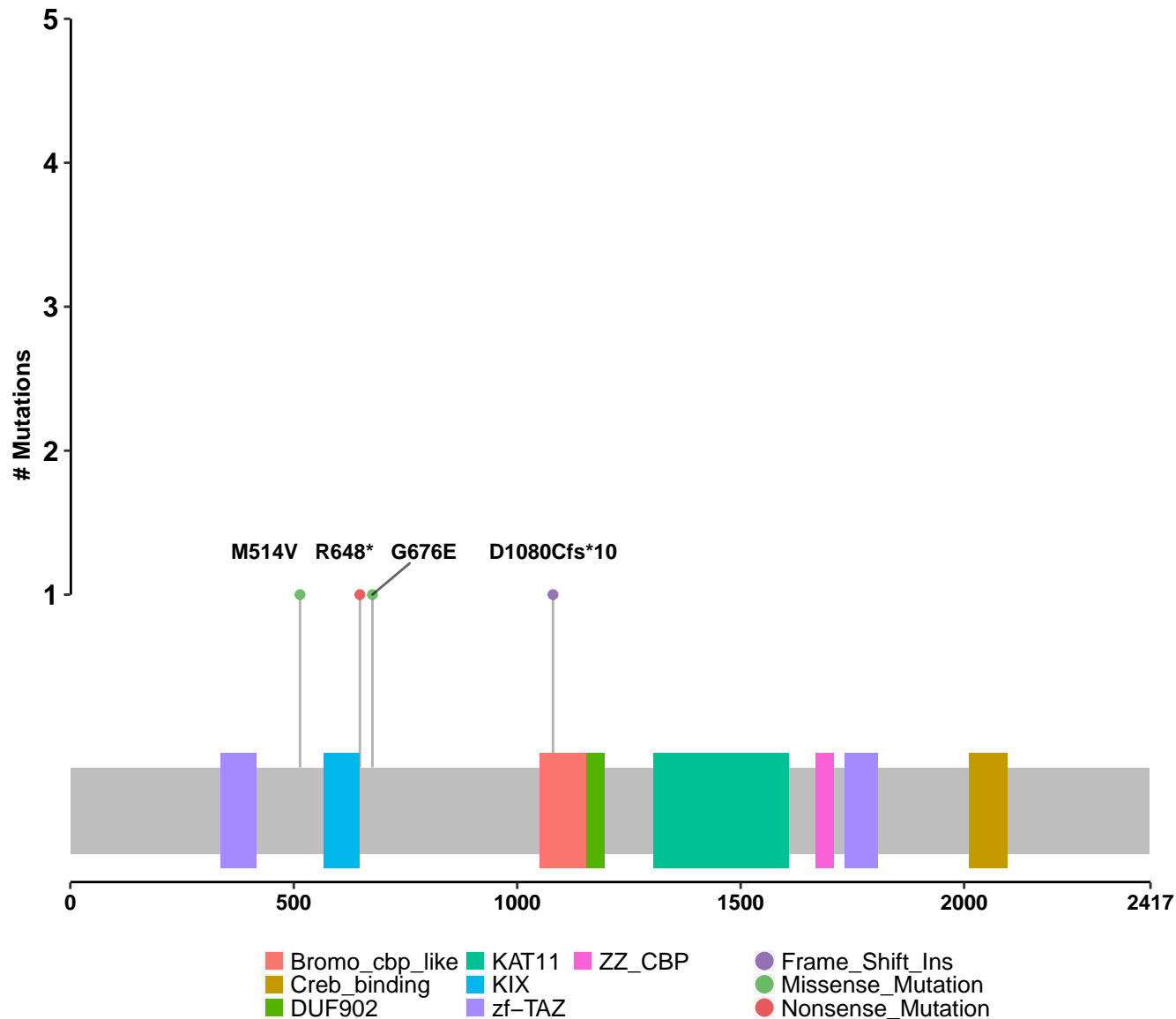
DNMT3A: [Somatic Mutation Rate: 9.09%]

