

1 **EPSTEIN-BARR VIRUS LMP1 ENHANCES LEVELS OF MICROVESICLE-**
2 **ASSOCIATED PD-L1**

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25 **Abstract:**

26 Extracellular vesicles (EVs) circulate throughout the body and carry cargo that can be
27 conferred to proximal or distant cells, making them major delivery vehicles for cellular
28 communication. Epstein-Barr virus (EBV) infected cells release EVs that contain viral proteins
29 such as the major viral oncogene, latent membrane protein 1 (LMP1). LMP1 has been shown
30 to regulate the cellular gene expression of programmed cell death protein 1 ligand (PD-L1).
31 PD-L1, a protein that suppresses the immune system by binding to PD-1, (a receptor found on
32 cytotoxic T cells). PD-L1 has been recently found to be packaged into small EVs contributing
33 to immune evasion of lung cancer cells. Recent studies establish that MVs are shed in very
34 large amounts by tumor cells, and that elevated levels of MVs correlate to disease metastasis
35 and cancers being more aggressive. Here, we demonstrate PD-L1 enrichment in MVs
36 released from nasopharyngeal carcinoma cells and an important function of EBV LMP1 in
37 regulating PD-L1 levels in MVs. These PD-L1+ MVs containing LMP1 likely contribute to the
38 immunosuppressive microenvironment found in EBV-associated cancers.

39

40 **Importance:**

41 Accumulating evidence over the past decade supports that viruses utilize EVs and associated
42 pathways to incorporate viral products to evade eliciting an immune response, while
43 concurrently enabling viral spread or persistence within the host. Considering that viral proteins
44 confer very strong antigenic peptides that will be recognized by T cells, the regulation of the
45 PD-1 pathway by the overexpression of MV-associated PD-L1 may be a strong immune
46 evasion tactic utilized by viruses. The discovery that EBV LMP1 increases PD-L1 microvesicle
47 secretion, identifies a new therapeutic target in immune blockade therapy. We expect that our

48 findings will begin to clarify the mechanism of LMP1-mediated enhanced packaging of PD-L1
49 into MVs and may produce more specific targets to treat EBV-associated cancers.
50 Consequently, identifying whether a disease is of viral origin through predictive MV biomarkers
51 could further allow for more targeted therapies.

52

53 **KEYWORDS:** Epstein-Barr virus, microvesicles, extracellular vesicles, human herpesviruses,
54 PD-L1, LMP1, oncosome, exosomes

55

56 **Introduction**

57 Epstein-Barr virus (EBV) is a human herpesvirus that persistently infects over 90% of the
58 world's population (1). Most individuals are asymptomatic; however, in immunocompromised
59 or genetically susceptible individuals, EBV infection can cause various lymphomas and
60 carcinomas (1). PD-L1 normally functions by suppressing an individual's immune system from
61 attacking their own cells within the body. Any pathogenic, viral, or foreign substance trying to
62 invade the body is combated by the immune system; however, certain cancer cells take
63 advantage of the functions of PD-L1 and overexpress this gene in order to escape immune
64 detection and maintain proliferation and survival. PD-L1 exists in the blood in two different
65 forms: extracellular vesicle-associated or a soluble protein. One of the first observations of PD-
66 L1 being expressed on small extracellular vesicles (EVs) was in 2011 where investigators
67 detected exosomal PD-L1 extracted from human samples of plasma and urine (2).
68 Additionally, PD-L1 has been found on the surface of antigen presenting cells such as B cells,
69 mast cells, and certain epithelial and endothelial cells (3, 4). It is highly expressed on the

70 surface of tumor cells, T lymphocytes and tumor associated macrophages (5). Additionally, it
71 can be found in many tissues such as muscles and nerves (6). PD-L1 suppresses the immune
72 system by binding to PD-1, a receptor found on cytotoxic T cells. The PD-1 pathway involves
73 several interactions leading to the inhibition of T-regulatory functions and the production of
74 interleukins which results in a reduced immune response, T cell apoptosis and exhaustion, and
75 the suppression of dendritic cells (7). These cumulative immunosuppressive effects create a
76 very strong protective barrier for cancerous cells to grow uncontrollably and eventually
77 metastasize throughout the body. PD-L1 may also play an important role in immune evasion
78 strategies adopted by viruses and other human pathogens.

79 Some of the more recent data has suggested an important role for the PD-L1 ligand as a
80 mechanism of achieving an immune resistant tumor microenvironment and establishing
81 latency within the host in EBV infection. Expression of PD-L1 is significantly higher in EBV
82 positive cells compared to EBV negative cells (8). It has been shown that high EBV copy
83 number per infected cell is correlated with PD-L1 expression such as in EBV associated
84 gastric carcinoma (9). The presence of high levels of PD-1 and PD-L1 in EBV+ patients is
85 directly linked to the development of high-risk Hodgkin lymphoma (10). Considering that LMP1,
86 (major viral oncogene expressed in EBV associated cancers), has been established in
87 regulating PD-L1 levels within the cell and manipulates EV cargo and functions, we
88 hypothesized that LMP1 may influence PD-L1 EV levels as an immune evasion mechanism.
89 Ultimately, this would result in an immunosuppressive tumor microenvironment favoring viral
90 sustainability and propagating infection, not only to neighboring cells, but cells throughout the
91 body as well.

92 Viruses share many similarities with EVs, such as the transfer of functional cellular proteins,
93 RNAs, and miRNAs into neighboring cells (11). The formation of large EVs or microvesicles
94 (MVs) involves transport of cargo to the plasma membrane, lipid membrane redistribution,
95 budding, and finally a form of vesicle pinching upon reaching the membrane which leads to the
96 release of the vesicle (12). Shed MVs are distinct in size, cargo, and mechanism of formation
97 from the other subpopulation of EVs known as small EVs. Both small EVs and MVs
98 encapsulate and transfer cargo including proteins, miRNAs, and RNA transcripts to other cells.
99 Caveolin-1 is essential for sorting of selected miRNAs into MVs (13). Both viruses and MVs
100 emerge from the plasma membrane at lipid raft organizing centers indicating a similar form of
101 biogenesis (14). Elevated levels of EVs in tumor microenvironments and within the circulation
102 correlate to a more advanced disease stage in cancers. MVs play a role in acting as a bridge
103 of cellular communication between cancer and the surrounding stroma to alter the surrounding
104 tumor environment in a way that enhances their growth and survival. MVs shed from a highly
105 metastatic melanoma cell line, were able to confer metastatic characteristics to poorly
106 metastatic cells (15). Recent data has indicated a role for PD-L1 expression in small EVs;
107 however, little is known about PD-L1 expression in MVs, the mechanism that leads to its
108 upregulation, and the localization of PD-L1 in these different EV subpopulations.

109 Previous studies have already implicated a role for MVs in immune suppression. For example,
110 MVs derived from colorectal carcinoma or human melanoma, suppressed monocyte
111 differentiation into antigen presenting cells and suppressed T lymphocytes through TGF- β ,
112 both *in vivo* and *in vitro* (16). LMP1, (a major viral oncoprotein present in EVs), has been
113 shown to be involved in indirectly inhibiting humoral immune response(17, 18). LMP1 has a
114 major role in the lifecycle of EBV, is an important contributor to many EBV-associated cancers,

115 and is packaged and released from infected cells into small EVs (19). LMP1 activates several
116 signaling pathways such as the JAK/STAT, MAPK, and NF- κ B pathways which have been
117 shown to upregulate PD-L1 expression as well and are known to be commonly constitutively
118 activated in a multitude of cancers (19). Here we demonstrate the enrichment of PD-L1 in MVs
119 in response to levels of LMP1 and clarify localization, co-immunoprecipitation, and the
120 regulation of these MVs in response to LMP1 levels.

121

122 **Results:**

123 **PD-L1 levels are elevated in MVs from NPC cells with LMP1 expression.**

124 EBV infected cells have different expression of viral transcriptional programs referred to as
125 latency I, II, and III. EBV Latency II, was originally identified in biopsies of NPC, which was
126 characterized by the co-expression of LMP1, LMP2, and EBNA1 transcripts (20). NPC tissues
127 expressing LMP1 are significantly associated with poor overall survival in NPC patients and
128 lymph node metastasis (21, 22). We decided to investigate two different NPC cell lines with
129 varying levels of LMP1. In the first model, an EBV-negative nasopharyngeal carcinoma cell line
130 (HK1) was compared to HK1 containing a GFP-tagged LMP1 tetracycline-inducible system
131 (HK1 LMP1). The HK1 LMP1 cells were treated with doxycycline to activate LMP1 expression
132 (Fig. 1 A). Additionally, to investigate PD-L1 expression in the context of lower stable
133 expression of LMP1, EBV-negative nasopharyngeal carcinoma (HNE-1) cells were used. HNE-
134 1 cells were transduced with a vector control (pBabe) or hemagglutinin (HA)-tagged LMP1
135 retroviral vector (HNE-1 pBabe LMP1) that constitutively expresses low levels of LMP1 (Fig. 1
136 B). LMP1 expression was detectable in the HNE-1 pBabe LMP1 but notably lower than the
137 HK1 LMP1 inducible model. The lower levels of LMP1 have been previously reported to

138 closely exhibit expression patterns found in EBV-infected cell lines (23). We harvested the cell
139 lysates, apoptotic bodies (2K), microvesicles (10K), and small EVs (100K), and analyzed them
140 by immunoblot (24). The results showed an increase in PD-L1 levels with elevated levels of
141 LMP1, with PD-L1 noticeably enriched within the MV subpopulation of EVs compared to small
142 EVs and apoptotic bodies (Fig 1.A and B). Quantification of the levels of LMP1 and PD-L1
143 specifically in the MV subpopulation normalized to levels of (HK1 and HNE-1) showed a
144 significant increase in PD-L1 and LMP1 in the MVs of the NPC cell lines expressing LMP1
145 compared to the wild type cell lines with no LMP1 (Fig. 1C and D). Quantification also
146 demonstrated higher PD-L1 expression in the MVs compared to the other two subpopulations
147 of EVs as seen in (Fig. 1 E and F). In conclusion, these results further support the correlation
148 between LMP1 expression and increased PD-L1 being released from the cell in association
149 with MVs.

