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Metabolic and transcriptional modules independently diversify plasma cell lifespan and function

Wing Y. Lam
Washington University School of Medicine in St. Louis

Arijita Jash
Washington University School of Medicine in St. Louis

Cong-Hui Yao
Washington University in St. Louis

Lucas D’Souza
University of Arizona

Rachel Wong
Washington University School of Medicine in St. Louis

See next page for additional authors

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Authors
Wing Y. Lam, Arijita Jash, Cong-Hui Yao, Lucas D'Souza, Rachel Wong, Ryan M. Nunley, Gordon P. Meares, Gary J. Patti, and Deepta Bhattacharya
Metabolic and Transcriptional Modules Independently Diversify Plasma Cell Lifespan and Function

Graphical Abstract

Highlights

- Plasma cells with varying lifespans are distinguished by fluorescent glucose uptake
- Lifespan is associated with antibody secretion, autophagy, and nutrient uptake
- Endoplasmic reticulum stress responses are similar across all plasma cell subsets
- Conserved transcriptional changes are not observed in long-lived subsets

Authors

Wing Y. Lam, Arijita Jash, Cong-Hui Yao, ..., Gordon P. Meares, Gary J. Patti, Deepta Bhattacharya

Correspondence
deeptab@email.arizona.edu

In Brief

Plasma cell survival and the consequent duration of immunity vary widely with infection or vaccination. Lam et al. demonstrate that short- and long-lived plasma cells are distinguished by metabolic properties such as nutrient uptake. In contrast, very few conserved transcriptional changes are observed between plasma cells of varying longevity.
SUMMARY

Plasma cell survival and the consequent duration of immunity vary widely with infection or vaccination. Using fluorescent glucose analog uptake, we defined multiple developmentally independent mouse plasma cell populations with varying lifespans. Long-lived plasma cells imported more fluorescent glucose analog, expressed higher surface levels of the amino acid transporter CD98, and had more autophagosome mass than did short-lived cells. Low amino acid concentrations triggered reductions in both antibody secretion and mitochondrial respiration, especially by short-lived plasma cells. To explain these observations, we found that glutamine was used for both mitochondrial respiration and anaplerotic reactions, yielding glutamate and aspartate for antibody synthesis. Endoplasmic reticulum (ER) stress responses, which link metabolism to transcriptional outcomes, were similar between long- and short-lived subsets. Accordingly, population and single-cell transcriptional comparisons across mouse and human plasma cell subsets revealed few consistent and conserved differences. Thus, plasma cell antibody secretion and lifespan are primarily defined by non-transcriptional metabolic traits.

INTRODUCTION

Upon infection or vaccination, naive B cells become activated by foreign antigens, and a subset of these cells differentiate into antibody-secreting plasma cells. Once formed, plasma cells secrete antibodies constitutively as long as they live (Manz et al., 1998; Sifka et al., 1998). Because these antibodies preexist subsequent exposures to pathogens, plasma cells have the ability to provide sterilizing immunity and prevent re-infection. As a result, plasma cells and the antibodies they produce are the primary determinants of humoral immunity following vaccination (Zinkernagel and Hengartner, 2006). The transience of plasma cell persistence and consequent antibody production is the major reason for the loss of immunity against infectious diseases such as malaria (Weiss et al., 2010; White et al., 2015). Reciprocally, long-lived plasma cells pose a major problem in certain autoimmune disorders and are the cell of origin in multiple myeloma (Winter et al., 2012). A mechanistic understanding of plasma cell survival may provide additional targets for the above disorders.

In T cell-dependent reactions, an initial wave of extrafollicular plasma cells tends to be relatively short-lived and produces germline-encoded antibodies (Sze et al., 2000). These cells form an early response to provide partial control of the infection until plasma cells encoding higher affinity antibodies emerge later from the germinal center reaction. As the germinal center progresses, there is a concomitant increase in both the affinity of the encoded antibodies as well as in the lifespans of the selected plasma cells (Weisel et al., 2016). Yet germinal centers are not required per se for the formation of long-lived plasma cells. T cell-independent responses, which yield neither germinal centers nor robust immunological memory, can also yield plasma cells of extended lifespans, as well as a proliferative subset of antibody-secreting cells that together maintain serum antibodies long after immunization (Bortnick et al., 2012; Reynolds et al., 2015; Savage et al., 2017). These and other data demonstrate substantial functional heterogeneity in ontogeny and lifespan within the plasma cell compartment (Amanna et al., 2007), but the underlying molecular basis is unclear.

We reasoned that coupling specific metabolic and transcriptional properties in conjunction with other markers would allow for prospective separation of new plasma cell subsets with a range of lifespans. This in turn would allow for an assessment...
RESULTS

Prospective Separation of Developmentally Distinct Plasma Cell Subsets with Varying Lifespans

We reasoned that prospectively separating plasma cells into functionally distinct groups would provide a cellular foothold to define pathways that regulate lifespan. Intracellular staining for immunoglobulin \( k \) (Igk) demonstrated very high levels of antibodies in almost all CD138\textsuperscript{high} cells (Figure S1A). We further separated polyclonal CD138\textsuperscript{+} plasma cells in the spleen and bone marrow, formed in response to natural infections in the colony, based on uptake of 2-((N-(7-nitrobenz-2-oxa-1,3-diazol-4-yl)amino)-2-deoxyglucose (2NBDG), a fluorescent glucose analog (Yoshioka et al., 1996), and expression of B220, which marks relatively short-lived and/or proliferative and immature cells (Chernova et al., 2014; Kallies et al., 2004). Using these criteria, splenic plasma cells could be readily separated into four distinct subsets (Figure S1B). Although all plasma cells imported 2NBDG above background levels, for simplicity we designate the subsets gated as in Figure S1B as either 2NBDG\textsuperscript{−} or 2NBDG\textsuperscript{+}. Bone marrow plasma cells were dominated by the B220\textsuperscript{−}2NBDG\textsuperscript{+} subset, whereas the other subsets were too rare to work with easily (Figure S1B). Therefore, the B220\textsuperscript{−}2NBDG\textsuperscript{+} subset was specifically purified for all subsequent analyses of bone marrow plasma cells.

To quantify the half-lives of plasma cell subsets, we performed pulse-chase experiments using bromodeoxyuridine (BrdU). Mice were provided BrdU in the drinking water for 1 week, followed by either 0, 1, or 2 weeks of water without BrdU (Figure 1A). Animals were then injected with 2NBDG and sacrificed 15 min later. The splenic B220\textsuperscript{−}2NBDG\textsuperscript{−} subset demonstrated the shortest half-life of approximately 3–4 days, followed by the B220\textsuperscript{−}2NBDG\textsuperscript{+} subset (4–6 days), B220\textsuperscript{+}2NBDG\textsuperscript{+} cells (5–18 days), B220\textsuperscript{−}2NBDG\textsuperscript{−} cells (8–12 days), and bone marrow (BM) plasma cells, which showed no turnover during this limited 3-week experiment (Figure 1A). For B220\textsuperscript{−}2NBDG\textsuperscript{−} and B220\textsuperscript{−}2NBDG\textsuperscript{+} cells, the BrdU decay rates varied between weeks 2 and 3. These data suggest additional heterogeneity within these subsets, with a fraction of cells that either proliferate or die rapidly, and another subset that persists more durably without division. Thus, plasma cells that import high levels of 2NBDG have longer half-lives than do their 2NBDG\textsuperscript{−} counterparts.

