The self-peptide repertoire plays a critical role in transplant tolerance induction

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Abstract

While direct allorecognition underpins both solid organ allograft rejection and tolerance induction, the specific molecular targets of most directly-alloreactive $CD8^+$ T cells have not been defined. In this study, we used a combination of genetically-engineered MHC I constructs, mice with a hepatocyte-specific mutation in the class I antigen-presentation pathway and immunopeptidomic analysis to provide definitive evidence for the contribution of the peptide cargo of allogeneic MHC I molecules to transplant tolerance induction. We established a systematic approach for the discovery of directly-recognised pMHC epitopes, and identified 17 strongly immunogenic H-$2K^b$-associated peptides recognised by $CD8^+$ T cells from B10.BR (H-2^k) mice, 13 of which were also recognised by BALB/c (H-2^d) mice. As few as five different tetramers used together were able to identify almost 40% of alloreactive T cells within a polyclonal population. To our knowledge, this represents the first example of such an approach in the context of direct allorecognition.

Introduction

Allorecognition may result in either graft rejection, graft versus host disease or transplantation tolerance, depending upon the context in which the recipient immune system encounters the allogeneic major histocompatibility complex (MHC). When donor MHC class I (MHC I) molecules are expressed in the hepatocytes of recipient mice, subsequent skin or pancreatic islet grafts bearing the same donor allomorph are accepted indefinitely[1, 2, 3]. Insights from this model can inform our understanding of allorecognition and transplant tolerance induction more broadly. MHC I molecules are ubiquitously expressed, and display a range of endogenous peptides (the class I immunopeptidome) reflecting protein turnover and normal cellular processes[4]. While tolerance induction depends upon recognition of intact donor MHC I molecules by recipient $CD8^+$ T cells[3], the contribution of the self-peptide cargo of these molecules to tolerance induction in this setting is unknown.

Many individual alloreactive T cell clones recognise epitopes comprising allogeneic MHC I molecules complexed with self-peptides[5, 6, 7, 8, 9, 10, 11, 12]. Conversely, peptide-independent direct allorecognition is also described[7, 13, 14], and the ability of peptide-independent cytotoxic T lymphocyte (CTL) clones to bring about rapid destruction of allogeneic skin grafts has been demonstrated[15]. At the level of a polyclonal alloresponse *in vivo*, there is limited information about the role of the donor's tissue-specific class I immunopeptidome in allorecognition and consequent immune responses that impact on graft survival.

In preceding studies[1, 3], we had used liver-specific adeno-associated viral (AAV) vectors encoding the donor MHC I heavy chain (HC). Within transduced hepatocytes, allogeneic HC associated with native β2 microglobulin (β2m) and the resulting heterodimers were loaded with a repertoire of endogenous peptides (Figure 1a). Here, we examined the role of the liver immunopeptidome in transplantation tolerance induction using two different approaches. In the first of these, we engineered liver-specific AAV vectors which would express H-2K^b or H-2K^d as a single chain trimer (SCT) comprising the polymorphic HC, β2m light chain and a defined covalently-bound peptide species[16, 17], thus excluding presentation of endogenous peptides by the allogeneic MHC I when these constructs were expressed in B10.BR (H-2^k) or C57BL/6 (H-2^b) recipient hepatocytes (Figure 1a). In parallel, we introduced a global shift in the repertoire of peptides bound to allogeneic H-2K^d. To accomplish this, we generated recipient mice in which the transporter associated with antigen processing (TAP1) protein was deficient only in hepatocytes (TAP1KOHep, H-2^b) to reduce the availability of high affinity K^d-binding peptides within the endoplasmic reticulum, and designed a construct expressing the H-2K^d HC with a modification (Y84C, A139C; subsequently termed YCAC) which stabilises the molecule and permits occupancy by lower affinity peptides[18]. Induction of tolerance to subsequent donor skin grafts was blocked by these manipulations, establishing that the endogenous peptide repertoire of hepatocytes makes an essential contribution to transplant tolerance induction.

Differential responses by alloreactive T cells to MHC I allomorphs expressed by various target tissues has been cited as evidence in support of peptide-specific allorecognition[6, 19, 20]. Based on the ability of H-2K^b or K^d HC expressed in recipient hepatocytes to induce tolerance to allogeneic skin grafts and to downmodulate responses against donor splenocyte stimulators[1, 3], we hypothesised that the peptides critical for allorecognition and tolerance induction would be found within a subset common to these three tissue types. We identified these peptides using immunoaffinity purification coupled with mass spectrometry and determined their ability to bind activated alloreactive T cells using tetramer staining. Of 100 peptides selected for tetramer screening, 17 bound more than 5% of this T cell population, and 13 of these peptide-MHC (pMHC) epitopes were also recognised by BALB/c mice. Strikingly, we demonstrated a cumulative increase in the proportion of alloreactive T cells bound when multiple pMHC tetramers were used together, whereby as few as five different pMHC tetramers were able to identify around 40% of alloreactive T cells within a polyclonal population. Development of multimer panels to capture a substantial proportion of directly alloreactive T cells will enable immune monitoring and a range of other downstream applications including T cell receptor (TCR) repertoire analysis, cloning and biophysical and structural studies. In short, the findings of this study represent a significant advance in our understanding of the role of endogenous peptides in direct T cell alloreactivity, and a springboard for further knowledge gain and technological development.

Results

Single chain trimer constructs exclude presentation of endogenous peptides.

To express allogeneic MHC I at high levels on recipient hepatocytes, while excluding the presentation of naturally processed peptides, we engineered SCT constructs, each encoding the HC of H-2K^b, β2m and a single, defined H-2K^b-restricted peptide [SIINFEKL (SIIN) or KIITYRNL (KIIT), Figure 1a], and packaged them in hepatocyte-specific AAV2/8 vectors. Sequences are shown in supplementary Figure 1. Transgene expression in hepatocytes was close to maximal by d7 following intravenous (iv) inoculation, and persisted through to at least d100, no significant increases in serum aspartate aminotransferase (AST) or alanine aminotransferase (ALT) levels

were observed, and minimal cellular infiltration was detected by histology (Figure 1b-c). SCT molecules were expressed on transduced hepatocytes at equivalent levels to the heterotrimer formed by transgenic H-2K^b HC with native β2m and peptide (Figure 2a). To demonstrate exclusion of naturally processed peptides, we co-transduced B10.BR (H-2^k) hepatocytes with AAV vectors encoding full-length chicken ovalbumin (OVA) and either HC-K^b or SCT-K^b-KIIT, and stained them with a monoclonal antibody, 25D-1.16, which is specific for the OVA peptide SIINFEKL complexed with K^b. K^b-SIINFEKL was only detected at the surface of cells co-transduced with HC-K^b and not those expressing SCT-K^b-KIIT (Figure 2b-c). We extended this analysis to the broader endogenous peptide repertoire of K^b-transduced hepatocytes using immunoaffinity purification with the H-2K^b-specific antibody K9-178, followed by reverse phase high performance liquid chromatography (RP-HPLC) to collect peptide-containing fractions that were then analysed using liquid chromatography with tandem mass spectrometry (LC-MS/MS) to identify bound peptides (Figure 2d). The K^b binding motif of peptides eluted from HC-K^b transduced hepatocytes mirrored that obtained from C57BL/6 (H-2^b) hepatocytes (Figure 2e). While there was greater diversity among the unique peptides isolated from HC-K^b transduced hepatocytes (Figure 2f), there was substantial overlap between the peptide repertoires, with >90% of the peptides from C57BL/6 hepatocytes also identified in HC-K^b transduced B10.BR (Figure 2g). In contrast, almost no K^b-bound peptides could be identified in association with SCT-K^b-KIIT, confirming exclusion of the endogenous peptide repertoire from presentation by this molecule (Figure 2f). Hepatocytes transduced with SCT-K^b-KIIT did not manifest any generalised defect in antigen processing, with both the numbers and repertoire of peptides isolated from the native allomorph H-2K^k being similar across all groups (Figures 2h-i). The full peptide dataset can be found in supplementary data 1.

SCT-K^b-KIIT induces tolerance in alloreactive T cells expressing the cognate T cell receptor but not in a polyclonal alloreactive population.

We first verified that SCT molecules were recognised by cells bearing their cognate TCRs in a manner analogous to the native epitope. Pulsing RMA-S cells with synthetic peptides KIITYRNL, SIINFEKL and AAAAFAAL (minimum binding requirement for H-2K^b) stabilised K^b expression on

the cell surface (Supplementary Figure 2a-b). Similar levels of surface expression were achieved by transient transfection of RMA-S cells with the corresponding SCT constructs (Supplementary Figure 2c). Using interferon-gamma (IFN-γ) ELISPOT, we found a strong, specific response to SCT-K^b-KIIT by Des-RAG TCR-transgenic T cells which express the cognate TCR; SCT-K^b-SIIN was similarly recognised by OT-I-RAG T cells (Supplementary Figure 2d). Following adoptive transfer into B10.BR mice transduced with SCT-K^b-KIIT, Des-RAG T cells proliferated vigorously, expanding more than those transferred to the positive control 178.3 (H-2^k + K^b) mice after 2 days ($p < 0.0001$, Supplementary Figure 2e-f). The polyclonal responder population of liver leukocytes from B10.BR mice also contained $CD8^+$ T cells, which were activated in response to transduction with SCT-K^b-KIIT. Naïve or primed B10.BR mice were inoculated with SCT-K^b-KIIT, and liver leukocytes isolated 7 days later (Figure 3a). Activated $CD8^+$ T cells, defined as $CD44^+$PD-1^{hi}, increased upon priming or transduction with SCT-K^b-KIIT, with a further augmentation when primed mice received SCT-K^b-KIIT vector (Figure 3b). Activated $CD8^+$ T cells from transduced mice recognised K^b-KIIT dextramers but not dextramers of the self-pMHC complex K^k-EEEPVKKI, while PD-1^- bystander $CD8^+$ T cells did not bind either dextramer (Figure 3c-d).

Next, we determined that Des-RAG T cells alone were capable of rejecting K^b-bearing 178.3 skin grafts upon adoptive transfer to B10.BR-RAG recipients (Figure 3e-f). Graft survival was inversely related to the T cell dose; 50,000 transferred cells yielded a median graft survival comparable to that in B10.BR mice with a polyclonal K^b-reactive T cell repertoire and this dose was used in subsequent experiments. All grafts to reconstituted B10.BR-RAG mice treated with SCT-K^b-KIIT survived indefinitely, whereas no graft survival prolongation was observed in reconstituted mice receiving the control vector SCT-K^b-SIIN (Figure 3g). Surviving grafts appeared normal macroscopically (Figure 3h) and upon histology (Figure 3i) with continued expression of H-$2K^b$. In contrast, transduction of wild-type B10.BR mice with either SCT-K^b-KIIT or SCT-K^b-SIIN only briefly delayed graft rejection (Figure 3j).

The YCAC mutation alters the repertoire of H-2K^d-bound peptides in both TAP1KOHep and C57BL/6 mice.

Mice with a conditional deletion of Tap1 in hepatocytes (TAP1KOHep, H-2^b) express trace amounts of the native MHC I allomorphs H-2K^b and H-2D^b at the hepatocyte surface (Figure 4a-d). Importantly, expression of these molecules on most other cell types within the liver, in other tissues (such as spleen, thymus and lymph node), and in TAP1$^{fl/fl}$ control mice was normal (Figure 4a-d and supplementary Figure 3a). Transduction of TAP1KOHep mice with a vector encoding the H-2K^d HC (HC-K^d) resulted in surface expression of H-2K^d which was clearly positive with respect to untransduced controls, yet was reduced in comparison to that in C57BL/6 or TAP1$^{fl/fl}$ mice (Figure 4e-f). Increasing the vector dose did not yield an appreciable increase in surface expression (data not shown), most likely because of instability of suboptimally-loaded H-2K^b molecules and their rapid recycling from the cell surface[21, 22, 23]. To counter this, we designed a construct where the point mutations Y84C and A139C (YCAC) in the H-2K^d HC result in the formation of a disulphide bridge, which stabilises the molecule when empty or loaded with lower affinity peptides[18]. This modification does not interfere with TCR recognition of the bound peptide[18]. The construct sequence is shown in supplementary Figure 1. Comparable strong expression of H-2K^d on the surface of hepatocytes was achieved in TAP1KOHep mice treated with HC-K^d-YCAC and in TAP1$^{fl/fl}$ mice receiving either the HC-K^d or HC-K^d-YCAC vectors (Figure 4e-g). Immunoaffinity purification and tandem LC-MS/MS were used to characterise the bound self-peptide repertoire of transduced hepatocytes. 9570 unique peptides were identified from C57BL/6 hepatocytes transduced with HC-K^d (B6/HC), compared with 7690, 7776, and 6417 unique peptides respectively, from C57BL/6, TAP1$^{fl/fl}$ and TAP1KOHep transduced with HC-K^d-YCAC (*i.e.* B6/YCAC, TAP1$^{fl/fl}$/YCAC and TAP1KO/YCAC). The full dataset can be found in supplementary data 1, while distribution of peptide lengths and spectral intensities is shown in supplementary Figure 4a-b, along with the gene ontology analysis of the subcellular location and function of the source proteins. Whilst the sequences of eluted 9-mer peptides from B6/HC, B6/YCAC and TAP1$^{fl/fl}$/YCAC corresponded to the canonical motif for H-2K^d, with tyrosine (Y) residues predominant at position 2, and leucine (L) and isoleucine (I) most frequently found at position 9,

this motif was not observed for the peptides eluted from TAP1KO/YCAC (Figure 5a-b). Compared to B6/HC, just under 45% of peptides were common to B6/YCAC or TAP1$^{fl/fl}$ /YCAC, while 22% were shared with TAP1KOHep/YCAC (Figure 5c). Similarity across peptide repertoires was increased when the comparison was weighted for peptide abundance (Figure 5c). The peptide SYFPEITHI (SYFP) was common to all K^d repertoires, and comparable proportions of CD8$^+$ T cells recognising K^d-SYFP could be detected among the liver leukocytes isolated from primed TAP1KO/YCAC as well as from primed B6/YCAC and B6/HC (Figure 5d) consistent with published reports that the YCAC mutation alters the peptide repertoire but does not interfere with TCR recognition of presented peptides[18, 24].

Increasing perturbation of the hepatocyte H-2K^d peptide repertoire correlates with progressive reduction of K^d-bearing skin graft survival in transduced mice.

Mice were inoculated with AAV-HC-K^d, AAV-K^d-YCAC, or an SCT vector encoding K^d with the single peptide SYFPEITHI (AAV-SCT-K^d-SYFP), seven days prior to transplantation with a B6.Kd skin graft. The construct sequence and expression data for AAV-SCT-K^d-SYFP are shown in supplementary Figures 1 and 5, respectively. The majority of C57BL/6 or TAP1$^{fl/fl}$ mice transduced with AAV-HC-K^d accepted K^d-bearing B6.Kd skin grafts indefinitely, whereas median survival of B6.Kd skin grafts to C57BL/6 or TAP1$^{fl/fl}$ mice treated with AAV-K^d-YCAC was reduced to 62.5 ± 5.3 days and 52.5 ± 9.2 days respectively ($p = 0.009$ and $p = 0.007$ compared to HC-K^d) (Figure 5e). Graft survival in TAP1KOHep mice inoculated with AAV-K^d-YCAC was further reduced to 20 ± 1.9 days, similar to that in C57BL/6 mice which received a vector encoding SCT-K^d-SYFP (17 ± 1.2 days). Median graft survival in no vector control mice was 12.5 ± 0.6 days for C57BL/6 and 10 ± 0.6 days for TAP1KOHep (Figure 5e). Failure to induce tolerance was not associated with loss of transgene expression in the transduced livers (supplementary Figure 5). Instead, progressive loss of ability of H-2K^d gene transfer to prolong B6.Kd skin graft survival correlated with increasing disturbance of the hepatocyte K^d peptide repertoire in the various experimental groups. These findings, along with the inability of SCT-K^b vectors to induce tolerance in polyclonal alloreactive T

cell populations demonstrate the importance of the hepatocyte immunopeptidome in transplantation tolerance induction following donor MHC I gene transfer to the liver.

Profiling the tissue-specific immunopeptidomes of hepatocytes, skin and spleen

Given the ability of H-2K^b or K^d HC expressed in recipient hepatocytes to induce tolerance to allogeneic skin grafts and to downmodulate responses against donor splenocyte stimulators[1, 3], we postulated that the peptides critical for allorecognition and tolerance induction would be found within a subset common to these three tissue types. The self-peptide repertoires of transduced hepatocytes, grafted donor skin and donor spleen were determined using a combination of immunoaffinity purification and RP-HPLC to liberate and collect peptide containing fractions from associated MHC I with LC-MS/MS for peptide identification, for both the 178.3 to B10.BR (K^b mismatch, H-2^k background) and B6.Kd to C57BL/6 (K^d mismatch, H-2^b background) strain combinations, as outlined in Figure 6a. The lists of common peptides are found in supplementary Table 2 (H-2K^d) and supplementary Table 3 (H-2K^b). For H-2K^d, 880 common peptides were identified across the three tissue types (Figure 6b), whereas there were 1083 common K^b-binding peptides (Figure 6c). The peptide length distributions (Figure 6d and f) and binding motifs (Figure 6e and g) were as anticipated for the respective allomorphs and were similar across tissue types. Of note, the common peptide pool was more limited when TAP-sufficient, or particularly TAP-deficient hepatocytes had been transduced with HC-K^d-YCAC (324, 347 and 36 unique peptides respectively), compared to TAP-sufficient hepatocytes transduced with HC-K^d (880 unique peptides) (Figure 6h). Comparison of the different tissue immunopeptidomes showed that in the two settings where skin graft tolerance was achieved in wild-type recipient mice following expression of allogeneic donor MHC I in hepatocytes, the proportion of skin peptides common to hepatocytes was 43% and 45% for H-2K^d (Figure 6b) and H-2K^b (Figure 6c), respectively. Conversely, only 1.6% of skin peptides were also found in TAP1KOHep hepatocytes transduced with AAV-HC-K^d-YCAC, while in the two groups with intermediate graft survival (TAP1$^{fl/fl}$ or C57BL/6 inoculated with AAV-HC-K^d-YCAC), the proportion of skin peptides present in

hepatocytes was in the order of 15-17%. Gene ontology analysis of source proteins is shown in supplementary Figure 4c.

H-2K^b peptides from the common peptide pool are recognised by activated alloreactive CD8$^+$ T cells.

A total of 100 peptides were selected for screening (listed in supplementary Table 4). 96 peptides were drawn from the common peptide pool, and their identity was confirmed by a direct comparison between the mass spectra obtained from synthetic and eluted natural peptides. Representative spectra from three peptide pairs, along with the Pearson correlation coefficient and the corresponding p-value between the $\log_{10}$ intensities of identified b- and y-ions in synthetic and sample-derived spectra is shown in Figure 7a. For all peptides, $p < 0.05$. A further four peptides had been previously identified as alloreactive CD8$^+$ T cell epitopes in B10.BR mice[11, 25]. Three of these four epitopes were detected within the common pool. Binding of pMHC tetramers was used to determine which peptides combined with H-2K^b to form immunogenic epitopes recognised by alloreactive B10.BR CD8$^+$ T cells. B10.BR mice were first primed by placement of a K^b-bearing 178.3 skin graft. Approximately 30 days after graft rejection, mice were inoculated with AAV-HC-K^b, and after a further 7 days, liver leukocytes were isolated and stained by flow cytometry (Figure 7b). The gating strategy is shown in Figure 7c. Activated CD8$^+$ T cells were defined as CD44$^+$PD-1^{hi}, whereas PD-1$^-$ cells were considered to be an internal control population, which had been exposed *in vivo* to H-2K^b expressed on hepatocytes but were not activated. Peptides were deemed immunogenic when ≥2% of CD44$^+$PD-1^{hi} CD8$^+$ T cells were bound by pMHC tetramer. Representative flow plots demonstrating T cell recognition of immunogenic and non-immunogenic peptides are shown in Figure 7d, and data summarising the results are shown in Figure 8a and supplementary Table 4. Allorecognition of K^b-bound peptides was then examined in recipient mice of a second background haplotype (BALB/c, H-2^d) (Figures 8a-b and Supplementary Table 4).

Of 100 peptides screened, 17 peptides were recognised by >5% of activated recipient CD8$^+$ T cells from male B10.BR mice (termed strongly immunogenic), and a further 39 were bound by 2-5% of

cells (moderately immunogenic). These responses were mirrored in female B10.BR recipients (Figures 8a-b). A number of pMHC epitopes were recognised by BALB/c mice as well as B10.BR (Figures 8a-b). All peptides recognised by >5% of B10.BR responder cells and 42/43 of those binding > 5% of BALB/c cells were 8-mers. For 8-mer peptides, there was a strong correlation between overall peptide abundance (as estimated by the product of the spectral intensity across the three tissue types) and the percentage of T cells with specificity for a given pMHC ($r = 0.52$, $p < 0.0001$, Figure 8c). No such relationship was observed for 9-mers. Predicted peptide binding affinity for H-2K^b (measured by IC_{50}) did not differ significantly between strongly, moderately or non-immunogenic peptides (Figure 8d, $p = 0.098$ by one-way ANOVA), nor was a correlation observed between IC_{50} and spectral abundance (Figure 8e). Simultaneous staining with two different pMHC tetramers was used to evaluate the proportion of T cells recognising more than one pMHC specificity, with a total of six peptides being evaluated. A substantial proportion of T cells recognised two peptides (SGYIYHKL and/or SVYVYKVL) in addition to SNYLFTKL (86.7% of T cells recognising SGYIYHKL-PE could recognise SNYLFTKL-APC and 66.8% of T cells recognising SVYVYKVL-PE could also recognise SNYLFKTKL-APC), whereas cross-reactivity between VGPRYTNL, INFDFPKL and RTYTYEKL was considerably lower (Figure 8f-g). When 5 of these 6 peptides (excluding SGYIYHKL), each binding between 7.2 and 15.2% of T cells, were used together as a panel the proportion of alloreactive CD8$^+$ T cells bound increased to 39.1% (Figure 8i, $p= 0.002$ compared with SNYLFTKL). This cumulative increase in binding is consistent with alloreactive T cell recognition of epitopes comprising both a self-peptide and allogeneic MHC I molecule, and suggests that the development of pMHC multimer panels for the identification and tracking of alloreactive T cell populations is feasible.

Discussion

Direct allorecognition refers to the engagement of recipient TCRs by intact allogeneic MHC molecules on the surface of donor cells. In some settings, intact, unprocessed donor MHC is transferred to the surface of recipient APC, a variant known as the semi-direct pathway of allorecognition[26]. While direct/semi-direct allorecognition is a critical driver of both solid organ

allograft rejection[26] and tolerance induction[3], the specific molecular targets of most directly-alloreactive CD8+ T cells have not been defined, limiting our understanding of these phenomena. In this study, we provide definitive evidence for the contribution of the peptide cargo of allogeneic MHC I molecules to transplant tolerance induction. Moreover, we demonstrate the feasibility of a systematic approach incorporating mass spectrometry-based identification of alloantigen-presented peptides, alloreactive T cell enrichment and pMHC multimer screening for the discovery of pMHC epitopes that are directly recognised by alloreactive CD8+ T cells. To our knowledge, this represents the first example of such an approach in the context of direct allorecognition.

Studies over many years using T cell clones suggested that most directly alloreactive CD8+ clones recognise allogeneic MHC I molecules complexed with an endogenous peptide, while peptide-independent direct allorecognition was also reported. Our recent findings that direct recognition of hepatocyte-expressed donor MHC I by recipient CD8+ T cells was required for donor skin graft tolerance induction provided us with a unique opportunity to examine the role of the hepatocyte immunopeptidome in transplant tolerance induction, and by extension, in alloresponses more broadly. We used two complementary approaches to separate expression of donor MHC I molecules from presentation of their usual peptide cargo. In the first approach, we utilised an AAV vector encoding H-2K^b HC, β2m and the single peptide KIITYRNL to express high levels of K^b on the surface of recipient hepatocytes, while excluding presentation of naturally-processed endogenous peptides. Tolerance to K^b-bearing skin grafts was able to be induced in reconstituted mice with a monoclonal population of T cells all recognising the K^b-KIIT epitope, but not in wild-type mice possessing a full TCR repertoire. Secondly, we expressed a mutated version of the H-2K^d HC, which is permissive to loading with suboptimal peptides in a purpose-bred mouse strain (TAP1KOHep) with a hepatocyte-specific deletion of Tap1. This combination resulted in a significant alteration of the K^d-bound peptide repertoire and prevented tolerance induction. Graft survival was shortened to a lesser extent in TAP1-sufficient mice transduced with AAV-HC-K^d-YCAC, in keeping with the lesser perturbation of the K^d peptide repertoire observed in these mice. The point mutations Y84C and A139C in the K^d HC permit the creation of a disulphide bridge which

stabilises the peptide binding groove when empty or populated by a low-affinity peptide[18]. The presence of these mutations alters the composition of the K^d-associated peptide repertoire but does not impede T cell responses to a given pMHC ligand[24]. Accordingly, the ubiquitous peptide SYFPEITHI was present within the repertoires of all hepatocytes transduced with either AAV-HC-K^d or AAV-HC-K^d-YCAC and comparable proportions of T cells isolated from the livers of these mice bound K^d-SYFP dextramers.

Having demonstrated the importance of the peptide cargo of allogeneic MHC I molecules for transplant tolerance induction, we set about identifying the subset of peptides responsible for modulating the anti-graft alloresponse, using an immunoproteomic approach to identify and characterise the immunopeptidomes of relevant tissues. We hypothesised that hepatocyte expression of peptides that were also presented by cells in the grafted skin underpinned tolerance induction. Consistent with this hypothesis, in conditions where tolerance was achieved, 43% of K^d-associated peptides and 45% of K^b-bound peptides from transduced hepatocytes were also expressed in donor skin. When survival prolongation was minimal, only 1.6% of hepatocyte K^d-bound peptides were common to donor skin, and this shared proportion increased to 15-17% in the groups with intermediate graft survival. This data in combination with our previous observations that expression of allogeneic MHC I in recipient liver reduces IFN-γ ELISPOT responses against donor splenocyte stimulators, implied that the critical set of self-peptides would be concentrated amongst those common to all three tissue types.

We next set out to determine which peptides from this shared subset would be recognised by alloreactive T cells using tetramer binding assays. We generated an enriched population of alloreactive $CD8^+$ T cells in the liver by priming mice with a skin graft expressing H-2K^b, followed by boosting with liver-specific AAV-HC-K^b. Co-expression of CD44 with high levels of PD-1 allowed us to distinguish between activated cells and bystander cells which had been exposed to the alloantigens, but had not responded. Of the 100 K^b-binding peptides selected for tetramer screening, 17 were recognised by >5% of the enriched alloreactive T cell population. INFDFNTI,

previously reported to be recognised by a large proportion of the polyclonal alloreactive T cell population of B10.BR mice[25] was bound by an average of 3.7% of male B10.BR cells.

