

Supplementary Material**Biochemical analysis of human *POLG2* variants associated with mitochondrial disease**

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Supplementary Table: *POLG2* sequencing primers. Primer sequences were designed using genomic sequence from the Genbank database. All primers are M13 linked.

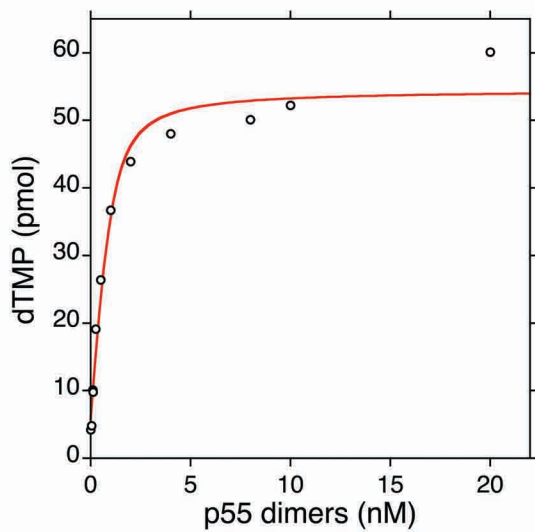
Exons	Primer Names	Primer Sequences (5'-3')	Length
E1	POLG2-E1F2	CTC GT TGT AAA ACG ACG GCC AGT AACGGTAGTGGTGGCTTGTT	43
	POLG2-E1R2	CTG CT CAG GAA ACA GCT ATG ACC CCAGTTGCAATCCCCAAG	41
E2-3	POLG2-E2-3F	CTC GT TGT AAA ACG ACG GCC AGT CCACCAAGCTTAGCCAACAT	43
	POLG2-E2-3F3	CTC GT TGT AAA ACG ACG GCC AGT TAGGCGTGAGCCACCAAG	41
	POLG2-E2-3R	CTG CT CAG GAA ACA GCT ATG ACC ACACATCTGAGCCCAACAAA	43
E4	POLG2-E4F	CTC GT TGT AAA ACG ACG GCC AGT TGCTGAATAAAAAGTATCGGACAA	47
	POLG2-E4R	CTG CT CAG GAA ACA GCT ATG ACC GGCTCTGTGGCAATAGTGGA	43
E5	POLG2-E5F	CTC GT TGT AAA ACG ACG GCC AGT CCGTCTCAAAAACAAACAAACA	45
	POLG2-E5R2	CTG CT CAG GAA ACA GCT ATG ACC AGAAACCGAGCACACTAACATT	45
E6	POLG2-E6F	CTC GT TGT AAA ACG ACG GCC AGT CTGCCAAACATCTAAGTGGAGA	45
	POLG2-E6R	CTG CT CAG GAA ACA GCT ATG ACC TGAGTTCAAAGGAAATGCTCA	44
	POLG2-E6R2	AACTCACCTGTCTTAGTTC	20
E7	POLG2-E7F	CTC GT TGT AAA ACG ACG GCC AGT TTGAAGAGGGTGATTTGTGG	43
	POLG2-E7R	CTG CT CAG GAA ACA GCT ATG ACC TTCTGTAAAAGGGAAACTGAGGA	46
E8	POLG2-E8F	CTC GT TGT AAA ACG ACG GCC AGT CCCTGAGTCTGTGACTCTTGA	44
	POLG2-E8R	CTG CT CAG GAA ACA GCT ATG ACC AATGAAAGCAAGCACCACAA	43

Figure Legends

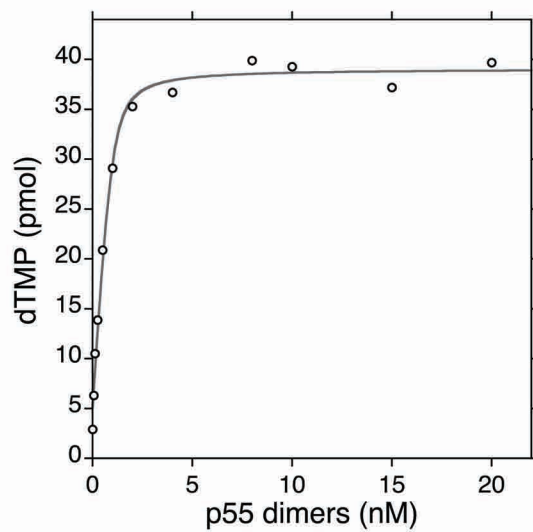
Figure S1. Determination of the affinities of p55 variants for p140 ($K_{d(p140)}$). Representative p140-binding isotherms for wild-type and each of the p55 variants. Reactions (50 μ l) contained 1 nM of p140 and varying amounts (0 – 20 nM) of dimeric p55 or variant at the fixed concentration of 220 mM NaCl. Reaction times were 10 minutes at 37°C. On the Y-axis, pmol dTMP represents the amount of dTMP incorporated into the poly(rA)•oligo(dT)₁₂₋₁₈ (polymerase activity) as measured by counting TCA-insoluble radioactivity. Using the KaleidaGraph program each $K_{d(p140)}$ value was estimated from the quadratic curve fits by nonlinear regression analysis as described in Materials and Methods. Each version of p55 was measured at least twice and the average $K_{d(p140)}$ value \pm the standard deviation is reported in Table 2.