Loss of BrdU retention during the chase period could have been caused by death, proliferation, or differentiation to a distinct plasma cell subset. To distinguish between these possibilities, we first quantified antigen-specific plasma cell numbers over time in each subset after immunization with alum-adjuvanted 4-hydroxy-3-nitrophenylacetyl-ovalbumin (NP-OVA), a T cell-dependent antigen. The initial NP-specific response at 1 week was dominated by the 2NBDG\textsuperscript{−} groups, with nearly 80% of antigen-specific plasma cells contained within B220\textsuperscript{−}2NBDG\textsuperscript{−} and B220\textsuperscript{−}2NBDG\textsuperscript{+} subsets (Figure 1B). Nevertheless, NP-specific cells could also clearly be found within the B220\textsuperscript{−}2NBDG\textsuperscript{+} and B220\textsuperscript{+}2NBDG\textsuperscript{−} subsets (Figure 1B), suggesting the contemporaneous generation of each of these four plasma cell populations. At these early time points, very few NP-specific bone marrow plasma cells were found (data not shown). Subsequent weeks revealed that NP-specific cells were rapidly lost from the 2NBDG\textsuperscript{−} subsets, whereas after an initial decay, antigen-specific cell numbers were relatively stable in both 2NBDG\textsuperscript{−} subsets (Figure 1B). These data mirror the BrdU pulse-chase experiments above and suggest that the major portion of plasma cell turnover in each of these subsets is driven by death. Moreover, the contemporaneous formation of multiple plasma cell subsets argues against a strict developmental hierarchy between these groups.

Initial efforts to determine whether plasma cell subsets can interconvert failed because of poor cell recovery after adoptive transfer. Therefore, as an alternative approach, we quantified CD93 expression. CD93 is a marker of developmental maturity and is itself required for long-term maintenance of plasma cells (Chevrier et al., 2009). The percentage of CD93\textsuperscript{+} cells was somewhat lower in 2NBDG\textsuperscript{−} plasma cell subsets, but each subset displayed a substantial fraction of mature CD93\textsuperscript{+} cells (Figure 1C). These data again suggest that each plasma cell subset defined by B220 expression and 2NBDG uptake is formed and matures independently of one another.

To further examine the developmental relationships between plasma cell subsets, we performed immunoglobulin repertoire sequencing of polyclonal populations. Within the immunoglobulin G (IgG) isotypes, we observed very little overlap (<10% for most comparisons) between B220\textsuperscript{−} and B220\textsuperscript{−} subsets, both within the spleen and bone marrow (Figures 1D and S1C). These data are consistent with previous studies demonstrating differential light chain usage between B220\textsuperscript{−} and B220\textsuperscript{−} subsets (Chernova et al., 2014). IgM-expressing plasma cells showed somewhat more overlap (15%–25%) between all subsets (Figures 1D and S1C). Although this may reflect somewhat more interconversion across immunoglobulin M\textsuperscript{+} (IgM\textsuperscript{+}) plasma cell subsets, it seems likely that this overlap occurs because these cells arise from precursor B-1 cells (Savage et al., 2017), which have relatively restricted repertoires (Yang et al., 2015). Within the B220\textsuperscript{−} or B220\textsuperscript{−} subsets, we observed 15%–20% overlap between CDR3 nucleotide sequences of 2NBDG\textsuperscript{−} and 2NBDG\textsuperscript{+} cells (Figures 1D and S1C). Two of the most diverse subsets were the B220\textsuperscript{−}2NBDG\textsuperscript{−} IgG and the B220\textsuperscript{−}2NBDG\textsuperscript{+} IgG groups (Figure S1D). Despite their diversity, these two populations showed the most overlap (~25%) of all sets of comparisons (Figure 1D). Reciprocally, the bone marrow IgG group was among the least diverse (Figure S1D), yet showed minimal overlap with any other subset in the same animal (Figure 1D). Thus, it does not appear that diversity per se artificially suppresses the clonal overlap between two groups. These data suggest that developmental interconversion might account for a minor portion of ontogeny, but that the majority of plasma cell immunoglobulin sequences in each subset are unique. We conclude that fluorescent glucose uptake can be used to purify plasma cells of...
Figure 1. Glucose Uptake Correlates with Long Half-Lives in Plasma Cell Subsets

(A) Mice were fed BrdU in the drinking water for 1 week and assessed for incorporation and retention at 0, 1, and 2 weeks post-BrdU withdrawal. Half-lives of each plasma cell population were calculated at weeks 1 and 2 of the chase period and are shown above each dataset. Data are cumulative from two independent experiments. Mean values ± SEM are shown.

(B) Mice were immunized with NP-OVA, and antigen-specific plasma cells were assessed 1, 2, and 3 weeks thereafter. Example flow cytometric plots (left) and quantification (right) are shown from CD138-enriched cells and surface NP staining. Data are cumulative from two independent experiments. Mean values ± SEM are shown, as are the fold decreases relative to the previous time point.

(C) Representative CD93 staining of each plasma cell subset is shown to the left. Cumulative data from two independent experiments are shown to the right. Each data point represents cells from one mouse, and subsets from the same mouse are connected by lines. *p < 0.05, by paired one-way ANOVA with post hoc Tukey’s multiple comparisons test.

(D) Heatmap showing percent clonal overlap between CDR3 nucleotide sequences of plasma cell populations. Plasma cell populations were sorted and immunoglobulin heavy chain VDJ sequences were amplified with common V region primers and either Cm- or pan-Cγ-specific primers. Heatmap is derived from one individual mouse out of a total of three analyzed. Data from the remaining mice are shown in Figure S1.
differing lifespans and to help define other pathways that regulate survival, independently of developmental relationships.

Amino Acids Are Limiting for Plasma Cell Respiration and Antibody Secretion

Imported glucose is used both to glycosylate antibodies and to provide spare respiratory capacity, thereby allowing long-lived plasma cells to survive (Lam et al., 2016). This suggests a model in which the very nutrients used to synthesize immunoglobulins are also used to promote survival and energy metabolism in antibody-secreting cells (Lam and Bhattacharya, 2018). To extend upon this model, we assessed plasma cell metabolism of amino acids. We first assessed CD98/SLC3A2 expression, a common subunit for many amino acid transporters (Mastroberardino et al., 1998), and thus a marker of amino acid availability. CD98 expression is controlled by the transcription factor BLIMP1 and thus is very high in plasma cells (Shi et al., 2015; Tellier et al., 2016). CD98 deficiency leads to severe antibody defects, mostly as a function of its adhesion domain being required for activated B cell proliferation (Cantor et al., 2009), but amino acid transport is likely to be essential at the plasma cell stage (Tellier et al., 2016). 2NBDG− plasma cells expressed modestly but consistently lower cell surface levels of CD98 than did 2NBDG+ cells (Figure 2A). This difference was not simply a function of cell size, because B220+2NBDG−, B220+2NBDG+, and bone marrow plasma cells all showed comparable forward scatter measurements (Figure S2). Amino acids can also be derived intrinsically by autophagy as cellular components are recycled. Although autophagy is normally inversely correlated with extra-cellular amino acid uptake, 2NBDG− plasma cells modestly but consistently stained more brightly with a dye that marks autophagosomes (An et al., 2017) than did 2NBDG+ cells (Figure 2B). These autophagy data are consistent with previous human plasma cell studies (Halliley et al., 2015).

The changes in CD98 expression and autophagy dye staining were subtle and of unclear functional significance. Moreover, many amino acids are transported independently of CD98 and would not be accounted for in these analyses. Therefore, we sought to perform functional assays to test the sensitivity of plasma cell subsets to extracellular amino acid concentrations. Plasma cells that are genetically deficient in autophagy display reduced levels of ATP (Pengo et al., 2013), suggesting that 2NBDG− cells may also display reduced energy metabolism when amino acids are limiting. Indeed, a retrospective analysis of our previous work revealed that primary plasma cells assayed under physiological amino acid concentrations have lower levels of respiration than cells in standard RPMI media (Figure 2C), which have supraphysiological concentrations of amino acids (Lam et al., 2016). This difference was most pronounced in 2NBDG− plasma cells (Figure 2C). To determine whether amino acid availability also limits antibody secretion by plasma cells, we cultured each subset with physiological or supraphysiological concentrations of amino acids in otherwise identical media. A clear association was observed between elevated amino acid concentrations and antibody production (Figure 2D).