NM_175629



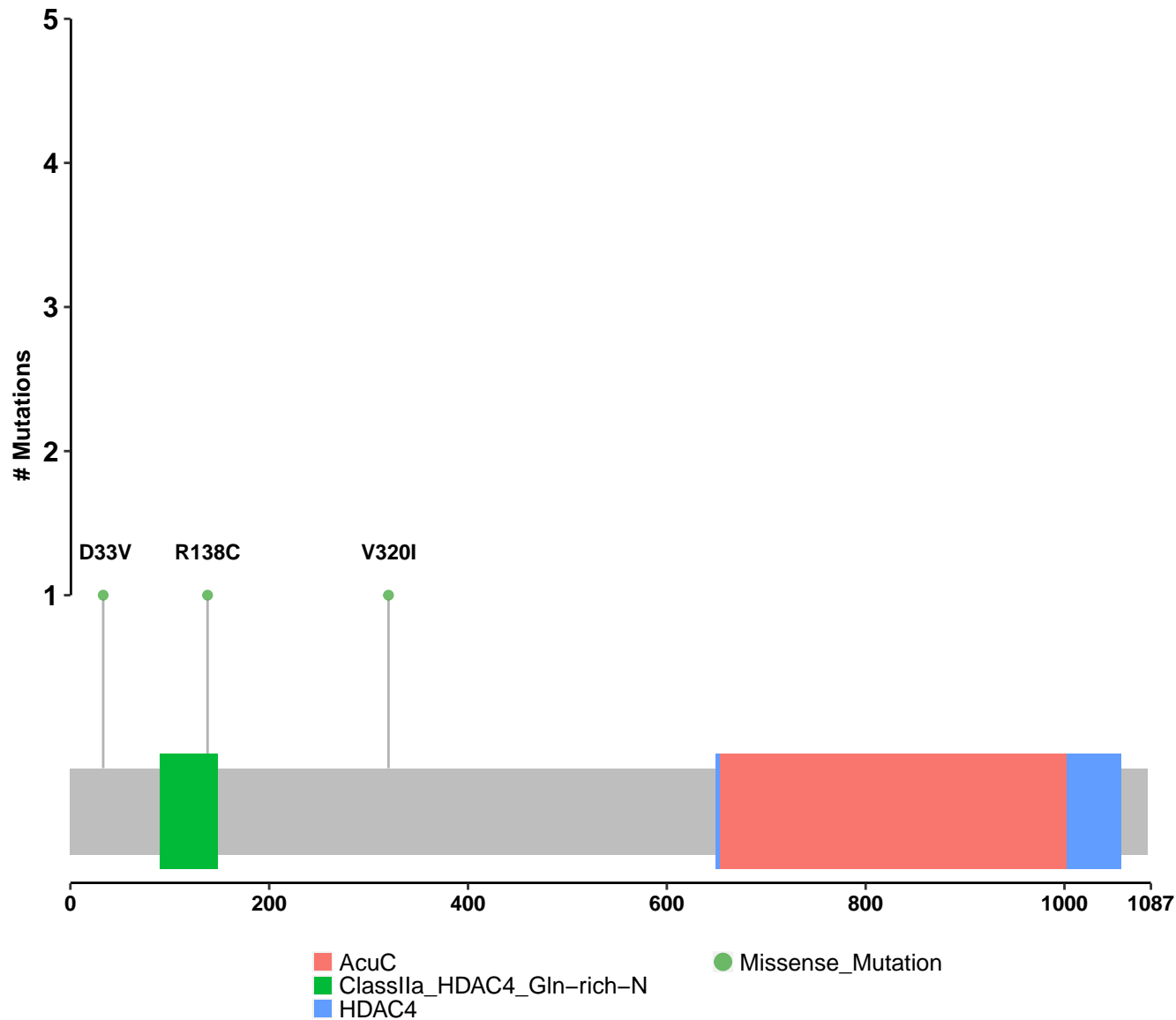
EP300: [Somatic Mutation Rate: 6.06%]

NM_001429



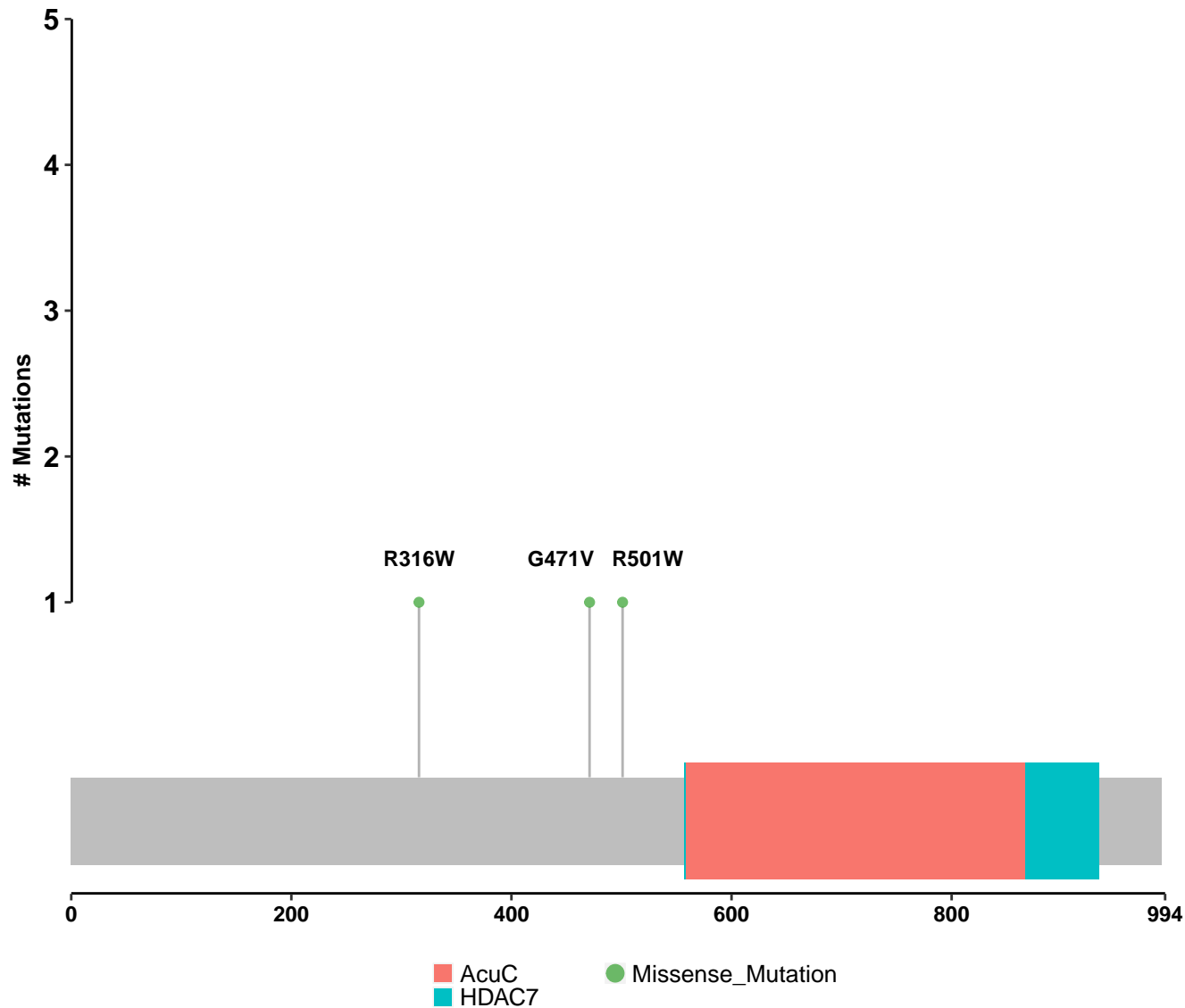
HDAC4: [Somatic Mutation Rate: 9.09%]