Figure S2. Determination of the dissociation constants for DNA binding ($K_{d(DNA)}$) of p55 and p55 variants. Representative DNA-binding isotherms for wild-type and each of the p55 variants. Electrophoretic mobility shift assays were performed to estimate the $K_{d(DNA)}$ values using various concentrations of p55 or p55 variant (0 – 160 nM dimers) incubated separately with 15 nM of double stranded oligonucleotide in 20 μ l binding reactions (Materials and Methods). The fraction of DNA bound is plotted against the concentration of p55 or variant dimers and binding isotherms were fit to a quadratic equation by nonlinear regression analysis using the KaleidaGraph program to estimate $K_{d(DNA)}$ values. Each version of p55 was measured at least twice and the average $K_{d(DNA)}$ value \pm the standard deviation is reported in Table 2.

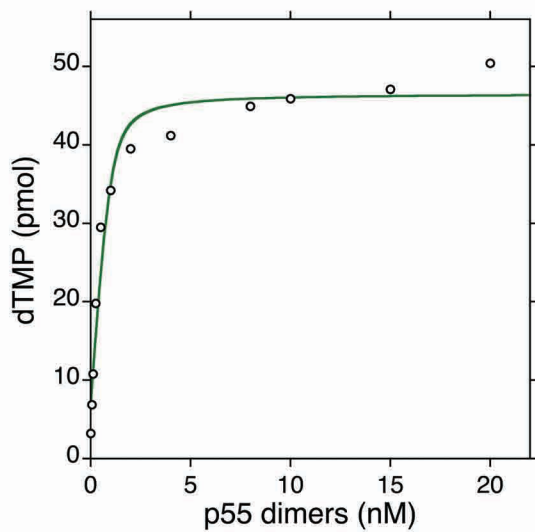
WT p55



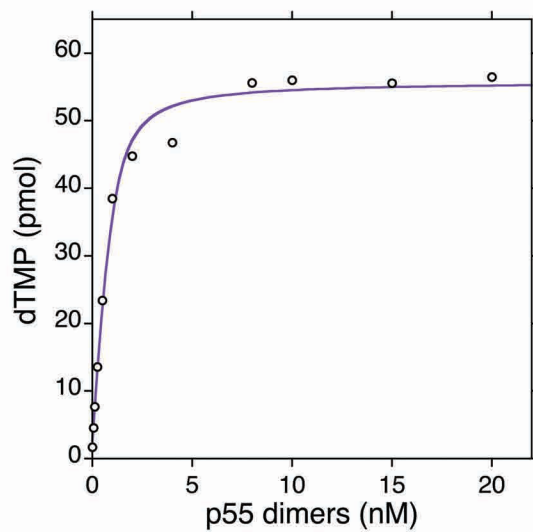
G103S p55