![Figure 2. Amino Acids Are Limiting for Plasma Cell Respiration and Antibody Secretion](image-url)
concentrations and antibody secretion rates in most subsets (Figure 2D). 2NBDG+ plasma cells continued to secrete more antibodies than did 2NBDG− cells under both low- and high-amino acid conditions (Figure 2D). This enhanced secretion by 2NBDG+ cells occurred despite apparently elevated levels of autophagy (Figure 2C), which is known to limit immunoglobulin production (Pengo et al., 2013).

Previous studies on myeloma cell lines have demonstrated that glutamine catabolism is essential for energy metabolism, amino acid production, and survival (Garcia-Manteiga et al., 2011; Thompson et al., 2017). 13C-glutamine tracing experiments on primary human long-lived plasma cells demonstrated robust contributions to glutamate and aspartate synthesis, and labeled carbons were readily observed in the tricarboxylic acid (TCA) cycle intermediates malate and fumarate (Figure 3A). However, no label was detected in citrate or aconitate (Figure 3A).

Thus, glutamine is used for anaplerotic reactions to generate glutamate and aspartate (Figure 3B). By contributing to succinate oxidation, glutamine also provides electrons for respiration (Lehniger et al., 2013). Although glutamine alone is unlikely to account for the entirety of the link, these data confirm that the same nutrients used to maintain mitochondrial function are also used to generate the amino acid building blocks for immunoglobulin synthesis. It is also likely that amino acid availability promotes antibody secretion through other mechanisms aside from immunoglobulin translation (Zacharogianni et al., 2011).

ER Stress Responses Are Similar across Plasma Cell Subsets

To define how metabolic modules integrate with transcriptional outputs, we first focused on ER stress responses, which can link these pathways. 13C tracing experiments in human bone marrow plasma cells revealed that a substantial portion of uridine diphosphate N-acetylglucosamine (UDP-GlcNac), a precursor to glycosylation sugars, is generated by import of extracellular glucose (Figure S3). Reductions in protein glycosylation and subsequent misfolding of antibodies trigger ER stress responses in plasma cells (Hickman et al., 1977). Given that short-lived plasma cells import relatively little glucose, we reasoned that they may underglycosylate proteins and antibodies, and thus be subject to more ER stress than are their long-lived counterparts. ER stress responses are necessary for high levels of antibody secretion, but they can also limit the lifespan of plasma cells (Auner et al., 2010; Reimold et al., 2001).

Splicing of XBP1 to XBP1s by IRE1α, cleavage of ATF6α into an active transcription factor, and phosphorylation of eIF2α by eukaryotic translation initiation factor 2 alpha kinase 3/protein kinase R-like endoplasmic reticulum kinase (EIF2AK3/PERK) represent the three arms of the ER stress response (Ron and Walter, 2007). Expression of ATF6α targets, such as HSPA5, varied
slightly across subsets, with the lowest levels in B220+2NBDG- and bone marrow plasma cells (Figure 4A), but XBP1s and downstream targets such as EDEM1 were similarly expressed by all groups (Figure 4A). This analysis revealed no significant changes in ER stress responses that correlated with 2NBDG uptake and, as a result, with lifespan (Figure 4A). Previous studies have suggested that caspase-12 activation might promote ER stress-dependent apoptosis in short-lived plasma cells (Auner et al., 2010). Yet cleavage of a caspase-12 substrate was similar across all plasma cell subsets (Figure 4B). These data demonstrate that the XBP1s and ATF6α-dependent ER stress pathways are similar between short- and long-lived plasma cells. We next examined the remaining ER stress pathway, mediated by phosphorylation of elf2α. Although previous studies using in vitro cultures found minimal phosphorylation of elf2α (Ma et al., 2010), we observed clear activation of this pathway in all plasma cell subsets ex vivo (Figure 4C). B220+ plasma cells displayed slightly elevated levels of p-elf2α relative to their B220- counterparts (Figure 4C). However, no changes were observed in p-elf2α as a function of 2NBDG uptake (Figure 4C).

We considered the possibility that short-lived plasma cells succumb to apoptosis because of a relative inability, rather than an excessive propensity, to mount ER stress responses. Neither XBP1 nor ATF6α are required for plasma cell survival (Aragon et al., 2012; Taubenheim et al., 2012), yet the necessity of elf2α phosphorylation in plasma cells in vivo remains unresolved (Gass et al., 2008; Mielke et al., 2011; Scheuner et al., 2001). Therefore, we first defined the relevant kinases involved in elf2α phosphorylation in plasma cells. We isolated human bone marrow plasma cells, due to their abundance, and examined the effects of pharmacological inhibitors of each of the kinases involved in elf2α phosphorylation (Ron and Walter, 2007). Inhibition of PERK, but not of general control nonderepressible 2 (GCN2), protein kinase R (PKR), or Heme-regulated inhibitor (HRI), completely eliminated p-elf2α (Figure 4D). Thus, PERK is solely responsible for elf2α phosphorylation in plasma cells.

Consistent with previous in vitro-generated plasma cells in lipopolysaccharide (LPS) cultures (Gass et al., 2008), we observed no effect of PERK inhibition on survival or antibody...
secretion ex vivo (Figures S4A and S4B). To test the importance of PERK for plasma cell survival in vivo, we utilized conditional Perkfl/fl mice crossed to transgenic animals ubiquitously expressing tamoxifen-inducible CreERT2 (Guthrie et al., 2016). Equal numbers of CD45.2 Perkfl/fl or Perkfl/fl CAGG-CreERT2 bone marrow cells were mixed with wild-type competitor CD45.1 bone marrow cells and transplanted into irradiated CD45.1 recipients. At 8 weeks post-transplant, mice were given tamoxifen-containing chow for 2 weeks. CD45.2 chimerism was then measured of B lymphocytes and plasma cells formed in response to natural infections in the colony. Chimerism of splenic B cells was similar irrespective of Perk genotype (Figure 4E). Within the plasma cell subsets, we observed a small but consistent reduction in PERK-deficient B220−2NBDG− and B220−2NBDG+ plasma cells relative to controls (Figures 4E and S4C). In contrast, no statistically significant reductions were observed in PERK-deficient B220−2NBDG− or B220−2NBDG+ plasma cells (Figure 4E). Bone marrow plasma cell chimerism was also similar between genotypes, but we were unable to confirm efficient deletion of Perk in these cells (Figure S4D). These data demonstrate that PERK promotes either survival or formation of B220+ plasma cells in vivo. However, this dependency on PERK is not correlated with glucose uptake, and thus fails to explain inherent differences in survival between plasma cell subsets.

ER stress in 2NBDG− cells could potentially be mitigated by reducing overall rates of protein and antibody production. Indeed, examination of electron micrographs revealed no consistent alterations in ER lumenal distension (Figures S5A and S5B), a marker of misfolded protein accumulation (Oslowski and Urano, 2011). Each plasma cell subset also displayed similar total levels of Igκ protein and mRNA (Figures 5A and S5C). To test whether the rates of protein translation differ between cell types, we employed in vivo ribopuromycylation in which puromycin is incorporated into nascent polypeptides, leading to chain termination (Seedhom et al., 2016). Mice were injected with puromycin and 2NBDG, sacrificed 15 min later, and intracellular...
levels of puromycin were measured. All plasma cell subsets had similar levels of puromycin labeling, and there was no correlation between 2NBDG uptake and translation rates (Figure 5B). Consistent with these findings, each subset displayed similar levels of phosphorylated S6 (Figure S5D), a marker of mammalian target of rapamycin (mTOR) activation, which promotes translation and antibody synthesis in plasma cells (Jones et al., 2016). Together, these data demonstrate that despite marked differences in glucose uptake, no compensatory changes are engaged in plasma cell subsets to modulate immunoglobulin synthesis and protein translation.