150 **PD-L1 is upregulated at the transcriptional level in LMP1 expressing cells and detected**
151 **in MVs.**

152 To further understand whether PD-L1 is also being impacted at an mRNA level due to LMP1
153 expression, RT-qPCR was performed on cells and MVs from both HK1 wild type cells and HK1
154 LMP1 induced cells. HK1 LMP1 containing cells significantly increased the expression of PD-
155 L1 and EV biogenesis related genes (CD9, CD63, CD81, Sytenein-1, and HRS) compared to
156 HK1 cells (Fig. 2A). Interestingly, LMP1 expression did not influence the mRNA levels of PD-
157 L1 in MVs but did have significantly higher levels of CD9, CD63, CD81, Syntenin-1, and HRS
158 mRNA when compared to HK1 (Fig. 2B). CD9, CD63 and CD81 are endosome-specific
159 tetraspanins that are enriched in exosome (samall EV) membranes. CD63 has been found to
160 regulate EBV LMP1 exosomal packaging (18) and HRS and Syntenin-1 have previously been

161 shown to induce EV formation through EBV LMP1 (25). Altogether, this data suggests that PD-
162 L1 is upregulated at the transcriptional level in LMP1 expressing cells but the level of mRNA
163 transcripts in the MVs remain unchanged.

164

165 **Characterization of MVs from NPC cells.**

166 MVs are characterized as being within the 100 to few micrometers size range (26). In order to
167 confirm size range of these MVs harvested from NPC cells with or without LMP1, Transmission
168 Electron microscopy (TEM) imaging was performed. Both the HK1 and HK1 GFP LMP1
169 inducible MV subpopulations were visualized to be around 200nm and exhibited similar
170 phenotypes under the microscope, as seen in (Fig. 3A and B). Additionally, nanoparticle
171 tracking was performed to further validate the EM results and to identify differences in MVs
172 harvested from NPC cells expressing LMP1 compared to wild type NPC cells. The tracking
173 data in (Fig. 3C) revealed that there was a significant increase in particles/ml for the MVs
174 harvested from the high expressing LMP1 NPC cell line compared to the wild type cell line,
175 however, there was no significant difference in particles/cell between the two cell lines (Fig.
176 3D). This is different than what was previously observed for enhancement of small EV
177 production due to LMP1 expression (27). The reasoning to why increased particles per ml is
178 observed could be due to the fact that NPC cells expressing LMP1 grow at a faster rate than
179 the wild type cells resulting in more MVs being released per ml of media. Both the mean and
180 mode size of the MVs secreted from the high LMP1 expressing cell line was significantly
181 increased compared to wild type MVs (Fig. 3E and F). This led us to question whether these
182 larger secreted MVs carry more protein cargo. The tracking and protein analyses revealed that
183 the MVs from the high expressing LMP1 cell line had a significant increase in total protein

184 content compared to the wild type MVs (Fig. 3F). The nanoparticle tracking data suggests that
185 there are not more MVs secreted per cell in the high expressing LMP1 cells but there is more
186 protein per MV. Therefore, cells expressing LMP1 secrete larger MVs with increased protein
187 content that may alter the immune response within the infected microenvironment.

188 **PD-L1 is enhanced on the surface of MVs due to LMP1.**

189 PD-L1 has previously been reported to be expressed on the surface of small EVs similar to cell
190 surface PD-L1 membrane topology, in which the extracellular domain of PD-L1 is surface
191 exposed (28). PD-L1 extracellular exposure is required for it to exert its immunosuppressive
192 effects, since PD-L1 needs to be exposed on the surface to bind to its receptor PD-1 which is
193 found on cytotoxic T cells. Flow cytometry on MVs from HK1 wild type cells and HK1 LMP1
194 induced cells expressing LMP1 was done. The MVs from both cell lines were incubated with
195 surface PD-L1 antibody or isotype control. Flow cytometry analyses revealed elevated surface
196 PD-L1 expression in the MVs from HK1 GFP tagged LMP1 (green) compared to the MVs from
197 the HK1 wild type cells (blue) (Fig. 4A). In order to further understand PD-L1 localization on
198 these MVs, scanning transmission electron microscopy (STEM) was undertaken to observe
199 the MVs after immunogold labelling of PD-L1 with antibodies that specifically bind to PD-L1 on
200 the extracellular domain. Upon examination of both the prepared EM grids, gold labelling of
201 PD-L1 was only observed on the HK1 LMP1 MVs (Fig. 4B and C). Quantification of gold
202 particles per MV revealed a significant increase in gold particles in the HK1 LMP1 MVs
203 compared to the wild type MVs (Fig. 4D). Research has shown PD-L1 localization to be on the
204 surface of small EVs; however, more current studies have found PD-L1 to be present on both
205 the surface and within small EVs (29). To further understand PD-L1 localization within the MV,
206 a protease protection experiment was done using two different PD-L1 antibodies. For this

207 experiment, Syntenin and CD71 were used as the positive and negative controls, respectively.
208 Syntenin is a cytosolic adaptor located within EVs that binds to the intracellular domain (ICD)
209 of syndecans (30), and CD71 is a transferrin receptor found on the surface of EVs. In (Fig. 4E),
210 a PD-L1 antibody that recognizes endogenous levels of PD-L1 showed a decrease in band
211 size upon the addition of trypsin. In (Fig. 4F) a PD-L1 antibody that recognizes the extracellular
212 domain of PD-L1 was used, and upon trypsin addition little PD-L1 is observed. This reveals
213 that there is some PD-L1 surface exposure on these MVs secreted from high LMP1 expressing
214 cells; however, some PD-L1 may also be present inside MVs or is resistant to Trypsin
215 cleavage. Taken together, LMP1 seems to play a role in increasing PD-L1 exposure to the
216 surface of MVs which may influence the immunosuppressive effects of MVs released from
217 EBV infected cells.

218 **LMP1 and PD-L1 localize within the same MV subpopulation.**

219 LMP1 and PD-L1 have previously been demonstrated to be expressed on small EVs (28, 31).
220 Here, we aimed to investigate whether LMP1 was present in PD-L1 positive MVs following
221 LMP1 induction of NPC cells. First, Optiprep density gradient purification of MVs was
222 performed. This technique uses iodixanol and ultra-centrifugal force to further purify EV
223 subpopulations into fractions based on their buoyant density (24) . This can be used to
224 determine the exact density and fractions within the MV pellet that contain PD-L1 and whether
225 it co-migrates with LMP1 in the gradient. MVs were harvested from doxycycline-treated HK1
226 GFP-LMP1 tetracycline-inducible cells and separated by density. The vesicles were purified on
227 an iodixanol density gradient to separate larger MV subpopulation according to the method of
228 Kowal et al (24). Two major populations of vesicles were observed in fractions 3 (F3) and 5
229 (F5) of the gradients, corresponding to densities 1.115 g/mL (third fraction = F3) and 1.145

230 g/mL (fifth fraction = F5) of iodixanol. MV subpopulations, F3 and F5 have previously been
231 determined to be enriched with specific proteins. F3 usually contains unique ribosome and
232 proteasome proteins with F5 containing more mitochondrial and ER proteins (24). In these
233 experiments, F3 and F5 MV subpopulation of EVs were enriched for protein markers LMP1,
234 PD-L1, and Caveolin-1 (Fig. 5A). LMP1 is present in both small EVs and larger shed
235 microvesicles (31, 32). Furthermore, we demonstrate the co-migration of LMP1 and PD-L1 in
236 fractions 3, 4 and 5. Fractions 3 and 5 were enriched with LMP1, PD-L1 and Caveolin-1 more
237 so than the other fractions indicating that both LMP1 and PD-L1 co-migrate within the same
238 density fractions in MVs. If LMP1 is present in PD-L1 positive MVs, then MVs immuno-
239 precipitated with PD-L1 specific antibodies should contain LMP1. To test this, MVs were
240 harvested from cells expressing LMP1 and recovered by the addition of anti-PD-L1 antibody.
241 Ten percent of the MV input sample was used to compare to the PD-L1 immuno-precipitated
242 MVs. Immunoblot analysis further revealed LMP1 to be present in the PD-L1 pulldown (Fig.
243 5B). EGFR was also pulled down in these PD-L1 positive MVs which was interesting since it
244 has been recently demonstrated that EGFR activity can control PD-L1 surface presentation in
245 breast cancer cells (33). Together, this data suggests that LMP1 and PD-L1 are likely in the
246 same MV population (mostly in fractions 3 and 5) and are localized to the same vesicle within
247 MVs.