NM_006037



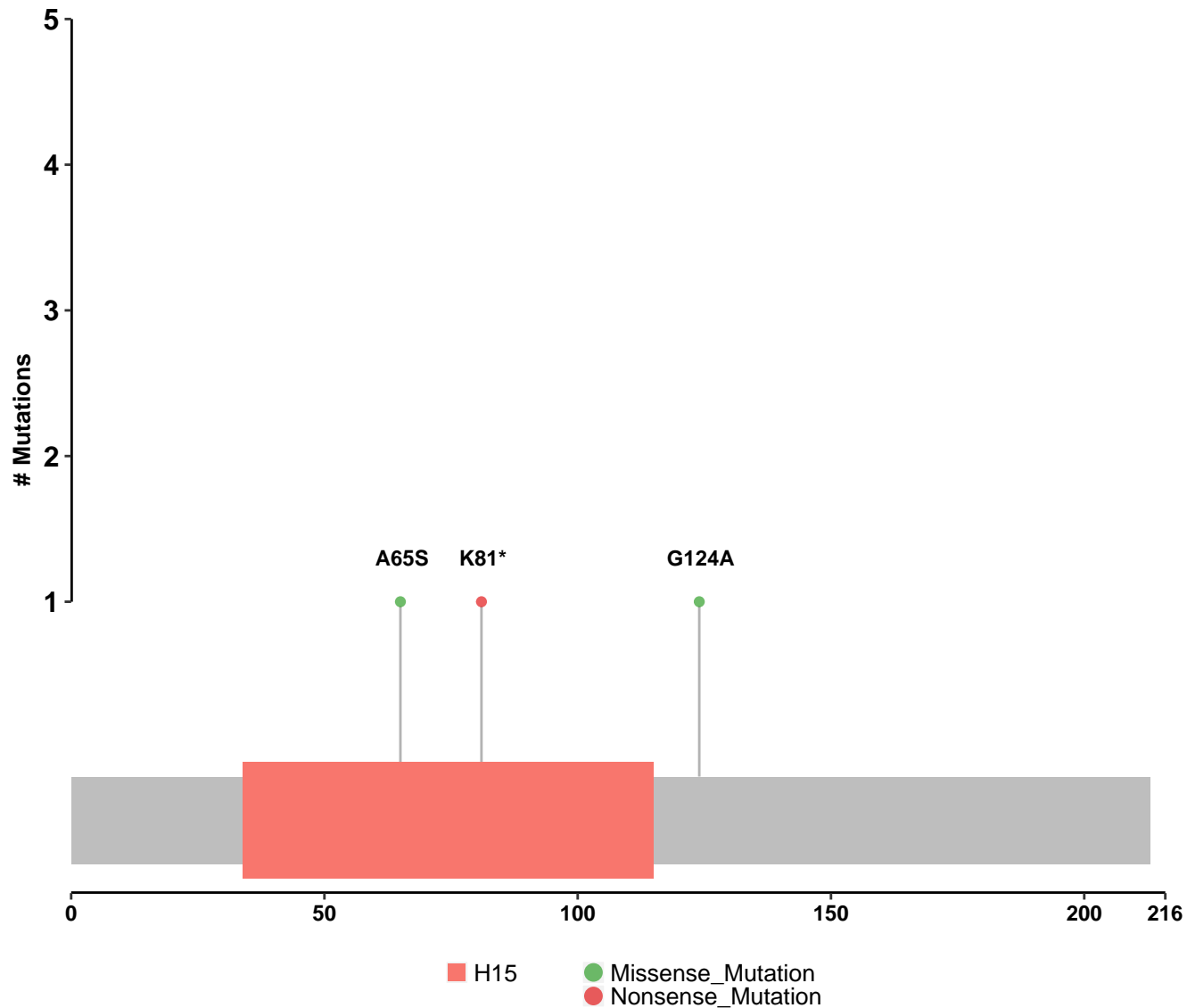
HDAC7: [Somatic Mutation Rate: 9.09%]