To examine factors which might contribute to the immunogenicity of different pMHC, we used spectral intensity as an approximation for relative peptide abundance and IC_{50} to predict binding affinity of the peptide for H-2K^b. An overall measure of abundance, was derived by multiplying the spectral intensity recorded in each of the three tissues. For 8-mer peptides, a strong correlation was found between abundance and the proportion of $CD8^+$ T cells recognising particular peptides. This is at variance with observations of $CD8^+$ T cell recognition of K^b-associated viral epitopes, where the frequency of T cells responding to a given epitope corresponds weakly at best to epitope abundance[27, 28]. In contrast, while there was a tendency for the strongly immunogenic peptides to have high predicted affinity for K^b, there was no significant difference in IC_{50} between the strongly-, moderately- and non-immunogenic groups, nor was there an association between IC_{50} and peptide abundance. While a prediction of immunogenicity based on peptide abundance is no substitute for direct measurement, these findings suggest that the likelihood of finding strongly immunogenic peptides is greater if the search is targeted towards the most highly-represented peptide species. The relationship between abundance and immunogenicity did not apply to 9-mer peptides. A staining panel comprising only five strongly immunogenic pMHC epitopes identified nearly 40% of T cells in an enriched alloreactive population; we anticipate that an expanded panel will capture an even greater proportion of alloreactive cells, and that such panels could be used to enumerate, track and phenotype polyclonal alloreactive T cell populations.

One intriguing finding of this study was the broad overlap between strongly immunogenic K^b-peptide epitopes recognised by BALB/c and those first identified in B10.BR mice (13/17 peptides). Further studies in mouse and human subjects will be needed to establish the prevalence of such ‘super-epitopes” recognised by allogeneic T cells across several genetic backgrounds. While extensive cross-reactivity is a feature of self MHC-restricted T cells, the range of possible cross-reactive epitopes is constrained by peptide length, with T cell clonotypes showing a strong

preference for a single length peptide[29]. Alloreactive T cell clones have undergone positive selection during thymic development based on self-MHC. The majority of peptides eluted from H-2K^k are 8-mers ([30] and supplementary data 1) which aligns with the result that in male B10.BR mice (H-2^k) 17/79 8-mer peptides but 0/21 9-mers were strongly immunogenic. Most peptides associated with the H-2^d allomorphs D^d, L^d and K^d are nonamers[30], yet 42/79 8-mers and only 1/21 9-mers were strongly immunogenic in BALB/c (H-2^d) mice. Possible explanations for this asymmetry are that cross-reactivity involving an allogeneic MHC molecule is not subject to the same peptide length limitations as cross-reactivity between self MHC-restricted peptide epitopes, or that a small number of octamer-preferring CD8$^+$ T cells from BALB/c mice expand preferentially in the presence of H-2K^b presenting mainly 8-mers. While the mean H-2K^b IC_{50} among the 9-mer peptides was greater than that of the 8-mers, a number of 9-mer peptides were in the same IC_{50} range as the strongly immunogenic 8-mers, so this is unlikely to fully explain the reduced frequency of recognition of 9-mer peptides.

The findings of this study open a number of avenues for future research. Firstly, they suggest an approach for the systematic discovery of pMHC epitopes for directly alloreactive CD8$^+$ T cells which may be adapted to additional MHC I allomorphs in mice, humans and other species. Identification of large numbers of allogeneic pMHC epitopes will enable the characterisation of alloreactive TCR repertoires, including biophysical and structural studies with many more receptor-ligand pairs than the handful currently known, which in turn will provide further insights into the fundamental basis of alloreactivity. Systematic allogeneic pMHC epitope discovery is complemented by the recent advent of methodologies such as oligonucleotide barcoding permitting the use of pMHC multimers for parallel tracking and enumeration of >1000 individual pMHC specificities, with options for coupling to single cell TCR sequence and gene expression analyses[31, 32]. pMHC multimers conjugated with radionuclides are sensitive tools which could be applied to *in vivo* imaging of specific alloresponses[33]. Beyond their potential as research reagents, allospecific pMHC multimers could enhance post-transplant immune monitoring and immunophenotyping of directly alloreactive T cells in a clinical setting. Finally, pMHC multimers

are not only reagents for antigen-specific T cell detection, but potential vehicles for antigen-specific therapy, which may be employed for the depletion or immunomodulation of alloreactive T cells[34]. In conclusion, the findings of this study represent a significant advance in our understanding of the role of endogenous peptides in direct T cell alloreactivity. They will enable exploration of the alloreactive T cell repertoire and potential translation to clinically-applicable tools.

Methods

Peptides, antibodies and reagents

Peptides were synthesised with an average of 98% purity (GL Biochem Shanghai Ltd.). The lyophilised peptides were reconstituted in 10% DMSO and all peptides were stored at -80°C. Dasatinib (Sigma-Aldrich, catalogue# CDS023389) was reconstituted in DMSO and 5 mM stock was stored at -80°C. Antibodies used in experiments are summarised in Supplementary Table 4.

Cell Lines

The *Tap2* deficient T lymphoma cell line RMA-S was cultured in RPMI 1640 medium supplemented with L-glutamine (Lonza, catalogue# 12-702F), penicillin-streptomycin (Invitrogen, catalogue# 15140) and 10% FCS (Sigma-Aldrich, catalogue# 13K179) at 37°C with 5% CO_2.

RMA-S peptide stabilisation and transfection

RMA-S cells were grown to confluence and passaged to a concentration of 3×10^5 cells/mL then transferred to flat-bottomed 24 well culture plates. The cells were incubated at 27°C for 20 hours with 5% CO_2, then pulsed with 6 different concentrations of peptides ranging from 0.0001 – 10 µM. The cells were incubated with peptides at 27°C for 1 hour then returned to 37°C for 2 hours. The surface expression of stabilised H-2K^b was quantified using flow cytometry with the conformation-dependent mAb Y-3 antibody, which binds to correctly folded K^b molecules stabilised with peptides. For transient transfection of RMA-S cells, 2×10^6 cells were nucleofected with 2 µg of pcDNA3.1$^+$ plasmid carrying a gene insert of interest per reaction (Lonza-AMAXA program X-001, Nucleofector 2b). 24 hours after transfection, the expression of the transgene was checked using flow cytometry.

Mice

Unless otherwise stated, mice were bred at the University of Sydney (Camperdown, Australia). 178.3 mice (originally provided by Drs. W. Health and M. Hoffman, Walter and Eliza Hall Institute, Melbourne, Australia) express a transgenic MHC class I molecule H-2K^{b} ubiquitously, under the control of its own promoter, on a B10.BR (H-2^{k}) background. Des-TCR mice express an H-2K^{b}-specific TCR, which recognises the peptides KVITFIDL, KVLHFYNV and KIITYRNL restricted by H-2K^{b} and Des-TCR is identifiable by a clonotypic mAb (Désiré). Des-RAG mice were obtained by crossing Des-TCR mice with CD45.1$^{+/+}$ RAG1$^{-/-}$ mice, which are both on a B10.BR (H-2^{k}) background. OT-I mice carry a TCR which recognises the peptide SIINFEKL presented by H-2K^{b}. OT-I were crossed with RAG1$^{-/-}$ mice to create the OT-I-RAG line. These mice were bred at the Centenary Institute. C57BL/6J^{Arc} (H-2^{b}) and BALB/c (H-2^{d}) mice (termed C57BL/6 and BALB/c) were purchased from the Animal Resources Centre, Perth, Australia. B6.Kd mice express an H-2K^{d} transgene ubiquitously on a C57BL/6 (H-2^{b}) background. B6.Kd mice were originally developed by R. Pat Bucy at the University of Alabama (Tuscaloosa, Alabama, USA) and were provided by Robert Fairchild, Cleveland Clinic (Cleveland, Ohio, USA). B6.Kd mice were backcrossed for 4 generations to C57BL/6J, prior to use. TAP1KOHep mice were generated based on the conditional-ready strain 09400, C57BL/6N-Tap1<tm2a(EUCOMM)Hmgu>/Ieg, developed as part of the European Conditional Mouse Mutagenesis programme (EUCOMM)[35]. Mice heterozygous for the Tap1tm2a allele on the C57BL/6N genetic background were obtained from the European Mutant Mouse Archive, based at Helmholtz Zentrum. These mice were backcrossed to C57BL/6J^{Arc}, then intercrossed with FLPo deleter (B6.129S4-*Gt(ROSA)26SOR*$^{tm2(FLPo)Sor}$/J) mice[36] (imported from the Jackson Laboratory, Bar Harbor, ME) to generate mice carrying the Tap1tm2c (floxed) allele. FLPo was bred out by backcrossing to C57BL/6J^{Arc}, following which the mice were crossed to Albumin-Cre mice (B6.FVB(129)-Tg(Alb1-cre)1Dlr/J)[37]. TAP1KOHep mice are homozygous for the floxed Tap1 allele (Tap1tm2c) and have one copy of Cre, which is expressed exclusively in hepatocytes resulting in hepatocyte-specific deletion of the floxed Tap1 allele. Genotyping and genetic background testing was performed on earpunch tissue, isolated hepatocytes or spleen by Transnetyx (Cordova, TN, USA). The genetic background of TAP1KOHep and TAP1$^{fl/fl}$ control mice was at least 91.3% C57BL/6J (91.3-97.9%) and these mice did

not reject syngeneic skin grafts from C57BL/6J donors (not shown). Further characterisation of this strain is shown in Figure 4 and Supplementary Figure 3.

Male and female mice aged between 8 and 12 weeks were used in this study. Male mice were used unless stated otherwise. At the termination of each experiment, tissues were collected under general anaesthesia. Frozen tissues were stored at -80°C. All animal procedures were approved by the University of Sydney Animal Ethics Committee (protocol 2017/1253) and carried out in accordance with the Australian code for the care and use of animals for scientific purposes.

AAV vectors

H-2K^b and H-2K^d were cloned as previously described[3]. An SCT construct with a disulphide trap consists of a defined peptide sequence, β2m and MHC I HC joined together by flexible linkers[16]. The construct encodes a signal peptide sequence followed immediately by a defined peptide sequence, then a linker of GCGAS$(G_4S)_2$, a β_2m sequence, a linker of $(G_4S)_4$ and either a HC H2-K^b or H2-K^d sequence. A tyrosine to cysteine substitution at HC position 84 and a cysteine at the second position of the peptide-β_2m linker form the disulphide trap[17]. dt-SCT (H-2K^b) constructs with defined peptide sequences KIITYRNL or SIINFEKL and a dt-SCT (H-2K^d) construct with a defined peptide sequence SYFPEITHI were designed *in silico* (termed SCT-K^b-KIIT, SCT-K^b-SIIN and SCT-K^d-SYFP, respectively), codon-optimised and were synthesised by GeneArt (Thermo Fisher Scientific). Also, H2-K^d sequence incorporating the Y84C and A139C mutations were created *in silico* (termed K^d-YCAC), codon optimised and was synthesised by GenScript. All synthesised genes were delivered in pcDNA3.1$^+$ plasmids. The full-length native chicken ovalbumin (OVA) gene inserted in a pcDNA3.1$^+$ plasmid (clone ID: OGa28271) was purchased from GenScript. Gene inserts from pcDNA3.1$^+$ plasmids were cloned into the pAM2AA backbone incorporating the human α-1 antitrypsin, liver-specific, promoter and human ApoE enhancer flanked by AAV2 inverted terminal repeats. Each gene was then packaged into an AAV2/8 vector, purified, and quantitated as previously described[38]. AAV Vectors were either produced in-house or by the Vector and Genome Engineering Facility, Children's Medical Research Institute, Westmead, Australia. AAV2/8 vector aliquots were stored at -80°C. All vectors were used at a dose of 5×10^{11} vgc except AAV-SCT-K^b-KIIT which was used at 2×10^{12} vgc. AAV2/8 vectors

in 500 µL sterile PBS were administered to male mice via penile vein intravenous injection and to female mice via tail vein intravenous injection under general anaesthesia.

Skin transplantation

Skin transplantation was performed as described previously[3]. In short, full-thickness grafts of 1x1cm^2 tail skin from donor mice were grafted onto the dorsum of anaesthetised recipient mice whose graft bed has been shaved and a small 1 x 1 cm^2 area excised to accommodate the donor skin graft. The graft was fixed using cyanoacrylate tissue adhesive (Dermabond, Ethicon, catalogue# ANX12) and bandaged. Mice received analgesia with buprenorphine (Temgesic, Schering-Plough, 0.05 mg kg^{-1} s.c.), prophylactic ampicillin (Alphapharm, 100 mg kg^{-1} s.c.) and 0.5 ml of warmed saline. The bandage was removed 7-10 days later and the grafts were regularly monitored for 100 days post-transplant. Grafts were deemed rejected when less than 20% of the viable skin graft remained. B10.BR and B10.BR-RAG mice (H-2^k) received H-2K^b singly-mismatched allogeneic skin grafts from 178.3 strain donor mice. C57BL/6, TAP1$^{fl/fl}$ and TAP1KOHep mice (H-2^b) received H-2K^d singly-mismatched allogeneic skin grafts from B6.Kd donor mice. BALB/c mice (H-2^d) received fully allogeneic skin grafts from C57BL/6 donor mice. Skin transplant donors and recipients were sex-matched.

Hepatocyte isolation

Retrograde perfusion of the liver was achieved by cannulating the inferior vena cava (IVC) and allowing the perfusate to flow out of the liver via the transected hepatic portal vein. The liver was sequentially perfused with the following solutions at a flow rate of 5 ml/min (administered using a Masterflex L/S 7528-30, Thermo Fisher Scientific); firstly with 25 ml of HBSS (Lonza, catalogue# 10-543F), then with 25 ml of HBSS with 0.5 mM EDTA (MilliporeSigma, catalogue# E6758), followed by 25 ml of HBSS, and finally with 25 ml of HBSS plus 5 mM $CaCl_2$ (calcium chloride, MilliporeSigma, catalogue# C5670) and 0.05% of collagenase Type IV (Thermo Fisher Scientific, catalogue# 17104019). All solutions were warmed to 37°C. The gallbladder was removed and the liver was gently agitated in cold RPMI 1640 medium containing 2% FCS (RPMI/FCS2) to collect the hepatocytes. The hepatocyte slurry was centrifuged at 50 *g* for 3 minutes and washed twice. The hepatocyte slurry was resuspended in isotonic Percoll PLUS (GE Healthcare Life Sciences)/PBS and centrifuged at 500 *g* for 15 minutes at RT. The

hepatocyte pellet was collected, washed twice, resuspended in RPMI/FCS2 medium and analysed using flow cytometry. Hepatocytes for immunoaffinity purification experiments underwent further washing with cold PBS before being stored at -80°C.

Leukocyte isolation from liver, spleen, and draining lymph nodes

For liver leukocyte isolation, the IVC was cannulated and the hepatic portal vein was transected. The liver was flushed with 20 ml of PBS at RT and after gall bladder removal, the liver was meshed through a 100 µm cell strainer and washed through with cold RMPI/FCS2 medium. The liver slurry centrifuged at 400 *g* for 10 minutes and washed twice. The liver slurry was purified using isotonic Percoll PLUS gradient separation as described above. The supernatant was discarded, and the liver leukocyte pellet was then washed before being resuspended in red cell lysis buffer for 2 minutes at RT. Following this, the liver leukocytes were washed twice and analysed using flow cytometry. For splenocyte isolation, the spleen was pressed through a 70 µm nylon mesh strainer, washed and resuspended in red cell lysis buffer for 2 minutes at RT. The splenocytes were washed twice and analysed using flow cytometry. For isolating lymphocytes from draining lymph nodes, the nodes were ruptured through a 40 µm nylon mesh strainer and then prepared as for splenocytes, with the omission of the red cell lysis step.

Adoptive transfers

Lymphocytes from portal and mesenteric lymph nodes were collected and processed as detailed above. Cells resuspended in RPMI 1640 medium containing 10% FCS was labelled with 10 µM CFSE dye (Thermo Fisher Scientific, catalogue# C34570) for 4 minutes at RT. The reaction was quenched by adding more RPMI 1640 medium containing 10% FCS. CFSE-labelled lymphocytes were washed with cold RMPI/FCS10 medium, filtered through 40 µm nylon mesh and resuspended in 500 µL cold sterile PBS. CFSE-labelled lymphocytes were administered via penile vein intravenous injection under general anaesthesia. CFSE-labelling and cell viability were assessed using flow cytometry.

Histology and immunostaining

For immunohistochemical staining, OCT-embedded frozen tissues were cut into 6 µm thick sections. Sections were allowed to air dry for 1 hour at room temperature (RT) prior to fixation in acetone for 8

minutes at RT. Sections were blocked with 20% normal mouse serum (MilliporeSigma, catalogue# M5905) and 5% normal porcine serum (Thermo Fisher Scientific, catalogue# 31890) for 20 minutes at RT and they were stained with FITC-conjugated primary antibodies against H-2K^b (AF6-88.5, BioLegend), H-2K^d (SF1-1.1, BD Biosciences), CD4 (GK 1.5, BD Biosciences), CD8α (53-6.7, BioLegend), F4/80 (BM8, BioLegend), B220 (RA3-6B2, BD Biosciences), CD11c (N418, BioLegend) or CD19 (6D5, BioLegend) or the corresponding isotype controls for 30 minutes at RT. Sections were then stained with horseradish peroxidase-conjugated rabbit-anti-FITC secondary antibody (Bio-Rad, catalogue# 4510-7864) before development with diaminobenzidine (DAB) substrate chromogen system (Dako, catalogue# K3468). Sections were counterstained in Mayer's hematoxylin solution (MilliporeSigma, catalogue# MHS16) for 2 minutes and mounted with Fronine safety mount No.4 (Thermo Fisher Scientific, catalogue# FNNII068). Tissue processing and H&E staining were performed by the Histopathology Laboratory, Discipline of Pathology, Sydney Medical School. For H&E staining, 5 µm thick sections from formalin fixed paraffin embedded tissues were used.

Confocal imaging

The livers of freshly-sacrificed mice were perfused retrogradely via the IVC (as above) with 3 ml of PBS and then 10 ml of 2% paraformaldehyde (Sigma, catalogue# 30525-89-4) in PBS. The gallbladder was removed and the liver was fixed in 2% paraformaldehyde in PBS for 8 hours. A section of the liver was embedded in 3% agarose (Fisher Biotec, catalogue# AGR-LM-50) and 150 µm thick sections were cut using a Vibratome 1000 Plus Sectioning System (Harvard Apparatus, Holliston MA). Sections were blocked with 4% bovine serum albumin (Tocris bioscience, catalogue# 9048-46-8), 5% normal goat serum (Invitrogen, catalogue# 31873) and 0.3% Triton-X 100 (Sigma, catalogue# 9002-93-1) in PBS for 20 hours at 4°C. Sections were stained with primary antibodies; anti-mouse CD31-AF488 (PECAM-1, BioLegend), anti-mouse CD45-AF647 (30-F11, BioLegend), anti-mouse CK19 purified (EPNCIR127B, Abcam) and anti-mouse H-2K^b purified (Y-3, WEHI), for 20 hours at 4°C. Sections were washed, then incubated with secondary antibodies [anti-rabbit IgG-AF750 (polyclonal, catalogue# A21039, Invitrogen) and anti-mouse IgG2b-PE (RMG2b-1, BioLegend)], for 20 hours at 4°C, followed by staining with DAPI (Sigma, catalogue# 28718-90-3) for 1 hour at 4°C. Primary and secondary antibodies were made in blocking buffer. Washing buffer comprised 0.1% Triton-X 100 in PBS. Images

were acquired using a Leica SP8 confocal microscope at 93x objective magnification with a numerical aperture of 1.35. The images were analysed using Imaris v9.5 (Oxford instruments).

Flow cytometry

Cells resuspended in cold staining buffer (2% FCS in PBS) were blocked with mouse Fc Block (BD Biosciences, catalogue# 553141) for 10 minutes at 4°C and stained with a panel of antibodies (Supplementary Table 1). Cells were washed twice with PBS before staining with Zombie NIR viability dye (BioLegend, catalogue# 423105) for 15 minutes at RT. Cells were washed with the staining buffer before analysis. The samples were analysed using LSR Fortessa X-20 (BD Biosciences) and analysis of data was performed using FlowJo v10 (BD).

ELISpot

IFN-γ ELISpot assays were performed according to the manufacturer's protocol (U-Cytech, catalogue# CT317-PR5). RMA-S cells either pulsed with peptides or transiently transfected with dt-SCT plasmids, were irradiated with a dose of 3000 rad. Responders were either OT-I-RAG or Des-RAG splenocytes. For pre-stimulation, 1×10^6 irradiated stimulator cells and 1×10^6 responder splenocytes were suspended in 250 µL of RPMI/FCS10 medium with penicillin-streptomycin in each well of a 96-well U-bottom plate (Corning, catalogue# 3788). They were cultured at 37°C with 5% CO_2 for 24 hours and then transferred into an antibody-coated polyvinylidene difluoride (PVDF) plate, serially diluted, and incubated for a further 16 hours. The plates were then developed, and the spots were counted using an AID iSpot plate reader as previously described[1].

pMHC multimer staining

The pMHC multimer staining method has been adapted from that of Dolton *et al.*[39]. Cells were incubated with a protein kinase inhibitor, 50 nM dasatinib, for 30 minutes at 37°C. PE- or APC-conjugated tetramers or dextramers were centrifuged at 16,000 *g* for 1 minute to remove aggregates. The cells were stained with 0.5 µg of pMHC tetramer or pMHC dextramer at 6.4 nM in 50 µL unless stated otherwise for 30 minutes on ice. Following pMHC multimer staining, the cells were washed with cold FACS staining buffer twice. Blocking with mouse Fc Block (BD Biosciences, catalogue# 553141) was

performed for 10 minutes at 4°C and either or both of mouse anti-PE (clone PE001, BioLegend) and anti-APC (clone APC003, BioLegend) biotin-conjugated antibodies were added at 0.5 µg/100 µL to the cells depending on the pMHC multimer conjugates used. The cells were washed and the following antibodies were then added for 30 minutes at 4°C: anti-PD-1-BV421 (29F.1A12, BioLegend), anti-CD8-FITC (KT-15, Invitrogen), anti-CD14-BV605 (rmC5-3, BD Bioscience), anti-CD19-BV605 (6D5, BioLegend), anti-CD44 (IM7, BioLegend) and anti-CD90.2-PerCPCy5.5 (53-2.1, BioLegend). Cells were washed twice with PBS before staining with Zombie NIR viability dye (BioLegend, catalogue# 423105) for 15 minutes at RT. Cells were washed with staining buffer before analysis. The samples were analysed using LSR Fortessa X-20 (BD Biosciences) and analysis of data was performed using FlowJo v10.

Dextramers were purchased from Immudex. QuickSwitch Custom Tetramer Kits (MBL International) were utilised to generate multiple tetramers with selected peptides in order to screen an array of pMHC epitopes. Quantitation of peptide exchange with selected peptides was performed according to the manufacturer's protocol.

Immunoaffinity purification

Two replicate samples were prepared for each tissue or experimental group. Around 1×10^8 purified hepatocytes from 4 - 5 mice were pooled per sample. Hepatocytes were lysed in 0.5% IGEPAL, 50 mM Tris (pH 8), 150 mM NaCl and protease inhibitors (Roche cOmplete Protease Inhibitor Cocktail; Merck, catalogue# 11836145001). Spleens, skin grafts (on d7 post-transplant) or tail skins from 5 - 9 donors were pooled per sample. Spleen and skin samples were ground in a Retsch Mixer Mill MM 400 under cryogenic conditions and then lysed in 0.5% IGEPAL, 50 mM Tris (pH 8), 150 mM NaCl, and protease inhibitors. Lysates were incubated for 1 hour at 4°C, then cleared by ultracentrifugation (40,000 rpm, 30 min) and MHC complexes were isolated from supernatant by immunoaffinity purification using solid-phase-bound monoclonal antibodies SF1-1.1.10 (anti H-2K^d), K9-178 (anti H-2K^b), Y3 (anti H-2K^b/K^k) and 28.14.8s (anti H-2D^b) as described previously[40]. Peptides were dissociated from the MHC with 10% acetic acid. For purified hepatocyte and spleen samples, the mixture of peptides, class I HC and β2m was fractionated on a 4.6 mm internal diameter × 100 mm monolithic C18 column (Chromolith SpeedROD; Merck Millipore, catalogue# 1021290001) using an ÄKTAmicro RP-HPLC (GE Healthcare)

system, running a mobile phase consisting of buffer A (0.1% trifluoroacetic acid; Thermo Fisher Scientific) and buffer B (80% acetonitrile, 0.1% trifluoroacetic acid; Thermo Fisher Scientific), running at 1 mL min^{-1} with a gradient of B of 2–40% over 4 min, 40–45% over 4 min and 45–99% over 2 min, collecting 500 µL fractions. Peptide-containing fractions were either unpooled or combined into pools, vacuum-concentrated and reconstituted in 0.1% formic acid (Thermo Fisher Scientific) for mass spectrometry analysis. For tail skin samples, the mixture of peptides, class I HC and β2m was purified using Millipore 5 kDa Amicon centrifugal units (Human Metabolome Technologies; catalogue# UFC3LCCNB_HMT) in 0.1% trifluoroacetic acid. Peptides were extracted and desalted from the filtrate using ZipTip C18 pipette tips (Agilent Technologies, catalogue# A57003100K) in a final buffer of 30% acetonitrile, 0.1% trifluoroacetic acid. Peptide samples were vacuum-concentrated and reconstituted in 0.1% formic acid for mass spectrometry analysis.

Mass Spectrometry

Reconstituted peptides were analysed by LC-MS/MS using an information-dependent acquisition strategy on a Q-Exactive Plus Hybrid Quadrupole Orbitrap (Thermo Fisher Scientific, Bremen, Germany) coupled to a Dionex UltiMate 3000 RSLCnano system (Thermo Fisher Scientific) as described previously[31]. Briefly, peptides were trapped on a 2 cm Nanoviper PepMap100 trap column at a flow rate of 15 min using a RSLC nano-HPLC. The trap column was then switched inline to an analytical PepMap100 C18 nanocolumn (75 µm x 50 cm, 3 µm 100 Å pore size) at a flow rate of 300 nL/min using an initial gradient of 2.5% to 7.5% buffer B (0.1% formic acid 80% ACN) in buffer A (0.1% formic acid in water) over 1 min followed with a linear gradient from 7.5% to 32.5% buffer B for 58 min followed by a linear increase to 40% buffer B over 5 min and an additional increase up to 99% buffer B over 5 min. Survey full scan MS spectra (m/z 375–1800) were acquired in the Orbitrap with 70,000 resolution (m/z 200) after the accumulation of ions to a 5×10^5 target value with a maximum injection time of 120 ms. For Data Dependant Acquisition (DDA) runs, the 12 most intense multiply charged ions ($z \geq 2$) were sequentially isolated and fragmented by higher-energy collisional dissociation (HCD) at 27% with an injection time of 120 ms, 35,000 resolution and target of 2×10^5 counts. An isolation width of 1.8 m/z was applied and underfill ratio was set to 1% and dynamic exclusion to 15 sec. For Data Independent Acquisition (DIA) runs, the MS1 survey scan and fragment ions were acquired using

variable windows (Supplementary Table 6) at 35,000 resolution with an automatic gain control (AGC) target of 3e6 ions. The mass spectrometry data will be deposited to the ProteomeXchange Consortium via the PRIDE[41] partner repository.