248 **LMP1 and PD-L1 colocalize in NPC cells and are enriched in lipid rafts.**

249 NPC cells have enhanced levels of PD-L1 fluorescence expression in cells that are EBV+
250 compared to EBV- (34). Based on the above, it was hypothesized that LMP1 might be
251 responsible for this observation possibly even altering PD-L1 subcellular localization. Similarly,
252 the results from (Fig. 6A-E) demonstrate enhanced PD-L1 expression and perinuclear

253 colocalization with LMP1 in two different NPC cell lines (HK1 and HNE-1). Maximum intensity
254 orthogonal projections of Z-stack colocalization images demonstrate PD-L1 and LMP1
255 perinuclear localization in live and fixed cell images (Fig. 6A and C). HNE-1 cells were
256 transfected with RFP-tagged LMP1 and GFP-tagged PD-L1 and were examined by live cell
257 confocal microscopy. The cells exhibited a distinct punctate perinuclear signal for LMP1 and
258 PD-L1 (Fig. 6A). To confirm these results with endogenous levels of PD-L1 expression, and to
259 understand what LMP1 does to PD-L1 localization within the cell, fixed cell imaging was done
260 for HK1 LMP1 cells that were induced and un-induced with doxycycline. As seen in (Fig. 6B),
261 PD-L1 is mostly localized perinuclearly when LMP1 is present. It seems to aggregate to one
262 side of the cell in accordance to where LMP1 is also being accumulated. However, in the un-
263 induced images lacking LMP1, PD-L1 was found to be mostly dispersed throughout the cell
264 rather than localized within a sub-region like when LMP1 is present (Fig. 6C). Pearson's
265 correlation coefficient between LMP1 and PD-L1 in the HNE-1 transfected cells and the
266 induced HK1 LMP1 cells, was around 0.7 and 0.8 respectively, indicating a strong correlation
267 between these two variables (Fig. 6B and D). Additionally, CTCF values were calculated for
268 HK1 LMP1 cells with and without doxycycline and showed very high significance in levels of
269 PD-L1 fluorescence in the doxycycline induced HK1 LMP1 cells compared to the un-induced
270 (Fig. 6E).

271 LMP1 accumulates in lipid raft microdomains within the cell to engage signaling pathways (35).
272 Lipid rafts are distinct lipid domains enriched in cholesterol and glycosphingolipids that are
273 involved in many roles which include but are not limited to signal transduction, membrane
274 trafficking and the lateral compartmentalization of molecules at the cell surface (35, 36). Both
275 viruses and MVs emerge from the plasma membrane at lipid raft organizing centers indicating

276 a similar mechanism of biogenesis (14). The formation of MVs involves the transport of specific
277 cargo to the plasma membrane, lipid membrane redistribution and finally a form of vesicle
278 pinching off upon reaching the membrane which leads to the release of the vesicle (12). To
279 test whether PD-L1 also accumulates in membrane microdomains, lipid rafts were isolated
280 from wild type HK1 or HK1 LMP1 cells following induction of LMP1 based on their detergent-
281 resistant biochemical properties and analyzed by immunoblot. In both cell lines raft isolates
282 were enriched in lipid raft scaffolding protein Caveolin-1 (37). The adaptor protein Syntenin-1
283 was probed for since it is required for efficient LMP1 EV incorporation (25). As seen in (Fig.
284 6F), LMP1 and PD-L1 are enriched in lipid rafts; however, very little PD-L1 is present in wild
285 type HK1 cells or rafts lacking LMP1. Based on this data, we conclude that PD-L1 is not only
286 enhanced by LMP1 at the cellular level but also shifts PD-L1 localization from dispersed
287 throughout the cell to colocalizing with LMP1 at perinuclear regions within the cell; additionally,
288 PD-L1 and LMP1 may share a similar lipid raft associated mechanism of MV incorporation.

289

290 **Discussion:**

291 In this study, we examined the impact of EBV oncoprotein LMP1 on MV associated PD-
292 L1 levels using a number of techniques. LMP1 has previously been found to contribute
293 to immune evasion strategies and protect virus infected cells through the activation and
294 upregulation of multiple immune-associated proteins (38). Moreover, LMP1 modified
295 EVs are found to contribute to tumor progression through shaping the tumor
296 microenvironment by enhancing tumor cell growth, migration, invasion, and suppressing
297 the anti-tumor host response (39). LMP1 from infected cancer cells accumulate in small
298 EVs (40). Numerous observations indicate that full-length LMP1 protein is secreted from

299 the cell in larger EVs shed from the cell surface called microvesicles (MVs) (41). The
300 release of LMP1 from the cell through EV pathways has been suggested as a method of
301 escape from degradation and cell-to-cell transmission of LMP1 and associated proteins
302 (2, 3).

303 Recently, LMP1 has been found to regulate PD-L1 expression at the cellular level
304 through STAT3, AP-1, and NF- κ B pathways (34). Cytokines such as tumor necrosis
305 factor- α (TNF- α), interferon- γ (IFN- γ), and interleukin 4 (IL-4) upregulate PD-L1
306 expression through the STAT and NF- κ B pathways (43–45). IFN- γ also has been shown
307 to have a synergetic effect with LMP1 in up-regulating PD-L1 in NPC (34). PD-L1
308 upregulation has been implicated in numerous roles with regards to immune
309 suppression (28, 43, 44). Constitutive expression of PD-L1 on tumor cells is an innate
310 immunity mechanism activated by several pro-survival pathways: MAPK (45),
311 ATM/ATR/Chk1 (46), JAK/STAT (43), and PI3/AKT(44); or by genetic aberrations such
312 as CDK5 disruption (47), loss of PTEN (48), or truncation of the 3'-UTR that stabilizes
313 an increase in PD-L1 transcripts (49). However, constitutive expression of PD-L1 is far
314 less common than IFN induced PD-L1 expression. PD-L1 is expressed in various
315 cancers: gastric cancer (50), melanoma (51), nasopharyngeal carcinoma (52), post-
316 transplant lymphoproliferative disorder (53), non-small cell lung cancer (54), pancreatic
317 cancer (55), lymphomas (56), bladder cancer (57), kidney cancer (58), breast cancer
318 (59), and Hodgkin lymphoma (60) . Other than EBV, multiple human herpes virus
319 infections have also been found to result in increased PD-L1 expression such as herpes
320 simplex virus (61), Varicella zoster virus (62), Cytomegalovirus (63), Human herpesvirus
321 6 (64), and Kaposi's sarcoma-associated herpesvirus (65). Interestingly, in addition to

322 human herpes viruses, infection with human immunodeficiency virus (HIV), influenza
323 virus, Ebola virus, and adenovirus also leads to elevated PD-L1 expression (66), (67).
324 Altogether, the wide array of diseases viral and non-viral, that are associated with
325 increased PD-L1 expression emphasizes the need for elucidating the mechanism of
326 pathway regulation, activation, and localization of PD-L1.

327 In immune competent hosts, EBV efficiently infects B lymphocytes, this initiates a strong
328 cytotoxic T cell response against lytic and latent antigens, leading to the expansion of
329 EBV-transformed B cells. To establish and maintain latency, EBV has adopted many
330 immune evasion mechanisms. To further understand the function of PD-L1 in EBV
331 related cancers in response to EBV viral oncogene LMP1, we characterized the
332 subpopulations of extracellular vesicles expressing PD-L1 following LMP1 expression.
333 In our experiment we determined PD-L1 enrichment in MVs in response to LMP1 levels
334 in both a high LMP1 expressing cell line construct (HK1 GFP-tagged inducible LMP1)
335 and by a LMP1 expressing cell line (HNE-1 pBabe LMP1) which constitutively
336 expresses lower levels of LMP1, similar to levels found in EBV infected cells. It was
337 observed that LMP1 and PD-L1 accumulated in a subpopulation of EVs called MVs.
338 Additionally, we determined that the upregulation of PD-L1 in the MV subpopulation was
339 in response to EBV LMP1. MVs from NPC cells were confirmed through size, density
340 and the detection of MV markers. Flow cytometry analyses indicated an approximately
341 10-fold increase in PD-L1 associated MVs from the NPC cell line expressing LMP1
342 compared to the wild type. LMP1 upregulated the cellular expression of PD-L1 at the
343 transcriptional level; however interestingly, PD-L1 mRNAs were detected in MVs. PD-L1
344 is post-transcriptionally regulated in an indirect way through TNF α -activated NF- κ B (68).

345 LMP1 is a CD40 receptor mimic that constitutively activates NF- κ B (69, 70). This
346 depicts a mechanism in which PD-L1 is possibly being upregulated at the transcriptional
347 level in MVs through the activation of NF- κ B by LMP1.

348 Moreover, we demonstrate that LMP1 expression in NPC cells results in total elevated
349 levels of EV secretion and enhanced packaging of proteins within the MV. One possible
350 explanation for the increase in protein per MV may be that EVs released from virally
351 infected cells can package more proteins involved in suppressing the immune response
352 toward the virus and consequently enhancing viral spread. LMP1 also appears to play a
353 role in enhancing PD-L1 surface exposure in MVs. Enhanced PD-L1 surface levels
354 could depict the mechanism in which LMP1 contributes to immune suppression by
355 enhancing PD-L1-PD-1 interaction and T cell inactivation. LMP1 and PD-L1 also co-
356 migrate within the same density gradient, and immuno-isolation of this MV
357 subpopulation confirmed the presence of LMP1 in PD-L1 containing vesicles from an
358 LMP1 expressing NPC cell line. EGFR was also immuno-isolated within the same MV
359 with LMP1 and PD-L1. Recently, EGFR has been found to play a vital role in
360 upregulating PD-L1 once activated, mediating immune escape in non-small cell lung
361 cancer (71). LMP1 signaling occurs through localization in lipid rafts and by recruiting
362 key signaling components to internal lipid raft containing membranes (35, 72). Our
363 observations indicate that both LMP1 and PD-L1 colocalize perinuclearly within the cell
364 and are enriched in lipid rafts which suggests a similar signaling platform between these
365 two proteins, bringing together numerous signaling components that drive immune
366 evasion mechanisms, and facilitates their interaction. These findings lead us to
367 conclude that LMP1 might have different roles in different subpopulations of EVs, and

368 that LMP1 modified MVs may act as an instrumental component contributing to immune
369 suppression and evasion of EBV viral infected cells, by the enhanced packaging of
370 proteins into these MVs, with one of them being PD-L1.