NM_015401



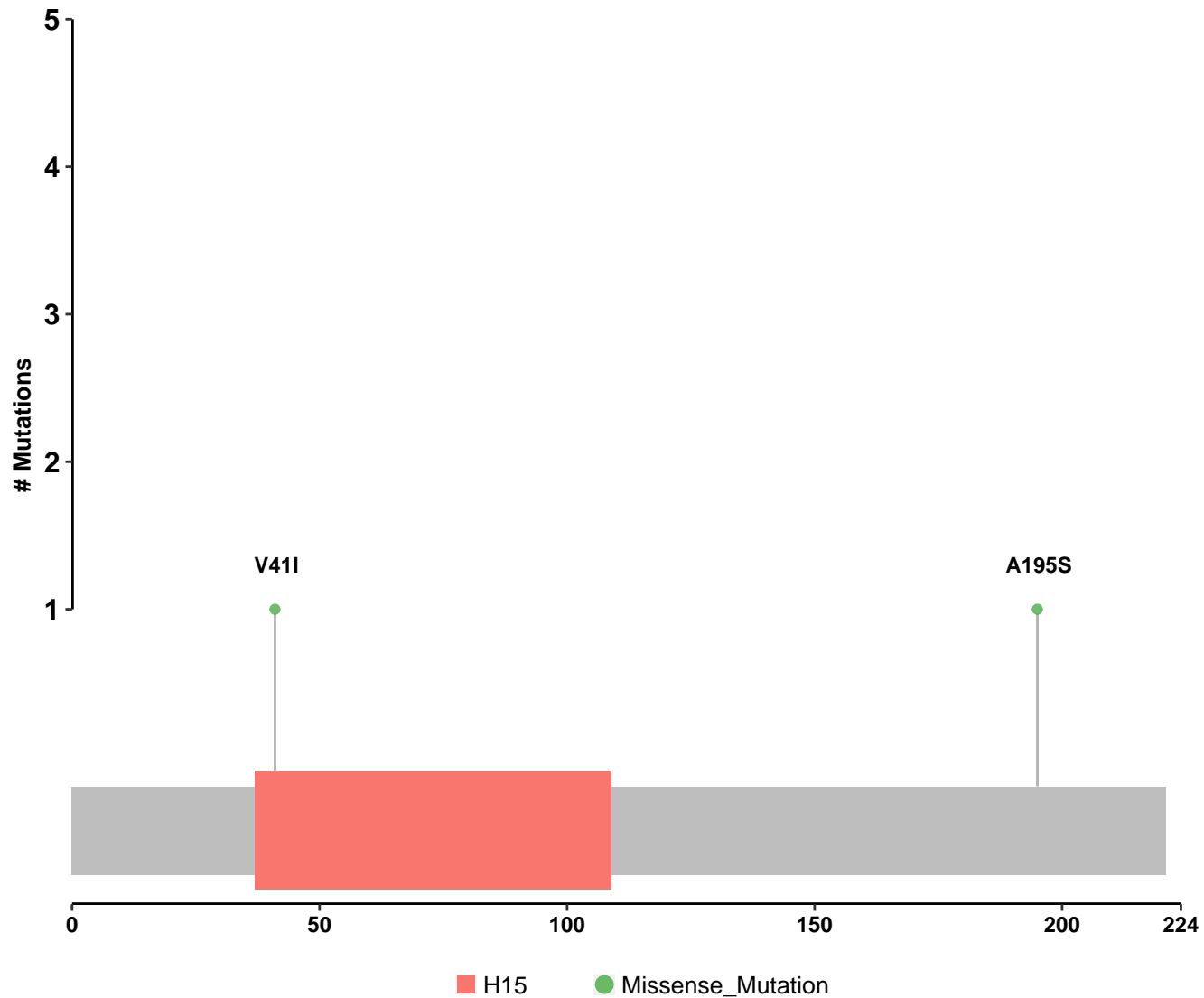
HIST1H1C: [Somatic Mutation Rate: 9.09%]