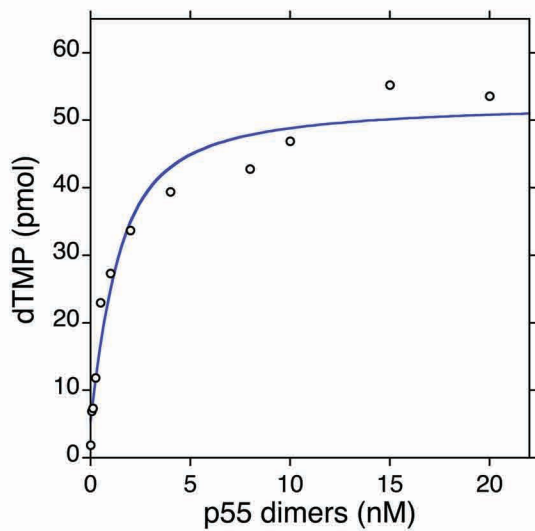
L153V p55



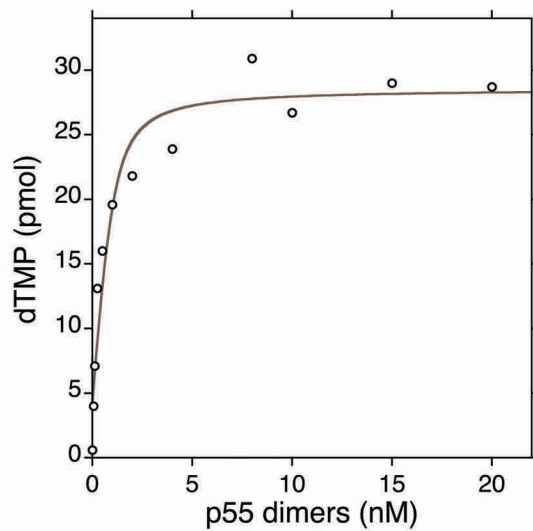
P205R p55



R369G p55



D386E p55



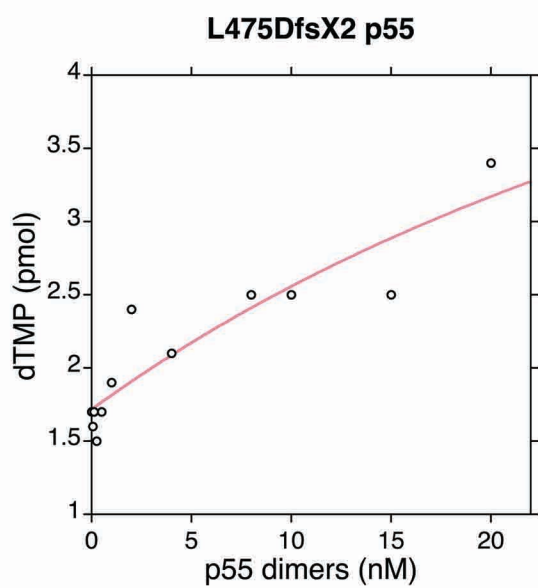
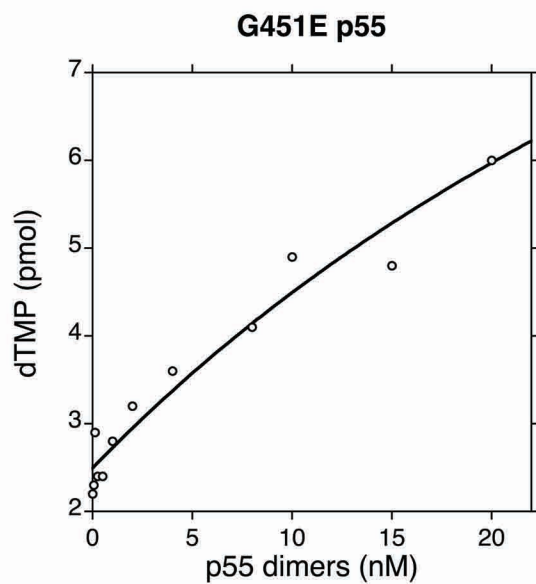
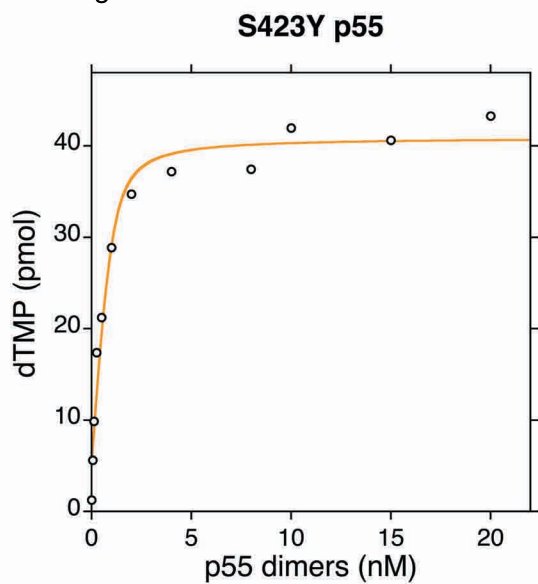
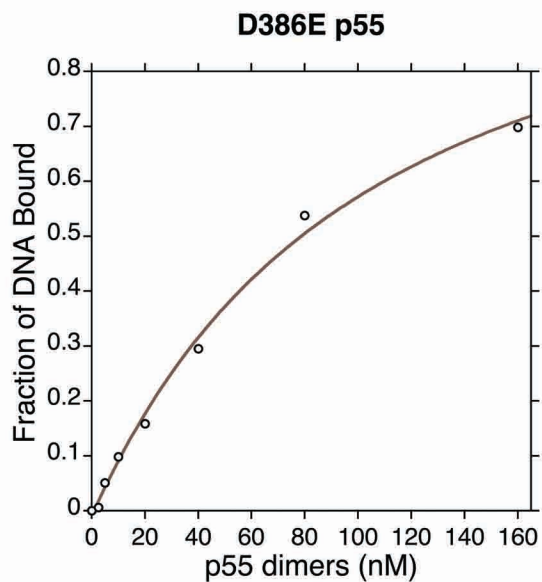
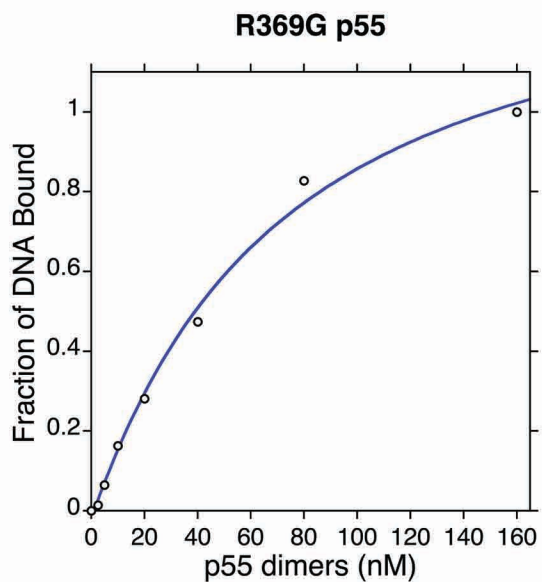
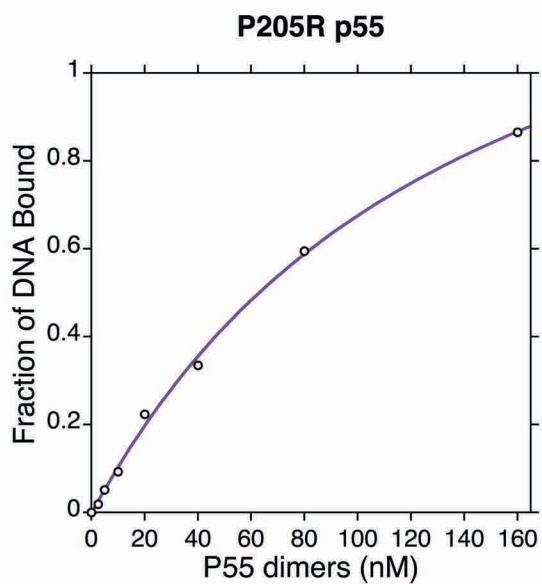
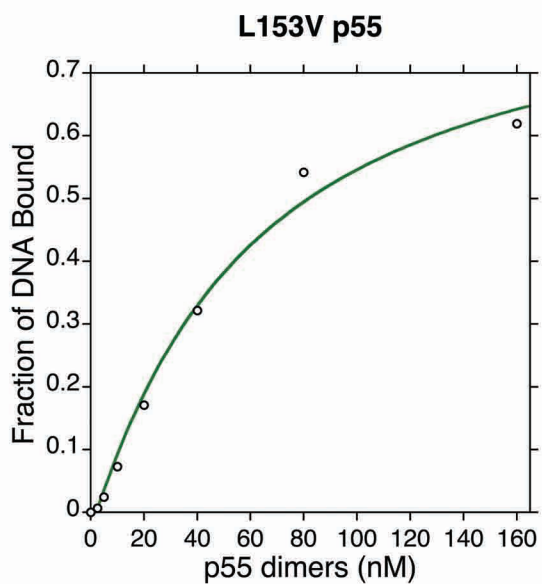
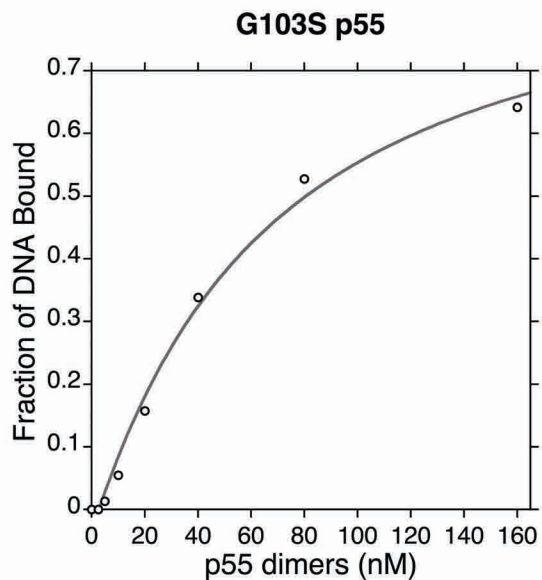
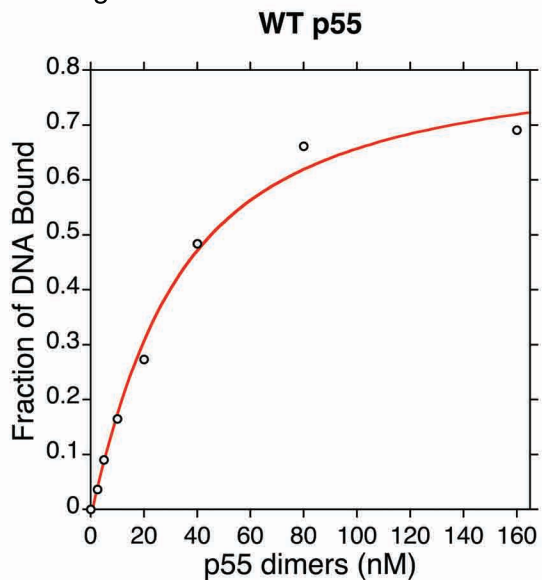