371 Altogether, the above data suggests that EBV+ related diseases are largely dependent
372 on PD-L1 for disease progression and possibly immune protection, and identifies a
373 more specific target for treating these diseases. Therefore, any immunotherapy
374 treatments targeted at disrupting this pathway could lead to better outcomes for patients
375 suffering from EBV related diseases. One form of treatment for cancers that induce PD-
376 L1 expression is immunotherapy which serves to boost the immune antitumor response
377 and has fewer side effects than alternative cancer therapies, such as chemotherapy,
378 surgery, and radiation. FDA approved antibodies pembrolizumab (73) and nivolumab
379 (74) that target PD-1 and atezolizumab (75) that targets PD-L1, improve survival against
380 Hodgkin's lymphoma (73, 75). Anti-PD-1 antibody is effective in several other cancers,
381 such as glioblastoma (76), and metastatic melanoma (28). In addition to cancer, anti-
382 PD-1/PD-L1 treatment has also been considered as a possible treatment for patients
383 with dementia and Alzheimer's (77). Moreover, monoclonal antibodies targeting PD-1 or
384 PD-L1 are now in phase I-II trials as a therapeutic treatment for patients with
385 metastatic/recurrent NPC (78). Using anti-PD-1 or anti-PD-L1 ligands alone is usually
386 insufficient. Unfortunately, using several immune blockade therapies increases the
387 patient's likelihood of experiencing unwanted side effects (79).

388 Now that EBV's role in the regulation of PD-L1 has been established, exploring other
389 viral functions that might be inducing MV associated PD-L1, such as EBV microRNAs,

390 EBNA-1/2, and LMP1/2A should be investigated. Targeting both LMP1 and PD-L1
391 expressing MVs and small EVs in EBV+ tumors might lead to a synergistic inhibitory
392 effect on tumor growth and metastasis. Identifying post-treatment levels of MV levels of
393 PD-L1 with anti- PD-L1 blockade therapy could help distinguish patients who respond to
394 this specific type of therapy early on. Tumor genomic profiling is therefore necessary in
395 order to prescribe the most effective treatment that will confer the best results with the
396 least amount of toxicity and side effects to the patient. Additionally, determining the best
397 way to overcome PD-L1 blockade resistance and detect/target MV associated PD-L1
398 are the necessary next steps to take in the PD-L1 therapeutic research domain. These
399 results highlight the crucial role that MV associated PD-L1 might be playing in creating
400 an immunosuppressive environment that cancers and possibly other diseases exploit.
401 As more research on MV associated PD-L1 in EBV related cancers is conducted, its
402 vital role in facilitating tumor progression can be elucidated.

403 The results from this research contribute to the EV field and PD-L1 immune-targeted
404 therapies in several ways. Determining that MVs derived from EBV+ cell lines express
405 PD-L1, identifies a new therapeutic target in immune blockade therapy. Consequently,
406 determining whether PD-L1 localization is based on cell line, or on levels of LMP1 will
407 help clarify the mechanisms that promote immune suppression since PD-L1 surface
408 exposure is necessary for T cell inactivation. The next steps include determining the
409 immunosuppressive functions of MV surface expressed PD-L1 in EBV related cancers
410 and determining if they differ from PD-L1 function within small EVs. This
411 immunosuppressive contribution could equate to exosomal levels of PD-L1 or may play
412 a more vital role in immune suppression. In conclusion, we expect that our findings will

413 begin to clarify the mechanism of LMP1-mediated enhanced packaging of PD-L1 into
414 MVs and the functions of LMP1-modified MVs. In terms of clinical applications, it could
415 also serve as a potential therapeutic target or diagnostic biomarker for identifying
416 whether or not the patient will respond well to immunotherapy treatment and predict
417 tumor responses.

418

419 **Materials and Methods:**

420 **Retrovirus production.**

421 Retrovirus particles for transduction and stable cell generation were produced in HNE-1
422 cells following JetPrime transfection of expression plasmids (pBabe neo, pBabe-HA-
423 LMP1 neo) and packaging plasmids pMD2.G (Addgene; number 12259; a gift from
424 Didier Trono) and PSPAX2 (Addgene; number 12260; a gift from Didier Trono)
425 according to the manufacturer's instructions (Polyplus). Medium was collected at 48, 72,
426 and 96 h post-transfection, centrifuged for 10 min at 1,000 × *g*, filtered through a 0.45-
427 μm filter, and frozen at -80°C until use. Stable HNE1 cell lines expressing pBabe-HA-
428 LMP1 were created by retrovirus transduction as described above and were selected
429 and maintained in 1 mg/ml of G418 sulfate.

430 **Generation of GFP-LMP1-inducible cells**

431 HK1 cells that stably express GFP-LMP1 under control of a tetracycline-inducible
432 promoter were created by first being transduced with lentivirus particles containing
433 pLenti CMV TetR BLAST (Addgene; 17492) as previously described in (18). Stable cells
434 were selected with medium containing 10 μg/ml of blasticidin (InvivoGen; ant-bl-1) and
435 then transduced with retrovirus particles containing pQCXP GFP-LMP1. Doubly stable

436 cells were selected with medium supplemented with blasticidin (10 µg/ml) and
437 puromycin (2 µg/ml) for 2 weeks. LMP1 expression was induced for 24 h with the
438 addition of doxycycline to a final concentration of 1 µg/ml or 0.5 µg/ml.

439 **Cell culture.**

440 HNE1 cells were cultured in 1:1 mixture of Dulbecco modified Eagle medium (DMEM;
441 Lonza; 12-604Q) and Ham's F-12. HK1 (a gift from George Tsao, Hong Kong
442 University). All cell culture Medium was supplemented with 10% fetal bovine serum
443 (FBS; Seradigm; 1400-500), 2 mM L-glutamine (Corning; 25-005-CI), 100 IU of
444 penicillin-streptomycin (Corning; 30-002-CI), and 100 µg/ml:0.25 µg/ml
445 antibiotic/antimycotic (Corning; 30-002- CI). The cells were maintained at 37°C with 5%
446 CO₂.

447 **Transient Transfection**

448 HK1 grown in 100 mm plates were transfected with 5 µg of RFP-LMP1 or GFP-PD-L1
449 plasmid using Lipofectamine 3000 transfection kit (Invitrogen, L3000015). Lipofectamine
450 reagents were diluted in Opti-MEM medium (Gibco, 31,985–070) and added according
451 to manufacturer's instructions. Twenty-four hours after transfection, cells were
452 harvested and lysed in RIPA buffer, as previously described (25, 47). Cell-conditioned
453 medium was harvested for extracellular vesicle enrichment.

454 **Immunofluorescence assay**

455 Cells were stained as previously described (47). The coverslips were coated with poly-
456 L-lysine (Sigma; P1955) as according to manufacturer's instructions, then cells were
457 seeded. The next day, cells had GFP-LMP1 induced using 0.5 µg/ml of doxycycline.
458 The next day, cells were fixed in 100% ice-cold methanol or 4% paraformaldehyde for

459 10 minutes. Cells were then washed again with PBS 3 times before being permeabilized
460 with 0.2% Triton-X in PBS. Cells were then placed in a blocking buffer (5% goat serum
461 in PBS with 0.2% Tween [PBST]) for 30 minutes. Next, cells were stained with primary
462 antibodies in blocking buffer PD-L1 D8T4X (1:200) for 2 hours. Cells were washed 3
463 times in PBST then placed in secondary antibody rabbit IgG (A48254; Thermo Fisher)
464 diluted in the blocking buffer for 1 hour. Cells were washed 3 times with PBST before
465 being incubated with Red DNA stain (52406; ENZO) diluted in PBS for 10 minutes.
466 Cells were washed 2 times with PBS, and once with water before being mounted on a
467 glass slide with mounting medium (4% propyl gallate, 90% glycerol in PBS) for confocal
468 microscopy imaging. Confocal images were taken using a Zeiss LSM 880 microscope
469 and processed using Zen 2.1 Black software.

470 **Extracellular-vesicle enrichment.**

471 Extracellular vesicles were harvested from conditioned cell culture media by differential
472 centrifugation and polyethylene glycol (PEG) precipitation as previously described
473 (80),(81). Briefly, apoptotic bodies/cell debris (2K), microvesicles (10K), and small EVs
474 (100K) were harvested from cell-conditioned media by ultra-centrifugation at 2,000 RPM
475 for 10 min, 10,000 RPM for 30 min, and by the ExtraPEG method respectively.

476 **Protease Protection Experiment**

477 After the washing step the MV pellet is resuspended in a 1:1 ratio of 0.25% trypsin and
478 particle free PBS and left at 37°C for 30 minutes. This cleaves the surface membrane of
479 the EV sample. Antibodies: (PD-L1 E1J2J; Cell Signaling) for extracellular domain of
480 PD-L1, and (PD-L1 E1L3N; Cell Signaling) was used for endogenous levels of PD-L1.
481 Sample is then resuspended in lysis buffer for immunoblot analysis.