Another mechanism that could mitigate stress responses is protein degradation. To quantify the rates of antibody turnover, we treated plasma cells with the protein translation inhibitor cycloheximide for 24 hr and quantified intracellular levels of Igκ. Although Igκ light chain itself is infrequently glycosylated, it is degraded unless paired with properly folded and glycosylated immunoglobulin heavy chain isotypes (Chillarón and Haas, 2000). As in Figure 5A, antibody levels were similar in all subsets in the untreated control group (Figure 5C). Upon cycloheximide treatment, however, both 2NBDG⁻ subsets showed a substantial loss in Igκ relative to their 2NBDG⁺ counterparts (Figure 5C). The loss of antibodies in 2NBDG⁻ plasma cells after cycloheximide could be driven by degradation or by antibody secretion. However, consistent with Figure 2D, 2NBDG⁻ cells secreted substantially fewer antibodies than did their 2NBDG⁺ counterparts (Figure 5D). Thus, 2NBDG⁻ plasma cells degrade antibodies more rapidly than do their 2NBDG⁺ counterparts, and this may be a mechanism by which they avoid excessive ER stress.

Transcriptional Profiles Are Similar between Plasma Cell Subsets

Given that ER stress responses were similar between short- and long-lived plasma cell subsets, we examined the global transcriptional profiles of these subsets in an unbiased way to identify other genes that are correlated with glucose uptake and lifespan. After excluding immunoglobulin genes, RNA-sequencing (RNA-seq) comparisons of short-lived B220⁻2NBDG⁻ and long-lived B220⁻2NBDG⁺ plasma cells revealed remarkably similar transcriptional profiles. A total of 29 genes, representing 2486 genes consistently elevated in mouse 2NBDG⁺ plasma cells and genes elevated in human long-lived plasma cells (Figure 6D). Thus, we find no evidence for an evolutionarily conserved transcriptional signature associated with enhanced glucose uptake or plasma cell longevity.

Pathway overrepresentation analyses on individual comparisons between plasma cell subsets revealed elevations in cell-cycle gene expression in B220⁻2NBDG⁻ cells and, unexpectedly, an elevation in neutrophil degranulation genes in bone marrow plasma cells (Figure 6E). This was surprising given that Ly6g and CD11c-expressing neutrophils and other myeloid cells were specifically excluded from the cells sorted for RNA-seq. Because the levels of transcripts for many of these neutrophil degranulation genes were low, the data suggested that potentially only a subset of plasma cells expressed this unusual signature.

Single-Cell RNA-Sequencing Reveals Plasma Cell Subsets with Distinct Isotypes and Antimicrobial Peptide Expression

We next performed single-cell RNA-seq on approximately 1,000 cells of each plasma cell subset to define transcriptional heterogeneity. Igκ constant region transcripts represented an average of 30% of the total transcriptome of each cell (Figure S6A; consistent with previous plasma cell RNA-seq studies (Shi et al., 2015). Other plasma cell markers including IGJ (Rinkenberger et al., 1996), LY6A/E (Wilmore et al., 2017), TNFRSF13B (Pracht et al., 2017), and XBP1 (Reimold et al., 2001) were highly expressed, confirming the identity and purity of these cells (Figures S6A and S6B).

After excluding immunoglobulin transcripts, t-distributed stochastic neighbor embedding (t-SNE) analysis on concatenated sequences revealed nine clusters (Figure 7A). Three hundred fifty-two genes were preferentially expressed (p < 0.1, t test with Benjamini-Hochberg correction for multiple tests) by at least one cluster relative to the rest of the population. Pearson distance measurements using this set of genes revealed that clusters 9 and 6 were related and distinct from each of the other clusters (Figure 7B). The remaining clusters were distinguished from one another by a much smaller group of genes (Figure 7B). We next overlaid data points from each plasma cell population onto the t-SNE plot to determine the composition of each subset and cluster (Figure 7C). The B220⁻2NBDG⁻ subset, which is the shortest lived plasma cell population (Figure 1A), was mainly distributed between the unique clusters 6 and 9 (Figures 7C and S6C). In contrast, the long-lived bone marrow plasma cell subset was concentrated in clusters 1.
and 5 (Figures 7C and S6C). Each of the other plasma cell populations showed more heterogeneous distributions across the clusters (Figures 7C and S6C). These data demonstrate that despite marked metabolic differences, each plasma cell subset, defined by B220 expression and 2NBDG uptake, is distributed across most of these transcriptionally defined clusters.

Thus, plasma cell metabolic properties do not correlate with transcriptional profiles.

To determine how this transcriptional heterogeneity relates to other markers and strategies to separate plasma cell subsets that have been used by others, we examined expression of CD93, major histocompatibility complex class II (MHC class II),...
CXCR3, and mKi67. CD93 mRNA expression did not uniquely associate with or exclude any clusters (Figure 7D). MHC class II/H2-Aa and CXCR3, which mark BLIMP1low plasmablasts (Kallies et al., 2004; Shi et al., 2015), were preferentially expressed by clusters 6 and 9 (Figure 7D). In contrast, the proliferation marker mKi67 was expressed primarily in cluster 9 (Figure 7D). Other markers, such as CD19 and BLIMP1 itself (Chernova et al., 2014; Kallies et al., 2004; Pracht et al., 2017), were near the lower limit of detection for single-cell RNA-seq, which captures only ~10% of mRNAs (Macosko et al., 2015), and thus did not resolve the populations further (Figure S6B).

We next used all 352 genes that were preferentially and statistically significantly expressed by at least one cluster to perform over-representation analysis, using the Consensus Pathway database (Herwig et al., 2016), to determine the biological significance of the heterogeneity. Biological pathways that were significantly over-represented (q value < 10^{-5}) included translation, ER protein processing, cell cycle, mRNA splicing, electron transport chain, proteasome, and, as noted above, neutrophil degranulation (Figure 7E). Clusters 6 and 9, which compose most of the short-lived B220^+2NBDG^− subset (Figure 7D), preferentially expressed genes in the translation, ER protein processing, electron transport chain, and proteasome pathways (Figure 7E). Clusters 6 and 9 were distinguished from each other by genes involved in cell-cycle and mRNA splicing (Figure 7E), consistent with mKi67 expression observed in cluster 9 (Figure 7D). These data suggest that cluster 9 is composed of proliferative B220^+2NBDG^- plasmablasts, whereas cluster 6 is composed of non-cycling B220^-2NBDG^- cells. Indeed, reports by others and our own previous data suggest that a subset of the B220^+ plasma cells is proliferative (Chernova et al., 2014; Lam et al., 2016). As above in Figure 6E, only the neutrophil degranulation pathway was able to distinguish the remaining clusters (Figure 7E). Other highly expressed granulocyte transcripts such as CSF3R and LY6G were undetectable (Figure S6B), arguing against neutrophil contamination.

Inclusion of immunoglobulin constant region genes in the single-cell RNA sequencing (scRNA-seq) analysis revealed differences in isotype usage across plasma cell subsets. For example, 75% of B220^+2NBDG^- plasma cells used IgM, whereas nearly 60% of bone marrow plasma cells were IgA^+ (Figure S6D), consistent with previous reports (Wilmore et al., 2018). However, each isotype was observed at some frequency in every plasma cell subset, demonstrating that antibody class does not strictly
define plasma cell longevity or metabolic programs. Expression of neutrophil degranulation genes correlated somewhat with antibody isotype (Figure S6E), but in none of these cases was this correlation absolute. For example, IgG1+ plasma cells expressed on average higher levels of Slpi than did IgM+ plasma cells (Figure S6E). However, a small subset of IgM+ cells expressed very high levels of Slpi (Figure S6F). Thus, transcriptional programs and antibody isotype independently diversify plasma cell function.