Figure S1.



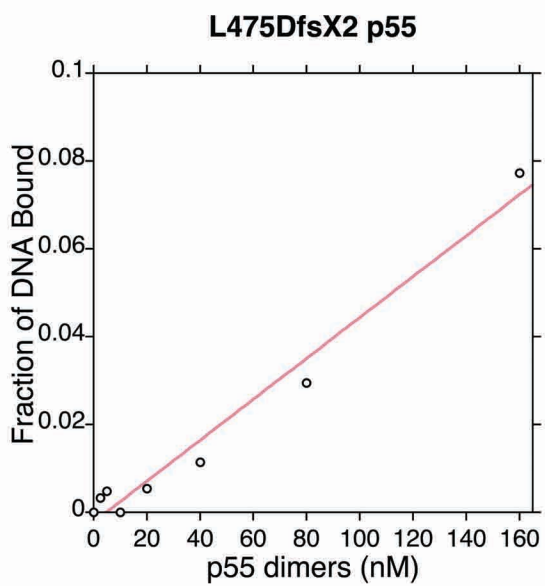
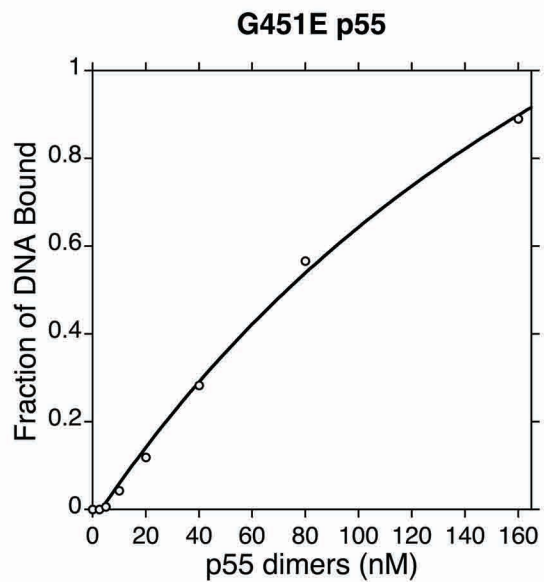
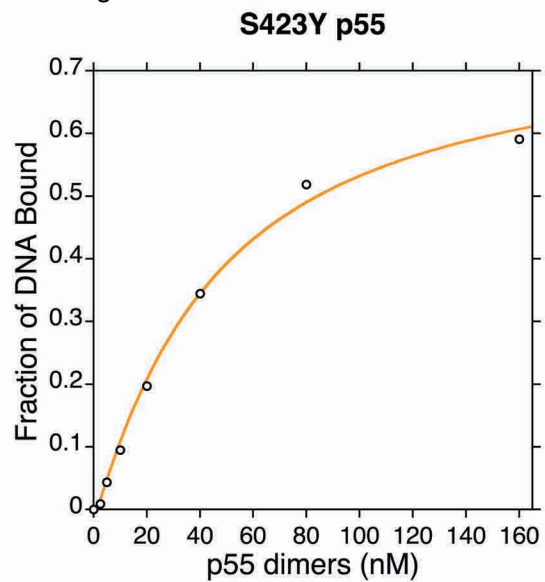


Figure S2.