Supplemental Figure legends

Supplemental Figure 1: String analysis of eIF4B interacting partners. The enlarged box represents eIF4B interaction with reported DUBs and E3 ligase (string.db.org). Light blue node indicates potential interaction from the curated database; the pink node indicates protein-protein interaction experimentally determined, green, red, and dark blue predicts gene neighborhood, gene fusions, and gene co-occurrence, respectively. Yellow, black and purple determines text mining (PubMed), co-expression, and protein homology.

Supplemental Figure 2: (A) The protein levels of eIF4B were shown in GM B-cells (2184, 3323, 1726), DLBCL (ABC-HLY-1, DS, OCI-Ly3, SUDHL-2 and GC-Toledo, Farage, SUDHL-4 and RC) cells and naïve B-cells (three cases of different donors). **(B)** Densitometric quantification of the immunoblots in Figure 1B. Values were first normalized with their respective loading controls and neutralized with the average of naïve B-cells and expressed as mean±SD, which was set at 1. **(C, E)** 293T cells were transfected with either GFP or PARK2 (A) and PARK2 or PARK2-CS (C) and treated with CHX in increasing time point and probed for indicated antibodies. **(D, F)** Densitometric quantification of Supplemental Figure 2A and 2C, respectively. Values were normalized with their corresponding loading controls and neutralized with GFP (B) or PARK2 (C) transfected untreated cells which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using Student's t-test (Unpaired two-tailed). *p<0.05, **p<0.01, ***p<0.005, vs corresponding control cells. **(G)** 293T cells were transfected with an increasing concentration of PARK2 for 48h. Post transfection, cells were treated with MG132 (10μM) for 4 h. Lysates were probed with the indicated antibodies. **(H)** Densitometric quantification of the immunoblots in Supplemental Figure 2E. Values were normalized with their corresponding loading controls and neutralized with GFP transfected cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using Student's *t*-test (Unpaired two-tailed) *p<0.05, ***p<0.005 vs. GFP transfected cells.

Supplemental Figure 3: (A) PARK2-depleted stable GMO cells (1528, 1760) were cultured in the presence of puromycin (3 μg/mL) for 30 min, and lysates were probed for defined antibodies. GAPDH was used as a loading control. **(B)** Densitometric quantification of the immunoblots in Supplemental Figure 3A. Values were normalized with their corresponding loading controls and neutralized with corresponding SCR infected cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Dunnett post hoc analysis. **p<0.01, ***p<0.005, ****p<0.001 vs SCR infected cells. **(C, E, G)** PARK2-depleted stable GMO cells (1528, 1760) were probed for defined antibodies. Actin was used as a loading control. **(D, F, H)** Densitometric quantification of the immunoblots in Supplemental Figure 3C, 3E, 3G, respectively. Values were normalized with their corresponding loading controls and neutralized with corresponding SCR infected cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-

way ANOVA followed by Dunnett post hoc analysis. [a]$p<0.05$, [b]$p<0.01$, [c]$p<0.005$, [d]$p<0.001$ vs SCR infected cells.

Supplemental Figure 4: qRT-PCR analysis for expression of defined genes in indicated stable cells infected with shRNA against PARK2 or SCR (scrambled). Results are normalized with corresponding 18S rRNA expression and neutralized with correspdonding SCR infected cells which was set as 1, and were represented as mean±SD (n=3). Statistical analysis was performed using one-way ANOVA followed by Dunnett post hoc analysis. [a]$p<0.05$, [b]$p<0.01$, [c]$p<0.005$, [d]$p<0.001$ vs SCR infected cells.

Supplemental Figure 5: Indicated PARK2-depleted stable cells were seeded 1 million per well in 6-well plates. Post 12 h, the cells were collected and counted using trypan blue. Values are expressed as mean ± SD (n = 3), *$p<0.05$, vs. SCR infected corresponding cells.

Supplemental Figure 6: (A-F) Indicated cells were cultured with either C75 (A), Ly284002 (C), Rapamycin (D), MK2206 (E), or PF470851 (F) for 16h or infected with shRNA against FASN (B) and lysed. Post-treatment/infection, cell lysates were probed for PARK2 expression. GAPDH was used as a loading control. The bar diagram beneath each figure represents the densitometric quantification of the immunoblots. Values were normalized with their corresponding loading controls and neutralized with corresponding DMSO (0.1%) or SCR infected corresponding cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Dunnett post hoc analysis. *$p<0.05$, **$p<0.01$, ***$p<0.005$, ****$p<0.001$ vs corresponding cells.

Supplemental Figure 7: (A-F) Indicated cells were cultured with either C75 (A), Ly284002 (C), Rapamycin (D), MK2206 (E), or PF470851 (F) for 16h or infected with shRNA against FASN (B) and lysed. Post-treatment/infection, cell lysates were probed for PARK2 expression. GAPDH was used as a loading control.

