

Figure S1: The results of normal mode analysis of ADAM33 proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S2: The results of normal mode analysis of D219V mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S3: The results of normal mode analysis of C388Y mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S4: The results of normal mode analysis of C444Y mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S5: The results of normal mode analysis of C475G mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S6: The results of normal mode analysis of C606G mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)

Figure S7: The results of normal mode analysis of C669G mutated proteins. Here, (a) deformability, (b) B-factor, (c) eigenvalues, (d) variance (red color indicates individual variances and green color indicates cumulative variances), (e) co-variance map (correlated (red), uncorrelated (white) or anti-correlated (blue) motions), and (f) elastic network (darker gray regions designate more stiffer regions)