NM_005319



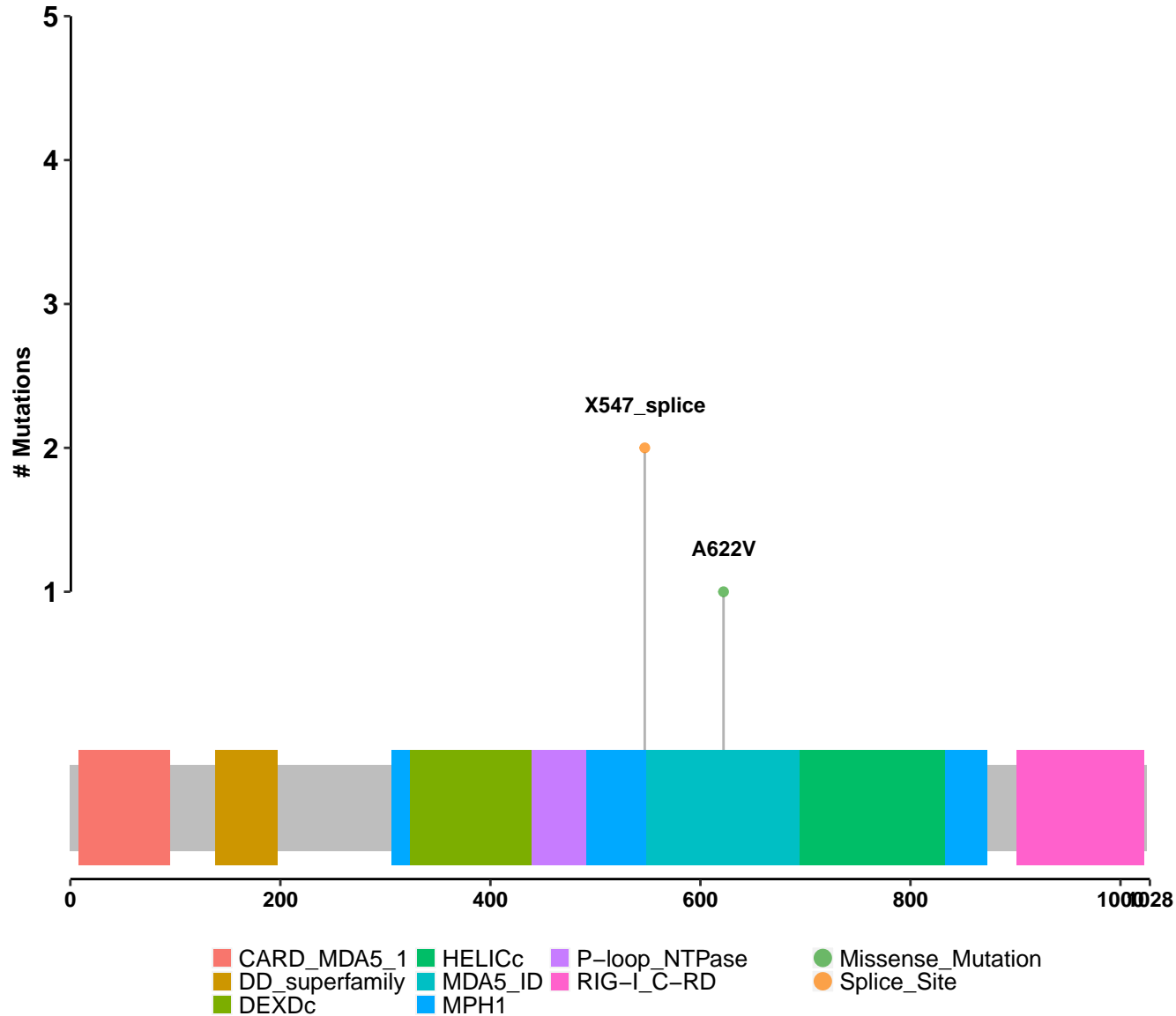
HIST1H1D: [Somatic Mutation Rate: 6.06%]