482 **Purification of membrane microdomains**

483 Lipid raft (LR) microdomains were harvested as previously described (82).

484 **Iodixanol density gradient.**

485 EVs from HK1 GFP-LMP1-inducible cells and HNE1-pBabe-HA-LMP1 cells harvested
486 by centrifugation for 10,000 \times g for 30 min were further purified on a density gradient,
487 according to the method of Kowal et al. (24). Briefly, EV pellets following the
488 centrifugation step were re-suspended in 1.5 ml of 0.25 M sucrose buffer (10 mM Tris
489 [pH 7.4]). A 60% stock (wt/vol) Optiprep (Sigma, D1556) solution was added 1:1 to EV
490 suspensions and transferred to an MLS-50 rotor tube (Beckman; 344057). Iodixanol
491 stock was then diluted in 0.25 M sucrose-Tris buffer to make 10% and 20% iodixanol
492 solutions, and then 1.3 ml of 20% iodixanol and 1.2 ml of 10% iodixanol solutions were
493 carefully layered on top of EV suspensions. Gradients were centrifuged for 90 min at
494 maximum MLS-50 rotor speed (268,000 \times g) and separated by collection of 490 μ l
495 fractions from the top of the gradient. Densities were measured with a refractometer
496 (Refracto 30PX). Individual fractions were washed with PBS and re-pelleted by
497 ultracentrifugation in an SW41 Ti rotor at 100,000 \times g for 2 h. Pellets were resuspended
498 in particle-free PBS for NTA or strong urea-containing lysis buffer for immunoblot
499 analysis.

500 **Immunoblot analysis.**

501 To prepare cell lysates, cells were washed and then scraped into cold PBS and
502 collected by centrifugation at 1,000 \times g for lysis in radio immune precipitation assay
503 (RIPA) buffer (20 mM Tris-HCl, 50 mM NaCl, 1% NP-40, 0.1% SDS, 0.5%
504 deoxycholate) with 1X proteinase inhibitor. EV samples were harvested as described

505 above. To prepare all cell lysates, and EV lysates run under reducing conditions for
506 SDS-PAGE, additional sample buffer (5x) also containing 0.2 M dithiothreitol (DTT) was
507 added to samples. Lysates were boiled for 5 min. An equal protein concentration or
508 equal volume of cell and EV lysate was run in an SDS 10% polyacrylamide gel and
509 subsequently transferred onto a nitrocellulose membrane (GE Healthcare). Total protein
510 was measured by Ponceau S stain. Blots were blocked with 5% (wt./vol.) nonfat dry milk
511 powder in Tris-buffered saline with Tween 20 (TBS-T). Blots were probed with primary
512 antibodies against the following: PD-L1 (E1L3N; Cell Signaling), Syntenin-1 (S-31;
513 Santa Cruz), HSC70 (B-6; Santa Cruz), Caveolin-1 (D46G3; Cell Signaling), CD63
514 (TS63; Abcam), LMP1 (CS1-4; Dako), CD81 (B399; GeneTex), CD9 (CBL162;
515 Millipore), CD71 (D7G9X; Cell Signaling), EGFR (SC-03; Santa Cruz). Blots were
516 subsequently probed with the following horseradish peroxidase (HRP)-conjugated
517 secondary antibodies: rabbit anti-mouse IgG (Genetex; 26728), or anti-mouse kappa
518 light chain (H139-52.1; Abcam). Blots were imaged using an ImageQuant LAS4000
519 (General Electric) and processed with ImageQuant TL v8.1.0.0 software, Adobe
520 Photoshop CS6, and Adobe illustrator.

521 **Nanoparticle tracking.**

522 Nanoparticle tracking analysis (NTA), a technology used to quantify nanoparticle
523 concentrations and sizes consistent with EV populations, was used to determine
524 increases in vesicle secretion and confirm size range of EV pellets following PD-L1
525 expression in cells. Following EV enrichment, vesicles were resuspended in particle-
526 free PBS for quantitation using a Malvern NanoSight LM10 instrument as previously
527 described in detail (83)(81). The camera level was set to 13, and the threshold was

528 maintained at 3 for all samples. The quantity of particles measured by NTA was
529 normalized to the number of live cells counted at the time of harvest to generate a
530 measure of the number of EVs secreted per cell. For nanoparticle tracking experiments,
531 live cells were counted with an automated cell counter (Cellometer Vision, software
532 version 2.1.4.2; Nexcelom Biosciences) at the time of harvest by staining with a 0.2%
533 final concentration of trypan blue (Sigma; T8154) in phosphate-buffered saline (PBS) in
534 a 1:1 ratio. Relative vesicle secretion was obtained by normalization of EV levels to
535 control cells in each experiment.

536 **Transmission electron microscopy.**

537 Following enrichment of EVs by the ExtraPEG method, pellets were resuspended in 100
538 μ l of particle-free PBS for electron microscopy imaging. Samples were prepared as
539 described by Lässer et al. (84) and visualized on an FEI CM120 transmission electron
540 microscope. For immunogold labelling, EV pellet was resuspended in anti-PD-L1
541 antibody (D8T4X; Cell Signaling) (1:60) in blocking buffer (1% BSA in PBS) for 2 hours.
542 The EV suspensions were applied to formvar/carbon-coated nickel grids 200 mesh for 3
543 min. Then grids were washed with 5 separate drops (50 μ l, 10 min per drop) of PBS
544 with 0.1% BSA. Transferred a drop of the secondary antibody conjugated to 10 nm gold
545 particle (Goat F(ab')₂ Anti-Rabbit IgG H&L (10nm Gold; ab39601) (1:100 in PBS with
546 0.1%BSA) to grids for 1 hour. Repeat washing steps. Next wash with 2 separate drops
547 of fresh MilliQ. Finally, negative stain with uranyl acetate for 1 min.

548 **Live cell imaging.**

549 HNE-1 cells were seeded into 35-mm glass well plates (Greiner Bio-One; number
550 627860), co-transfected 24 h later with 1 μ g of GFP tagged PD-L1 and RFP tagged

551 LMP1, and imaged 24 h post transfection using a Zeiss LSM 880 microscope with a
552 live-cell imaging chamber. Hoechst 33342 nuclear staining (5 µg/ml; Thermo Scientific;
553 number 62249) was added 15 min prior to imaging. Confocal images were taken and
554 processed using Zen 2.1 Black software.

555 **Immunoprecipitation**

556 The MV sample obtained after centrifugation was resuspended in 1%BSA in PBS. 100
557 µl of magnetic G beads were washed 3 times with (0.1%BSA in PBS). Rabbit (DA1E)
558 mAb IgG XP® Isotype Control or PD-L1 (Extracellular Domain Specific) (D8T4X)
559 antibodies were diluted in PBS with 0.1% BSA and then mixed with 1.0 µg magnetic
560 beads. The antibodies and magnetic beads were incubated with rotation for 20 min at
561 room temperature. This was followed by three washes with 0.1% BSA in PBS. The
562 Microvesicle sample was then added to the beads and left in the cold room for 3 hours
563 with rotation. This was followed by another three washes with 0.1% BSA in PBS.
564 Resuspended in 2x reducing buffer and then heat for 7 min at 90 °C before running on
565 gel for immunoblot analysis.

566 **Flow cytometry**

567 Microvesicles from HK1 or HK1-LMP1 cell were first blocked with flow buffer (1% BSA
568 in PBS) stained with either isotype control Ig or anti-PDL1 at 2g/mL for one hour at 4 °C.
569 After wash with flow buffer, samples were stained with PE conjugated anti-rabbit
570 antibody at 4 °C for 30 mins. Wash to remove unbound antibodies, samples were run on
571 FACSC onto flow cytometer (BD) in Translational lab College of Medicine FSU. The
572 data were analyzed by FACSDiva software (BD).

573 **RNA Isolation and Reverse Transcription**

574 Total RNA of cell or EV samples were isolated by Trizol reagent (ThermoFisher,
 575 15596018) and quantified by nanodrop. Less than 1 µg of total RNA was used for
 576 reverse transcription by qScript cDNA SuperMix (Quantabio, 95048). CDNAs were store
 577 in -20°C until further use.

578 Quantitative Real-Time PCR and Data analysis

579 Standard 3-step cycles protocol (40 cycles of 95 °C for 5 s, 60 °C for 10 s, 72 °C for 20 s)
 580 was used in all qPCR reactions. PerfeCTa SYBR Green FastMix (Quantabio, 95072-
 581 012), assay primers (250 nM) and cDNA (1.0 µL) of cell or EV were prepared in 20 µL
 582 reaction and run on CFX96 qPCR machine (Bio-Rad). Gene expression level were first
 583 normalized to housekeeping gene GAPDH and then calculated with $\Delta\Delta C_t$ method.

584 qPCR primer sequence:

Gene ID (Aliases)	Sequence	Reference Primer Bank ID
GAPDH	GGAGCGAGATCCCTCCAAAAT	378404907c1
	GGCTGTTGTCATACTTCTCATGG	
CD274 (PD-L1)	CCTACTGGCATTGCTGAACGCAT	PNAS December 30, 2008 105 (52) 20852- 20857
	ACCATAGCTGATCATGCAGCGGTA	
CD9	TTCCTCTTGGTGATATTCGCCA	319738657c2
	AGTTCAACGCATAGTGGATGG	
CD63	CAGTGGTCATCATCGCAGTG	91199544c1
	ATCGAAGCAGTGTGGTTGTTT	
CD81	TTCCACGAGACGCTTGACTG	62240999c2
	CCCGAGGGACACAAATTGTTC	

SDCBP (Syntenin-1)	TGGCTCCTGTA ACTGGTAATGA	55749522c2
	CTCAGACCAACCAATGAGGCT	
HRS	AACGACAAGAACCCACACGTC	315138978c2
	GGCCTGGATCAGGTACAGGA	

585

586 **Data and statistics analysis**

587 Statistical analysis was performed using the GraphPad Prism 8 (GraphPad Software, San
588 Diego, CA) or Microsoft Excel with a significant threshold of $p \leq 0.05$. Pearson correlation
589 coefficient (PCC) was determined using an ImageJ colocalization plugin, with a minimum of 10
590 cells analyzed. The ImageJ software (NIH) was used to calculate the CTCF by applying this
591 formula: CTCF = integrated density (indicated by the software)-(Area of selected cell x Mean
592 fluorescence of background readings), as previously described (85). Statistical significance of
593 results was evaluated by unpaired t test with Welch's correction. Figures were constructed using
594 Adobe illustrator.