**DISCUSSION**

Plasma cells vary greatly in lifespan, depending on the type of infection or vaccine, the timing of ontogeny, and their anatomical location. Defining pathways that promote plasma cell longevity is a major goal for vaccine development, especially for immunizations that lead to very transient protection against infections. Reciprocally, identifying ways to antagonize long-lived plasma cells in the context of multiple myeloma and autoimmunity is also an important clinical goal. We observed that fluorescent glucose analog uptake correlates with plasma cell lifespan and allows for further purification and prospective isolation of long- and short-lived subsets when coupled with B220 expression. The usage of fluorescent glucose uptake thus helps facilitate the prospective isolation of short- and long-lived plasma cells.

Clearly, however, much still remains unresolved regarding the mechanisms of plasma cell survival. Although glucose uptake correlates with plasma cell longevity, it does not fully explain the heterogeneity. We observed substantial differences in lifespans among plasma cells that import the same amount of glucose. This led us to explore other pathways, such as ER stress and transcriptional regulation of survival genes, which may integrate with metabolism and nutrient uptake to tune plasma cell lifespan. Yet against all our predictions, we found almost no consistent changes in ER stress or transcription between mouse long- and short-lived plasma cell subsets. Although transcriptional changes are essential during plasma-blast differentiation to establish a metabolic program (Guo et al., 2018; Jash et al., 2016; Price et al., 2018; Wang and Bhat-tacharya, 2014), these changes seem not to further distinguish mature plasma cell subsets (Valor et al., 2017).

The transcriptional changes we did observe were mainly linked to cell proliferation and, unexpectedly, genes traditionally involved in neutrophil effector functions. Although we observed no evidence of neutrophil-like granules in plasma cells, it is possible that these proteins are constitutively released and allow certain plasma cell subsets to perform non-canonical effector functions to help clear pathogens and resolve damage. Such properties are reminiscent of tumor necrosis factor alpha (TNF-α) and inducible nitric oxide synthase (iNOS)-producing IgA+ plasma cells in the intestine, which help maintain microbial homeostasis (Fritz et al., 2011). iNOS itself promotes plasma cell survival (Saini et al., 2014), yet it seems unlikely that the innate immune pathways identified here would be directly tied to plasma cell lifespan given that the differences are not correlated with metabolic properties. The functional importance of these unusual signatures clearly needs to be explored more deeply.

The major pathways that consistently distinguish long- from short-lived plasma cells are non-transcriptional. Long-lived plasma cells that import high levels of glucose and also express high cell surface levels of CD98, a common subunit to many amino acid transporters (Mastroberardino et al., 1998), are less sensitive to reductions in extracellular amino acid concentrations and secrete more antibodies than do their short-lived counterparts. As in human long-lived plasma cells (Halliley et al., 2015), mouse long-lived plasma cells also have elevated autophagosome content. Glucose is used predominantly to glycosylate antibodies, but also to generate pyruvate for spare respiratory capacity, which in turn promotes survival (Lam et al., 2016). Similarly, glutamine is used as a carbon source for mitochondrial anaplerotic reactions and respiration, as well as a building block for antibodies. Together, our findings suggest a metabolic link between antibody secretion and lifespan. The discovery of new pathways that enhance or unlink these properties can potentially be exploited to prolong immunity or antagonize autoimmunity and plasma cell malignancies.

**STAR METHODS**

Detailed methods are provided in the online version of this paper and include the following:

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**SUPPLEMENTAL INFORMATION**

Supplemental Information includes six figures and can be found with this article online at https://doi.org/10.1016/j.celrep.2018.07.084.

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Washington University School of Medicine for help with genomic analysis. The Center is partially supported by NCI Cancer Center Support Grant P30 CA91842 to the Siteman Cancer Center and by ICTS/CTSA Grant UL1TR000448 from the National Center for Research Resources (NCRR), a component of the NIH, and NIH Roadmap for Medical Research. This publication is solely the responsibility of the authors and does not necessarily represent the official view of NCRR or NIH.

AUTHOR CONTRIBUTIONS


DECLARATION OF INTERESTS

D.B. is a co-founder of Cloak Therapeutics and owns significant equity. A patient application related to the current work has been filed (PCT/US18/23288). G.J.P. is a scientific advisory board member for Cambridge Isotope Laboratories, Integra Sciences; Medtronic; Smith & Nephew; and Wright Medical Technology, Inc. W.Y.L. is an employee of Amgen Inc.

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REFERENCES


## STAR METHODS

### KEY RESOURCES TABLE

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### Experimental Models: Organisms/Strains

| Mouse: C57BL/6N | Charles River Labs | Strain code 027 |
| Mouse: B6-Ly5.1/Cr | Charles River Labs | Strain code 564 |
| Mouse: Eif2ak3-tm1.2Dr/J | Jackson Labs | Stock No: 023066 |
| Mouse: B6.Cg-Tg(CAG-cre/Esr1*)5Amc/J | Jackson Labs | Stock No: 004682 |
| Mouse: B6.Cg-Gpi1a Thy1a Igha/J | Jackson Labs | Stock No: 001317 |

### Oligonucleotides

- Primers for XBP1s: 5’-CTGAGTCCGaaATCAGGTGCAG-3’ (forward) and 5’-GTCATGGGAAGATGTTCTGG-3’ (reverse)
- Primers for XBP1: 5’-TGCCGGGTCTGCTGAGTCCG (forward) and 5’-GTCATGGGAAGATGTTCTGG-3’ (reverse)
- Primers for HSPA5: 5’-TCAGCAGTATTATCGGAAACTCT (forward) and 5’-TTTCTGTATGATCTCTCACCAGT-3’ (reverse)
- Primers for DDIT3: 5’-CATACACCACACACCAGAAAG (forward) and 5’-CCGTCTTCTTCTTCTTGC-3’ (reverse)
- Primers for EDEM1: 5’-CCTCAATGTTGGAAGATGTTCTG (forward) and 5’-GTCATGGGAAGATGTTCTGG-3’ (reverse)
- Primers for HPRT: 5’-TTATGGACAGGACTGAAAGAC (forward) and 5’-GTCATGGGAAGATGTTCTGG-3’ (reverse)
- Primers for msVHEstdseq1 forward: 5’-TCTTTCCCTACACGATCTGGGAATT CGAGGTGCAGCTGCAGGAGTCTGG-3’
- Primers for P5 forward Stdseq: 5’-AATGATACGGCGACCACGCTGGAC-3’
- Primers for PERK qRT-PCR: forward 5’-GAAATCTCTGACTACATACGGAC-3’ and reverse 5’-ACACTGAAATTCCACTTCTCAC-3’
- Index seq: 5’-GATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3’
- Common Gamma reverse primer: 5’-TGACTGGAGTTCACTCAGCTGACGGCATGGAC-3’
- Stdseq1: 5’-ACACTTCTTCTACACGACCAGCTTCTCCCGATCT-3’
- Stdseq2: 5’-TGACTGGAGTTCACTCAGCTGACGGCATGGAC-3’
- Index seq: 5’-GATCGGAAGAGCACACGTCTGACGGCATGGAC-3’

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Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Deepta Bhattacharya (deeptab@email.arizona.edu).

**EXPERIMENTAL MODEL AND SUBJECT DETAILS**

All animal procedures in this study were approved by the Institutional Animal Care and Use Committee at Washington University (protocol 20160259) and at The University of Arizona (protocol 17-266). 8-12 week old mice of both sexes were used, were age- and sex-matched for each experiment, and littermates were used and chosen randomly in all experiments. C57Bl6/N and B6-Ly5.2/Cr (CD45.1) mice were purchased from Charles River Laboratories, IgHa allotype mice were purchased from Jackson Laboratories, and then housed in specific pathogen-free facilities for wild-type bone marrow and splenic plasma cells. Perkfl/fl mice and CAGG-CreERT2 mice were purchased from Jackson Laboratories. Mice were maintained under specific pathogen-free conditions. Euthanasia was performed by administering carbon dioxide at 1.5 L/minute into a 7 L chamber until 1 minute after respiration ceased. After this point, cervical dislocation was performed to ensure death.