DDA data analysis

For peptide identification, the acquired raw files were searched with PEAKS Studio X+ (Bioinformatics Solutions) against the *Mus musculus* (SwissProt) database. The parent mass error tolerance was set to 10 ppm and the fragment mass error tolerance to 0.02 Da. Oxidation of methionine (M) was set as variable modifications and a false-discovery rate (FDR) cut-off of 5% was applied.[42]

DIA data analysis

PEAKS Studio X+ was used to generate a spectral library from all DDA data. DIA raw files were imported to Spectronaut 11 Pulsar (Biognosys). The parent mass error tolerance was set to 10 ppm and the fragment mass error tolerance to 0.02 Da. Oxidation of M was set as variable modifications and a peptide list was exported at Q-value=1%.

Immunopeptidome analysis

Known contaminants were removed from the analysis. Unique peptides from the DDA (replicate 1) and DIA (replicate 2) datasets were combined to increase the coverage of the tissue immunopeptidomes. For analysis requiring spectral intensity values, only DDA datasets were used. Binding motifs of 8-mer peptides from samples that were immunoaffinity purified with K9-178 antibody (H-2K^b group) and 9-mer peptides from samples that had been immunoaffinity purified with SF1-1.1.10 antibody (H-2K^d group) were visualised using the GibbsCluster2.0 algorithm (NetMHC4.0)[43]. For comparison of unique H-2K^b peptides between different tissues, 8-mer to 11-mer peptides with a predicted half-maximum inhibitory concentration (IC_{50}) of binding to H-2K^b less than 500 nM (NetMHC4.0 database) were selected. For comparison of unique H-2K^d peptides between tissues, all 9-mer peptides were used. The source proteins associated with the eluted peptides were analysed using the PANTHER Gene Ontology classification system[44]. Function classification analysis and statistical over-representation tests were performed[45].

Validation of peptide identification using retrospectively synthesised peptides

We validated the identity of a panel of peptides by comparing chromatographic retention and MS/MS spectra of synthesised peptides (GL Biochem, Shanghai) with those of the corresponding eluted peptides. The PKL files of the synthetic and eluted peptides were exported from PEAKS X plus studio software. To evaluate the similarity between two spectra, we predicted all b- and y-ions for each sequence and then extracted the intensity for each ion (with a fragment mass error tolerance of 0.02 Da). The Pearson correlation coefficient and the corresponding p-value between the $\log_{10}$ intensities of identified b- and y-ions in the synthetic and sample-derived spectra were calculated[46]. The closer the correlation coefficient to 1, the greater identity between paired spectra. All tested peptides were found to have a *p*-value of less than 0.05.

Statistical Analysis and Data Visualisation

Data are represented as mean ± SEM unless otherwise stated. Unpaired Student's t-tests were performed to calculate statistical differences in a single variable between the means of two groups and one-way analysis of variance (ANOVA) in conjunction with Sidak's multiple comparison tests were used to calculate statistical differences between the means of three or more groups. For analysis of 2 variables, two-way ANOVA with Sidak's multiple comparison tests were used. Graft survival curves were compared using Mantel Cox log-rank tests. Synthetic and corresponding eluted peptide spectra were compared using Pearson correlation tests. The relationship between overall peptide abundance and alloreactive T cell binding, and the impact of differences in sexes and strains on alloreactive T cell binding, were analysed using linear regression and Pearson correlation tests. Statistical tests were performed using GraphPad Prism version 8.01 (GraphPad Software, La Jolla CA). Heatmaps were generated using Morpheus software (https://software.broadinstitute.org/morpheus).

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Author contributions

A.W.P., N.A.M., E.T.S., P.B., D.B. and A.F.S. designed experiments. E.T.S., M.P-H., P.F., S.H.R., M.L., K.E., A.B., N.L.D. and N.A.M. performed experiments. A.W.P., L.L., I.E.A. and P.B. provided reagents and/or samples. E.T.S., P.F., S.H.R., A.W.P., N.A.M. and A.F.S. analysed data. P.F., S.H.R., N.A.M., E.T.S. and A.F.S. wrote the manuscript. All authors read and approved the manuscript.

Competing Interests

E.T.S., M.P-H., A.F.S. (University of Sydney) and N.A.M., A.W.P., P.F., N.L.D. (Monash University) are named as co-inventors in a patent application filed by the University of Sydney and Monash University (PCT/AU2020/051221) covering the identification and use of certain peptides described in the publication.

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Figure Legends

Figure 1. Expression of SCT-K^b-peptide in mouse hepatocytes is robust and persistent

(a) Schematic diagram of SCT pMHC constructs. MHC I HC expressed in hepatocytes can bind endogenous peptides and associate with endogenous β2m to form a wide repertoire of pMHC complexes (left). Conversely, SCT constructs exclude binding of endogenous peptides and present a single type of pMHC epitope on the cell surface (right). B10.BR mice were inoculated with AAV-SCT-K^b-KIITYRNL **(b)** or AAV-SCT-K^b-SIINFEKL **(c)**. On days 2, 4, 7, 14, 28 and 100 post-inoculation, tissues were collected for analysis (n = 3 for each time point). Representative immunostained (IHC) and H&E images show transduced liver sections. Robust expression of H2-K^b or H-2K^d was present through day 100 post-inoculation. Histologic examination of the liver sections was normal. Levels of aspartate transaminase (AST) and alanine transaminase (ALT) did not increase significantly from baseline in mice treated with AAV-SCT-K^b-KIITYRNL (one-way ANOVA, p = 0.4 for AST and p = 0.21 for ALT) or in mice receiving AAV-SCT-K^b-SIINFEKL (one-way ANOVA, p= 0.13 for AST and p = 0.02 for ALT, due solely to a decrease in ALT on d4). Minimal infiltration with cells expressing the markers CD4, CD8, CD11c or CD19 was detected.

Figure 2. SCT-K^b-KIIT constructs exclude presentation of endogenous peptides

(a-c). B10.BR mice were transduced with either AAV-SCT-K^b-SIIN, AAV-SCT-K^b-KIIT or AAV-HC-K^b with or without AAV-OVA. Hepatocytes were isolated on day 7 post-inoculation, then subjected to antibody staining and flow cytometric analysis. **(b)** Equivalent levels of H-2K^b cell surface expression were demonstrated using the monoclonal antibody (mAb) AF6-88.5. **(b, c)** Detection of SIINFEKL ($OVA_{257-264}$) peptide bound to H-2K^b was carried out using an anti-K^b-SIINFEKL mAb (25D-1.16). Co-transduction with a vector encoding full length chicken ovalbumin (AAV-OVA) permitted presentation of SIINFEKL by hepatocytes transduced with AAV-HC-K^b. Conversely, the SCT-Kb-KIIT construct excluded presentation of endogenously processed SIINFEKL peptide. For panels **(a)** and **(c)**, data were obtained from three independent experiments with a total of n = 3 biological replicates per group, and are displayed as the mean ± SEM of the geometric mean fluorescent intensity (MFI). Panel **(b)** depicts one representative experiment (from n = 3). **(d)**

depicts the workflow for the immunoaffinity purification assay. **(e, f, g, h, i)** Control B10.BR hepatocytes, B10.BR hepatocytes transduced with either AAV-HC-K^b or AAV-SCT-K^b-KIIT and control C57BL/6 hepatocytes underwent immunoaffinity purification in order to identify unique H-2K^b and H-2K^k peptides. A false discovery rate (FDR) of 5% was employed. Two replicate experiments were performed. A total of 4 mice were pooled per group for each replicate, and combined lists of peptides present in either or both replicates were generated. **(e)** Peptide-binding motifs for H-2K^b peptides were generated from a non-redundant list of 8-11-mer peptides using the GibbsCluster-2.0 (DTU bioinformatics) algorithm. The binding motif obtained from B10.BR hepatocytes transduced with AAV-HC-K^b closely reflected that from C57BL/6 (H-2^b) hepatocytes. **(f, g)** Whereas similar numbers of K^b-binding peptides were isolated from AAV-HC-K^b-transduced B10.BR hepatocytes and C57BL/6 hepatocytes, with significant overlap between the two repertoires, very few K^b-binding peptides could be eluted from B10.BR hepatocytes transduced with AAV-SCT-K^b-KIIT, comparable to untransduced control B10.BR group. **(h, i)** Comparable numbers of K^k-binding peptides were eluted from all B10.BR hepatocyte samples, but not from C57BL/6 mice which do not express this allomorph. Values represent mean ± SEM. **(a, c)** Statistical analysis was performed (one-way analysis of variance (ANOVA) in conjunction with Sidak's multiple comparison test: ns, not significant, *$p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, *** $p < 0.0001$).

Figure 3. Expression of the SCT-K^b-KIIT construct in recipient hepatocytes prevents skin graft rejection mediated by alloreactive $CD8^+$ T cells expressing the cognate TCR but does not induce tolerance in a polyclonal alloreactive population.

(a) Inoculation with SCT-K^b-KIIT vector not only activates a clone of transgenic Des-RAG T cells bearing the cognate receptor, but also activates a proportion of the polyclonal T cell repertoire of normal B10.BR mice. B10.BR mice were primed against allogeneic H-2K^b (178.3 skin graft). Approximately 30 days post-graft rejection, some of the primed or naïve B10.BR mice were inoculated with AAV-SCT-K^b-KIIT. Liver leukocytes were analysed on day 7 post-inoculation. **(b)** Activated $CD8^+$ T cells, defined as $CD44^+PD\text{-}1^{hi}$, increased in number following priming or

transduction with SCT-K^b-KIIT, with a further increase in primed mice receiving SCT-K^b-KIIT. **(c-d)** Inoculation of naïve or primed B10.BR mice with AAV-SCT-K^b-KIIT generated populations of activated ($CD44^+PD\text{-}1^{hi}$) $CD8^+$ T cells which bound K^b-KIITYRNL dextramers specifically. Dextramers of the syngeneic pMHC K^k-EEEPVKKI were used as negative controls. Data from one representative experiment is shown in **(c)**, while two independent experiments with a total of $n = 3$ biological replicates per group are shown in **(d)**. **(e)** B10.BR-RAG mice were reconstituted with doses of Des-RAG lymphocytes ranging from 1.0×10^4 to 2.5×10^5 cells, 3 days prior to receiving a skin graft from a K^b-bearing 178.3 donor. Some mice were also inoculated with AAV vectors as shown. **(f)** 178.3 skin grafts survived indefinitely on unreconstituted B10.BR-RAG hosts. A progressive shortening in survival accompanied the adoptive transfer of increasing cell numbers (Mantel-Cox log-rank test for trend: ****$p < 0.0001$, $n = 6$ per group). A dose of 50,000 cells yielded skin graft survival approximating that in immunosufficient B10.BR mice, and was used in subsequent experiments. **(g)** Inoculation of reconstituted B10.BR-RAG recipients with AAV-SCT-K^b-KIIT resulted in indefinite graft survival, whereas treatment with AAV-SCT-K^b-SIIN offered no survival prolongation compared with that in untransduced recipients; median survival time (MST) of 18.5 days versus 20 days (Mantel-Cox log-rank test: ns, $p = 0.2$, $n = 6$ per group). ***$p = 0.0005$, Mantel-Cox log-rank test between B10.BR-RAG mice receiving AAV-SCT-K^b-KIIT versus AAV-SCT-K^b-SIIN ($n = 6$ per group). **(h)** Representative macroscopic images of syngeneic (B10.BR-RAG) and allogeneic (178.3) skin grafts on transduced B10.BR-RAG mice reconstituted with Des-RAG lymphocytes demonstrate continued allograft survival in mice treated with AAV-SCT-K^b-KIIT but not other groups at 100 days after transplantation. **(i)** Representative IHC and H&E images showing sections of syngeneic (B10.BR-RAG) and allogeneic (178.3) skin grafts on transduced B10.BR-RAG mice reconstituted with Des-RAG lymphocytes 100 days post-transplant. Skin grafts are morphologically normal, with persistent expression of H-$2K^b$ within allogeneic 178.3 transplants. **(j)** Immunosufficient B10.BR mice were inoculated with either AAV-HC-K^b, AAV-SCT-K^b-KIIT or AAV-SCT-K^b-SIIN or were not transduced ($n = 6$ per group). 7 days post-inoculation, the mice received 178.3 skin grafts. In these mice, expression of either SCT-K^b-KIIT or SCT-K^b-SIIN led to a modest increase in graft survival (MST of 25 days versus 17 days in no vector controls,

Mantel-Cox log-rank test: ***p = 0.0007, n = 6 per group). However, only expression of H-2K^b loaded with the endogenous peptide repertoire was able to induce tolerance to 178.3 skin graft. ***p = 0.0005, Mantel-Cox log-rank test between B10.BR inoculated with AAV-HC-K^b and B10.BR inoculated with either AAV-SCT-K^b-KIIT or AAV-SCT-K^b-SIIN, n = 6 per group.

Figure 4. Hepatocytes from TAP1KO Hep mice express high levels of H-2K^d following transduction with AAV-HC-K^d-YCAC.

TAP1KOHep mice do not express the native H-2^b allomorphs H-2K^b or H-2D^b in hepatocytes **(a-d)**. Isolated hepatocytes, liver leukocytes, or splenocytes from TAP1KOHep mice, floxed control littermates, or negative control B10.BR mice were stained with the K^b-specific mAb AF6-88.5 **(a-b)**. Expression of K^b on the surface of liver leukocytes and splenocytes was equivalent between the two strains, while much lower levels were detected on hepatocytes from TAP1KOHep, compared with those from floxed littermates (representative flow plots from 1/3 experiments are shown). **(c)** TAP1KOHep and floxed control livers are morphologically normal. IHC staining with the antibodies AF6-88.5 and 28-8-6 demonstrate expression of K^b and D^b in nonparenchymal cells from TAP1KOHep livers, while K^b and D^b are absent from hepatocytes in these mice (200x). **(d)** Thick sections (150 µm) from TAP1KOHep or floxed control livers, perfused *in situ* with 4% paraformaldehyde in PBS were stained with antibodies against H-2K^b (Y-3), CD31, CK19 and CD45. Confocal micrographs were obtained at 93x objective magnification and Numerical Aperture 1.35 using a Leica SP8 confocal microscope and analysed using Imaris v9.5 software (Oxford Instruments). K^b is ubiquitously expressed in floxed controls, but absent from hepatocytes in TAP1KOHep livers (93x). **(e-f)** H-2K^d expression on isolated hepatocytes was detected using the antibody SF1-1.1. While K^d was clearly present on hepatocytes from TAP1KOHep transduced with AAV-HC-K^d, the expression levels did not reach those of TAP-sufficient mice transduced with the same vector. To achieve more robust cell surface expression of K^d, we designed a construct where two point mutations (Y84C and A139C; YCAC) stabilise expression of K^d when empty or loaded with low-affinity peptides. Inoculation of TAP1KOHep mice with an AAV vector encoding this

construct (AAV-HC-K^d-YCAC) yielded comparable expression to that of TAP-sufficient mice transduced with AAV-HC-K^d. Flow plots shown are representative of 3 separate experiments.

(g) Thick sections of TAP1KO/YCAC and TAP1$^{fl/fl}$/YCAC livers were obtained and stained with SF1-1.1 and antibodies against CD31, CK19 and CD45 as above. Equivalent strong expression of K^d in hepatocytes, but not other cell types within the liver, was observed for both treatment groups (93x, representative image shown, from 3 replicates).

Figure 5. Alteration in the endogenous peptide repertoire impedes transplantation tolerance induction.

(a) Cartoon representing the differences in peptide presentation between TAP-sufficient and deficient hepatocytes transduced with AAV vectors encoding one of three H-2K^d constructs. From left to right, the images show a single presented peptide (SYFPEITHI), a substantially-altered repertoire resulting from the combination of K^d-YCAC expression and absence of TAP, a moderately altered repertoire when K^d-YCAC is expressed in cells where TAP is active, and the repertoire normally associated with K^d in TAP-sufficient hepatocytes. Both empty and peptide-loaded K^d-YCAC molecules are expected to be present at the cell surface. **(b)** Peptide-binding motifs for H2-K^d peptides were generated from a non-redundant list of 9-mer peptides using the GibbsCluster-2.0 (DTU bioinformatics) algorithm. Peptides eluted from B6/HC, B6/YCAC or TAP1$^{fl/fl}$/YCAC, hepatocytes displayed the canonical K^d binding motif of tyrosine (Y) at position 2 and leucine (L) or isoleucine (I) at the C-terminus while no clear binding motif was discernible in the sequences for peptides eluted from TAP1KO/YCAC hepatocytes. **(c)** Compared to B6/HC peptides, just under 45% were common to the B6/YCAC TAP1$^{fl/fl}$/YCAC or TAP1$^{fl/fl}$/YCAC repertoires, while 22% were shared with TAP1KO/YCAC. Similarity across peptide repertoires was increased when the comparison was weighted for peptide abundance. The peptide SYFPEITHI was present in all repertoires. **(d)** Comparable proportions of activated $CD8^+$ T cells able to recognise K^d-SYFPEITHI were detected among the liver leukocytes of primed C57BL/6 mice inoculated with AAV-HC-K^d or AAV-HC-K^d-YCAC and those of TAP1KOHep mice treated with AAV-HC-K^d-YCAC. **(e)** TAP1KOHep, TAP1$^{fl/fl}$ or C57BL6 mice were inoculated with AAV-HC-K^d-

YCAC or were not transduced. Another group of C57BL/6 were transduced with AAV-SCT-K^d-SYFP, while C57BL6 and $TAP1^{fl/fl}$ controls received AAV-HC-K^d (n = 6 per group). 7 days post inoculation, the mice were challenged with B6.Kd skin grafts. In C57BL/6 and $TAP1^{fl/fl}$, only expression of HC-K^d loaded with the endogenous peptide repertoire was able to induce tolerance to B6.Kd skin grafts in the majority of recipients. Increasing perturbation of the H-2K^d bound peptide repertoire progressively shortened graft survival of H-2K^d bearing skin grafts. Statistical analysis of graft survival was carried out using the Mantel-Cox log-rank test ***p = 0.009, between C57BL/6 inoculated with AAV-HC-K^d (MST: indefinite) and C57BL/5 inoculated with either AAV-HC-K^d-YCAC (MST: 62.5 days), n = 6 per group. ***p = 0.007, between C57BL/6 inoculated with AAV-HC-K^d (MST: indefinite) and $TAP1^{fl/fl}$ inoculated with either AAV-HC-K^d-YCAC (MST: 52.5 days), n = 6 per group. ***p = 0.0005, between C57BL/6 inoculated with AAV-HC-K^d (MST: indefinite) and TAP1KOHep inoculated with AAV-HC-K^d-YCAC (MST: 20 days), n = 6 per group.

Figure 6: Profiling of the H-2 K^d and H-2 K^b-associated peptide repertoires of transduced hepatocytes, skin and spleen

(a) A schematic diagram illustrating the immunoaffinity purification workflow. **(b-c)** Unique peptides were identified from transduced hepatocytes, skin and spleen. For H-2K^d the peptide repertoires of C57BL/6 hepatocytes transduced with AAV-HC-K^d, B6.Kd spleen and B6.Kd skin grafts collected 7 days after transplantation were determined, while for the H-2K^b, the corresponding tissues were B10.BR hepatocytes transduced with AAV-HC-K^b, 178.3 spleen and 178.3 skin grafts removed 7 days post-transplant. Data from two experiments are shown. Within each replicate experiment, samples from 3-4 mice were pooled per condition. For K^d, 880 9-mer peptides were found to be shared across all three tissue types, while 1083 K^b peptides (8-11 mer, $IC_{50} < 500nM$) were common to the three tissues. **(d)** Length distribution of filtered H-2K^d peptides from hepatocytes, spleen and skin graft tissue samples. The number of peptides of each length identified with a 5% FDR cut-off are shown. **(e)** Peptide-binding motifs for H2-K^d peptides generated from a non-redundant list of 9-mer peptides using GibbsCluster-2.0 (DTU bioinformatics) algorithm. **(f)** Length distribution of H-2K^b peptides from hepatocytes, spleen and

skin graft tissue samples (as for **d**). Most eluted peptides are 8-mers, with 9-mers also relatively frequent. **(g)** Peptide-binding motifs for H2-K^b peptides generated from a list of 8-11-mer peptides using the GibbsCluster-2.0 algorithm as above. The canonical binding motifs were observed for all three tissues for both H2-K^d and H2-K^b. **(h)** The extent of peptide sharing between the H2-K^d repertoires of hepatocytes, spleen and skin was substantially reduced when TAP1KOHep, TAP1$^{fl/fl}$ or C57BL6 mice inoculated with AAV-HC-K^d-YCAC were substituted for C57BL/6 transduced with AAV-HC-K^d. This reduction was particularly striking for the combination of TAP1KOHep with AAV-HC-K^d-YCAC.

Figure 7. Identification of pMHC epitopes recognised by alloreactive CD8$^+$ T cells.

(a) We validated the identity of a panel of eluted peptides by comparing chromatographic retention and MS/MS spectra with those of the corresponding synthetic peptides. To evaluate the similarity between two spectra, we predicted all b- and y-ions for each sequence and then extracted the corresponding intensity for each ion. Example spectra for three pairs of synthetic and eluted peptides are shown at left. The Pearson correlation coefficients between the $\log_{10}$ intensities of identified b- and y-ions in the synthetic and sample-derived spectra are shown on the right. The corresponding p-value was <0.05 for each peptide pair. **(b)** Male B10.BR mice were primed with male 178.3 skin grafts and 30 days after rejection, mice were transduced with AAV-HC-K^b. Liver leukocytes were isolated and pMHC tetramer binding was analysed using flow cytometry. **(c)** shows the gating strategy that was employed to identify and stratify CD8$^+$ T cells into two groups; CD44$^+$PD-1^{hi} and CD44$^+$PD-1$^-$. CD44$^+$PD-1^{hi} cells are activated alloreactive CD8$^+$ T cells and CD44$^+$PD-1$^-$ cells are non-activated bystander CD8$^+$ T cells which serve as internal controls. **(d)** examples of pMHC tetramer binding by CD44$^+$PD-1^{hi} and CD44$^+$PD-1$^-$ CD8$^+$ T cells. Representative FACS plots for the selected pMHC epitopes are shown. K^b-SNYLFTKL (Epas$_{387-394}$), K^b-VGPRYTNL (Mapk1$_{19-26}$) and K^b-RTYTYEKL (Ctnnb1$_{329-336}$) were recognised by a large proportion of activated alloreactive T cells, whereas few T cells bound K^b-ASYEFVQRL (Dync1h1$_{1379-1387}$).

Figure 8. Immunogenic pMHC are recognised by mice from different allogeneic backgrounds and can be combined to enhance detection of alloreactive T cells within a polyclonal population.

(a) 100 peptides were screened for recognition by activated alloreactive T cells. T cells from female B10.BR mice primed with a female 178.3 skin graft and male BALB/c mice primed with a male C57BL/6 skin graft were used in parallel with T cells from primed male B10.BR. A heatmap was generated in order to compare how pMHC epitopes are recognised by alloreactive $CD8^+$ T cells across different sexes and strains. pMHC epitopes are ordered from the top to the bottom by the average of pMHC tetramer binding across all samples. Here, 13 pMHC were recognised by ≥5% of activated alloreactive T cells across all three groups. Full peptide screening data can be found in Supplementary Table 4. **(b)** Strong correlation of T cell binding to each pMHC was found between male and female B10.BR (Pearson correlation coefficient (r) = 0.76, ***$p < 0.0001$) and between male B10.BR and male BALB/c (r = 0.62, ***$p < 0.0001$). **(c)** For male B10.BR mice, 8-mer pMHC tetramer binding levels were proportional to the product of the spectral intensity values for each peptide across three different tissues (r = 0.52, ***$p < 0.0001$). Conversely, 9-mer pMHC tetramer binding levels did not correlate with peptide spectral intensity (r = 0.059, p = 0.65). For each pMHC epitope, data was obtained from one - two independent experiments with a total of 3 biological replicates. Values represent mean ± SEM. ns, not significant; *$p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Predicted peptide binding affinity for H-$2K^b$ (measured by IC_{50}) did not differ significantly between strongly, moderately or non-immunogenic peptides (p=0.098 by one-way ANOVA, line at mean, **(d),** nor was a correlation observed between IC_{50} and spectral abundance. (r = 0.11, p = 0.34, **e**). **(f,g)** Staining with two different pMHC tetramers was used to evaluate the proportion of T cells recognising more than one pMHC specificity. Six strongly immunogenic peptides were tested. 86.7% of $SNYLFTKL^+$ T cells recognised SGYIYHKL in addition to SNYLFTKL, while SVYVYKVL tetramers bound 66.8% of $SNYLFTKL^+$ T cells and SGYIYHKL tetramers bound 75.8% of $SVYVYKVL^+$ cells. Conversely, cross-reactivity between VGPRYTNL, INFDFPKL and RTYTYEKL was considerably lower (4.0 and 8.4% of T cells recognised VGPRYTNL in addition to INFDFPKL and RTYTYEKL, respectively). **(h,i)** When 5 of these 6 peptides (excluding SGYIYHKL), each

binding between 7.2 and 15.2% of T cells were used together as a panel, the proportion of alloreactive $CD8^+$ T cells bound increased to 39.1% (p= 0.002 compared with SNYLFTKL). Each tetramer was two-fold less concentrated compared to other multimer staining experiments due to the obligatory increase in staining volume (0.5 µg/100 µL versus 0.5 µg/50 µL, respectively).

Supplementary Figure 1.

Amino acid sequences for the SCT-K^b-SIIN, SCT-K^b-KIIT, SCT-K^d-SYFP and HC-K^d-YCAC constructs.

Supplementary Figure 2.

Recognition of dt-SCT peptide-MHC ligands *in vitro* and *in vivo*.

