Supporting Information

The newborn mouse lens proteome and its alteration by lysine 6 mutant ubiquitin

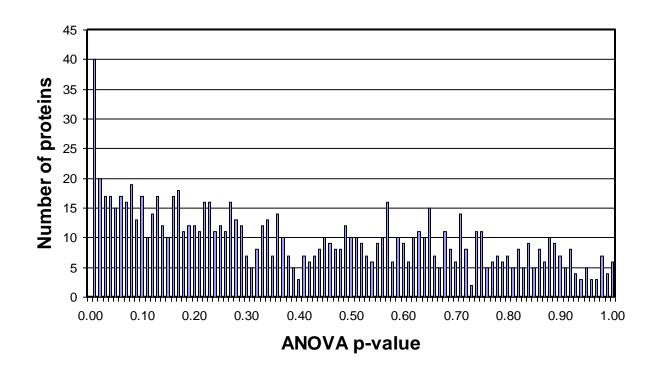
Fu Shang^{1,4}, Phillip A. Wilmarth², Min-lee Chang¹, Ke Liu¹, Larry L. David², Maria Andrea Caceres¹, Eric Wawrousek³, Allen Taylor^{1,4}

¹ Jean Mayer USDA Human Nutrition Research Center on Aging, Tufts University, Boston MA 02111;

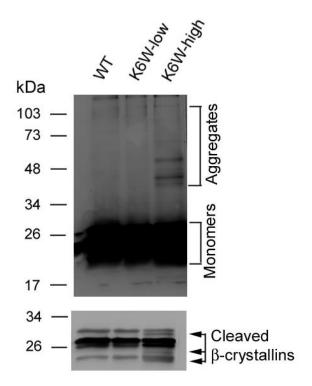
² Department of Biochemistry & Molecular Biology, Oregon Health Sciences University, Portland, OR 97239;

³ Genetic Engineering Core, National Eye Institute, National Institutes of Health, DHHS, Bethesda, MD 20892

⁴ To whom communication should be addressed.



Supplemental Fig. 1. Density histogram of ANOVA test p-value of the quantified 996 proteins. The p-value distribution is composed of a uniform (flat) density from 0 to 1 for the non-differentially expressed proteins and a standout density of low p-value associated with the true differential expressed proteins. The average of proteins in each interval of 0.01 p-value was 9.86, suggest that ~10 proteins with p<0.01 could be detected by chance.



Supplemental Fig. 2. Expression of high levels of K6W-ubiquitin results in aggregation and cleavage of β -crystallins. Lenses from WT and K6W-Ub transgenic newborn (P1) mice were homogenized and proteins were separated by SDS-PAGE on 12% gel. After transfer to nitrocellulose membrane, the blot was probed with antibodies to total β -crystallins. Panel A was the longer exposure of the blot, which shows the aggregated form of β -crystallins in K6W-Ub high expressers. Panel B was the shorter exposure of the blot, which shows the monomer and cleaved forms of β -crystallins. The arrows indicate the fragmented forms.