All human sample procedures in this study were approved by the Human Research Protection Office at Washington University. Bone marrow was obtained from total hip arthroplasty samples from patients undergoing elective surgery (Barnes Jewish Hospital). All samples were kept anonymous with no identifying information. The sex and age of the donors were not determined.

**METHOD DETAILS**

**Tissue Processing**

For mouse long-lived plasma cells, femurs, tibiae, humerus, and pelvic bones were isolated and crushed with a mortar and pestle. Spleens were dissected and dissociated using frosted glass microscope slides. Non-cellular debris was removed from bone marrow samples by gradient centrifugation for 10 minutes at 2000 g using Histopaque 1119 (Sigma-Aldrich). Interface cells were collected and red blood cells were lysed using a 0.15 M NH4Cl, 10 mM KHCO3, 0.1 mM EDTA (pH 7.2) solution (ACK). Cells were washed and filtered through 70-μM nylon mesh and stained with 1 µL/10^7 cells anti-CD138-PE (Biolegend). Antibody-bound cells were enriched using 1 µL/10^7 cells anti-PE microbeads and LS columns (Miltenyi Biotec) prior to flow cytometric analysis and sorting. Human bone marrow plasma cells were isolated using CD138 enrichment beads (Miltenyi Biotec) as previously described (Lam et al., 2016).
Bone Marrow Chimeras
For competitive reconstitutions, 5 × 10^6 bone marrow cells from either Perk<sup>fl/fl</sup> or Perk<sup>fl/fl</sup>:CAGG CreER littermates were mixed with 5 × 10^6 bone marrow cells from B6.Ly5.2 CD45.1+ mice and injected retro-orbitally into isoﬂurane-anesthetized 800 cGy-irradiated B6.Ly5.2 CD45.1+ recipients. At 8 weeks post-transplant, mice were fed tamoxifen-containing chow (400 citrate; Envigo) for 2 weeks before sacriﬁce and analysis.

Plasma Cell Cultures
Sorted plasma cells were cultured overnight (18-20 hours) in hypoxic conditions (37°C, 5% CO2, 5% O2) in 100µl of indicated media. Physiological amino acid media is a custom preparation supplemented with 1% penicillin/streptomycin solution, 10% FBS, and either 5µM or 25µM glucose as indicated and previously described (Lam et al., 2016). Supraphysiological amino acid media refers to RPMI 1640 (Corning Cellgro 90-022-PB). For p-eIF2α inhibition experiments, cells were cultured for 1 hr in the presence of 4 nM GSK2606414 (for PERK inhibition; Sigma-Aldrich [Axtén et al., 2013]; 500 µM SP600125 (for GCN2 inhibition; Calbiochem [Robert et al., 2009]); 500 µM indirubin-3’-monoxime (for GCN2 inhibition; Calbiochem [Robert et al., 2009]); 100 µM imidazole-oxindole C16 (for PKR inhibition; Sigma-Aldrich [Jammii et al., 2003]); and 50 µM hemin (for HRI inhibition; Sigma-Aldrich [Fagard and London, 1981]) before flow cytometric analysis. Cycloheximide was used at 50 µM concentrations. Autophagy Blue was used according to manufacturer’s instructions (Sigma-Aldrich).

Bromodeoxyuridine Experiments
Mice were fed with 2 mg/mL BrdU in the drinking water for the durations indicated. Animals were injected with 100 µg 2NBDG intravenously and euthanized 15 min later. Because formaldehyde ablates 2NBDG fluorescence (data not shown), plasma cell subsets were puriﬁed by ﬂuorescence activated cell sorting prior to ﬁxation, permeabilization, and intracellular analysis of BrdU incorporation and retention. Splenic plasma cells, memory B cells and CD138-enriched bone marrow plasma cells were ﬁrst stained for surface expression of respective antibodies. Cells were then puriﬁed by Fluorescence-activated cell sorting and then ﬁxed, permeabilized, and stained for incorporated BrdU with the FITC BrdU Flow kit (BD Biosciences) according to the manufacturer’s instructions. 2NBDG does not survive ﬁxation, allowing for the use of ﬂuorescein derivative-conjugated antibodies for intracellular analysis after cells were puriﬁed by FACS.

Immunizations
Mice were immunized intraperitoneally with 100 µg NP-Ova (Biosearch), adjuvanted with Alhydrogel (Invivogen). NP-APC used for staining was made by conjugating allopheocyanin (Sigma-Aldrich) with 4-hydroxy-3-nitrophenylacetyl-O-succinimide ester (Biosearch Technologies).

ELISAs
Supernatant collected was serially diluted 1:4, 1:16, 1:64 in antibody buffer (PBS + 2% BSA + 0.05% Tween). Standard curves were made with unlabeled mouse IgG (Southern Biotech) to 100, 20, 4, 0.8, 0.16, and 0.032 ng/ml. Ninety-six well high binding plates (Corning) were coated with purified rat μ-mouse Ig kappa, light chain (BD Pharmingen) at 5 µg/mL in ELISA coating buffer (0.1M bicarbonate, pH 9.5) overnight at 4°C. Plates were washed four times with PBS + 0.05% Tween before blocking for one hour with PBS + 2% BSA. Blocking buffer was flicked out and samples were plated for one hour at room temperature. Plates were washed four times with PBS + 0.05% Tween. Plates were coated with 0.13 µg/mL Biotin-SP-conjugated AffiniPure Donkey Anti-Mouse IgG (H+L) (Jackson Immunoresearch) in antibody buffer and incubated for one hour at room temperature. This secondary antibody recognizes all isotypes due to light chain reactivity. Plates were then washed four times with PBS + 0.05% Tween. Wells were incubated with 1:1000 streptavidin HRP (BD Pharmingen) in antibody buffer for one hour at room temperature. After incubation, wells were washed 3 × with PBS + 0.05% Tween and 3 × with PBS followed by development with 100 µl of 3,3′,5,5′-Tetramethylbenzidine dihydrochloride hydrate (TMB) (Dako) and quenched with 2N H2SO4. ELISA absorbance values were analyzed at 450 nm. Antibody titers were calculated using standard curves generated with known mouse IgG concentrations.

Flow Cytometry/Sorting
All ﬂuorescence activated cell sorting was performed on a BD FACS Aria II. Cells were sorted into phosphate-buffered saline containing 5% bovine serum. All ﬂow cytometric analysis was performed on a BD FACS Aria II, LSR II, or LSR Fortessa. Data was analyzed using FlowJo software (FlowJo Enterprise). The following μ-mouse antigen antibodies were used in this study: CD138-phycocerythrin (PE) (281-2; Biolegend); B220-allophycocyanin (APC)-Cy7 (RA3-6B2; Biolegend); CD93-PE-Cy7 (AA4.1; Biolegend); p-S6-V450 (N7-548, BD Biosciences); p-eIF2α-Alexa 647 (E90; Abcam); Igκ-PE-Cy7 (187.1, BD Biosciences); CD45.2-BV510 (104; Biolegend); CD45.1-BV605 (A20; Biolegend). For intracellular stains of p-S6 and p-eIF2α, plasma cell subsets were first puriﬁed by FACS, ﬁxed with 2% paraformaldehyde (Electron Microscopy Services), and permeabilized with cold 100% methanol prior to staining. For intracellular stains of Igκ, cells were ﬁxed with 2% paraformaldehyde and permeabilized with 0.1% saponin (Sigma-Aldrich) prior to staining.
qRT-PCR
Total RNA was prepared from double-sorted bone marrow plasma cell (20,000-60,000) and four different splenic plasma cell (10,000–100,000) populations using NucleoSpin RNA isolation kit (Macherey-Nagel) and first strand cDNA synthesis was performed with Superscript III Reverse transcription kit using oligo (dT) primers or random hexamers (Life Technologies) according to the manufacturer’s instructions. qRT-PCR was performed using SYBR Green PCR master mix (Applied Biosystems) on a StepOnePlus Real-Time PCR system (Applied Biosystems). The primer sequences, reported previously (Oslowski and Urano, 2011), are as follows: XBP1s, 100,000) populations using NucleoSpin RNA isolation kit (Macherey-Nagel) and first strand cDNA synthesis was performed with qRT-PCR custom physiological media supplemented with 1% Pen/Strep, 5 mM glucose, 500 µM glutamine, and 10% FBS and 1 µL of FITC-ATAD-FMK (from kit) for 1 hr in hypoxic conditions (5% O2, 5% CO2, 37°C). Cells were analyzed by flow cytometry and FITC-positive cells indicate active caspase-12.