(a) RMA-S cells were pulsed with different concentrations of the peptides KIITYRNL ($Pcid2_{318-325}$), SIINFEKL ($OVA_{257-264}$) or AAAAFAAL (synthetic negative control), or were untreated. Stabilisation of H-$2K^b$ surface expression was assessed by flow cytometry following staining with a conformation-dependent anti-H-$2K^b$ mAb (clone Y3). Samples were acquired using a LSR Fortessa X-20 (BD Biosciences) and analysed using FlowJo v10 (BD). **(b)** Flow plots shown are representative of 3 separate experiments. Peptide concentrations required to achieve equivalent H-$2K^b$ surface expression levels were determined. **(c)** RMA-S cells were transiently transfected with constructs encoding SCT-K^b-KIIT, SCT-K^b-SIIN and SCT-K^b-AAAA using a Lonza-AMAXA Nucleofector 2b. Transgene expression was assessed by flow cytometry (as above) 24 hours after transfection. Flow plots shown are representative of 3 separate experiments. **(d)** The proportion of cells secreting IFN-γ upon recognition of their cognate antigen was determined using ELISPOT assays. Splenocytes from Des-RAG or OT-I-RAG mice were cultured with irradiated stimulators; RMA-S pulsed with selected peptides or expressing SCT constructs after transient transfection. SCT recognition by cognate TCRs mirrored recognition of the native H-$2K^b$-peptide complex. SCT constructs were recognised in a peptide-specific manner *in vitro*. Data from two independent experiments with a total of n = 3 biological replicates per group are shown. **(e)** Des-RAG lymphocytes were labelled with CFSE, adoptively transferred into recipient mice and recovered

from the recipient liver two days later. Some recipient mice were treated with AAV encoding SCT-K^b-KIIT or SCT-K^b-SIIN prior to adoptive transfer, as shown. **(f)** Flow cytometry analysis of CFSE-labelled Des-RAG lymphocytes demonstrates peptide-specific activation and proliferation of adoptively transferred $CD8^+$ Des-RAG T cells upon encounter with their cognate antigen in the liver, confirming that recognition of the SCT-K^b-KIIT ligand *in vivo* was analogous to that of the native pMHC complex. Data from three experiments with a total of $n = 3$ biological replicates per group are shown. Values represent mean ± SEM. **(d,f)** Statistical analysis was performed (ANOVA in conjunction with Sidak's multiple comparison test: ns, not significant; *$p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, *** $p < 0.0001$).

Supplementary Figure 3.

Characterisation of TAP1KOHep mice

(a) Gating strategy for determination of K^b expression on the surface of hepatocytes, liver leukocytes and splenocytes of TAP1KOHep and $TAP1^{fl/fl}$ mice. **(b)** Genotyping PCR performed by Transnetyx shows the presence of the Albumin-Cre transgene in hepatocytes, liver leukocytes and spleen from TAP1KOHep mice (above). Because Cre activity is restricted to hepatocytes, the recombined Tap1 sequence specifically detected by the L1L2-Bact-P EX probe is only amplified in hepatocytes and not other tissues from TAP1KOHep (below). **(c)** Genetic background analysis was undertaken by Transnetyx. TAP1KOHep and $TAP1^{fl/fl}$ control mice were at least 91.3% C57BL/6J (91.3-97.9%). **(d)** AST and ALT levels are comparable between TAP1KOHep and floxed littermate control mice. **(e)** H-$2K^b$ is expressed at normal levels in the spleen, thymus and lymph node of TAP1KOHep and $TAP1^{fl/fl}$ mice. **(f)** H-$2K^b$ is absent from the hepatocytes of TAP1KOHep mice, but detectable on other liver cells.

Supplementary Figure 4.

Features of H-$2K^d$-associated peptides

The length distribution for H-$2K^d$-associated peptides eluted from transduced hepatocytes in each of four vector/strain combinations is shown in panel **(a)**. Peptides eluted from C57BL/6 mice

expressing K^d-HC are predominantly nonamers – this preference was less strong for the peptide repertoires of hepatocytes expressing K^d-YCAC. **(b-d)** Gene Ontology annotations of the source proteins associated with eluted peptides were analysed using the PANTHER classification system[44]. Function classification analysis and statistical over-representation tests were performed[45]. **(b)** Cellular component and biological process analysis of source proteins corresponding to the same hepatocyte peptide repertoires shown in **(a)**. **(c)** Analysis of the source proteins giving rise to the H-2K^d and K^b-associated peptide repertoires of transduced hepatocytes, donor skin grafts and donor spleen. **(d)** A number of Gene Ontology terms were enriched or depleted when hepatocyte source proteins from AAV-HC-K^d-YCAC-transduced TAP1KOHep mice were compared with those from AAV-HC-K^d-treated C57BL/6. The most striking enrichment was in terms associated with mitochondria and mitochondrial metabolism. Significant enrichment was also found for the cellular component terms endoplasmic reticulum, extracellular region and cytoplasm.

Supplementary Figure 5.

Expression of AAV-SCT-K^d-SYFPEITHI and AAV-HC-K^d-YCAC is robust and persistent.

(a) C57BL/6 mice were inoculated with AAV-SCT-K^d-SYFPEITHI iv. On days 2, 4, 7, 14, 28 and 100 post-inoculation, tissues were collected for analysis ($n = 3$ for each time point). Representative IHC and H&E images show transduced liver sections. Robust expression of H-2K^d was present through day 100 post-inoculation. Histologic examination of the liver sections was normal. Levels of AST and ALT did not increase significantly from baseline (one-way ANOVA, $p = 0.14$ for AST and $p = 0.11$ for ALT in mice inoculated with AAV-SCT-K^d-SYFPEITHI). Minimal infiltration with cells expressing the markers CD4, CD8, CD11c or CD19 was detected. **(b)** Liver function tests remained within the normal range in mice transduced with AAV-HC-K^d-YCAC (here shown on d7 post-inoculation). Other expression data for this vector are shown in figure 4. **(c)** Expression of H-2K^d persisted in transduced livers through to at least d100 following B6.Kd skin transplantation in all vector/strain combinations.

Supplementary Data 1. Complete list of identified peptides

Supplementary Table 2. Common subset of peptides presented by H-2K^d

1083 K^d-binding peptides were identified in either or both replicate samples from C57BL/6 hepatocytes transduced with AAV-HC-K^d, B6.Kd donor skin grafts or B6.Kd donor spleen. Features of the common peptides are listed.

Supplementary Table 3. Common subset of peptides presented by H-2K^b

880 K^b-binding peptides were identified in either or both replicate samples from B10.BR hepatocytes transduced with AAV-HC-K^b, 178.3 donor skin grafts or 178.3 donor spleen. Features of the common peptides are listed.

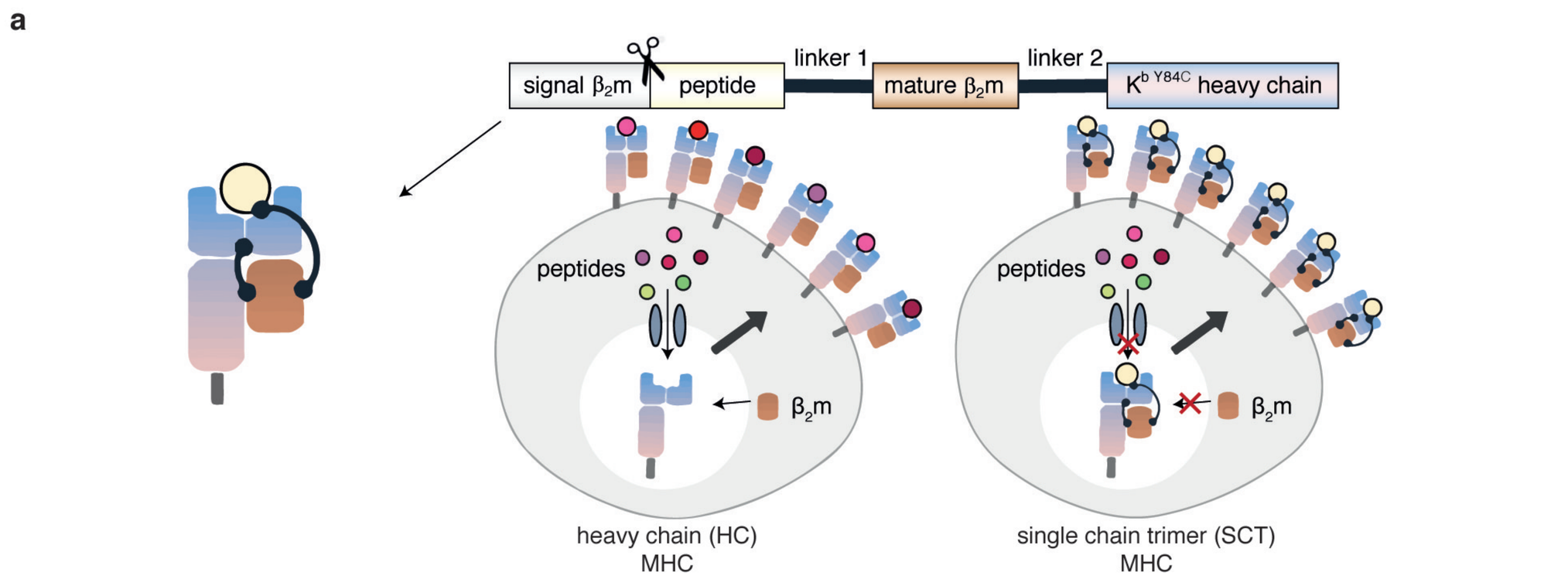
Supplementary Table 4. Tetramer screening of alloreactive CD8$^+$ T cells

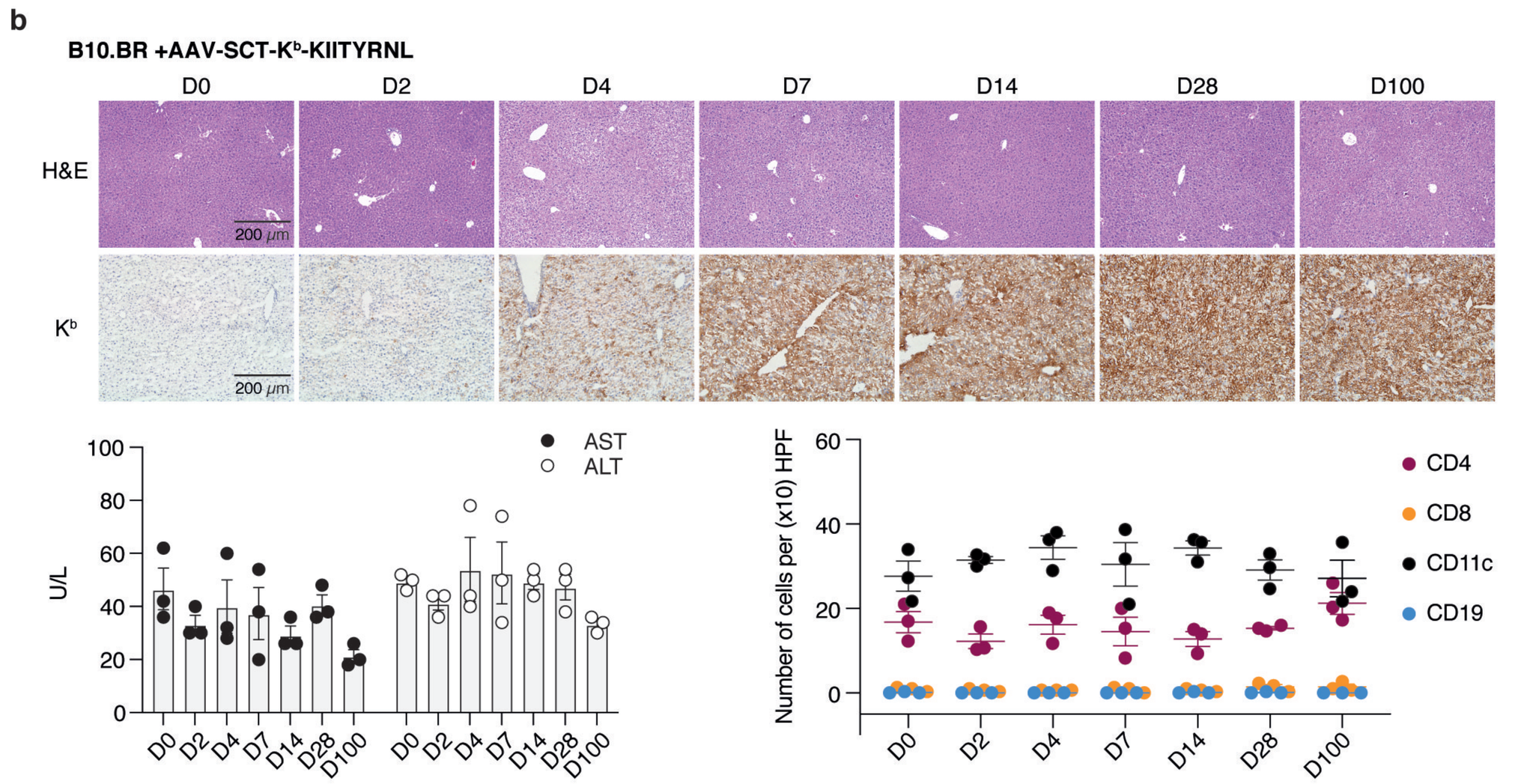
100 peptides were selected for evaluation of immunogenicity by pMHC tetramer staining of activated alloreactive CD8$^+$ T cells. Peptide characteristics and screening results in three different responder populations are shown. Values given for peptide screening results are the mean and the range (min-max). Peptides recognised by >5% of activated (CD44$^+$PD-1^{hi}) CD8$^+$ T cells are indicated in red.

Supplementary Table 5. List of Antibodies used in this study

Supplementary Table 6. Variable Window widths used for DIA acquisition

Figure 1


a
signal β2m
peptide
linker 1
mature β2m
linker 2
Kb Y84C heavy chain
peptides
β2m
heavy chain (HC) MHC
peptides
β2m
single chain trimer (SCT) MHC


b
B10.BR +AAV-SCT-Kb-KIITYRNL
D0
D2
D4
D7
D14
D28
D100
H&E
Kb
200 μm
AST
ALT
U/L
Number of cells per (x10) HPF
CD4
CD8
CD11c
CD19

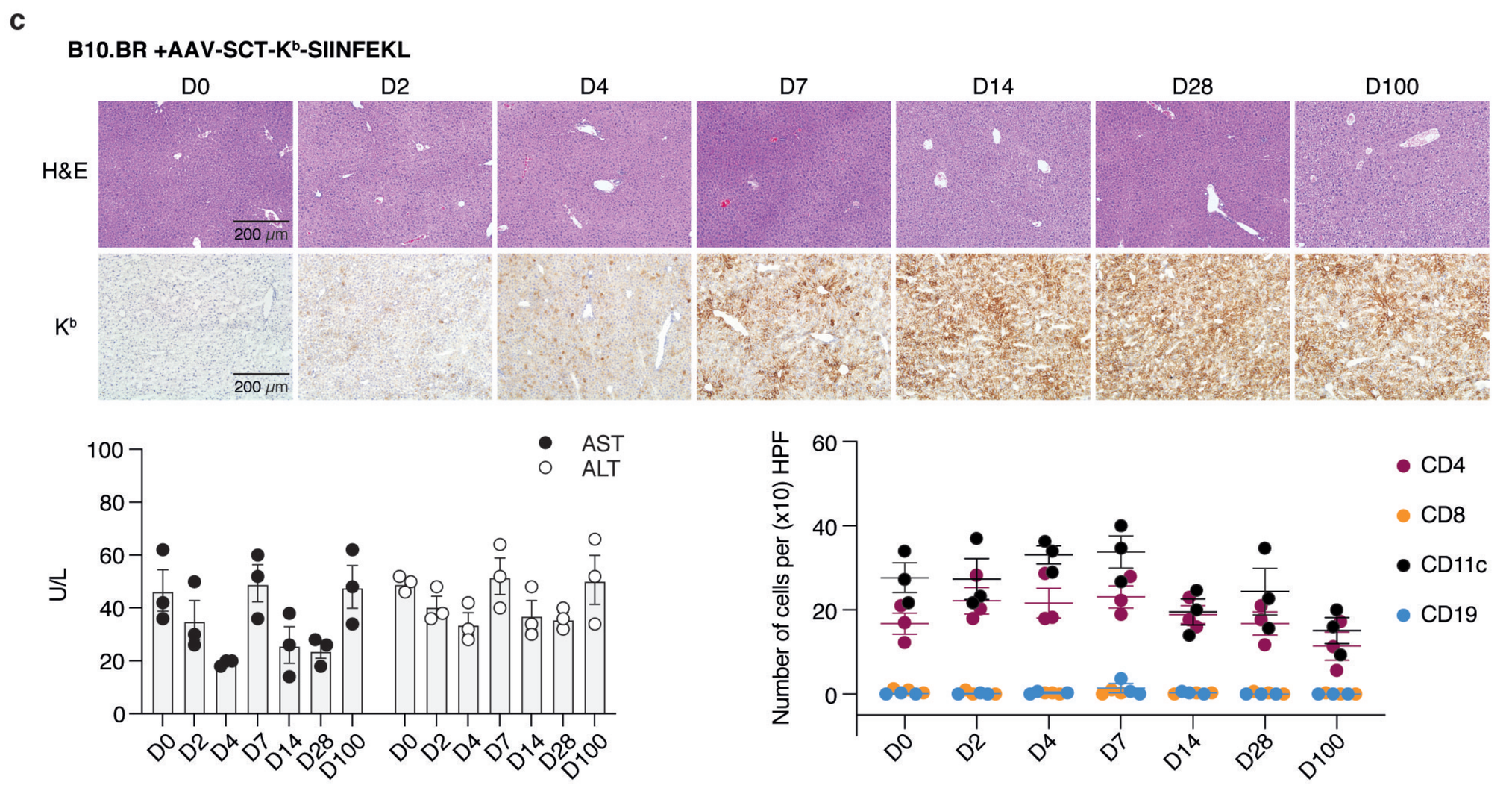

c
B10.BR +AAV-SCT-Kb-SIINFEKL
D0
D2
D4
D7
D14
D28
D100
H&E
Kb
200 μm
AST
ALT
U/L
Number of cells per (x10) HPF
CD4
CD8
CD11c
CD19

Figure 2

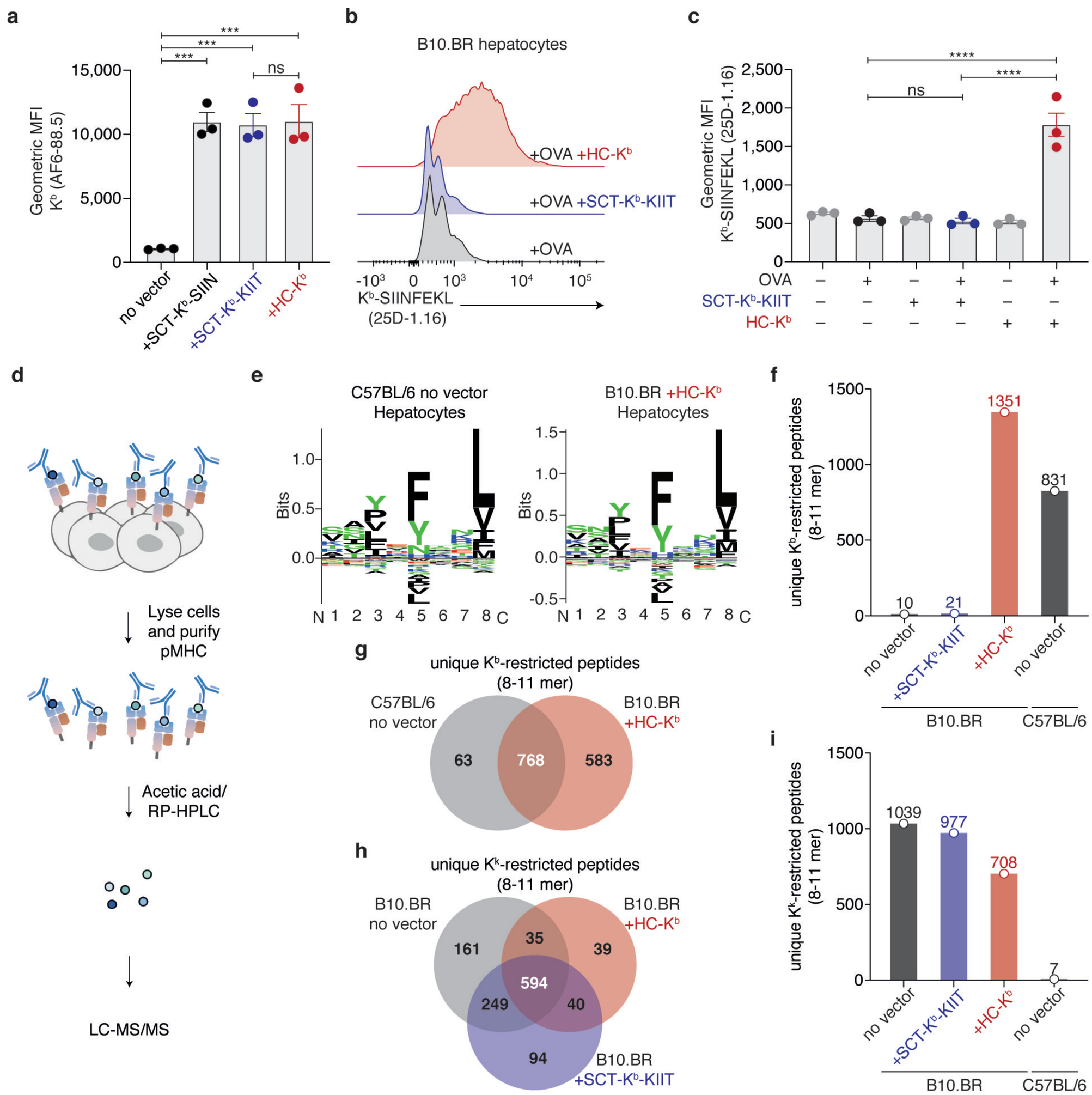

a
Geometric MFI
Kᵇ (AF6-88.5)
15,000
10,000
5,000
0
***
***
***
ns
no vector
+SCT-Kᵇ-SIIN
+SCT-Kᵇ-KIIT
+HC-Kᵇ
b
B10.BR hepatocytes
+OVA +HC-Kᵇ
+OVA +SCT-Kᵇ-KIIT
+OVA
-10³ 0 10³ 10⁴ 10⁵
Kᵇ-SIINFEKL
(25D-1.16)
c
Geometric MFI
Kᵇ-SIINFEKL (25D-1.16)
2,500
2,000
1,500
1,000
500
0
****
****
ns
OVA
SCT-Kᵇ-KIIT
HC-Kᵇ
d
Lyse cells
and purify
pMHC
Acetic acid/
RP-HPLC
LC-MS/MS
e
C57BL/6 no vector
Hepatocytes
B10.BR +HC-Kᵇ
Hepatocytes
Bits
N 1 2 3 4 5 6 7 8 C
f
unique Kᵇ-restricted peptides
(8-11 mer)
1500
1000
500
0
1351
831
10
21
no vector
+SCT-Kᵇ-KIIT
+HC-Kᵇ
no vector
B10.BR
C57BL/6
g
unique Kᵇ-restricted peptides
(8-11 mer)
C57BL/6
no vector
B10.BR
+HC-Kᵇ
63
768
583
h
unique Kᵏ-restricted peptides
(8-11 mer)
B10.BR
no vector
B10.BR
+HC-Kᵇ
B10.BR
+SCT-Kᵇ-KIIT
161
35
39
594
249
40
94
i
unique Kᵏ-restricted peptides
(8-11 mer)
1500
1000
500
0
1039
977
708
7
no vector
+SCT-Kᵇ-KIIT
+HC-Kᵇ
no vector
B10.BR
C57BL/6

Figure 3

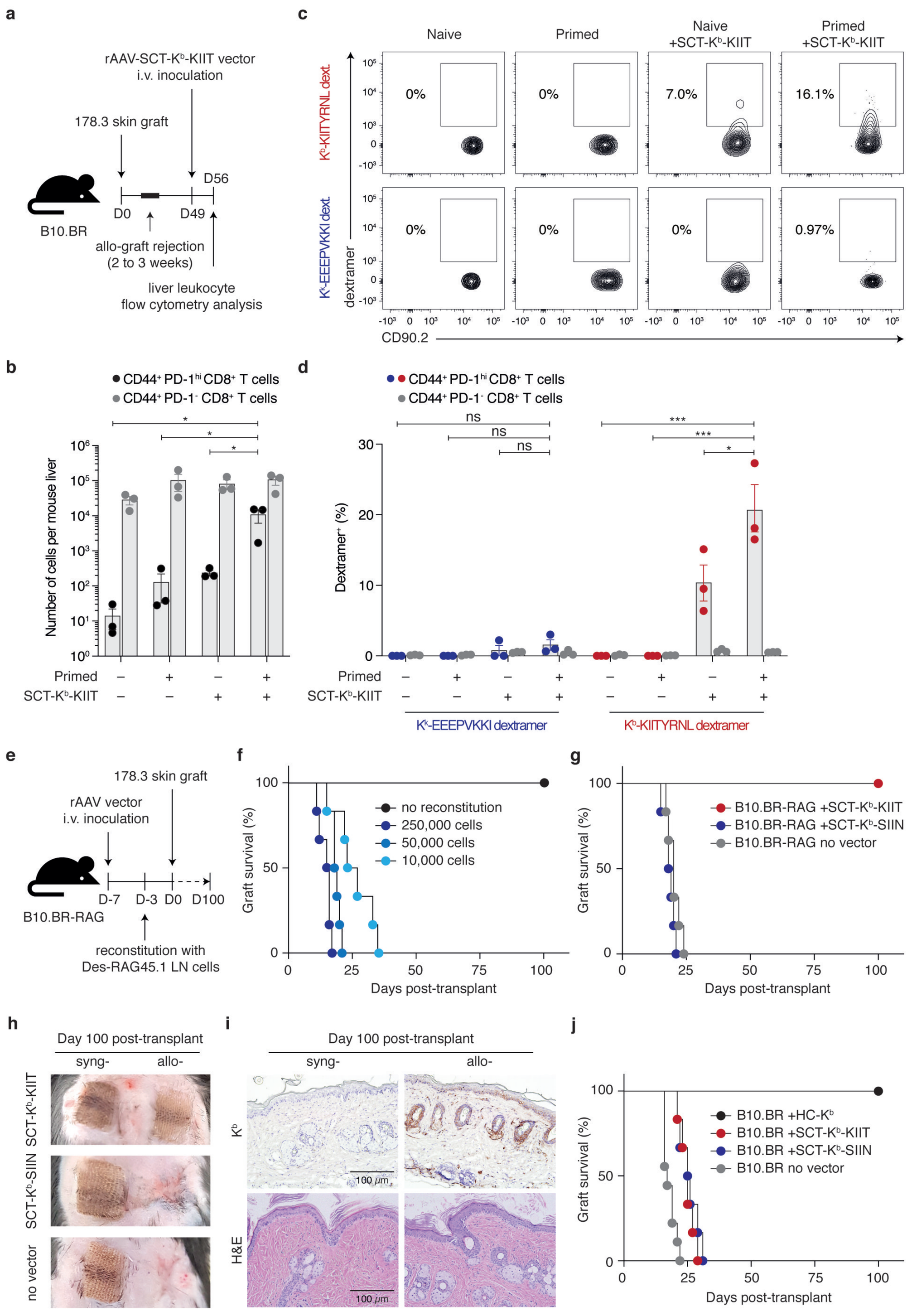

a
rAAV-SCT-Kᵇ-KIIT vector
i.v. inoculation
178.3 skin graft
D56
D0
D49
B10.BR
allo-graft rejection
(2 to 3 weeks)
liver leukocyte
flow cytometry analysis
c
Naive
Primed
Naive +SCT-Kᵇ-KIIT
Primed +SCT-Kᵇ-KIIT
Kᵇ-KIITYRNL dext.
Kᵏ-EEEPVKKI dext.
dextramer
CD90.2
0%
0%
7.0%
16.1%
0%
0%
0%
0.97%
b
CD44⁺ PD-1ʰⁱ CD8⁺ T cells
CD44⁺ PD-1⁻ CD8⁺ T cells
Number of cells per mouse liver
Primed
SCT-Kᵇ-KIIT
d
CD44⁺ PD-1ʰⁱ CD8⁺ T cells
CD44⁺ PD-1⁻ CD8⁺ T cells
Dextramer⁺ (%)
ns
ns
ns
***
***
*
Kᵏ-EEEPVKKI dextramer
Kᵇ-KIITYRNL dextramer
e
178.3 skin graft
rAAV vector
i.v. inoculation
D-7
D-3
D0
D100
B10.BR-RAG
reconstitution with
Des-RAG45.1 LN cells
f
Graft survival (%)
no reconstitution
250,000 cells
50,000 cells
10,000 cells
Days post-transplant
g
Graft survival (%)
B10.BR-RAG +SCT-Kᵇ-KIIT
B10.BR-RAG +SCT-Kᵇ-SIIN
B10.BR-RAG no vector
Days post-transplant
h
Day 100 post-transplant
syng-
allo-
SCT-Kᵇ-KIIT
SCT-Kᵇ-SIIN
no vector
i
Day 100 post-transplant
syng-
allo-
Kᵇ
H&E
100 μm
100 μm
j
Graft survival (%)
B10.BR +HC-Kᵇ
B10.BR +SCT-Kᵇ-KIIT
B10.BR +SCT-Kᵇ-SIIN
B10.BR no vector
Days post-transplant