Supplemental Figure 8: (A) Indicated cells were stably infected with the retroviral particles expressing GFP or PARK2 mutants and probed for the defined antibodies. (B) Densitometric quantification of the immunoblots in Supplemental Figure 8A. Values were normalized with GFP expressing cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post hoc analysis. [b]$p<0.01$, [d]$p<0.001$ vs GFP infected cells. [B]$p<0.01$, [C]$p<0.005$, [D]$p<0.001$ vs PARK2-W infected cells. **(C)** Indicated cells stably expressing the genes were challenged with puromycin. Post-treatment, cells were lysed, and the puromycin incorporation was studied using an anti-puromycin antibody. **(D)** Densitometric quantification of the immunoblots in Supplemental Figure 8D. Values were normalized with their corresponding loading controls and neutralized with corresponding GFP expressing cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post

hoc analysis. $^{a}p<0.05$, $^{b}p<0.01$ vs GFP infected cells. $^{B}p<0.01$, $^{C}p<0.005$, $^{D}p<0.001$ vs PARK2-W infected cells.

Supplemental Figure 9: qRT-PCR analysis for expression of *eIF4B* in indicated stable cells infected with PARK2 (wild type and mutants) or GFP. Results are normalized with corresponding 18SrRNA expressiobn and neutralized with correspdonding GFP infected cells which was set as 1, and were represented as mean±SD (n=3).

Supplemental Figure 10: (A) Indicated cells were stably infected with the retroviral particles expressing GFP or PARK2 mutants and probed for the defined antibodies. (B) Densitometric quantification of the immunoblots in Supplemental Figure 10 A. Values was normalized with GFP expressing cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post hoc analysis. $^{b}p<0.01$, $^{c}p<0.005$, $^{d}p<0.001$ vs GFP infected cells. $^{A}p<0.05$, $^{B}p<0.01$, $^{C}p<0.005$, $^{D}p<0.001$ vs PARK2-W infected cells.

Supplemental Figure 11: qRT-PCR analysis for expression of defined genes in indicated stable cells infected with PARK2 (wild type and mutants) or GFP. Results are expressed as mean±SD (n=3). Results are normalized with corresponding 18S rRNA expression and neutralized with corresponding SCR infected cells which was set as 1, and were represented as mean±SD (n=3). Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post hoc analysis. $^{a}p<0.05$, $^{b}p<0.01$, $^{c}p<0.005$, $^{d}p<0.001$ vs GFP infected cells. $^{A}p<0.05$, $^{B}p<0.01$, $^{C}p<0.005$, $^{D}p<0.001$ vs PARK2-W infected cells.

Supplemental Figure 12: (A) Indicated cells were stably infected with the retroviral particles expressing GFP or PARK2 mutants and probed for the defined antibodies. **(B)** Densitometric quantification of the immunoblots in Supplemental Figure 12 A. Values were normalized with their corresponding loading controls and neutralized with corresponding GFP expressing cells, which was set as 1 and were represented as mean±SD for n=3. Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post hoc analysis. $^{a}p<0.05$, $^{b}p<0.01$, $^{c}p<0.005$, $^{d}p<0.001$ vs GFP infected cells. $^{A}p<0.05$, $^{B}p<0.01$, $^{C}p<0.005$, $^{D}p<0.001$ vs PARK2-W infected cells.

Supplemental Figure 13: qRT-PCR analysis for expression of defined genes in indicated stable cells infected with PARK2 (wild type and mutants) or GFP. Results are expressed as mean±SD (n=3). Results are normalized with corresponding 18S rRNA expression and neutralized with corresponding SCR infected cells which was set as 1, and were represented as mean±SD (n=3). Statistical analysis was performed using one-way ANOVA followed by Bonferroni's post hoc analysis. $^{a}p<0.05$, $^{b}p<0.01$, $^{c}p<0.005$, $^{d}p<0.001$ vs GFP infected cells. $^{A}p<0.05$, $^{B}p<0.01$, $^{C}p<0.005$, $^{D}p<0.001$ vs PARK2-W infected cells.

Supplemental Figure 14 Indicated cells were stably infected with the retroviral particles expressing GFP, or PARK2 mutants were seeded 1 million per well in 6-well plates. Post 12 h, the cells were collected and counted using trypan blue. Values are expressed as mean ± SD (n = 3), $^{*}p<0.05$, vs. SCR, infected corresponding cells, $^{a}p<0.05$ vs. PARK2-W infected corresponding cells.

Supplemental Figure 15 (A, C) The same cohort as described in Figure 8E, 8F was segregated into molecular subgroups, and higher median PARK2 expression in GC- and Unclassified (UNC) DLBCL patients showed a similar trend of better prognosis than patients having lower than median expression; however was statistically not significant. **(B,D)** Progression-Free Survival analysis in GC and UNC-DLBCL patients showed a similar trend, albeit not statistically significant.