NM_005320



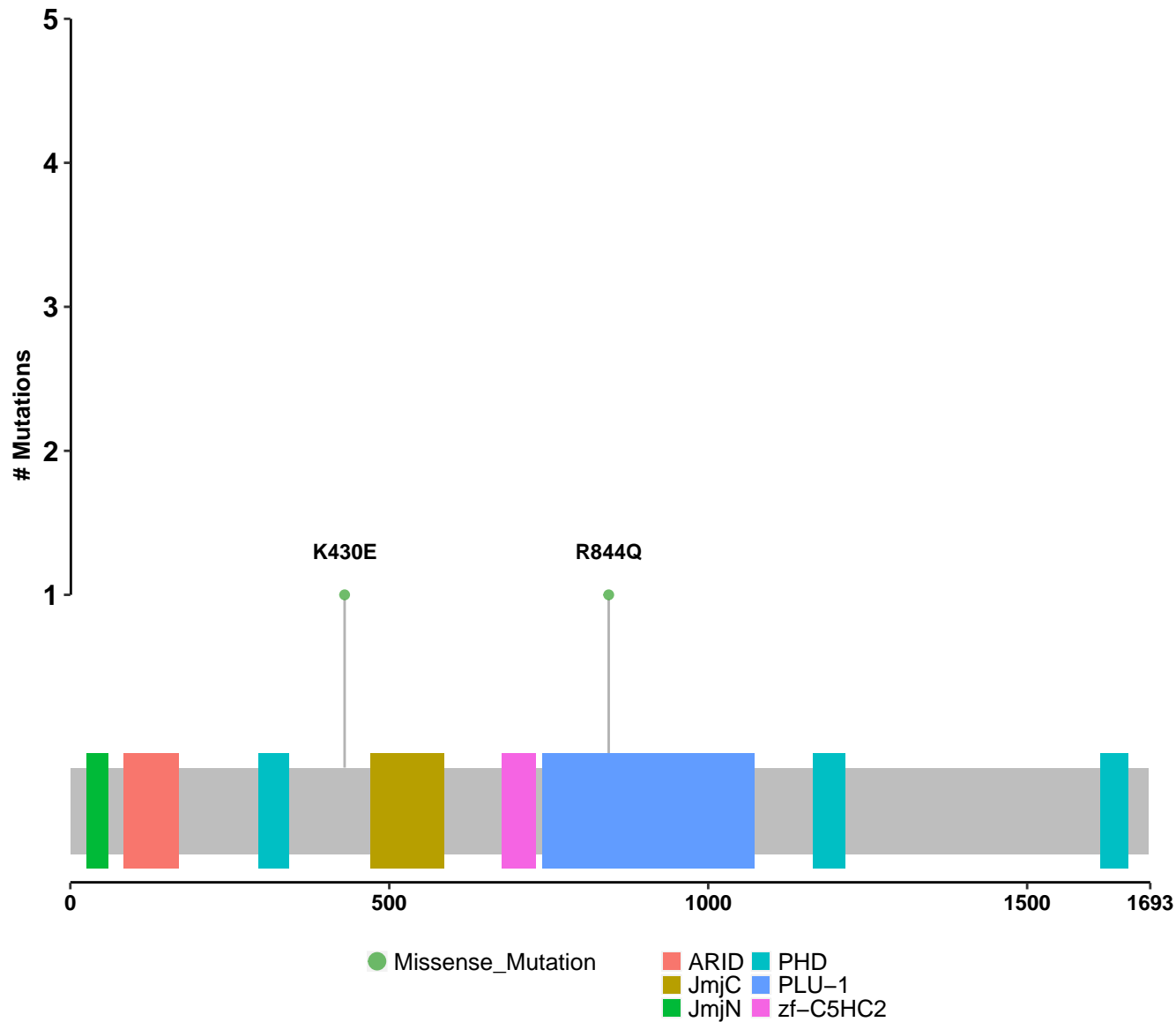
IFIH1: [Somatic Mutation Rate: 9.09%]

NM_022168



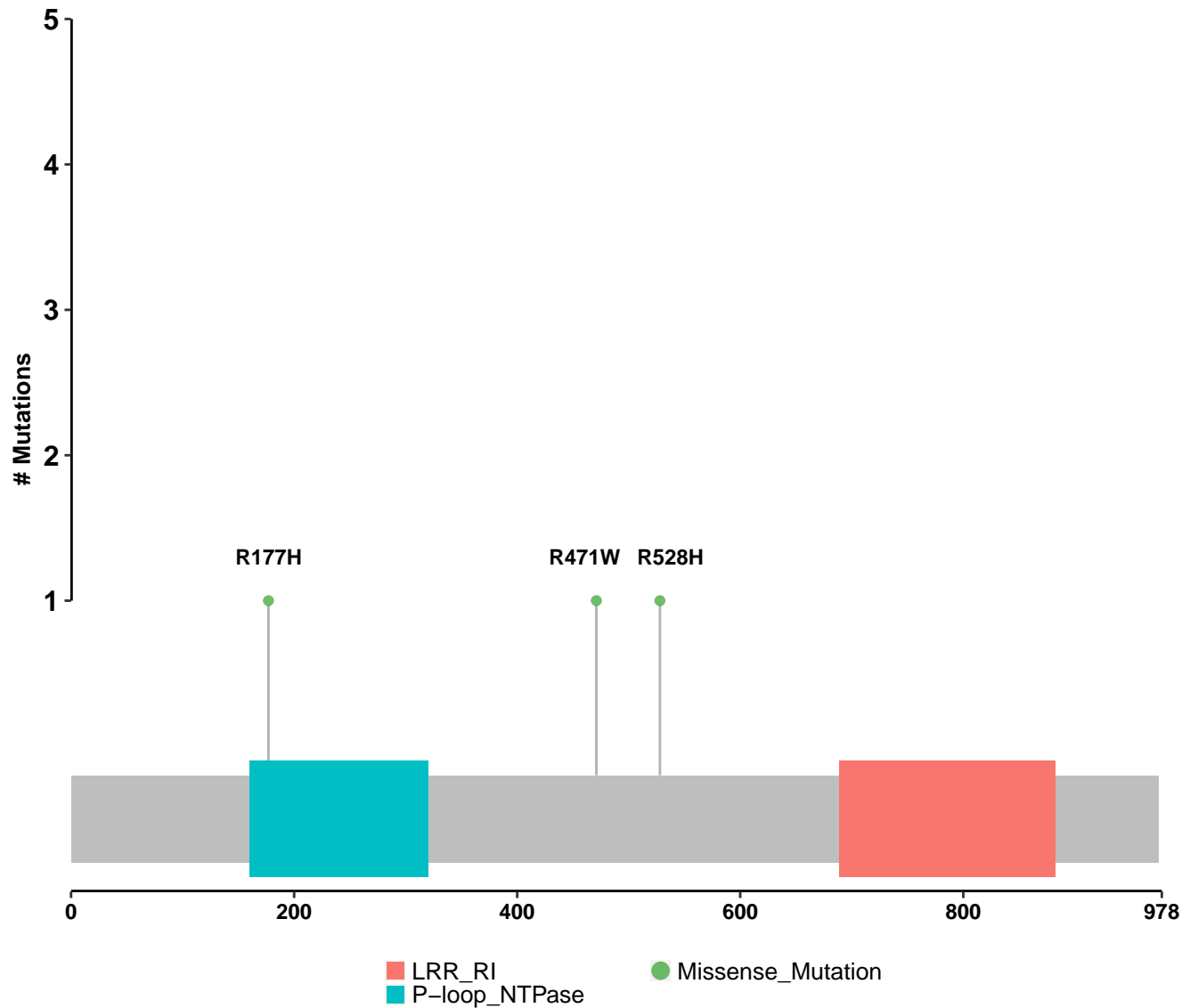
KDM5A: [Somatic Mutation Rate: 6.06%]