Electron Microscopy
Transmission electron microscopy of mouse splenic plasma cell subsets was performed by the Molecular Microbiology Imaging Facility at Washington University. For ultrastructural analysis, 3–5 x 10^5 sorted cells were fixed in 2% paraformaldehyde/2.5% glutaraldehyde (Ted Pella, Redding, CA, USA) in 100 mM cacodylate buffer (pH 7.2) for 1 hr at room temperature. Samples were washed in cacodylate buffer and postfixed in 1% osmium tetroxide (Polysciences, Warrington, PA, USA) for 1 hr. Samples were then rinsed extensively in dH2O prior to en bloc staining with 1% aqueous uranyl acetate (Ted Pella) for 1 hr. Following several rinses in dH2O, samples were dehydrated in a graded series of ethanol and embedded in Eponate 12 resin (Ted Pella). Sections of 95 nm were cut with a Leica Ultracut UCT7 ultramicrotome (Leica Microsystems, Bannockburn, IL, USA), stained with uranyl acetate and lead citrate, and viewed on a JEOL 1200 EX transmission electron microscope (JEOL USA, Peabody, MA, USA) equipped with an AMT 8 megapixel digital camera and AMT Image Capture Engine V602 software (Advanced Microscopy Techniques, Woburn, MA, USA). ER lumenal width analysis was performed using ImageJ software, and scored blinded to the cellular subset.

In Vivo Ribopuromycylation
Wild-type IgHa mice were injected with 1 mg of puromycin (EMD Millipore) intraperitoneally and euthanized 15 min later. Following fixation and permeabilization as previously described (Seedhom et al., 2016), puromycin incorporation was detected using a monoclonal antibody (clone 2A4 from the Developmental Studies Hybridoma Bank at the University of Iowa) followed by a biotin mouse anti-mouse IgG2a[b] (clone: 5.7 from BD Pharmingen) and finally BV605 streptavidin (BD Horizon).

CaspGLOW Assay
Caspase 12 activation was measured using the CaspGLOW staining kit (Biovision). Sorted cells were spun down and cultured in custom physiological media supplemented with 1% Pen/Strep, 5 mM glucose, 500 µM glutamine, and 10% FBS and 1 µL of FITC-ATAD-FMK (from kit) for 1 hr in hypoxic conditions (5% O2, 5% CO2, 37°C). Cells were analyzed by flow cytometry and FITC-positive cells indicate active caspase-12.

Immunoglobulin Repertoire Analysis
For these analyses, we sorted all recoverable plasma cells from spleen and bone marrow of femurs, tibiae, humerus, and pelvis bones, generating approximately 30,000 cells of each subset. Sorted cells were lyzed and RNA made using the NucleoSpin RNA XS kit (Macherey-Nagel) per manufacturer’s instruction. cDNA was generated using Superscript III First-Strand Synthesis System for FT (Thermo Fisher) with oligo dT per manufacturer’s instructions. PCR primers as previously reported were modified for MiSeq primer sequencing. PCR products were cleaned using gel/PCR DNA fragments extraction kit (IBI Scientific). PCR products were then used as templates for a second round of amplification with the following primers: msVHEstdseq1 5’-TCTTTCCCTACAGATCTGGGAATTCGAGGTGCAGCTGCAGGAGTCTGG-3’ and common mu stdseq2 5’-GTGACTGAGAGTACGATGTCCTTCCGATCTAGGGGGAACATTTGGGAAGGAC-3’. PCR products were cleaned using gel/PCR DNA fragments extraction kit (IBI Scientific). PCR products were then used as templates for a second round of amplification with the following primers: P5 forward Stdsq 5’-AATGATACGGAGACCCAGGATCTACAC TCTTTCCCTACAGACGC-3’ and P7 reverse Stdsq index 5’CAACGAGAAGACCGCATACGATNNNNNNNTGACTGGAG TTCAAGCGTGTTG-3’ where N represents a unique combination for barcoding purposes. For IgG repertoire analysis, cDNA was first amplified using the following primers: msVHEstdseq1 5’-TCTTTCCCTACAGATCTGGGAATTCGAGGTGCAGCTGCAGGAGTCTGG-3’ and a combination of

Cy1 primer 5’-GGAAGTGTCAGCAGCTGGAC-3’,
Cy2c primer 5’-GGAAGTGTCAGCAGCTGGAC-3’,
Cy2b primer 5’-GGAAGTGTCAGCAGCTGGAC-3’,
Cy3 primer 5’-AGACTGTCCGAGCACCAGCTGGAC-3’.
This was followed by a second round of PCR with: msVHEstdseq1 5'-TCTTTCCCTACACGATCTGGGAATTCGAGGTGCAGCTG
CAGGAGTCTGG-3' and a common Cγ primer: 5'- GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGGTGGATAGAGQ
CATCGATGGGG-3'. This was followed by a final amplification cycle with P5 forward Stdseq and P7 reverse Stdseq index. Samples
were then pooled, gel purified, and then sequenced using the Illumina Miseq 2 × 250 platform with the following primers: Stdseq1:
5'-ACACTCTTTCCCTACACGCTCTTCCGATCT-3'; Stdseq2: 5'-GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT-3'; and
Index seq: 5'-GATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3'. Repertoire information was extracted from fastq files using
Mixcr (Bolotin et al., 2015) and displayed using Cionplot (Fähnrich et al., 2017). Approximately 150,000 reads were obtained for
each sample, which when corrected for isotype usage corresponds to ~7–15 x coverage. Given that none of the subsets displayed
more than 4,000 distinct CDR3 regions, the data approach sequencing saturation.

RNA-Seq
RNA was prepared from approximately 30,000 plasma cells as described above. Human plasma cell RNA-seq data were obtained
from our previous studies (Jash et al., 2016; Lam et al., 2016). Sequencing libraries were generated using a Smart-Seq kit
and Nextera DNA library prep kit (Illumina). Single end 50bp reads were acquired using an Illumina HiSeq 2500. Reads were mapped
using Salmon (Patro et al., 2017), and differential gene expression analysis was performed using DESeq2 (Love et al., 2014). Refer-
ence transcriptomes and annotation files that include immunoglobulin variable and constant region genes were downloaded from the
Gencode Project: (ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M16/gencode.vM16.pc_transcripts.fa.gz). Inter-
section analysis was performed using Microsoft Access, and Venn Diagrams were generated using https://www.meta-chart.com/
venn#/data. Heatmaps were generated using http://www.heatmapper.ca/.

Single-Cell RNA-Seq
Approximately 5000 LY6G- CD11c- plasma cells of each subset were double-sorted and prepared for RNA-sequencing using a
Chromium Single Cell 3' Library & Gel Bead Kit and a Single Cell Controller from 10x Genomics according to manufacturer’s instruc-
tions. Sequencing libraries were prepared using Illumina Nextera kits, and each sample was sequenced in its own Illumina HiSeq
2500 lane. Sequencing files were aggregated, normalized, and processed using the Cell Ranger program (10x Genomics) and visu-
alized using Loupe Browser (10x Genomics). Minimum read cutoffs to focus the analysis on high-quality single cells were left at
default settings. Clusters were automatically defined by a graph-based method. Immunoglobulin isotypes and subset-specific
expression of neutrophil degranulation genes were visualized using SeqGeq (FlowJo).