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604 and D.G.M; project administration, D.G.M.; software, M.A. and L.S.; supervision,
605 D.G.M.; writing—original draft, M.A.; writing—review and editing, D.G.M. and L.S. All
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607 **Conflict of Interest**

608 The authors report no conflicts of interest. The funders had no role in the design of the
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861

862 **Figures:**

863 **Fig 1. LMP1 expression in NPC cells leads to enhanced PD-L1 levels in MVs.** Cell
864 lysates, 2K, 10K, and 100K were loaded at equal protein concentration of 20µg. (A and
865 B) Immunoblot analyses of HK1 GFP-tagged LMP1 and HNE-1 HA-tagged LMP1
866 demonstrate increased PD-L1 expression in the MV subpopulation compared to HK1

867 and HNE-1, respectively. (C and D) Quantification of 3 western blots from independent
868 experiments demonstrate significantly higher levels of PD-L1 expression in MVs
869 expressing LMP1 compared to control cell lines HK1 and HNE-1. (E and F)
870 Quantification of 3 western blots in NPC cells expressing LMP1 revealed significantly
871 higher levels of PD-L1 in the MVs compared to the other two EV subpopulations. **,
872 $P < 0.01$; *, $P < 0.05$.

873

874 **Fig 2. PD-L1 is upregulated at the transcriptional level in LMP1 expressing cells and is**
875 **detected in MVs.** RT-qPCR result of mRNA from normal HK1 cells or HK1 LMP1 induced
876 cells (A) and MVs (B). The results were normalized to GAPDH. ***, $P < 0.001$ **, $P < 0.01$; *,
877 $P < 0.05$.

878

879 **Fig 3. Characterization of MVs from NPC cells.** (A and B) MVs harvested by 10,000 RPM
880 spin from HK1 and HK1 LMP1 induced cells were examined by electron microscopy. (C-G)
881 Nanoparticle tracking analysis showed significant increase in particles/ml, microgram/particle,
882 mean, and mode size but not in particles/cell from MVs harvested from HK1 LMP1 cells
883 compared to HK1 control cells. ***, $P < 0.001$ **, $P < 0.01$; *, $P < 0.05$.

884

885

886 **Fig 4. LMP1 enhances PD-L1 MV-associated surface levels.** (A) Flow cytometry analysis on
887 MVs harvested from HK1 and HK1 LMP1 induced cells stained for either isotype control or PD-
888 L1 surface antibody. (B and C) PD-L1 immunogold labelling of HK1 and HK1 LMP1 MVs. (D)

889 Quantification of gold particles per MV from 10 HK1 and HK1 LMP1 induced MVs. (E and F)
890 Immunoblot analyses of HK1 LMP1 MVs with and without trypsin. Different PD-L1 antibodies
891 were used to probe for endogenous levels of PD-L1 (E) and extracellular domain specific PD-
892 L1 (F). CD71 and Syntenin-1 are used as negative and positive controls, respectively. **,
893 $P < 0.01$.

894

895 **Fig 5. LMP1 and PD-L1 localize within the same MV subpopulation.** (A) Immunoblot of
896 iodixanol density gradient fractions of HK1 LMP1 MVs demonstrating the presence of two
897 distinct populations enriched in LMP1, PD-L1, and Caveolin-1 corresponding to fractions (3
898 and 5), equal volumes loaded. (B) Immunoprecipitation of PD-L1, LMP1, and EGFR in HK1
899 LMP1 MVs. Equal volumes of control Rabbit IgG antibody, control rabbit IgG antibody and HK1
900 LMP1 MVs, and anti-PD-L1 antibody and HK1 LMP1 MVs were loaded. The first lane is 10%
901 of the HK1 LMP1 MV sample loaded for comparison.

902

903 **Fig 6. LMP1 and PD-L1 colocalize in NPC cells and are enriched in lipid rafts.** All confocal
904 images are Maximum Intensity Projections of Z-stacks, Scale bar: 10 μ m. (A) HNE-1 cells were
905 transfected with GFP-tagged PD-L1, RFP-tagged LMP1, and Hoechst nuclear stain, for live-
906 cell confocal microscopy. (C) HK1 GFP-tagged LMP1 cells induced or not induced with
907 doxycycline were fixed, stained for PD-L1 (Alexa Fluor plus 405) and Nuclear-ID Red DNA
908 stain and imaged by confocal microscopy. (B and D) Pearson's Correlation Coefficient for PD-
909 L1 and LMP1 in the HNE-1 transfected cells and induced HK1 LMP1 cells was measured in 10
910 cells with a value of around 0.7 and 0.8, respectively. (E) Induced HK1 LMP1 cells

911 demonstrate significantly higher PD-L1 fluorescence compared to un-induced cells.
912 Immunoblot analyses of whole cell lysates or lipid raft fraction of induced HK1 LMP1 cells or
913 HK1 control cells demonstrate lipid raft enrichment of LMP1, PD-L1, and Caveolin-1. ****,
914 $P < 0.0001$. CTCF=corrected total cell fluorescence.

915

Fig 1

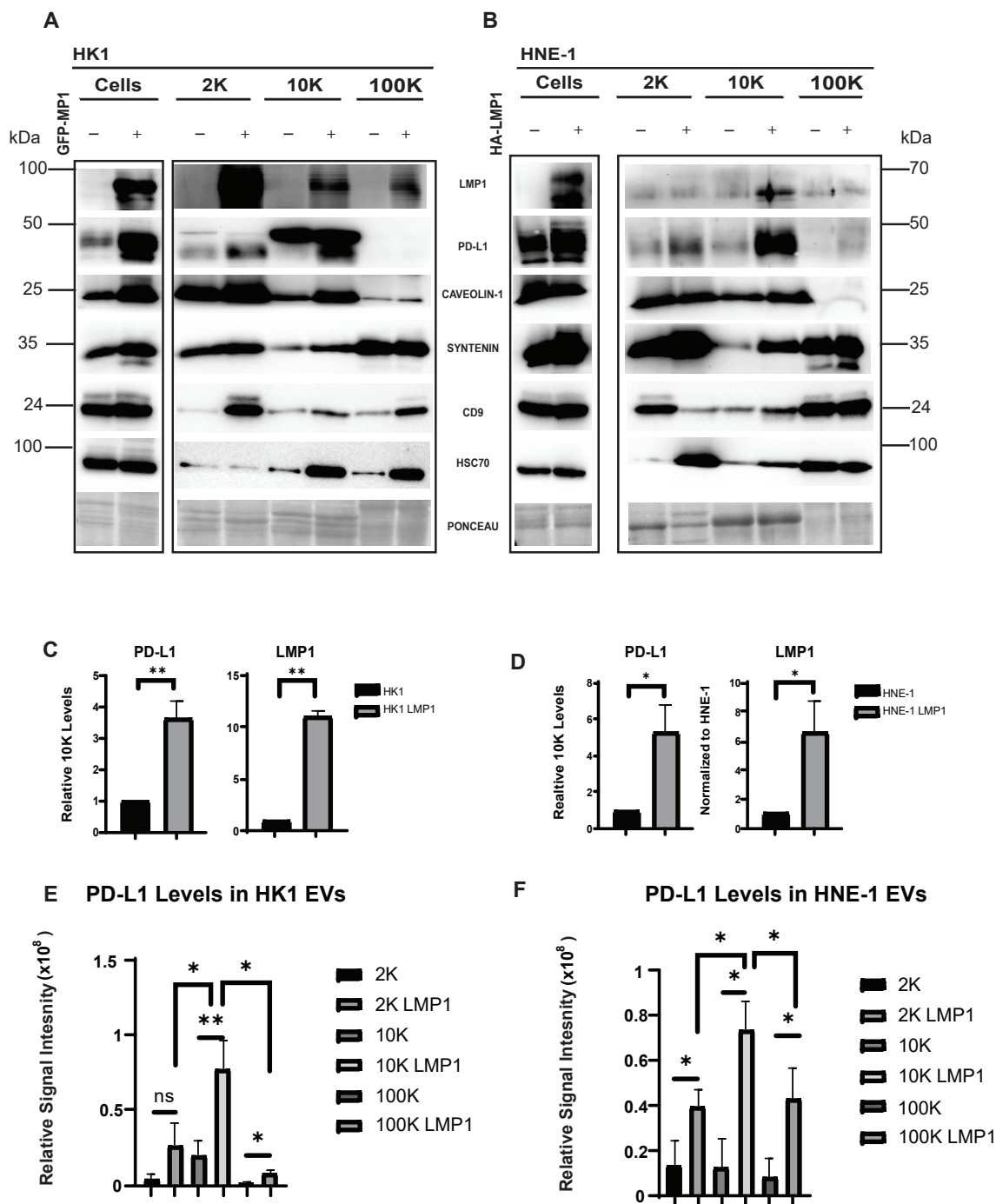


Fig 1. LMP1 expression in NPC cells leads to enhanced PD-L1 levels in MVs. Cell lysates, 2K, 10K, and 100K were loaded at equal protein concentration of 20µg. (A and B) Immunoblot analyses of HK1 GFP-tagged LMP1 and HNE-1 HA-tagged LMP1 demonstrate increased PD-L1 expression in the MVsubpopulation compared to HK1 and HNE-1, respectively. (C and D) Quantification of 3 western blots from independent experiments demonstrate significantly higher levels of PD-L1 expression in MVs expressing LMP1 compared to control cell lines HK1 and HNE-1. (E and F) Quantification of 3 western blots revealed significantly higher levels of PD-L1 in the MVs compared to the other two EV subpopulations. **, P<0.01; *, P<0.05.