NM_001042603



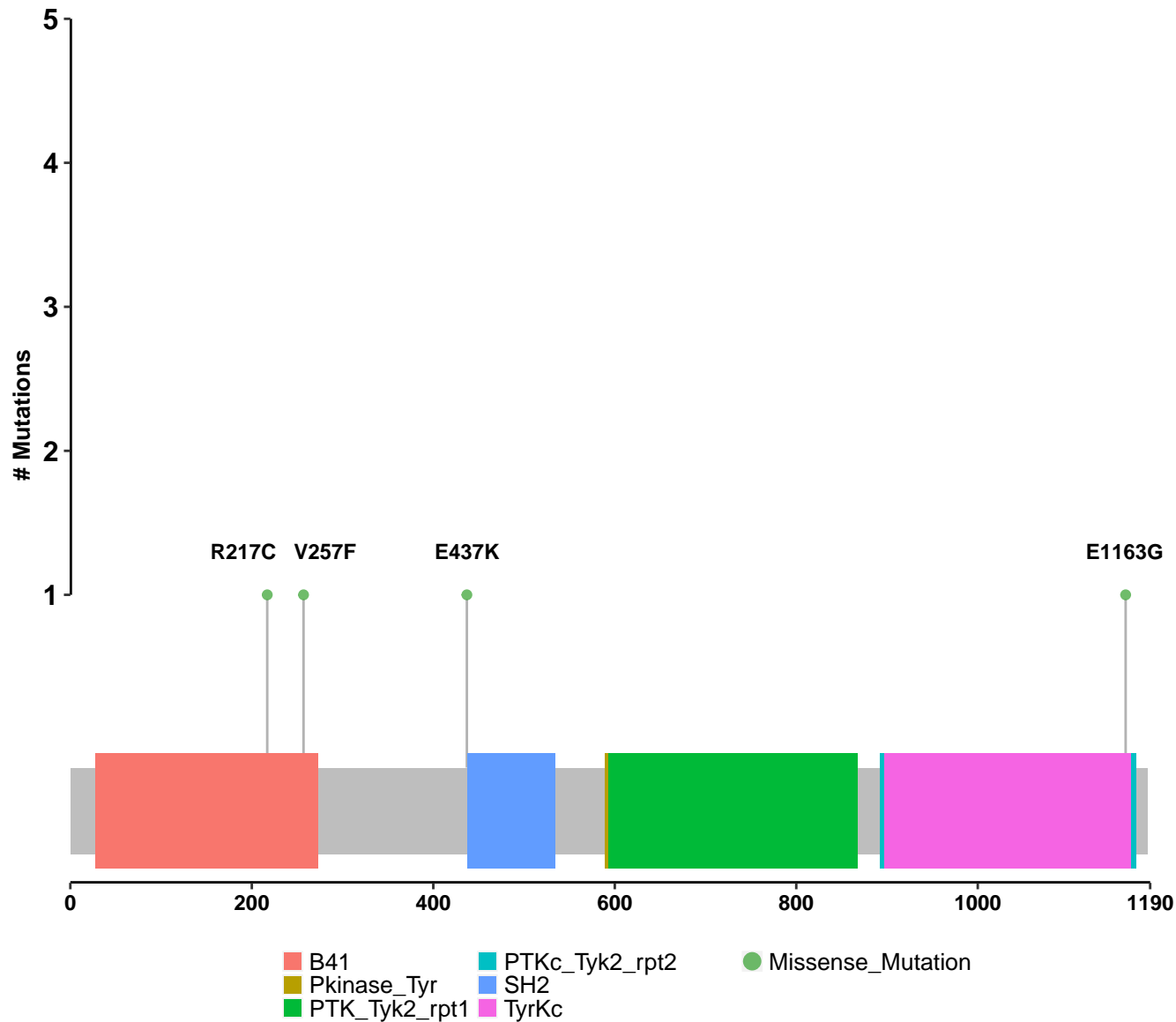
NLRX1: [Somatic Mutation Rate: 9.09%]