Figure 4

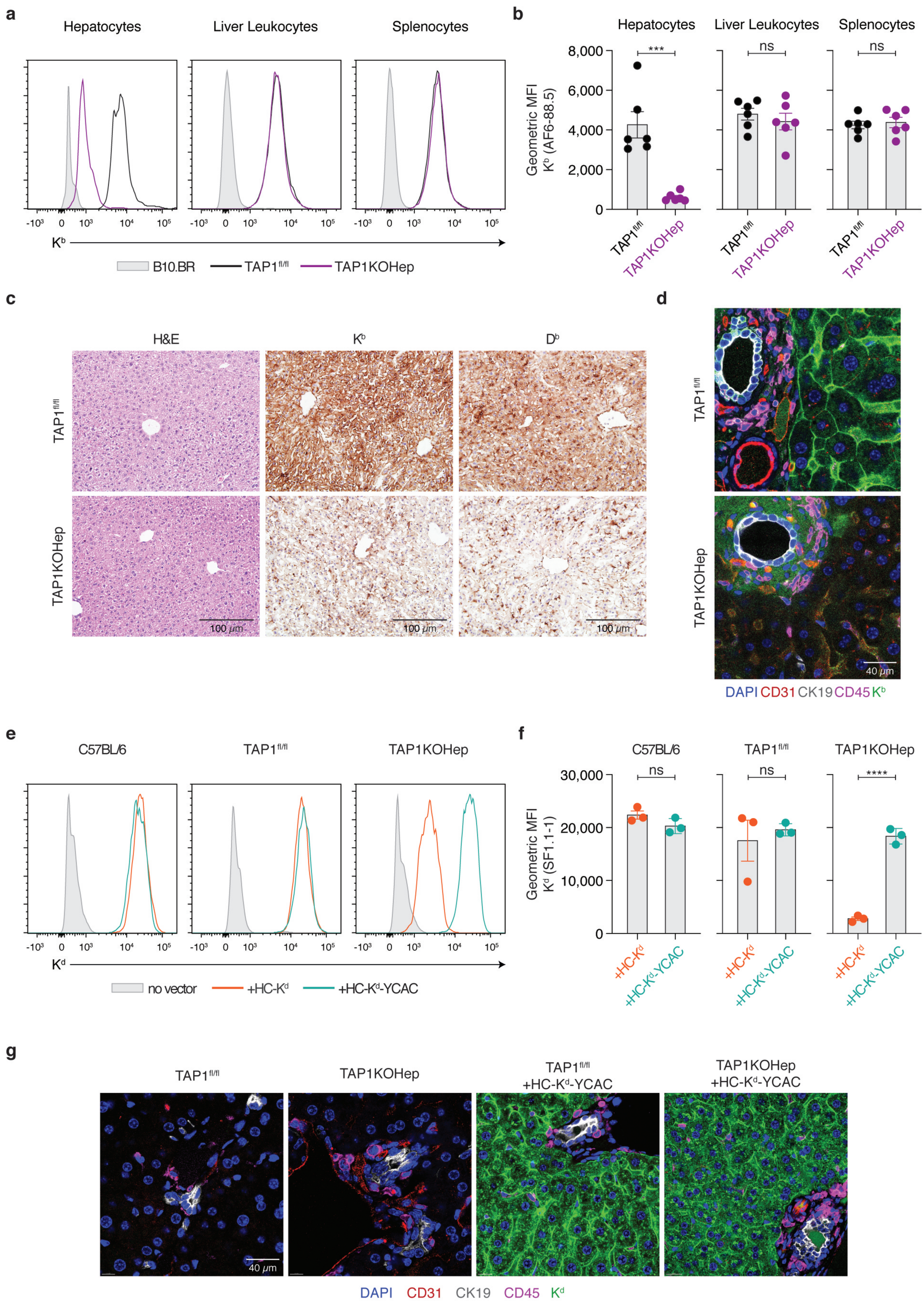

a
Hepatocytes
Liver Leukocytes
Splenocytes
Kᵇ
B10.BR
TAP1fl/fl
TAP1KOHep
b
Geometric MFI Kᵇ (AF6-88.5)
8,000
6,000
4,000
2,000
0
***
ns
ns
TAP1fl/fl
TAP1KOHep
c
H&E
Kᵇ
Dᵇ
TAP1fl/fl
TAP1KOHep
100 μm
d
DAPI CD31 CK19 CD45 Kᵇ
40 μm
e
C57BL/6
TAP1fl/fl
TAP1KOHep
Kᵈ
no vector
+HC-Kᵈ
+HC-Kᵈ-YCAC
f
Geometric MFI Kᵈ (SF1.1-1)
30,000
20,000
10,000
0
ns
ns
****
+HC-Kᵈ
+HC-Kᵈ-YCAC
g
TAP1fl/fl
TAP1KOHep
TAP1fl/fl +HC-Kᵈ-YCAC
TAP1KOHep +HC-Kᵈ-YCAC
40 μm
DAPI CD31 CK19 CD45 Kᵈ

Figure 5

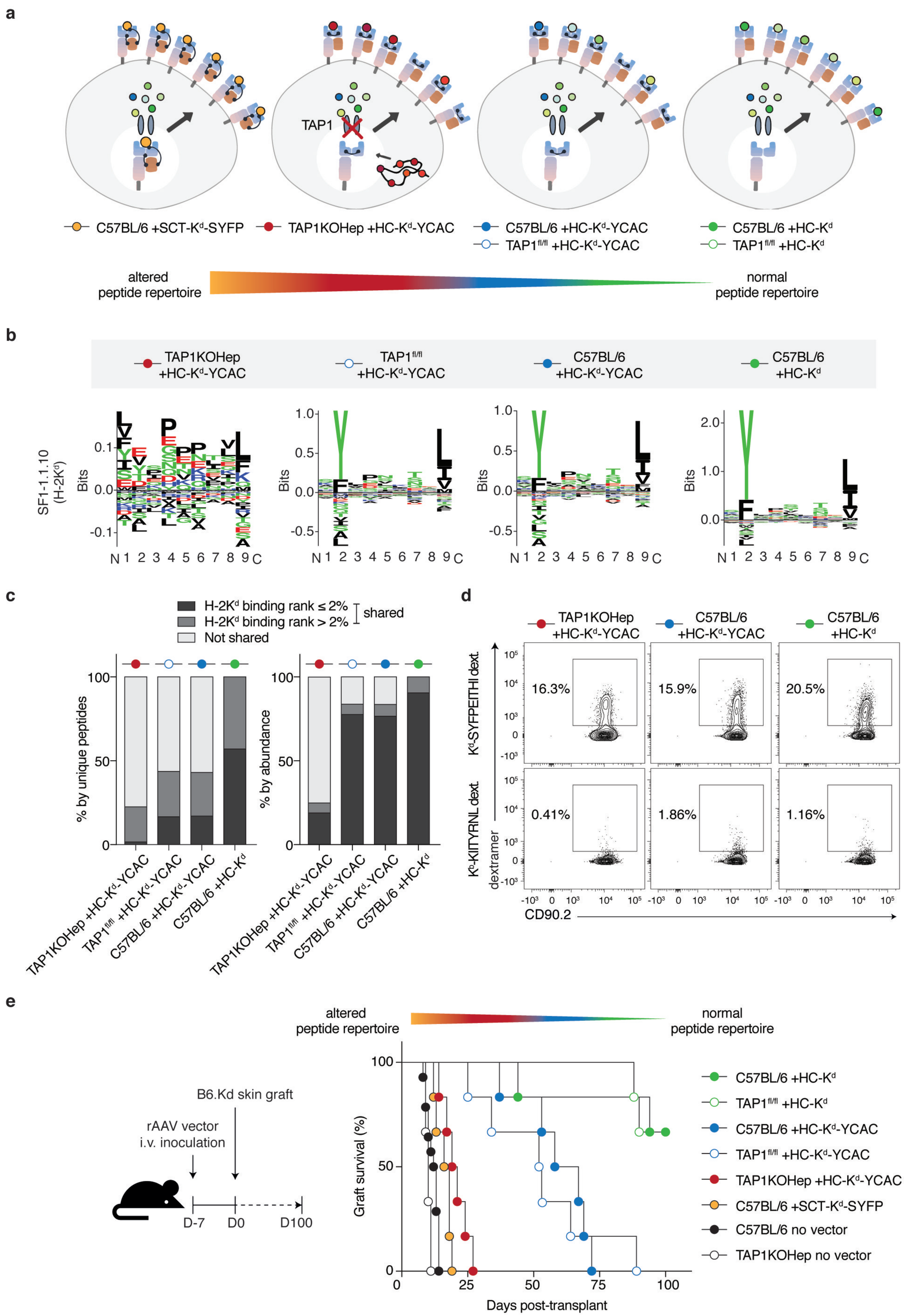

a
TAP1
C57BL/6 +SCT-Kd-SYFP
TAP1KOHep +HC-Kd-YCAC
C57BL/6 +HC-Kd-YCAC
TAP1fl/fl +HC-Kd-YCAC
C57BL/6 +HC-Kd
TAP1fl/fl +HC-Kd
altered peptide repertoire
normal peptide repertoire
b
TAP1KOHep +HC-Kd-YCAC
TAP1fl/fl +HC-Kd-YCAC
C57BL/6 +HC-Kd-YCAC
C57BL/6 +HC-Kd
SF1-1.1.10 (H-2Kd)
Bits
N 1 2 3 4 5 6 7 8 9 C
c
H-2Kd binding rank ≤ 2%
H-2Kd binding rank > 2%
shared
Not shared
% by unique peptides
% by abundance
TAP1KOHep +HC-Kd-YCAC
TAP1fl/fl +HC-Kd-YCAC
C57BL/6 +HC-Kd-YCAC
C57BL/6 +HC-Kd
d
Kd-SYFPEITHI dext.
Kb-KITYRNL dext.
dextramer
16.3%
15.9%
20.5%
0.41%
1.86%
1.16%
CD90.2
e
altered peptide repertoire
normal peptide repertoire
B6.Kd skin graft
rAAV vector i.v. inoculation
D-7
D0
D100
Graft survival (%)
Days post-transplant
C57BL/6 +HC-Kd
TAP1fl/fl +HC-Kd
C57BL/6 +HC-Kd-YCAC
TAP1fl/fl +HC-Kd-YCAC
TAP1KOHep +HC-Kd-YCAC
C57BL/6 +SCT-Kd-SYFP
C57BL/6 no vector
TAP1KOHep no vector

Figure 6

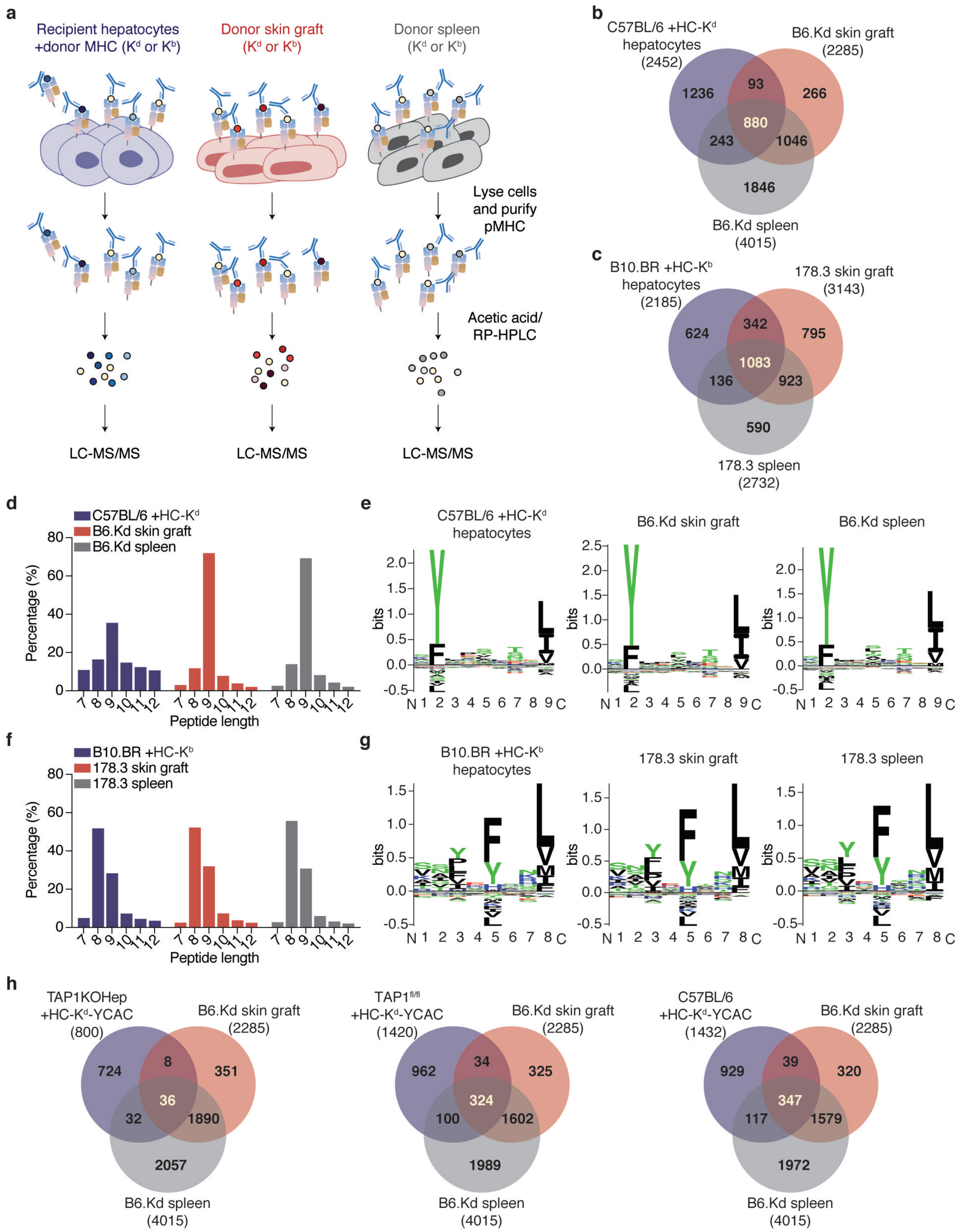

a
Recipient hepatocytes +donor MHC (Kd or Kb)
Donor skin graft (Kd or Kb)
Donor spleen (Kd or Kb)
Lyse cells and purify pMHC
Acetic acid/ RP-HPLC
LC-MS/MS
LC-MS/MS
LC-MS/MS
b
C57BL/6 +HC-Kd hepatocytes (2452)
B6.Kd skin graft (2285)
B6.Kd spleen (4015)
1236
93
266
880
243
1046
1846
c
B10.BR +HC-Kb hepatocytes (2185)
178.3 skin graft (3143)
178.3 spleen (2732)
624
342
795
1083
136
923
590
d
C57BL/6 +HC-Kd
B6.Kd skin graft
B6.Kd spleen
Percentage (%)
Peptide length
e
C57BL/6 +HC-Kd hepatocytes
B6.Kd skin graft
B6.Kd spleen
bits
f
B10.BR +HC-Kb
178.3 skin graft
178.3 spleen
Percentage (%)
Peptide length
g
B10.BR +HC-Kb hepatocytes
178.3 skin graft
178.3 spleen
bits
h
TAP1KOHep +HC-Kd-YCAC (800)
B6.Kd skin graft (2285)
B6.Kd spleen (4015)
724
8
351
36
32
1890
2057
TAP1fl/fl +HC-Kd-YCAC (1420)
B6.Kd skin graft (2285)
B6.Kd spleen (4015)
962
34
325
324
100
1602
1989
C57BL/6 +HC-Kd-YCAC (1432)
B6.Kd skin graft (2285)
B6.Kd spleen (4015)
929
39
320
347
117
1579
1972

Figure 7

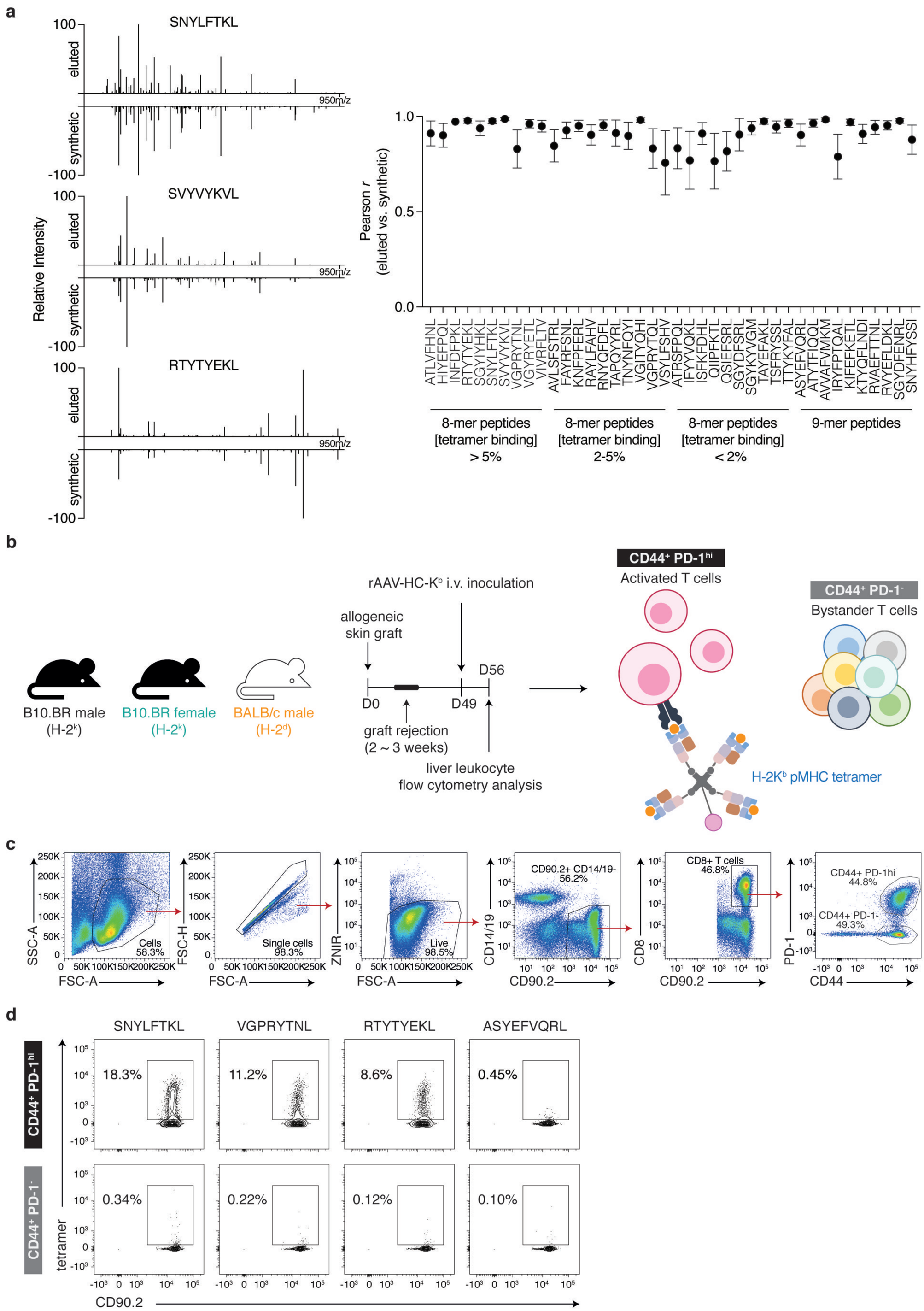
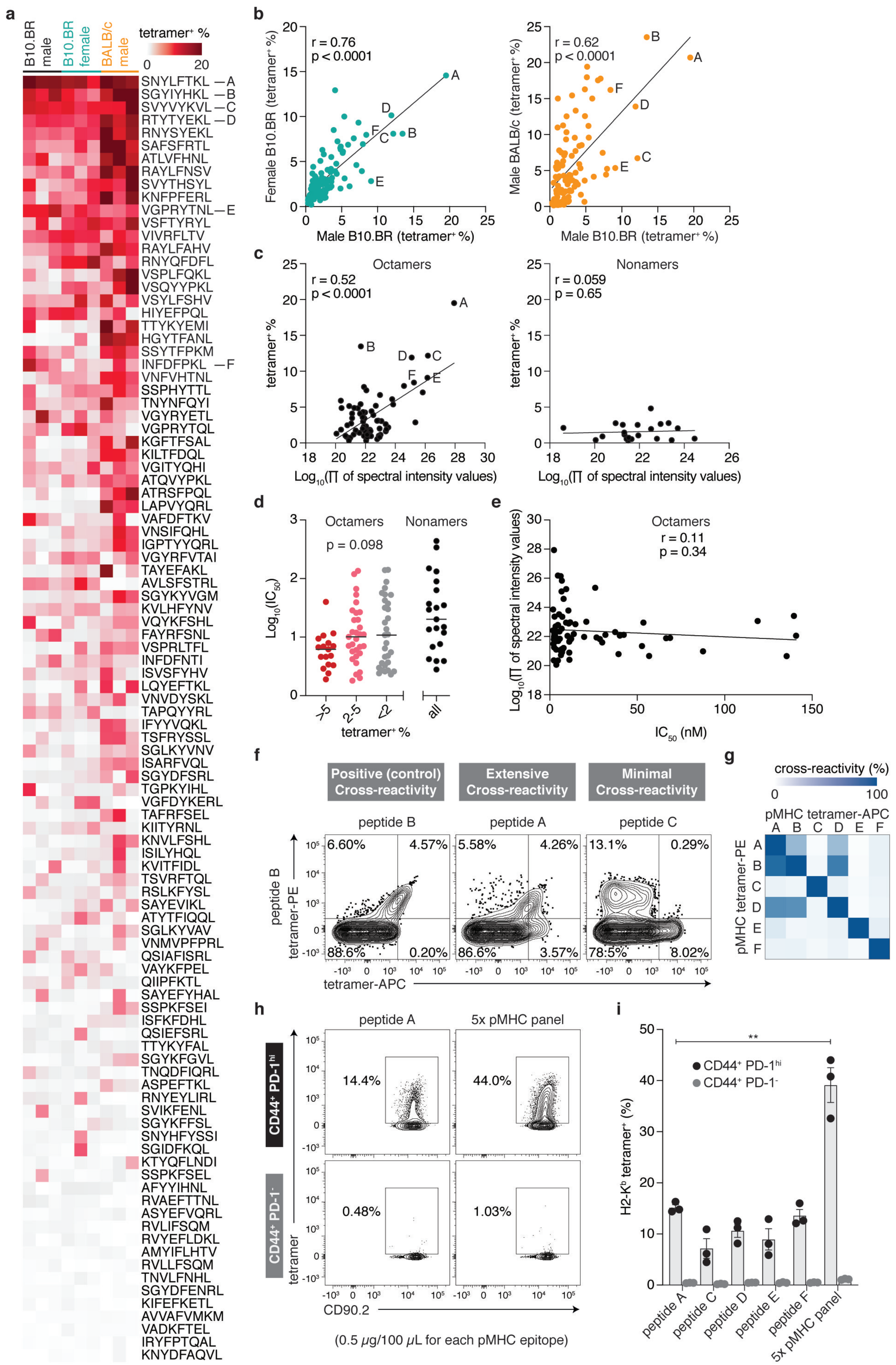

a
SNYLFTKL
SVYVYKVL
RTYTYEKL
eluted
synthetic
Relative Intensity
950m/z
Pearson r
(eluted vs. synthetic)
8-mer peptides [tetramer binding] > 5%
8-mer peptides [tetramer binding] 2-5%
8-mer peptides [tetramer binding] < 2%
9-mer peptides
b
B10.BR male (H-2k)
B10.BR female (H-2k)
BALB/c male (H-2d)
rAAV-HC-Kb i.v. inoculation
allogeneic skin graft
D0
D49
D56
graft rejection (2 ~ 3 weeks)
liver leukocyte flow cytometry analysis
CD44+ PD-1hi
Activated T cells
CD44+ PD-1-
Bystander T cells
H-2Kb pMHC tetramer
c
Cells 58.3%
Single cells 98.3%
Live 98.5%
CD90.2+ CD14/19- 56.2%
CD8+ T cells 46.8%
CD44+ PD-1hi 44.8%
CD44+ PD-1- 49.3%
SSC-A
FSC-A
FSC-H
ZNIR
CD14/19
CD90.2
CD8
PD-1
CD44
d
SNYLFTKL
VGPRYTNL
RTYTYEKL
ASYEFVQRL
18.3%
11.2%
8.6%
0.45%
0.34%
0.22%
0.12%
0.10%
CD44+ PD-1hi
CD44+ PD-1-
tetramer
CD90.2