Fig 2

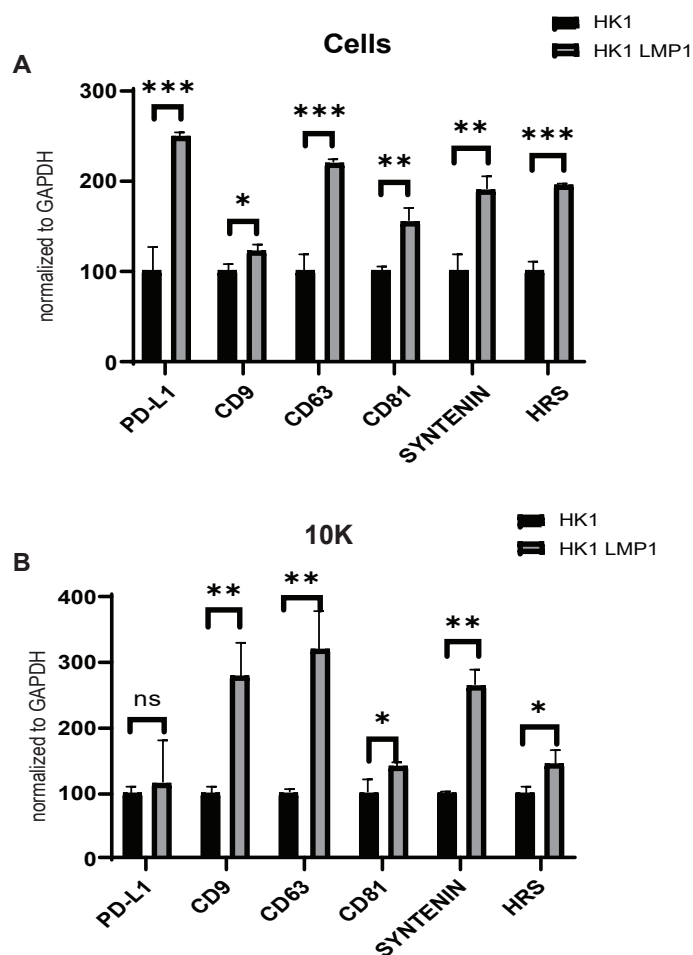


Fig 2. PD-L1 is upregulated at the transcriptional level in LMP1 expressing cells and detected in MVs. RT-qPCR result of mRNA from normal HK1 cells or HK1 LMP1 induced cells (A) and MVs (B). The results were normalized to GAPDH. ***, $P < 0.001$; **, $P < 0.01$; *, $P < 0.05$.

Fig 3

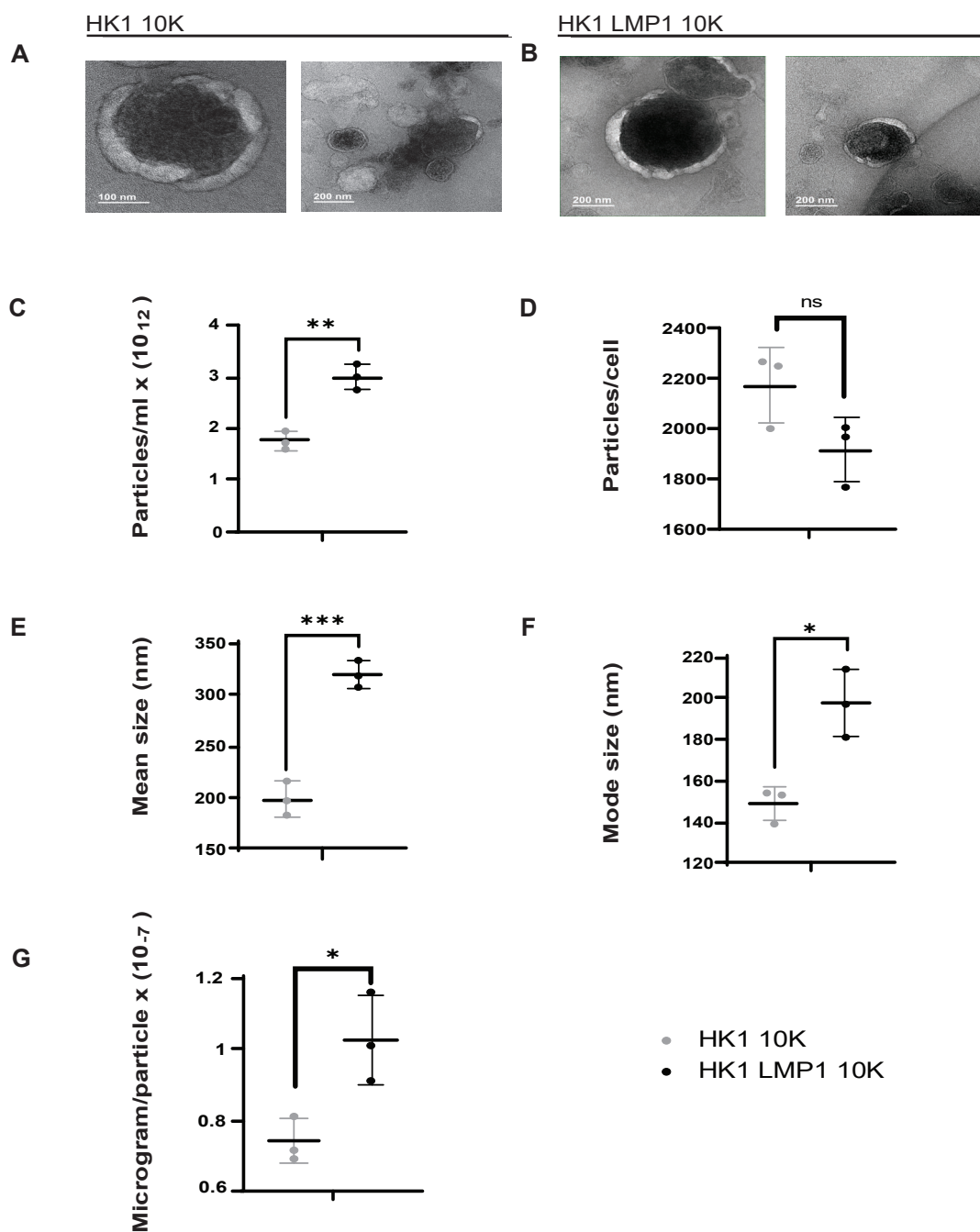


Fig 3. Characterization of MVs from NPC cells. (A and B) MVs harvested by 10,000 RPM spin from HK1 and HK1 LMP1 induced cells were examined by electron microscopy. (C-G) Nanoparticle tracking analysis showed significant increase in particles/ml, microgram/particle, mean, and mode size but not in particles/cell from MVs harvested from HK1 LMP1 cells compared to HK1 control cells. ***, P<0.001 **, P<0.01; *, P<0.05.