13C Tracing Experiments
Human bone marrow plasma cells were purified using CD138 beads as previously described (Lam et al., 2016). Approximately 2 ×
10⁶ cells were cultured in 2ml of physiological media containing either 5mM uniformly labeled 13C glucose or 500 μM uniformly
labeled glutamine for 24 hours. Cells were harvested and extracted as previously described (Yao et al., 2016). Samples were sepa-
rated on a Luna aminopropyl column (3 μm, 150 mm × 1.0 mm I.D., Phenomenex) coupled to an Agilent 1260 capillary HPLC system.
The Luna column was used in negative mode with the following buffers and linear gradient: A = 95% water, 5% acetonitrile (ACN),
10 mM ammonium hydroxide, 10 mM ammonium acetate; B = 95% ACN, 5% water; 100% to 0% B from 0-45 min and 0% B from
45-50 min; flow rate 50 μL/min. Mass spectrometry detection was carried out on an Agilent 6540 Q-TOF coupled with ESI source. The
identity of each metabolite was confirmed by comparing retention times and tandem MS data with standard compounds. The iso-
topologue distributions were corrected for natural abundance and isotope impurity.

QUANTIFICATION AND STATISTICAL ANALYSIS
Student’s t tests, 1-way ANOVAs with post hoc Tukey’s multiple comparison tests, and 2-way ANOVAs with post hoc Sidak’s mul-
tiple comparison tests were performed using Prism software (Graphpad). Figure legends specify the test used, criteria for statistical
significance, and experimental replicates. Figures and/or legends specify the number of technical and biological replicates per
experiment. Adjusted p values and fold changes for RNA-seq were calculated using DESeq2 (Love et al., 2014). Significant genes
in single cell RNA-seq experiments were identified using Loupe Browser, which applied a Benjamini-Hochberg correction for multiple
comparisons to generate adjusted p values.

DATA AND SOFTWARE AVAILABILITY
The accession number for the RNA-seq data reported in this paper is NCBI GEO: GSE115860.
Supplemental Information

Metabolic and Transcriptional Modules
Independently Diversify Plasma
Cell Lifespan and Function

Wing Y. Lam, Arijita Jash, Cong-Hui Yao, Lucas D'Souza, Rachel Wong, Ryan M. Nunley, Gordon P. Meares, Gary J. Patti, and Deepta Bhattacharya
Figure S1 refers to Figure 1. Plasma cell gating strategies and biological replicates of immunoglobulin repertoire sequencing.

(A) Representative flow cytometric plots of total surface and intracellular Igκ staining of fixed and permeabilized splenic and bone marrow CD138+ plasma cells. Cells were enriched with CD138 magnetic beads prior to analysis. (B) Representative flow cytometric plots of in vivo 2NBDG uptake by splenic and bone marrow plasma cell populations. Cells were pre-enriched using CD138 magnetic beads. (C) Heatmaps represent clonal overlap between plasma cell subsets. Sequencing and clonal overlap analysis was performed on 2 additional mice as in Figure 1. (D) Ecological diversity index for each subset calculated by Clonoplot. Data from the mouse analyzed in Figure 1D are shown.
Figure S2 refers to Figure 2. Plasma cell size does not correlate with CD98 expression. Forward scatter signal was plotted for plasma cell subsets shown in Figure 2A. No clear correlation was observed between FSC and CD98 surface levels.
Figure S3 refers to Figure 4. Hexosamine pathway intermediates are derived from extracellular glucose import.

Liquid chromatography-mass spectrometry analysis of $^{13}$C enrichment in human bone marrow plasma cell intermediary metabolites. Plasma cells were cultured for 18 hr with uniformly labeled $^{13}$C- glucose. Mean mass isotopomer distributions ± SEM from $^{13}$C-glucose and $^{12}$C-glucose controls are shown for 6 biological replicates.
Figure S4 related to Figure 4

A.

% DAPI+

B220+ 2NBDG- B220- 2NBDG- B220+ 2NBDG+ bone marrow

[Graph showing percentage DAPI+] (DMSO: black squares, PERK inhibitor: black diamonds)

B.

OD 450 nm

B220+ 2NBDG- B220- 2NBDG- B220+ 2NBDG+ bone marrow

[Graph showing optical density at 450 nm] (DMSO: black squares, PERK inhibitor: black diamonds)

C.

Perk^{+/+} Perk^{+/+} CAGG-CreERT2

CD45.1

CD45.2

[Flow cytometry dot plots for CD45.1 and CD45.2] (Perk^{+/+}: solid circles, Perk^{+/+} CAGG-CreERT2: solid squares)

D.

Perk mRNA (normalized to HPRT)

spleenic PC BM PC

[Graph showing Perk mRNA levels] (Perk^{+/+}: solid circles, Perk^{+-/} CreER+: solid squares)
Figure S4 refers to Figure 4. PERK inhibition \textit{in vitro} does not affect survival or antibody production by plasma cell populations.

(A) Plasma cell populations were sorted and cultured with either 4nM GSK2606414 PERK inhibitor or vehicle (DMSO). DAPI staining was used to determine cell viability. (B) Plasma cell populations were sorted and cultured with either 4nM GSK2606414 PERK inhibitor or vehicle (DMSO). Antibody secretion was measured by ELISA. (C) Representative flow plots of chimerism. Perk^{0/0} and Perk^{0/1} CAGG-CreERT2 are congenically marked with CD45.2. (D) qRT-PCR analysis of PERK expression in plasma cells isolated from Perk^{0/0} and Perk^{0/1} CAGG-CreERT2 chimeras.
Figure S5 refers to Figure 5. ER stress and mTOR signaling are similar between plasma cell populations.

(A) Representative electron microscopy images of splenic plasma cell populations. (B) Average ER lumen width of splenic plasma cell populations. Each dot represents the average of eleven randomly selected lumen widths of an individual cell. Mean values of biological replicates ± SEM are shown. (C) RNA-seq expression of the Ig constant region gene in plasma cell populations. TPM = transcripts per kilobase per million mapped reads. *p<0.05 by 1-way ANOVA with post-hoc Tukey’s multiple comparisons test. (D) Representative pS6 staining of plasma cell subpopulations (left) and quantification of MFI values (right). Data representative of 3 independent experiments. No statistically significant differences were observed by paired 1-way ANOVA.
Figure S6 related to Figure 7

A. 

B. Xbp1  Ly6a  Ly6e  Tnfrsf13b

     Prdm1  CD19  Ly6g  Csf3r

C. 

D. B220+2NB DG-  B220-2NB DG-  B220+2NB DG+  B220-2NB DG+  BM

E. Spi  Gliprl  Hmgb1  Plac8  Pro2  Pycard

F. IgG4
Figure S6 refers to Figure 7. Plasma cell purity and immunoglobulin isotype expression demonstrated by single cell RNA-seq.

(A) Expression of the Igκ constant region and IgJ as a fraction of the total number of transcripts in each cell. Each data point represents a unique cell within the B220-2NBDG- plasma cell population. (B) Expression of plasma cell and neutrophil marker genes are depicted as a heatmap overlaid onto the concatenated t-SNE plot of all plasma cell subsets. (C) Plasma cell subset composition within each t-SNE-identified cluster (top) and cluster composition of each plasma cell subset population (bottom). (D) Immunoglobulin isotype distribution across plasma cell subsets determined by scRNA-seq. (E) Average expression of neutrophil degranulation genes as a function of immunoglobulin isotype. (F) Example plot of Slpi expression as a function of IgM or IgG1.