Figure 8


a
B10.BR male
B10.BR female
BALB/c male
tetramer+ %
0
20
SNYLFTKL —A
SGYIYHKL —B
SVYVYKVL —C
RTYTYEKL —D
RNYSYEKL
SAFSFRTL
ATLVFHNL
RAYLFNSV
SVYTHSYL
KNFPFERL
VGPRYTNL—E
VSFTYRYL
VIVRFLTV
RAYLFAHV
RNYQFDFL
VSPLFQKL
VSQYYPKL
VSYLFSHV
HIYEFPQL
TTYKYEMI
HGYTFANL
SSYTFPKM
INFDFPKL —F
VNFVHTNL
SSPHYTTL
TNYNFQYI
VGYRYETL
VGPRYTQL
KGFTFSAL
KILTFDQL
VGITYQHI
ATQVYPKL
ATRSFPQL
LAPVYQRL
VAFDFTKV
VNSIFQHL
IGPTYYQRL
VGYRFVTAI
TAYEFAKL
AVLSFSTRL
SGYKYVGM
KVLHFYNV
VQYKFSHL
FAYRFSNL
VSPRLTFL
INFDFNTI
ISVSFYHV
LQYEFTKL
VNVDYSKL
TAPQYYRL
IFYYVQKL
TSFRYSSL
SGLKYVNV
ISARFVQL
SGYDFSRL
TGPKYIHL
VGFDYKERL
TAFRFSEL
KIITYRNL
KNVLFSHL
ISILYHQL
KVITFIDL
TSVRFTQL
RSLKFYSL
SAYEVIKL
ATYTFIQQL
SGLKYVAV
VNMVPFPRL
QSIAFISRL
VAYKFPEL
QIIPFKTL
SAYEFYHAL
SSPKFSEI
ISFKFDHL
QSIEFSRL
TTYKYFAL
SGYKFGVL
TNQDFIQRL
ASPEFTKL
RNYEYLIRL
SVIKFENL
SGYKFFSL
SNYHFYSSI
SGIDFKQL
KTYQFLNDI
SSPKFSEL
AFYYIHNL
RVAEFTTNL
ASYEFVQRL
RVLIFSQM
RVYEFLDKL
AMYIFLHTV
RVLLFSQM
TNVLFNHL
SGYDFENRL
KIFEFKETL
AVVAFVMKM
VADKFTEL
IRYFPTQAL
KNYDFAQVL
b
r = 0.76
p < 0.0001
Female B10.BR (tetramer+ %)
Male B10.BR (tetramer+ %)
r = 0.62
p < 0.0001
Male BALB/c (tetramer+ %)
Male B10.BR (tetramer+ %)
c
Octamers
r = 0.52
p < 0.0001
tetramer+ %
Log10(Π of spectral intensity values)
Nonamers
r = 0.059
p = 0.65
tetramer+ %
Log10(Π of spectral intensity values)
d
Octamers
Nonamers
p = 0.098
Log10(IC50)
>5
2-5
<2
all
tetramer+ %
e
Octamers
r = 0.11
p = 0.34
Log10(Π of spectral intensity values)
IC50 (nM)
f
Positive (control) Cross-reactivity
Extensive Cross-reactivity
Minimal Cross-reactivity
peptide B
peptide A
peptide C
6.60%
4.57%
88.6%
0.20%
5.58%
4.26%
86.6%
3.57%
13.1%
0.29%
78.5%
8.02%
peptide B tetramer-PE
tetramer-APC
g
cross-reactivity (%)
0
100
pMHC tetramer-APC
A B C D E F
pMHC tetramer-PE
h
peptide A
5x pMHC panel
CD44+ PD-1hi
CD44+ PD-1-
14.4%
44.0%
0.48%
1.03%
tetramer
CD90.2
(0.5 μg/100 μL for each pMHC epitope)
i
CD44+ PD-1hi
CD44+ PD-1-
**
H2-Kb tetramer+ (%)
peptide A
peptide C
peptide D
peptide E
peptide F
5x pMHC panel

Supplementary Figure 1

SCT - single chain trimer

Leader sequence----peptide----linker1(2C)----β2m----linker2----heavy chain H-2K^b/H-2K^d (Y84C)

SCT-K^b-SIINFEKL
(amino acid)
MARSVTLVFLVLVSLTGLYASIINFEKLGCGASGGGGSGGGGSIQKTPQIQVYSRHPPENGKPNILNCYVTQFHPP
HIEIQMLKNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTETDTYACRVKHASMAEPKTVYWDRDMGGGGSGGG
GSGGGGSGGGGSGPHSLRYFVTAVSRPGLGEPRYMEVGYVDDTEFVRFDSDAENPRYEPRARWMEQEGPEY
WERETQKAKGNEQSFRVDLRTLLGCYNQSKGGSHTIQVISGCEVGSDGRLLRGYQQYAYDGCDYIALNEDLKT
WTAADMAALITKHKWEQAGEAERLRAYLEGTCVEWLRRYLKNGNATLLRTDSPKAHVTHHSRPEDKVTLRCWAL
GFYPADITLTWQLNGEELIQDMELVETRPAGDGTFQKWASVVVPLGKEQYYTCHVYHQGLPEPLTLRWEPPPST
VSNMATVAVLVVLGAAIVTGAVVAFVMKMRRRNTGGKGGDYALAPGSQTSDLSLPDCKVMVHDPHSLA

SCT-K^b-KIITYRNL
(amino acid)
MARSVTLVFLVLVSLTGLYAKIITYRNLGCGASGGGGSGGGGSIQKTPQIQVYSRHPPENGKPNILNCYVTQFHPP
HIEIQMLKNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTETDTYACRVKHASMAEPKTVYWDRDMGGGGSGGG
GSGGGGSGGGGSGPHSLRYFVTAVSRPGLGEPRYMEVGYVDDTEFVRFDSDAENPRYEPRARWMEQEGPEY
WERETQKAKGNEQSFRVDLRTLLGCYNQSKGGSHTIQVISGCEVGSDGRLLRGYQQYAYDGCDYIALNEDLKT
WTAADMAALITKHKWEQAGEAERLRAYLEGTCVEWLRRYLKNGNATLLRTDSPKAHVTHHSRPEDKVTLRCWAL
GFYPADITLTWQLNGEELIQDMELVETRPAGDGTFQKWASVVVPLGKEQYYTCHVYHQGLPEPLTLRWEPPPST
VSNMATVAVLVVLGAAIVTGAVVAFVMKMRRRNTGGKGGDYALAPGSQTSDLSLPDCKVMVHDPHSLA

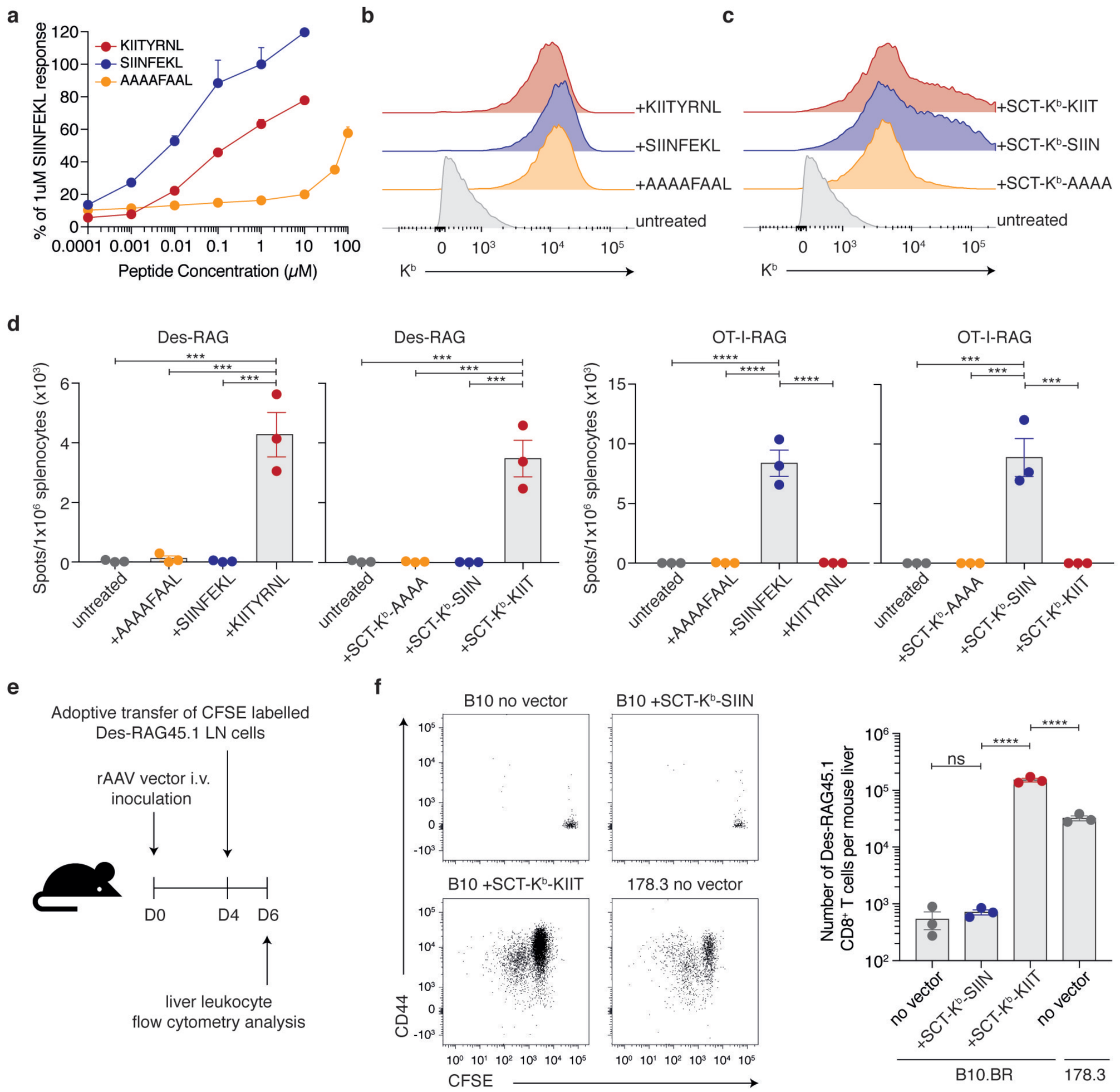
SCT-K^d-SYFPEITHI
(amino acid)
MAPCTLLLLLAAALAPTQTRASYFPEITHIGCGASGGGGSGGGGSIQKTPQIQVYSRHPPENGKPNILNCYVTQFH
PPHIEIQMLKNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTETDTYACRVKHASMAEPKTVYWDRDMGGGGSG
GGGSGGGGSGGGGSGPHSLRYFVTAVSRPGLGEPRFIAVGYVDDTQFVRFDSDADNPRFEPRAPWMEQEGPE
YWEEQTQRAKSDEQWFRVSLRTAQRCYNQSKGGSHTFQRMFGCDVGSDWRLLRGYQQFAYDGRDYIALNEDL
KTWTAADTAALITRRKWEQAGDAEYYRAYLEGECVEWLRRYLELGNETLLRTDSPKAHVTYHPRSQVDVTLRCW
ALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWAAVVVPLGKEQNYTCHVHHKGLPEPLTLRWKLPP
STVSNTVIIAVLVVLGAAIVTGAVVAFVMKMRRNTGGKGVNYALAPGSQTSDLSLPDGKVMVHDPHSLA

MHC (+YCAC mutation)

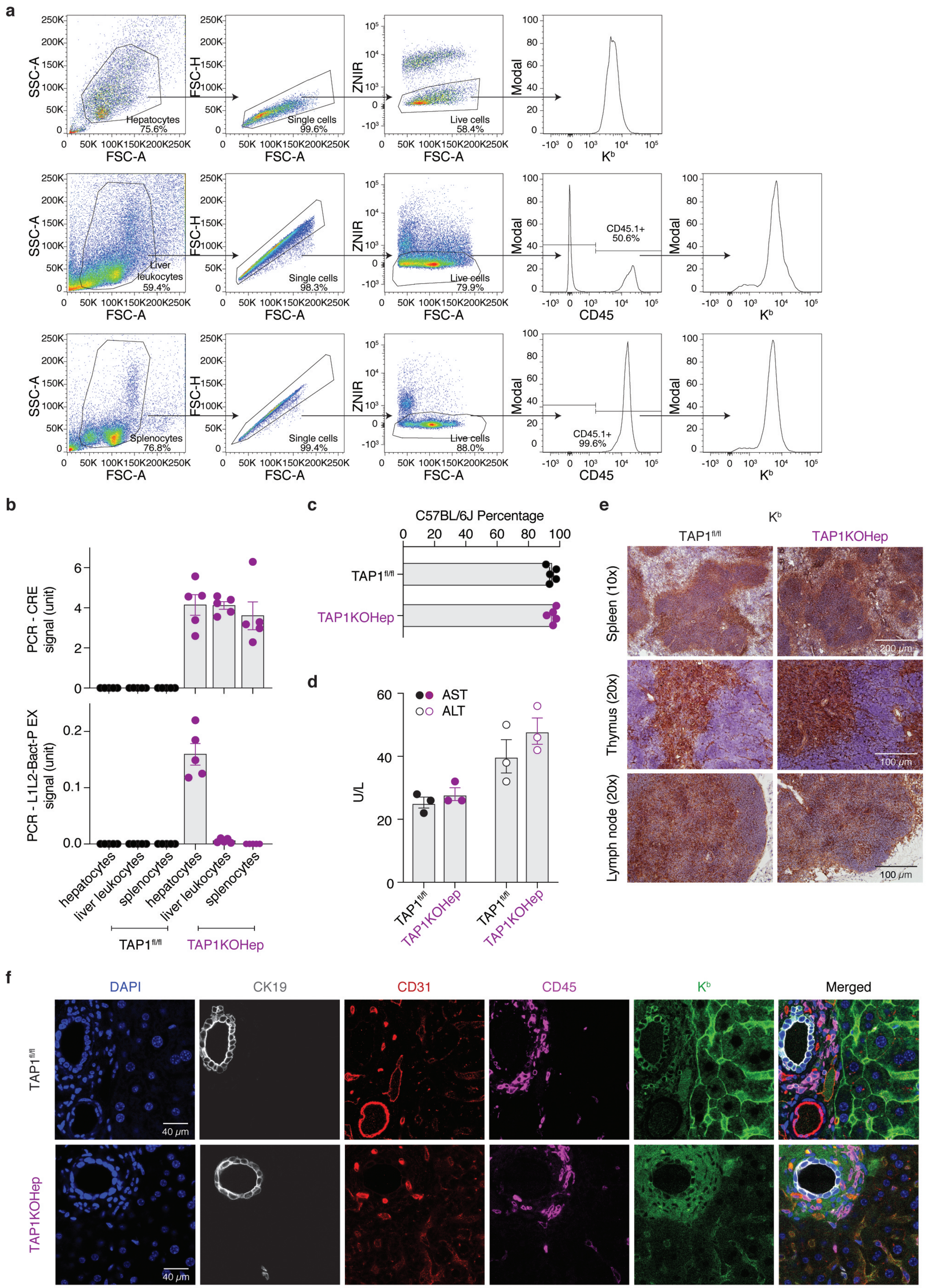
Leader sequence----heavy chain H-2K^d (Y84C, A139C)

HC-K^d-YCAC
(amino acid)
MAPCTLLLLLAAALAPTQTRAGPHSLRYFVTAVSRPGLGEPRFIAVGYVDDTQFVRFDSDADNPRFEPRAPWME
QEGPEYWEEQTQRAKSDEQWFRVSLRTAQRCYNQSKGGSHTFQRMFGCDVGSDWRLLRGYQQFAYDGRDYI
ALNEDLKTWTAADTCALITRRKWEQAGDAEYYRAYLEGECVEWLRRYLELGNETLLRTDSPKAHVTYHPRSQVD
VTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWAAVVVPLGKEQNYTCHVHHKGLPEPLTL
RWKLPPSTVSNTVIIAVLVVLGAAIVTGAVVAFVMKMRRNTGGKGVNYALAPGSQTSDLSLPDGKVMVHDPHSLA

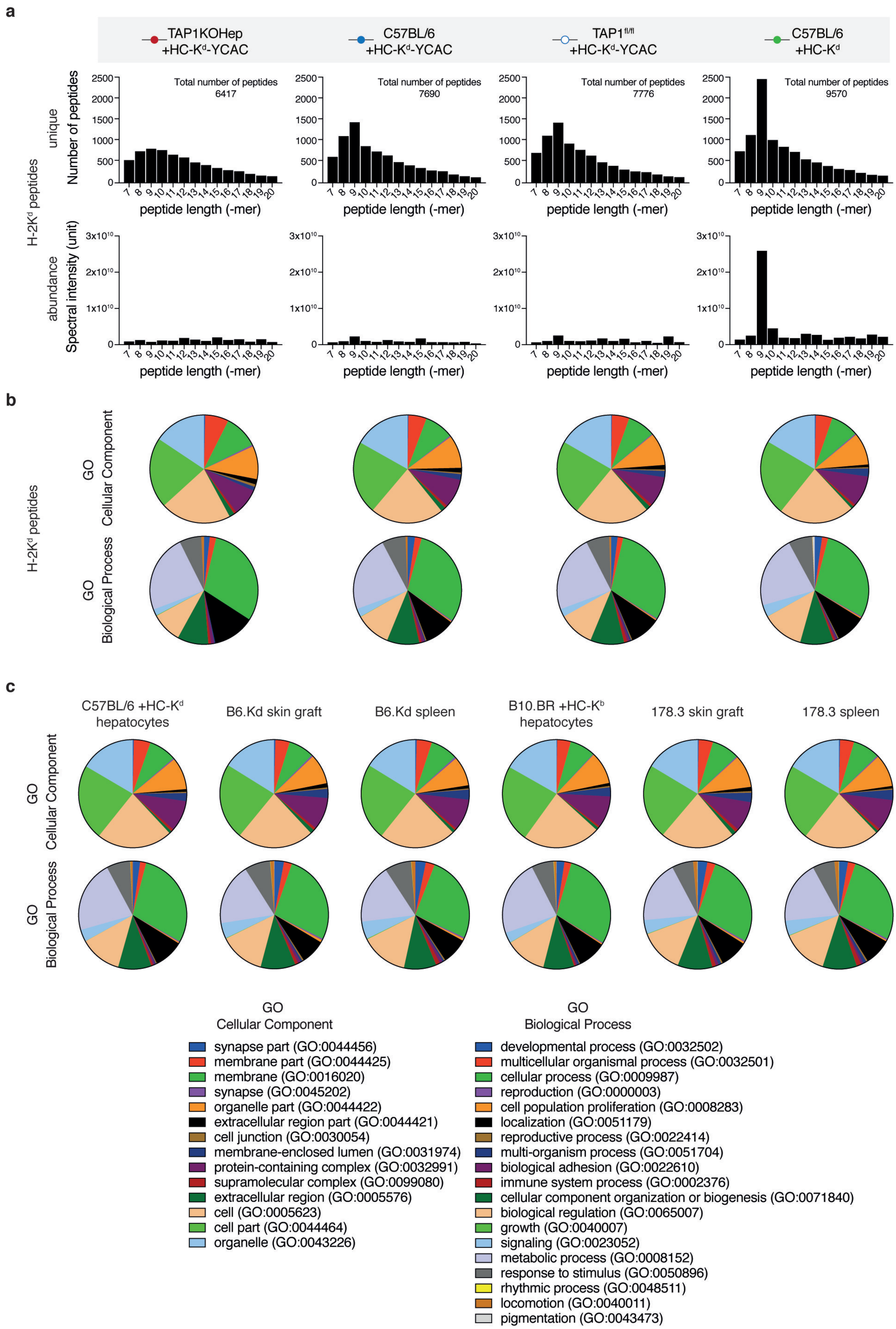
Supplementary Figure 2



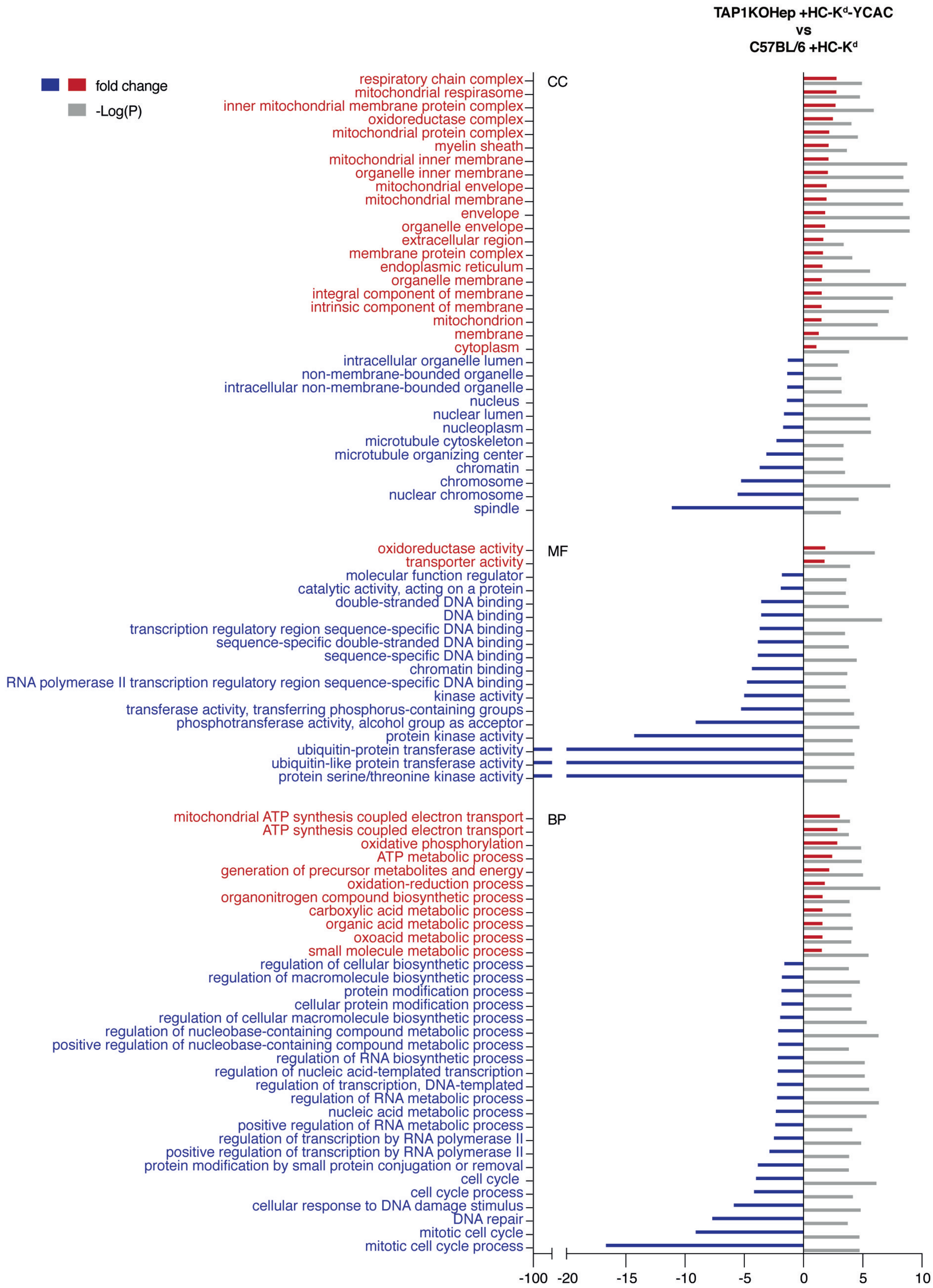
Supplementary Figure 3



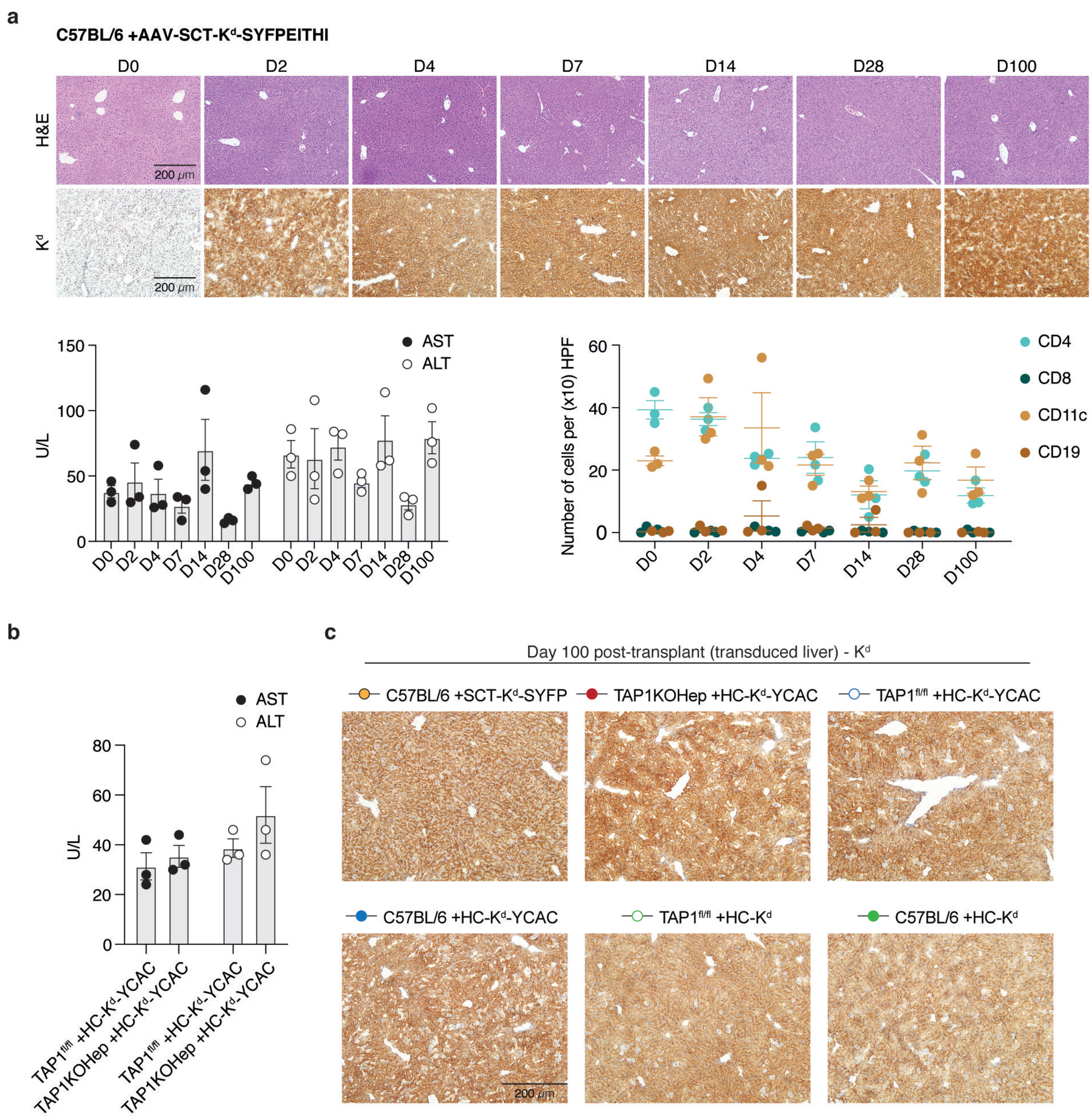
Supplementary Figure 4



Supplementary Figure 4



Supplementary Figure 5



Supplementary Table 2

AA SEQUENCE	Peptide	Length	H-2K^d IC50 (nM)	H-2K^d Rank	Spectral intensity value DDA (hep)	Present in DIA (hep)	Spectral intensity value DDA (skin	Present in DIA (skin)	Spectral intensity value DDA (spleen)	Present in DIA (spleen)	Accession
AFHPSKAYI	AFHPSKAYI	9	302.7	0.3	4801600	YES	224950	YES	27405000	YES	Q9ERG2
AFHPVHGTL	AFHPVHGTL	9	406.9	0.4		YES		YES	2174800	YES	Q8C570
AFHSSRTSL	AFHSSRTSL	9	39.1	0.03		YES	1219200	YES	32245000	YES	Q9QXZ0
AFIPTINAI	AFIPTINAI	9	202.2	0.175	386170	NO	39941000	YES	62111000	YES	P47930
AFLSSLTDV	AFLSSLTDV	9	228.5	0.25	919540	NO		YES	18927000	YES	Q3UVL4
AFQTILTEI	AFQTILTEI	9	53.5	0.05	273360	YES	8433500	YES	10894000	YES	P62492
AFVATGTNL	AFVATGTNL	9	292.2	0.3	979870	NO	766910	NO	2340900	NO	Q08024
AFVSMLNDI	AFVSM(+15.99)LNDI	9	227.8	0.25	12944000	YES	6645800	YES	41164000	YES	P19096
AFVSMLNDI	AFVSMLNDI	9	227.8	0.25	2013300	YES	1389400	YES		YES	P19096
AGLQFPVGR	AGLQFPVGR	9	40663.1	85	699580	NO	477890	YES	722300	YES	Q6GSS7:Q64523:C0HKE7:C0HKE6:C0HKE5:C0HKE3:C0HKE9:C0HKE2:C0HKE1:C0HKE4:C0HKE8:Q8BFU2:Q8CGP7:Q8R1M2:P27661:Q64522:P0C0S6
AISKLYSTI	AISKLYSTI	9	2926.9	1.7	1293300	YES	1583800	YES	23999000	YES	Q6P5B0
AKERLLLWT	AKERLLLWT	9	36992	60		YES		YES		YES	Q91ZU6
ALLPTITQL	ALLPTITQL	9	3507.2	2	400250	NO	12164000	YES	27669000	YES	C3VPR6
ALQANRTAL	ALQANRTAL	9	1290.7	0.9	49022	NO		YES	1400400	YES	Q6PB66
ALSRLFSSI	ALSRLFSSI	9	5105.7	3	423680	NO		YES	7906300	YES	Q3U308
ASLVNADKL	ASLVNADKL	9	21827.1	17		YES		YES		YES	P59016
ASVLNVNHI	ASVLNVNHI	9	13866.4	8		YES	881800	YES	6652900	YES	Q99NH0