Fig 4

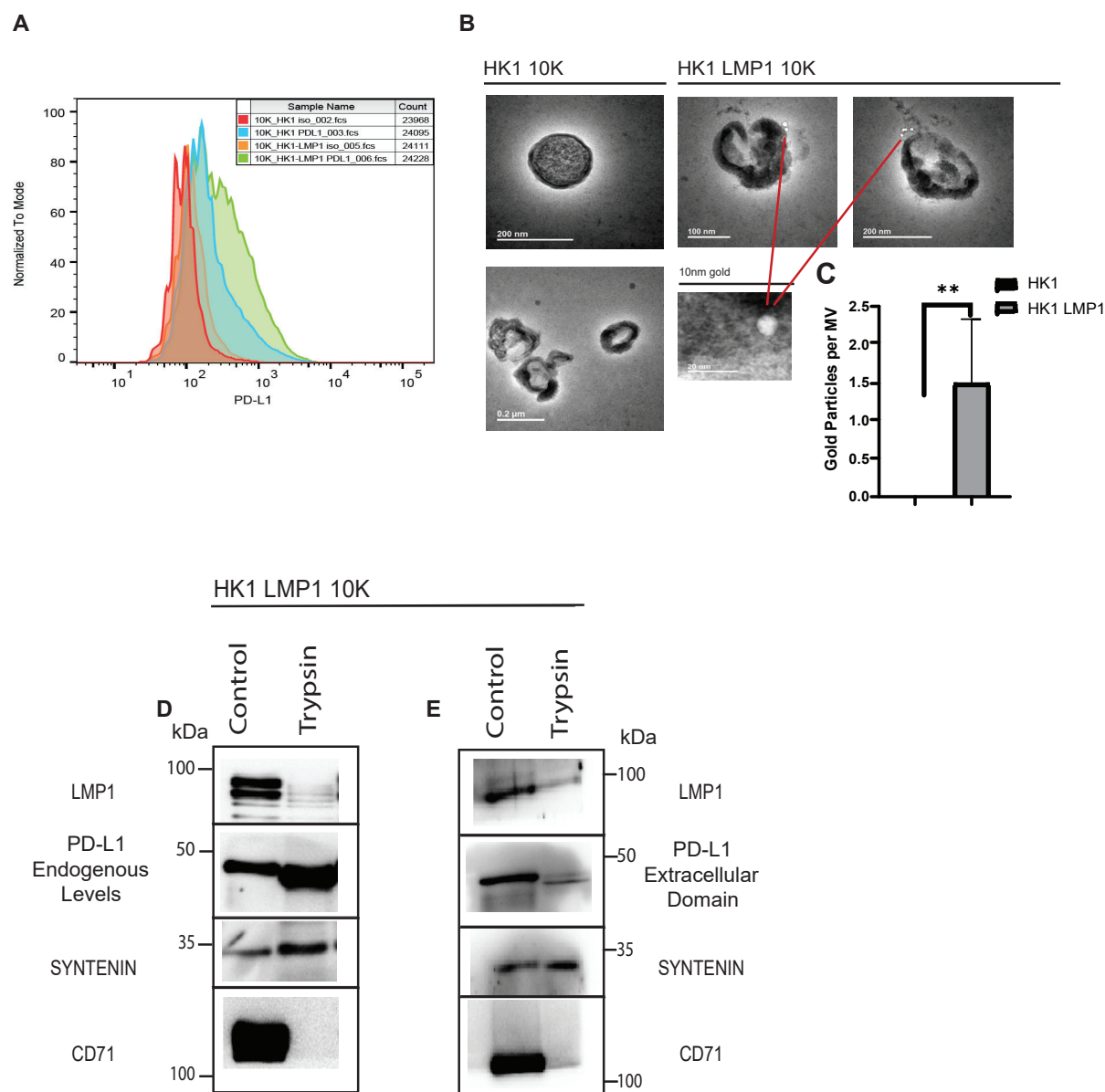


Fig 4. MV-associated PD-L1 surface expression is enhanced by LMP1 expression. (A) Flow cytometry analysis on MVs harvested from HK1 and HK1 LMP1 induced cells stained for either isotype control or PD-L1 surface antibody. (B and C) PD-L1 immunogold labelling of HK1 and HK1 LMP1 MVs. (D) Quantification of gold particles per MV from 10 HK1 and HK1 LMP1 induced MVs. (E and F) Immunoblot analyses of HK1 LMP1 MVs with and without trypsin. Different PD-L1 antibodies were used to probe for endogenous levels of PD-L1 (E) and extracellular domain specific PD-L1 (F). CD71 and Syntenin-1 are used as negative and positive controls, respectively. **, $P < 0.01$.

Fig 5

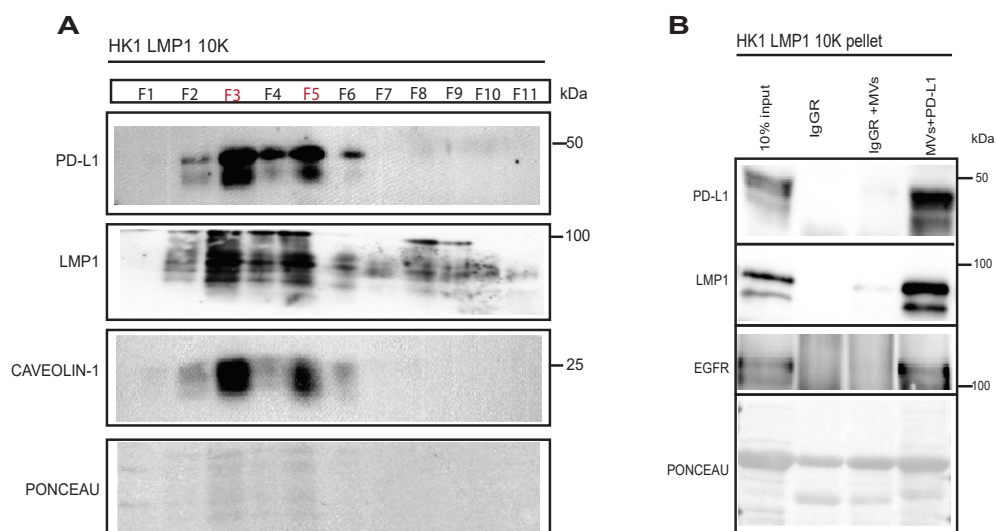


Fig 5. LMP1 and PD-L1 co-migrate and localize within the same MV subpopulation.

(A) Immunoblot of iodixanol density gradient fractions of HK1 LMP1 MVs demonstrating the presence of two distinct populations enriched in LMP1, PD-L1, and Caveolin-1 corresponding to fractions (3 and 5), equal volumes loaded. (B) Immunoprecipitation of PD-L1, LMP1, and EGFR in HK1 LMP1 MVs. Equal volumes of control Rabbit IgG antibody, control rabbit IgG antibody and HK1 LMP1 MVs, and anti-PD-L1 antibody and HK1 LMP1 MVs were loaded. The first lane is 10% of the HK1 LMP1 MV sample loaded for comparison.

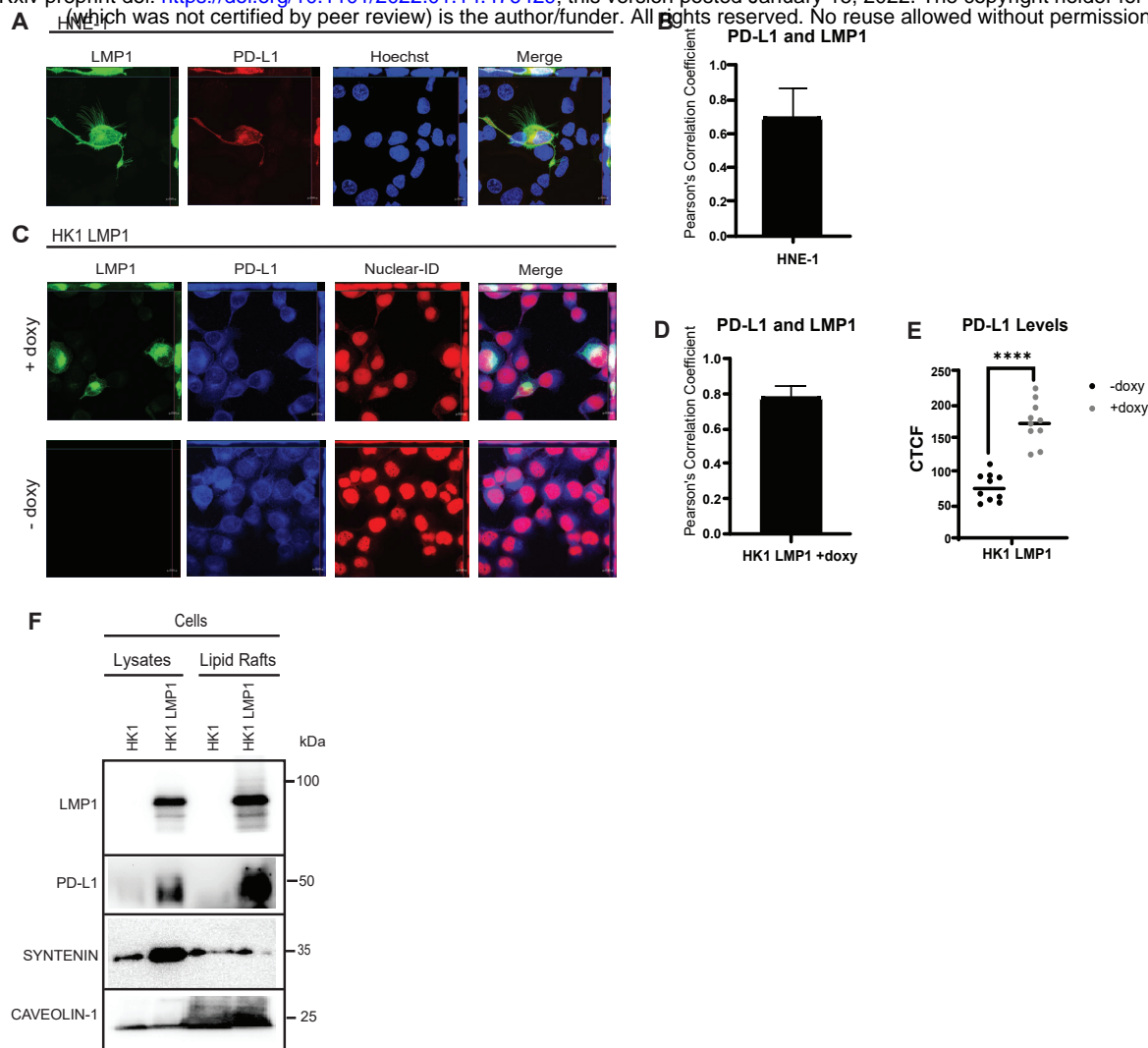


Fig 6. LMP1 and PD-L1 colocalize in NPC cells and are enriched in lipid rafts. All confocal images are Maximum Intensity Projections of Z-stacks, Scale bar: 10µm. (A) HNE-1 cells were transfected with GFP-tagged PD-L1, RFP-tagged LMP1, and Hoechst nuclear stain, for live-cell confocal microscopy. (C) HK1 GFP-tagged LMP1 cells induced or not induced with doxycycline were fixed, stained for PD-L1 (Alexa Fluor plus 405) and Nuclear-ID Red DNA stain and imaged by confocal microscopy. (B and D) Pearson's Correlation Coefficient for PD-L1 and LMP1 in the HNE-1 transfected cells and induced HK1 LMP1 cells was measured in 10 cells with a value of around 0.7 and 0.8, respectively. (E) Induced HK1 LMP1 cells demonstrate significantly higher PD-L1 fluorescence compared to un-induced cells. Immunoblot analyses of whole cell lysates or lipid raft fraction of induced HK1 LMP1 cells or HK1 control cells demonstrate lipid raft enrichment of LMP1, PD-L1, and Caveolin-1. ****, P<0.0001 CTCF=corrected total cell fluorescence.