NM_024618



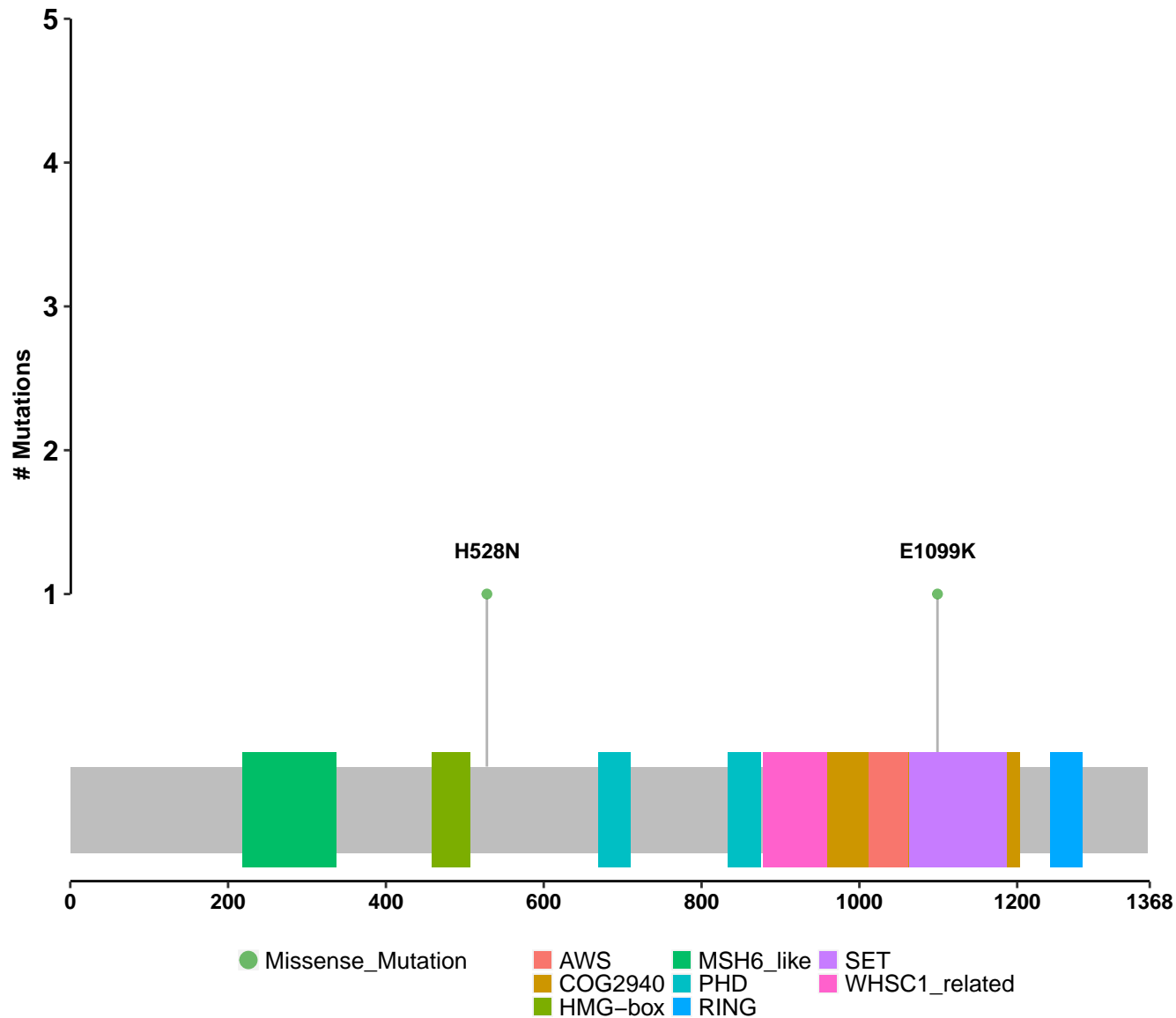
TYK2: [Somatic Mutation Rate: 9.09%]

NM_003331



WHSC1: [Somatic Mutation Rate: 6.06%]

NM_001042424



BRD4: [Somatic Mutation Rate: 6.06%]

NM_058243