ASYEFVQRL	ASYEFVQRL	9	28523.7	28		YES	4687600	YES		YES	Q9JHU4
AVFPSIVGR	AVFPSIVGR	9	36425.3	55	988750	YES	878000	YES	150920	YES	P60710:P63260:P68033:P62737
AVLSFSTRL	AVLSFSTRL	9	6750.8	4		YES		YES	2664100	YES	P46978
AWAKALTDI	AWAKALTDI	9	883.8	0.7	2017000	NO	1174600	YES	1154900	YES	O09117
AYAPAAATV	AYAPAAATV	9	31.6	0.02	15307000	YES	1207700	YES	42971000	YES	O88532
AYAPAIHQI	AYAPAIHQI	9	25.5	0.015	8671500	YES	3783900	YES	71931000	YES	E9Q7E2
AYAPSGNFV	AYAPSGNFV	9	37.7	0.03	19059000	YES	26714000	YES	46585000	YES	P62880:Q61011
AYAPSGNYV	AYAPSGNYV	9	22.2	0.01	4199800	YES	19868000	YES	91558000	YES	P62874:P29387
AYDGVRGSL	AYDGVRGSL	9	361.9	0.4	133580	NO	315290	YES	11411000	YES	Q8C4J7
AYFHLLNQI	AYFHLLNQI	9	51.1	0.04	4804500	YES	91785000	YES	159680000	YES	Q99K51
AYGSLFNSI	AYGSLFNSI	9	39	0.03	73719000	YES	2485800	YES	15326000	YES	Q71RI9
AYGVAVNKL	AYGVAVNKL	9	649.1	0.6	2016100	YES	403540	YES	3307600	YES	Q80XI6
AYHGGHLTI	AYHGGHLTI	9	43.6	0.04	8511100	YES	1852400	YES	14381000	YES	Q9CPX7
AYHQALSRV	AYHQALSRV	9	38.5	0.03	13361000	YES	3349900	YES	21002000	YES	P43883
AYHTQTTPL	AYHTQTTPL	9	12.8	0.01	164470	NO	212260	YES	6796200	NO	Q9WTP6
AYIPLNNYL	AYIPLNNYL	9	23.8	0.015	7756400	YES	9993000	YES	27978000	YES	Q8C878
AYITGKEDI	AYITGKEDI	9	19.4	0.01	421910	NO		YES	10259000	YES	Q60767
AYKANRDLI	AYKANRDLI	9	395.8	0.4	2276200	NO	7942100	NO	23426000	NO	P26231
AYKAVLNYL	AYKAVLNYL	9	43.8	0.04	1311500	NO	9871000	NO	87473000	NO	Q3TUU5
AYKFGKTVV	AYKFGKTVV	9	113.3	0.125	14182000	NO	4185100	NO	36495000	YES	Q8R3Q0
AYKVLKTEM	AYKVLKTEM	9	111	0.125	301280	NO	59993	NO		YES	Q8BI84
AYKWIRTSL	AYKWIRTSL	9	48.3	0.04	912120	NO	936360	NO	15429000	NO	Q8VE88
AYLAALTQL	AYLAALTQL	9	14.7	0.01	401190	NO	16738000	YES	99174000	YES	P54310
AYLGTITKT	AYLGTITKT	9	997.6	0.8	259800	NO		YES	588300	YES	O88545
AYLHAQHYI	AYLHAQHYI	9	28.4	0.02		YES	99485	YES	1034700	YES	Q9R117
AYLHSHNMI	AYLHSHNM(+15.99)I	9	17.8	0.01	96867	NO	415040	YES	4841000	YES	Q6ZQ29
AYLHSHTMI	AYLHSHTM(+15.99)I	9	10	0.01	547090	NO	698980	YES	9570100	YES	Q5F2E8

AYLHSHTMI	AYLHSHTMI	9	10	0.01	586530	NO	1169700	YES		YES	Q5F2E8
AYLLNLNHL	AYLLNLNHL	9	137.5	0.125	20372000	YES	21824000	YES	276160000	YES	Q91V04
AYLPQTSRL	AYLPQTSRL	9	65.8	0.06		YES	2246600	YES	60929000	YES	Q6NXY1
AYLPQYTHM	AYLPQYTHM(+15.99)	9	40	0.03	15770000	YES	51156000	YES	552720000	NO	Q91W59
AYLTDLTKL	AYLTDLTKL	9	75.4	0.07	669560	NO		YES	20522000	YES	G5E8P0
AYLVDIKTI	AYLVDIKTI	9	120	0.125	8257400	YES	17114000	YES	24060000	YES	Q6VH22
AYMKSSRYI	AYM(+15.99)KSSRYI	9	10.6	0.01	5584800	NO	102970	YES	4117800	YES	P10649
AYMKSSRYI	AYMKSSRYI	9	10.6	0.01	719650	NO	110900	YES		YES	P10649
AYNILIGEL	AYNILIGEL	9	766.3	0.6	198110	YES		YES	26291000	YES	Q5SV77
AYNPGQAVP	AYNPGQAVP	9	12730.9	7.5	2218500	NO		YES	4581600	YES	Q8VDP4
AYNRILDAL	AYNRILDAL	9	95.8	0.09	2140500	YES	3750600	NO	20923000	YES	Q68FD7
AYQELLRLI	AYQELLRLI	9	157.2	0.15		YES	3798900	YES	1990000	YES	Q9JLB2
AYQNNKELL	AYQNNKELL	9	304.4	0.3	7911200	YES	10425000	YES	172590000	YES	P57080
AYQRVFHSL	AYQRVFHSL	9	19.3	0.01	234370	NO	311020	YES	1952000	YES	Q3TUA9
AYQSIQSYL	AYQSIQSYL	9	19.1	0.01	59021000	YES	55445000	YES	134100000	YES	Q925U4
AYRQLRETL	AYRQLRETL	9	92	0.09	11090000	NO	4210400	NO	37984000	NO	Q9D083
AYSFGRTTI	AYSFGRTTI	9	15.1	0.01	13677000	YES	1371500	NO	5356100	NO	Q3TWI9
AYSGIKNQL	AYSGIKNQL	9	200.6	0.175	1395300	YES	1009700	YES	14226000	YES	Q9ERG2
AYSGVKNSL	AYSGVKNSL	9	60.3	0.06	1372700	YES	876020	YES	39980000	YES	G5E829
AYSIVIRQI	AYSIVIRQI	9	377.2	0.4	5487500	YES	13654000	YES	33996000	YES	Q80TP3
AYSKLGNYV	AYSKLGNYV	9	104.4	0.1	15272000	YES	4448600	NO	57828000	YES	Q8BJU0
AYSQAHLTL	AYSQAHLTL	9	96.6	0.09	1210300	NO		YES	8048900	YES	Q9DBE9
AYSRSMTKL	AYSRSM(+15.99)TKL	9	47	0.04	1457900	YES	1330500	YES	31203000	YES	Q3UQN2
AYSRSMTKL	AYSRSMTKL	9	47	0.04	119590	YES	1887500	YES		YES	Q3UQN2
AYSTLLSHI	AYSTLLSHI	9	16.6	0.01	10019000	YES	1997600	YES	34845000	YES	Q8CFX1
AYVAMNERL	AYVAM(+15.99)NERL	9	43.1	0.04	2529800	YES	3514000	YES	271380000	YES	Q9D7E4
AYVAMNERL	AYVAMNERL	9	43.1	0.04	6731200	YES		YES		YES	Q9D7E4

AYVAPTNDL	AYVAPTNDL	9	246.7	0.25	12962000	YES	118820	NO	159830	YES	Q5SW19
AYVETQDQL	AYVETQDQL	9	365.7	0.4	1502500	NO	3448500	YES	27736000	YES	F6ZDS4
AYVHVVTHF	AYVHVVTHF	9	357.8	0.4	1261200	YES	212630	YES	440820	YES	Q9D2C7
AYVPGFAHI	AYVPGFAHI	9	102.1	0.1	120030000	YES	170250000	YES	1010600000	YES	Q9CXX9
AYVPQQAWI	AYVPQQAWI	9	507.1	0.5	20734000	YES		YES	2886600	YES	Q8VI47:B2RX12:O35379
AYVPSHSDA	AYVPSHSDA	9	288.3	0.3		YES		YES	1951900	YES	Q8R420
AYWAGGLHL	AYWAGGLHL	9	92	0.09	10670000	YES	4115600	YES	26656000	YES	Q8BGH2
AYWPGLQSL	AYWPGLQSL	9	53.7	0.05	20978000	YES	1578700	YES	10007000	YES	Q8BJT9
DFHPSGTVV	DFHPSGTVV	9	936.9	0.7	2602900	YES		YES	21906000	YES	Q3UMY5
DFITVHTPL	DFITVHTPL	9	75.3	0.07		YES		YES	1777700	YES	Q61753
DLLPSHSTI	DLLPSHSTI	9	689.9	0.6	14804000	YES	841920	YES	1515000	YES	Q99MR8
DYHHIHTEI	DYHHIHTEI	9	35.5	0.025	448990	YES	367660	YES	3992400	YES	Q9EPE9
DYIALNEDL	DYIALNEDL	9	237.8	0.25		YES	3949300	YES	907390	YES	P01901
DYIITPHAL	DYIITPHAL	9	166.8	0.15	28525000	YES	36810000	YES	35211000	YES	Q3TWF6
DYIYGVTYI	DYIYGVTYI	9	25.6	0.015	5728600	YES		YES	2340300	YES	Q91ZX7
DYKESFNTI	DYKESFNTI	9	61.1	0.06	3436200	NO	81121000	YES	1310500	YES	Q921D9
DYLADKSYI	DYLADKSYI	9	31.2	0.02	111990000	YES	16793000	YES	68925000	YES	O70251
DYLGSRQYV	DYLGSRQYV	9	56.8	0.05	57315000	NO	27100000	NO	111590000	NO	P52332
DYLNVVNEL	DYLNVVNEL	9	130.2	0.125	1776300	YES	567220	YES	1365400	YES	Q6ZQB6
DYLPDRELV	DYLPDRELV	9	1829.5	1.2	6299900	NO	9177800	NO	27360000	NO	Q5SW75
DYLPSWQKI	DYLPSWQKI	9	171.6	0.175	5536600	NO		YES	327260	NO	Q91XC9
DYMEALTRL	DYM(+15.99)EALTRL	9	34.7	0.025	1207000	YES	4203400	YES	54106000	YES	Q99K70
DYMEALTRL	DYMEALTRL	9	34.7	0.025	4842100	YES	5164600	YES		YES	Q99K70
DYNRIGSSL	DYNRIGSSL	9	45	0.04	14104000	YES	7430600	YES	32374000	YES	Q6P8X1
DYNTAHNKV	DYNTAHNKV	9	109.6	0.1	614960	YES		YES	428560	YES	Q61510
DYQALRTSI	DYQALRTSI	9	8.7	0.01	44113000	YES	36431000	YES	802740000	YES	Q68FD5
DYQDVRNEI	DYQDVRNEI	9	42.6	0.04	763740	NO		YES	4406200	YES	G5E829
DYQPGITFI	DYQPGITFI	9	24	0.015	1956100	NO	9724600	YES	65946000	YES	Q8CJG0

DYQPGITYI	DYQPGITYI	9	15.1	0.01	7258000	YES	6303900	YES	17776000	YES	Q8CJG1:Q8CJF9
DYQRLLQTI	DYQRLLQTI	9	20.5	0.01	6339000	YES	11135000	YES	33648000	YES	Q6KAQ7
DYVVGFTDL	DYVVGFTDL	9	305.1	0.3	504840	NO		YES	398480	NO	Q9CQ79
DYYPDRTYI	DYYPDRTYI	9	29.8	0.02	2425300	NO	3058400	YES	94280000	YES	Q8JZL7
EGPVTEQVK	EGPVTEQVK	9	42038.8	90	5673300	NO		YES	1071600	YES	Q7TQH0
EYEKIKSQL	EYEKIKSQL	9	82.8	0.08	211480	NO		YES	469070	NO	B2RXS4
EYEPGKSSI	EYEPGKSSI	9	23.8	0.015	2963200	NO	83781	NO	10092000	NO	Q3UTJ2
EYIHALTLL	EYIHALTLL	9	96.2	0.09	1131600	NO		YES	10427000	YES	O35382
EYIHSKNFI	EYIHSKNFI	9	26.8	0.02	145970000	YES	59681000	YES	377220000	YES	Q9DC28:Q9JMK2
EYIKVITGL	EYIKVITGL	9	78.7	0.08	9480000	YES	17114000	YES	35285000	YES	Q6A070
EYLEGRNLI	EYLEGRNLI	9	90.2	0.09		YES	6789600	YES	12951000	YES	Q91Z67
EYLPSQITI	EYLPSQITI	9	67.2	0.06	6041700	YES	40351000	YES	32736000	YES	Q8R151
EYMKVQTEI	EYMKVQTEI	9	13.3	0.01	2485300	YES	1204200	YES		YES	Q62073
EYNDLKTEL	EYNDLKTEL	9	124.5	0.125	321160	NO	872110	YES	5006700	YES	Q8BU04
EYNELLTAI	EYNELLTAI	9	34.3	0.025	413120	NO	6739600	YES	49390000	YES	P70428
EYVANLTEL	EYVANLTEL	9	100.4	0.1	41849000	YES		YES	76108000	YES	Q3TKT4
EYVANLTNL	EYVANLTNL	9	101.7	0.1		YES	9411600	YES	29909000	YES	Q6DIC0
EYVATTFDI	EYVATTFDI	9	353.3	0.3	1559600	NO		YES		YES	Q922E6
EYVHTKNFI	EYVHTKNFI	9	65.8	0.06	42833000	YES	22258000	YES	141560000	YES	Q8BK63
EYVRNQQTI	EYVRNQQTI	9	76.3	0.07	294130	NO		YES	1334800	YES	Q9CQC6
EYWRLIGEL	EYWRLIGEL	9	458.4	0.4	1361900	NO	874200	YES		YES	P97352
FAYEGRDYI	FAYEGRDYI	9	4274.6	2.5		YES	11493000	YES	10900000	YES	P01899
FFSEIISSI	FFSEIISSI	9	477.5	0.4	489660	NO	531820	YES	372150	YES	Q925E7:Q6P1F6
FFSTIRTEL	FFSTIRTEL	9	151.6	0.15	42866000	YES	29077000	YES	551310000	YES	P50172
FFVENVSEL	FFVENVSEL	9	1873.6	1.2	551130	NO	1560300	YES	14915000	YES	Q6KCD5
FGPVNHEEL	FGPVNHEEL	9	27315.3	26	304380	NO		YES	30507000	YES	P46414
FLLPILSQI	FLLPILSQI	9	1108.5	0.8	1045300	YES	1365900	YES	7734300	YES	Q62167:Q62095

FYEPQKGSI	FYEPQKGSI	9	28.1	0.02	543420	NO		YES		YES	Q61102
FYFASKLVL	FYFASKLVL	9	32.7	0.025		YES	13400000	YES	15821000	YES	Q07813
FYFQQKGQL	FYFQQKGQL	9	43	0.04	1557800	NO	1789400	YES		YES	O55229
FYGDVQTHI	FYGDVQTHI	9	29.6	0.02	7727200	YES		YES		YES	Q6ZPE2
FYHPETTQL	FYHPETTQL	9	56.8	0.05	6473600	YES		YES		YES	Q61584
FYIGLGSRI	FYIGLGSRI	9	16	0.01	41374000	YES	23817000	YES	125600000	YES	Q8VCV1:Q7M759
FYLETQQQI	FYLETQQQI	9	29.4	0.02	1217300	NO		YES	10760000	YES	Q99MP8
FYLGSFDNI	FYLGSFDNI	9	34.2	0.025	1094800	YES	4021000	YES	12358000	YES	Q6GV12
FYLPAPGTL	FYLPAPGTL	9	18.8	0.01	781250	NO	1851900	YES	1631300	YES	Q80WC3
FYNPAVSRI	FYNPAVSRI	9	17	0.01		YES	3912800	YES	56969000	YES	Q80XR2
FYNQVSTPL	FYNQVSTPL	9	8.6	0.01	10580000	YES		YES	1776800	YES	Q61703
FYNVDISYL	FYNVDISYL	9	103.8	0.1	652900	YES		YES	5337700	YES	P10605
FYQKADHTL	FYQKADHTL	9	12.8	0.01	2423100	YES	688220	YES	3961700	YES	Q8K2Q7
FYQQQAGGL	FYQQQAGGL	9	119.8	0.125	114990	NO	525240	YES	4545800	YES	Q91YE7
FYSAGKNYL	FYSAGKNYL	9	26.1	0.015	3573000	YES		YES	43423000	YES	Q8R3N6
FYSNIQTVI	FYSNIQTVI	9	54.4	0.05		YES	31998000	YES	113460000	YES	P08775
FYSQDLTHL	FYSQDLTHL	9	73.6	0.07	926340	NO	3867900	YES	4288500	YES	Q8CHE4
FYSTTHGAL	FYSTTHGAL	9	35.9	0.025	1215300	YES		YES		YES	Q8C0L6
FYTPIPNGL	FYTPIPNGL	9	200	0.175	121730000	YES	48789000	YES	38209000	YES	O08573
FYTQLLQEL	FYTQLLQEL	9	69.7	0.07	92251	NO	615870	YES	809110	YES	Q5RJH6
FYVATSRQL	FYVATSRQL	9	37	0.025	38324000	YES		YES		YES	Q8VI47:B2RX12
FYVPSVSQL	FYVPSVSQL	9	20.6	0.01	3321900	YES		YES	23206000	YES	Q62136
GAVTNVKVI	GAVTNVKVI	9	17664	12		YES		YES	2167800	YES	P70372
GFHPSGSVL	GFHPSGSVL	9	601.8	0.5	3094100	YES	3561900	YES	67444000	YES	Q7TNG5
GFHRTISHL	GFHRTISHL	9	324.5	0.3	346380	NO	201600	NO	850400	YES	Q9DBU5
GFIASHVIV	GFIASHVIV	9	2437	1.5		YES	1744900	YES	2906200	YES	Q8VDR7
GFLKSISNV	GFLKSISNV	9	437.8	0.4	1660100	NO	1935900	NO	6027800	YES	Q8C176
GFNPALQLI	GFNPALQLI	9	2641.9	1.6	20014000	YES	96580000	YES	140080000	YES	Q9ER81

GFNSSISNI	GFNSSISNI	9	205.1	0.2		YES	1127100	YES	13727000	YES	A2AJ88
GGIQNVGHI	GGIQNVGHI	9	9776.3	5.5	113890	YES		YES	17747000	YES	P24547
GINEAGISR	GINEAGISR	9	35325.7	50		YES		YES		YES	P29533
GWGELQNTI	GWGELQNTI	9	7006.9	4	2588600	NO	1697500	YES	1220900	YES	P24527
GYAKLIAEL	GYAKLIAEL	9	255	0.25	3698100	YES	5673900	YES	27228000	YES	B1AZI6
GYALPHAIL	GYALPHAIL	9	1552.7	1	2056600	YES	1755600	YES	4444900	YES	P60710:P63260:Q8BFZ3
GYATLHHVI	GYATLHHVI	9	21.8	0.01		YES	1018700	YES	13564000	YES	Q925U4
GYATTYRQL	GYATTYRQL	9	49.2	0.04		YES		YES	5257900	YES	Q09200
GYEETLTRL	GYEETLTRL	9	81.3	0.08	2427400	YES		YES	1426400	YES	Q5XPI3
GYERIYNEI	GYERIYNEI	9	54.1	0.05	124340000	YES	4814800	YES	16195000	YES	Q61823
GYFEVTHDI	GYFEVTHDI	9	56.9	0.05	414680000	YES	11397000	YES	39391000	YES	P24270
GYFGSTQGL	GYFGSTQGL	9	311.3	0.3	2587900	YES		YES	12818000	YES	Q6KAR6
GYFNTYKLL	GYFNTYKLL	9	341.6	0.3	1505800	NO	2386400	YES	19343000	YES	Q8BT60
GYFPNKKQL	GYFPNKKQL	9	138.3	0.125	6191400	YES	1735700	YES	11806000	YES	P70388
GYGQGAGTL	GYGQGAGTL	9	101.9	0.1	1272900	NO		YES	20702000	YES	P97315
GYGRSILTV	GYGRSILTV	9	127.8	0.125	4729400	YES		YES	201240	NO	A2A8Z1
GYGTQKSSL	GYGTQKSSL	9	25.1	0.015	43231	NO		YES	5587100	YES	Q99KW3
GYIASLHEL	GYIASLHEL	9	24.4	0.015	30330000	YES	712280	YES	4194500	YES	Q920R0
GYIESIQHI	GYIESIQHI	9	22	0.01		YES	806020	YES	4452500	YES	Q9CXC3
GYIGGKKEI	GYIGGKKEI	9	37.6	0.03	1982400	YES	1776500	YES	7325400	YES	
GYIGGKKEL	GYIGGKKEL	9	80	0.08	1982400	YES	1776500	YES	7325400	YES	P97363
GYIGSHTVL	GYIGSHTVL	9	22	0.01	88165000	YES	9113400	YES	93856000	YES	Q8R059
GYILSIHRI	GYILSIHRI	9	49.6	0.04	9524200	YES	1254500	YES	6468000	YES	Q9Z0M5
GYIPSASMT	GYIPSASM(+15.99)T	9	74.7	0.07	520180	NO	308350	NO	4624600	NO	Q9QYF9
GYIQTGDRL	GYIQTGDRL	9	92.9	0.09	2273000	YES		YES		YES	Q69ZS7
GYISIANGL	GYISIANGL	9	57.1	0.05	5062200	YES	2643900	YES	9879100	YES	Q99LC2
GYKAGMTHI	GYKAGM(+15.99)THI	9	15	0.01	7341100	YES	9721800	YES	746490000	YES	P27659

GYKAGMTHI	GYKAGMTHI	9	15	0.01	6111700	YES	11103000	YES	2422300	YES	P27659
GYKESFSSI	GYKESFSSI	9	28.2	0.02	5685800	NO	618920	NO	17230000	NO	Q80YE7
GYLDGRLEP	GYLDGRLEP	9	5733.6	3.5	123760000	YES	2485300	YES	1563600	YES	P53566
GYLELLDHV	GYLELLDHV	9	138.2	0.125	8150400	YES	114840000	YES	751550000	YES	P26039
GYLGGENRV	GYLGGENRV	9	210	0.2	1495300	YES		YES	1061000	YES	E9Q5F9
GYLGQVTTI	GYLGQVTTI	9	15.1	0.01		YES	93831000	YES	344690000	YES	Q9Z1F9
GYLKGYTLV	GYLKGYTLV	9	45.2	0.04	6891400	YES	32833000	YES	114640000	YES	Q9CWZ3
GYLKLWDTV	GYLKLWDTV	9	71.6	0.07	528650	NO	3632000	YES	2715700	YES	P97499
GYLLDKETL	GYLLDKETL	9	167.7	0.15	2045500	YES	3492000	YES	15829000	YES	Q80ZJ6
GYLPGNEKL	GYLPGNEKL	9	164.4	0.15	47000000	YES	30146000	YES	181020000	YES	P97372
GYLPLAHVL	GYLPLAHVL	9	64.3	0.06	119230000	YES	123210000	YES	356670000	YES	Q9QUJ7:Q9CZW4
GYLPNKQVL	GYLPNKQVL	9	126.1	0.125	1231000000	YES	77832000	YES		YES	Q05915
GYLPTQQDV	GYLPTQQDV	9	193.7	0.175	1139300	NO		YES		YES	P21278
GYLPVQTVL	GYLPVQTVL	9	31.1	0.02	1492400	NO	47236000	YES	471550000	YES	P11531
GYLSSRVLL	GYLSSRVLL	9	95.1	0.09	15237000	YES	8758400	YES	88262000	YES	Q5NCS9
GYLTNPRSL	GYLTNPRSL	9	66.9	0.06		YES	484650	YES		YES	Q924Z5
GYMGHLTRI	GYM(+15.99)GHLTRI	9	42.3	0.04	945800	YES	182830	YES	1829700	YES	Q922D4
GYMRLLEFI	GYM(+15.99)RLLEFI	9	26.7	0.02	3700600	NO	17673000	YES	34678000	NO	Q9ER73
GYMGHLTRI	GYMGHLTRI	9	42.3	0.04		YES		YES		YES	Q922D4
GYNKAKAYI	GYNKAKAYI	9	33.7	0.025	40651	NO	158340	YES	1995900	YES	Q05909
GYNKQNTTL	GYNKQNTTL	9	16.3	0.01	622260	YES		YES	25708000	YES	E9Q3L2
GYNRVLQFL	GYNRVLQFL	9	77.5	0.07	2877000	YES	26707000	YES	6624200	YES	Q9R269
GYNSVQHLI	GYNSVQHLI	9	77.9	0.08	1264000	NO		YES	22084000	YES	Q91V83
GYQRLLELI	GYQRLLELI	9	73.8	0.07	1119500	NO	16437000	YES	36589000	YES	A2AIV2
GYQTAFSQL	GYQTAFSQL	9	14.4	0.01	1359600	NO	4738600	YES	21117000	YES	Q9ERK4
GYQTVKEAL	GYQTVKEAL	9	13.3	0.01	145620000	YES	7417000	YES		YES	P33267
GYQVLRSVL	GYQVLRSVL	9	35.9	0.025	745030	NO	7632300	YES	44588000	YES	Q8R5K4
GYSHILTNI	GYSHILTNI	9	61.6	0.06	1901500	YES	164500	YES	680790	NO	Q60866

GYSKLYDDI	GYSKLYDDI	9	403	0.4	4912000	YES	268340	NO	1581900	NO	O88822
GYSMNHQVI	GYSM(+15.99)NHQVI	9	434.8	0.4	5764000	YES	1507500	YES	8976600	YES	P46935
GYSMNHQVI	GYSMNHQVI	9	434.8	0.4	8292300	YES	1878800	YES		YES	P46935
GYSPQLQGL	GYSPQLQGL	9	1499.7	1	7576800	YES	3711900	YES	8228100	YES	Q8BRG8
GYTHGMHTL	GYTHGMHTL	9	64.2	0.06	2594400	YES		YES		YES	Q9R049
GYTITPNTL	GYTITPNTL	9	78	0.08	1281200	NO		YES	335610	NO	Q61139
GYVDNKEFV	GYVDNKEFV	9	785.1	0.6	152950000	YES	102660000	YES	459180000	YES	P01899:P01897
GYVETPRGL	GYVETPRGL	9	929.9	0.7	15489000	YES	7483300	YES	68411000	YES	P27659
GYVPSQADV	GYVPSQADV	9	558.5	0.5	3292300	YES	600450	YES	10131000	YES	O70251
GYVQGINDL	GYVQGINDL	9	191.6	0.175	20575000	YES	6004500	YES	17717000	YES	Q8R5A6
GYWNTYTEL	GYWNTYTEL	9	34.1	0.025	3198700	NO		YES	66718000	YES	Q3V2Q8
GYYNNSTKV	GYYNNSTKV	9	82.5	0.08	147360	NO	377760	YES	53721000	YES	P25911
GYYQANERV	GYYQANERV	9	102.9	0.1	153050	YES		YES	8398700	YES	O70378
HFIEGGRTV	HFIEGGRTV	9	819.3	0.7	6713500	YES		YES	2473000	YES	Q7TQI3
HFLPMLQTV	HFLPM(+15.99)LQTV	9	132.1	0.125	93378000	YES	180070000	YES	1572300000	NO	Q60605
HFLPMLQTV	HFLPMLQTV	9	132.1	0.125	54390000	YES	142220000	YES	368670	NO	Q60605
HFNPVQTQI	HFNPVQTQI	9	231	0.25		YES		YES	12779000	YES	E9PZJ8
HFSTVKTHL	HFSTVKTHL	9	94.9	0.09	346980	NO	854010	YES	3848200	YES	Q62348
HFVEGQTVV	HFVEGQTVV	9	2352.2	1.4	7210500	YES	1698000	YES	16198000	YES	Q6NS46
HFYSSISSL	HFYSSISSL	9	121	0.125	43117000	YES	59111000	YES	50938000	YES	Q60795
HFYSSKSEI	HFYSSKSEI	9	47	0.04	357840	NO	326900	YES	12292000	YES	P54276
HYEITKQDI	HYEITKQDI	9	133.7	0.125	6781400	YES	1472600	YES	10157000	YES	Q62245
HYFEDKENI	HYFEDKENI	9	169.8	0.15	3520100	YES	4116300	YES	572820	YES	P53351
HYGESITNI	HYGESITNI	9	36.6	0.025	4370600	YES	983690	YES	55329000	YES	Q80YA3
HYHQLLEKV	HYHQLLEKV	9	285.8	0.25	18213000	YES	663360	YES	8047100	YES	Q68FL6
HYLDMNTVL	HYLDM(+15.99)NTVL	9	21.1	0.01	3941200	YES	42293000	YES	75605000	NO	E9Q555
HYLDTTTLI	HYLDTTTLI	9	44.9	0.04	4970400	NO	12857000	YES	32580000	YES	P47941
HYLHSLSQA	HYLHSLSQA	9	226.4	0.2	771260	NO	598500	YES	6547800	YES	Q8K1X1

HYLPSYYHL	HYLPSYYHL	9	59.3	0.06	13251000	YES	3903400	YES	23000000	YES	Q9DAR7
HYQNMKHAI	HYQNM(+15.99)KHAI	9	8.1	0.01	1213700	NO	263900	YES	33853000	YES	Q8K0S9
HYQNMKHAI	HYQNMKHAI	9	8.1	0.01	396380	NO	113580	YES		YES	Q8K0S9
HYQQALTSA	HYQQALTSA	9	37.8	0.03	137920	NO	125550	YES	2987600	YES	Q8C181
HYQSIGSTL	HYQSIGSTL	9	10	0.01	8890500	YES	1176300	YES	33462000	YES	A3KGS3
HYSAIYSLL	HYSAIYSLL	9	202.4	0.175	3095800	YES	18774000	YES		YES	Q6P4S6
HYVAGLVGI	HYVAGLVGI	9	276.9	0.25	9046400	YES	2437200	YES	3603800	YES	P53798
HYVITARAL	HYVITARAL	9	121.4	0.125	2100000	YES	996850	YES	11734000	YES	Q9EQ61
HYWPVHNEL	HYWPVHNEL	9	36.4	0.025	2287500	NO	3738400	NO	103740000	NO	P97471
HYYETPTGI	HYYETPTGI	9	43.5	0.04		YES	1152500	YES	22383000	YES	Q5NCF2
IFDRVLTEL	IFDRVLTEL	9	1876.2	1.2	90057000	YES	70323000	YES	880290000	YES	P28700:P28704
IFIKIINTI	IFIKIINTI	9	136.9	0.125	1783600	NO	19772000	YES	69929000	YES	E9Q7G0
IFLLTNNNL	IFLLTNNNL	9	1689	1.1	517410	NO	1545400	NO	256420	NO	P46735
IFTSVRSEL	IFTSVRSEL	9	275.9	0.25	452130	YES	8862000	YES	177900000	YES	Q3UWM4
IGIENIHYL	IGIENIHYL	9	11116.3	6.5		YES	3897700	YES	12622000	YES	Q9DB27
IGPTYYQRL	IGPTYYQRL	9	31544	36		YES		YES	2032500	NO	Q8CFI7
ISPVNPVAI	ISPVNPVAI	9	27767	27		YES		YES	552350	YES	Q91WT8
IYASSKDAI	IYASSKDAI	9	12.9	0.01	1598100	YES		YES	67363000	YES	P18760:P45591
IYDKIKTGL	IYDKIKTGL	9	324.2	0.3	54964000	YES		YES	7706500	YES	O70503
IYEETRGVL	IYEETRGVL	9	416	0.4	6790300	YES	3419700	YES	22551000	YES	P62806
IYEGQITAV	IYEGQITAV	9	131.3	0.125	276650	NO		YES		YES	Q8K440
IYERAISTL	IYERAISTL	9	20.9	0.01	5633500	YES	2001900	YES	37566000	YES	Q99LI7
IYFPSVTGI	IYFPSVTGI	9	27.6	0.02	3868900	YES	2355800	YES	34081000	YES	Q9WVL3:Q91V14
IYGDVISNI	IYGDVISNI	9	158.4	0.15	5502900	YES	3752500	YES	1843500	YES	Q8CHW4
IYGGAHQTL	IYGGAHQTL	9	108.7	0.1	600170	NO	195090	YES	3038200	YES	Q80YV4
IYGGLTSKV	IYGGLTSKV	9	840	0.7	606430	NO	96860	YES	796360	YES	Q9WU78
IYHGLATLL	IYHGLATLL	9	80.6	0.08	5710800	YES	61807000	YES	51936000	YES	Q9QZQ1

IYHPNVDKL	IYHPNVDKL	9	1042.5	0.8	1732200	NO	475400	YES	488630	NO	P61089
IYKALQTAL	IYKALQTAL	9	54.4	0.05	497990	NO	2884200	YES	62823000	YES	Q3U0V2
IYKDSSTFL	IYKDSSTFL	9	92.3	0.09	13480000	YES	12467000	YES	46644000	YES	Q3UIK4
IYKGVIQAI	IYKGVIQAI	9	122.2	0.125	3535600	YES	48411000	YES	123410000	YES	Q99P72
IYKNSISKI	IYKNSISKI	9	84.2	0.08	1266200	NO	600750	NO	5588600	NO	Q8VCY6
IYKPGLSRL	IYKPGLSRL	9	148.8	0.15	1015400	NO	481980	YES		YES	P61406
IYLPAAQTM	IYLPAAQTM(+15.99)	9	26.8	0.02	11065000	NO	1321500	NO	3559900	NO	P58281
IYNQVKQII	IYNQVKQII	9	51.1	0.04	3757000	NO	678260	NO	7437200	NO	Q811D0
IYNRINNDL	IYNRINNDL	9	121.3	0.125		YES		YES	2543000	YES	Q6P4T0
IYQDIRHEA	IYQDIRHEA	9	788	0.6	238160	NO	94679	YES	242900	NO	P35821
IYQKVNERI	IYQKVNERI	9	26.4	0.015	91931	NO	539670	YES	6077200	YES	Q60931
IYRELEQSI	IYRELEQSI	9	225.9	0.2	35338000	YES	13543000	YES	104510000	YES	Q9WVE8
IYRPTINKL	IYRPTINKL	9	681.4	0.6	1599400	NO		YES	2267300	YES	Q7TMQ7
IYTSSVNRL	IYTSSVNRL	9	67.2	0.06	1314000	YES		YES		YES	O55029
IYVEQKQYI	IYVEQKQYI	9	39.1	0.03	31403000	YES	6139700	NO	88326000	YES	Q62018
IYWPNGLTI	IYWPNGLTI	9	76.7	0.07	3951400	YES	994390	YES	5098800	YES	Q91VN0
IYWPNGLTL	IYWPNGLTL	9	168.5	0.15	3951400	YES	994390	YES	5098800	YES	O88572
KALINADEL	KALINADEL	9	17699.8	12	194420	YES	3831800	YES	49146000	YES	P16546
KAPDNRETL	KAPDNRETL	9	24861.9	21	374430	YES		YES	5525400	YES	Q3TDQ1
KAPTNEFYA	KAPTNEFYA	9	36086.8	55		YES		YES		YES	O35988
KFAEGITKI	KFAEGITKI	9	329.4	0.3	17105000	YES	4155600	YES	47263000	YES	Q9CZU3
KFDKVLTAL	KFDKVLTAL	9	524.6	0.5	1558700	NO	3556800	YES	22754000	YES	Q9QZS8
KFFQTPEGL	KFFQTPEGL	9	3524.9	2	12967000	YES	21036000	YES	33950000	YES	Q60980
KFHPNGSTL	KFHPNGSTL	9	162.3	0.15	1256600	YES	1319400	YES	42569000	YES	Q6PE01
KFIATLQYI	KFIATLQYI	9	67.3	0.06	15393000	YES	42028000	YES	200480000	YES	Q9QUR6
KFIPLYSKV	KFIPLYSKV	9	674.1	0.6		YES	320010	YES	1346500	YES	P52479
KFITDCTGL	KFITDC(+119.00)TGL	9	301.1	0.3	3738800	NO	1749800	NO	28541000	NO	Q8CCJ3

KFLAAGTHL	KFLAAGTHL	9	39.7	0.03	1826700	YES	5135600	YES	131970000	YES	P14206
KFLPSSQEL	KFLPSSQEL	9	207.6	0.2	2362200	NO	11512000	YES	117980000	YES	O70472
KFLQDKDFL	KFLQDKDFL	9	3521	2	20327000	YES	427820	NO	1275000	NO	Q64471
KFNEVVSAL	KFNEVVSAL	9	410.2	0.4	909230	NO	1143200	YES		YES	Q64331
KFNPVETFL	KFNPVETFL	9	288.6	0.3	763950	NO	2062100	YES	1373000	NO	Q6PAC3
KFNQILTAL	KFNQILTAL	9	184.4	0.175	4664800	YES		YES	131450000	YES	Q9QZK2
KFQGMISEL	KFQGM(+15.99)ISEL	9	141.5	0.15	9388900	YES	6474800	YES	5951800	YES	P39061
KFQGMISEL	KFQGMISEL	9	141.5	0.15	6815500	YES	15583000	YES		YES	P39061
KFREDRSLL	KFREDRSLL	9	10221.8	6	312340	NO	328680	NO	41071000	NO	Q4LDD4
KFREIQQEL	KFREIQQEL	9	8047.7	4.5	635480	NO	43470	NO	1905000	NO	Q9QX47
KFSETATAI	KFSETATAI	9	113.1	0.125	761180	NO	695290	YES	16586000	YES	Q80YV3
KFSQQYSTI	KFSQQYSTI	9	205	0.2	156180	NO	560390	YES	11405000	YES	Q9QXZ0
KFTETLTNI	KFTETLTNI	9	183.5	0.175		YES	147280000	YES	253400000	YES	Q80SU7
KFTNSLTTV	KFTNSLTTV	9	74.3	0.07		YES	2257500	YES	17519000	YES	Q9D281
KFVDGVSTV	KFVDGVSTV	9	602.1	0.5	188300	NO	3277000	YES	57981000	YES	Q8CG48
KFVSTRSLI	KFVSTRSLI	9	100.2	0.1	3495900	NO	11130000	NO	135200000	YES	P56383
KFVTDIDEL	KFVTDIDEL	9	4542.4	2.5	2034800	YES	9059000	YES	1030900	YES	Q64261
KIADTKSSI	KIADTKSSI	9	770	0.6	1840000	NO	38576	YES	1536100	YES	Q8BPM0
KITESLSLL	KITESLSLL	9	8417.5	4.5	368210	NO		YES		YES	P58281
KLGPAGTTI	KLGPAGTTI	9	461.8	0.4	6754100	YES		YES	24397000	YES	Q6GQV7
KLIANNTTV	KLIANNTTV	9	410.1	0.4	1811800	YES	297300	YES	2777100	YES	Q9Z2N8
KLIESKENL	KLIESKENL	9	3387.3	2	123190	NO		YES	5438200	YES	Q61334
KLIESKHEV	KLIESKHEV	9	2078.9	1.3	745260	YES	98357	YES	1008100	YES	P62257
KLIPGLNNL	KLIPGLNNL	9	3679.7	2.5	8751100	YES		YES	2299700	YES	Q9JLV2
KLKGTLSFI	KLKGTLSFI	9	6251.1	3.5	157840	NO		YES		YES	O54774
KLLDIRSYL	KLLDIRSYL	9	2349.2	1.4	757470	NO	5622600	YES	7239600	YES	P26516
KLLETKNEL	KLLETKNEL	9	2982.4	1.8	473070	NO		YES	12559000	YES	Q9JJA4

KLLPGFTTL	KLLPGFTTL	9	621.8	0.5	894110	NO	5541500	YES	40444000	YES	Q3UQU0
KLLPSVTEL	KLLPSVTEL	9	1243.1	0.9	2801600	YES		YES	47099000	YES	Q80UV9
KLQEAFTKI	KLQEAFTKI	9	1665.7	1.1	439900	NO		YES		YES	Q8VDR9
KLVEGRTHI	KLVEGRTHI	9	423.7	0.4	16709000	YES	2212100	YES	27276000	YES	P01029
KLVPLKETI	KLVPLKETI	9	994.6	0.8	11935000	YES	5163100	YES	18665000	YES	P56480
KLVTTVTEI	KLVTTVTEI	9	439.2	0.4	3909300	YES	15372000	YES	302690000	YES	P40124
KMPILISKI	KM(+15.99)PILISKI	9	16285.6	10	1390600	YES	111330	YES	7200300	YES	Q99L88
KMTQLFTKV	KM(+15.99)TQLFTKV	9	5547.4	3	932730	YES	6418200	YES	25834000	YES	Q61221
KMPILISKI	KMPILISKI	9	16285.6	10	1201300	YES	401030	YES	55761	YES	Q99L88
KMTQLFTKV	KMTQLFTKV	9	5547.4	3	912440	YES	7513200	YES		YES	Q61221
KQLEDGRTL	KQLEDGRTL	9	8166.6	4.5		YES		YES	500360	YES	P62983
KWSSLLQVI	KWSSLLQVI	9	5162.7	3	916820	YES		YES	2138600	YES	Q6A009
KYAHMINGF	KYAHM(+15.99)INGF	9	846.8	0.7	3595400	YES	1967500	YES	19030000	YES	P46664
KYAHMINGF	KYAHMINGF	9	846.8	0.7	1240600	YES	2200200	YES		YES	P46664
KYAMMFAEL	KYAM(+15.99)M(+15.99)FAEL	9	58	0.05	151630	NO	1196500	YES	126590000	NO	Q7TMY8
KYAPSGFYI	KYAPSGFYI	9	15.2	0.01		YES	28637000	YES	72935000	YES	O88342
KYATGENTV	KYATGENTV	9	12.1	0.01	4109600	YES		YES	25514000	YES	A2A8Z1
KYDEAASYI	KYDEAASYI	9	22.1	0.01	4288800	YES	24519000	YES	209880000	YES	P08752
KYDELKNDL	KYDELKNDL	9	333.2	0.3	1723700	YES	2111100	YES	1871000	YES	E9Q555
KYDEVLHMV	KYDEVLHMV	9	205.1	0.2	1251200	NO	601500	YES		YES	Q8CIE6
KYDPINSML	KYDPINSM(+15.99)L	9	64.3	0.06	37307000	YES	11325000	YES	42934000	YES	Q91VC9
KYDPINSML	KYDPINSML	9	64.3	0.06	27689000	YES	16885000	YES		YES	Q91VC9
KYEAAGTLV	KYEAAGTLV	9	29.3	0.02	4103100	YES		YES	6086800	YES	Q9JIF7
KYEALKTYA	KYEALKTYA	9	42.5	0.04	1148800	YES	550810	YES	7120200	YES	Q9D1R1
KYEELLQVI	KYEELLQVI	9	90.6	0.09	2116500	NO	2639500	YES	7138300	YES	P97478
KYEEVARKL	KYEEVARKL	9	163.3	0.15	1083200	NO	542080	YES	1251100	NO	P21107:P58774
KYEHAFNSI	KYEHAFNSI	9	26.4	0.015	1492900	NO	511820	NO	1613400	NO	Q8BZ60

KYEIIASDL	KYEIIASDL	9	98	0.09		YES	3492000	NO	15829000	YES	Q64435
KYEPIFQDI	KYEPIFQDI	9	97.7	0.09	2144900	NO	1920400	YES	13220000	YES	Q64700
KYESVIATL	KYESVIATL	9	32.3	0.02	3530900	NO		YES	601550	YES	O35643
KYFEVPSVL	KYFEVPSVL	9	27.7	0.02	4198400	YES	23378000	YES	110500000	YES	Q9QZB7
KYFKGLMHV	KYFKGLM(+15.99)HV	9	38	0.03	170640	NO	1580100	NO	8790700	NO	Q9CRC9
KYFKMGDHV	KYFKMGDHV	9	16.2	0.01	503600	NO	265210	YES		YES	O55201
KYFPSRVSI	KYFPSRVSI	9	12.5	0.01	64830000	YES	29452000	YES	411230000	YES	Q6PEB6
KYGIPFSRI	KYGIPFSRI	9	225.8	0.2	1000600	NO		YES		YES	Q91VY5
KYGPVVSLL	KYGPVVSLL	9	107.2	0.1	1775300	YES	3917000	YES	78927000	YES	P97343
KYGVTMEQI	KYGVTM(+15.99)EQI	9	75.1	0.07	1140300	NO	2601100	YES	21818000	YES	Q9D7V2:Q9D0E3
KYGVVLDEI	KYGVVLDEI	9	80.5	0.08	362310000	YES	196050000	YES	508340000	YES	O89079
KYHGNVTLL	KYHGNVTLL	9	130	0.125	1022700	YES	752400	YES	2604700	YES	P19096
KYHLLLQEI	KYHLLLQEI	9	40.7	0.03	868430	NO	2609100	YES	64714000	YES	Q4VAC9
KYHLLLQEL	KYHLLLQEL	9	88.4	0.08	868430	NO	2609100	YES	64714000	YES	P27870:Q9R0C8
KYHSQYHTV	KYHSQYHTV	9	16.4	0.01	458080	NO	101700	YES	11023000	YES	E9Q3L2
KYIAEKTEF	KYIAEKTEF	9	189.1	0.175	119740	NO		YES	467640	YES	Q8BL99
KYIDQKFVL	KYIDQKFVL	9	226.7	0.2	30001000	NO	14492000	YES	52504000	YES	Q60996:Q61151
KYIDVGNTI	KYIDVGNTI	9	9.4	0.01	127610	YES		YES		YES	A2RTF1
KYIEDKDVF	KYIEDKDVF	9	3421.8	2	4346200	NO	127640	NO	443310	NO	Q9WTX6
KYIEGVSDF	KYIEGVSDF	9	585.7	0.5	50458000	YES	1585000	YES	250520	NO	P28575
KYIHSADII	KYIHSADII	9	23.6	0.015	5792100	YES	1989400	YES	76240000	YES	P47811
KYIHSANVL	KYIHSANVL	9	19.8	0.01	128430000	YES	46794000	YES	569820000	YES	P63085:Q63844:Q61532:Q6P5G0
KYIKSHYKV	KYIKSHYKV	9	56.5	0.05	2691500	NO	24387	NO	691450	NO	P10922
KYIPAARHL	KYIPAARHL	9	15.8	0.01	146950	YES	320280	YES	3086300	YES	O54692
KYIPNRGPL	KYIPNRGPL	9	27.1	0.02		YES	477050	YES	4455800	YES	Q6ZWV3
KYITNTDVL	KYITNTDVL	9	57.9	0.05	4298900	YES		YES	2729200	YES	Q9CXE7
KYKASENAI	KYKASENAI	9	16.9	0.01	3994900	YES	176790	YES	24457000	YES	P84091

KYKASIAAL	KYKASIAAL	9	78.8	0.08	753930	NO	10417000	NO	127400000	NO	Q8VDD5
KYKDIYTEL	KYKDIYTEL	9	91.9	0.09	55831000	YES	99603000	YES	1278200000	YES	P97434
KYKDSETRL	KYKDSETRL	9	84.7	0.08	12132000	YES		YES	2718400	YES	Q91XD7
KYKELGEKL	KYKELGEKL	9	502.3	0.5	668000	NO	967910	YES	7419300	YES	P27773
KYLATLERL	KYLATLERL	9	39.1	0.03	687950	YES	559870	YES	7942600	YES	Q9R117
KYLENPNAL	KYLENPNAL	9	50.9	0.04	25230000	YES	8442500	YES	148310000	YES	Q8BX02
KYLGLMENL	KYLGLMENL	9	82.1	0.08	387670	NO	25237000	YES		YES	Q9WTI7
KYLGQLHYL	KYLGQLHYL	9	40	0.03	1780700	NO	6151600	YES	15720000	YES	Q6PB44
KYLGQLTSI	KYLGQLTSI	9	10.8	0.01	2096600	YES	2465400	YES	198840000	YES	Q8K2Y9
KYLPLLDRA	KYLPLLDRA	9	795.7	0.6	1887300	YES		YES	3155900	YES	Q8C4V4
KYLQNDLYI	KYLQNDLYI	9	49.3	0.04	4228000	NO	17689000	YES	64621000	YES	O89050
KYLQSKEDL	KYLQSKEDL	9	27.2	0.02	364980	NO	344200	YES	6356500	YES	Q6ZWQ0
KYLSDNVHL	KYLSDNVHL	9	101.4	0.1	15529000	YES	9586500	YES	172790000	YES	Q61081
KYLSQKNVV	KYLSQKNVV	9	23.2	0.01	455110	NO		YES	6687300	YES	A2AN08
KYLSVQGQL	KYLSVQGQL	9	31.5	0.02	20312000	YES	21373000	YES	67291000	YES	Q791T5
KYLVGQRLV	KYLVGQRLV	9	295.2	0.3	2283300	YES	553460	YES	6194800	YES	Q6ZQ89
KYMEPLQEI	KYM(+15.99)EPLQEI	9	28	0.02	586610	NO	557240	YES	8041700	YES	Q80TY5
KYMETIEKL	KYM(+15.99)ETIEKL	9	78	0.08	1769600	YES	1033600	YES	87331000	YES	Q3TDD9
KYMEPLQEI	KYMEPLQEI	9	28	0.02	2141700	NO	1091600	YES		YES	Q80TY5
KYMETIEKL	KYMETIEKL	9	78	0.08	151640	YES	2155900	YES		YES	Q3TDD9
KYNDVSHQL	KYNDVSHQL	9	51.5	0.04	1879100	YES	619550	YES	8231400	YES	O09053
KYNGAVNEI	KYNGAVNEI	9	34.8	0.025	1072200	NO	447080	YES	22999000	YES	Q3URD3
KYNILIATL	KYNILIATL	9	137.3	0.125	359210	NO		YES	7498900	YES	Q99J21
KYNIMLVRL	KYNIM(+15.99)LVRL	9	186.1	0.175	10205000	YES	11276000	YES	135910000	YES	P42932
KYNIMLVRL	KYNIMLVRL	9	186.1	0.175	6567900	YES	15476000	YES		YES	P42932
KYNNGSTEL	KYNNGSTEL	9	16.3	0.01		YES		YES	27875000	YES	Q7TSH2
KYNPDKHYI	KYNPDKHYI	9	29.8	0.02	221180	NO	1268200	YES	11074000	YES	Q61194
KYNRGLTVV	KYNRGLTVV	9	24.5	0.015	64903000	YES	2547500	YES	31519000	YES	Q920E5

KYPPSATTL	KYPPSATTL	9	19.7	0.01	695690	NO	69661	YES	5573200	YES	Q7TMY8
KYQAAMERL	KYQAAMERL	9	24.9	0.015	6411400	YES		YES		YES	Q8BGC4
KYQDILNEI	KYQDILNEI	9	27.8	0.02	1280700000	YES	31909000	YES	660100000	YES	Q3UQ44
KYQDSLQSI	KYQDSLQSI	9	14.7	0.01	13373000	YES	3150000	YES	140550000	YES	Q6ZWR6
KYQEALDVI	KYQEALDVI	9	31	0.02	4777600	YES	25132000	YES	61705000	YES	Q8BWZ3
KYQEVTNNL	KYQEVTNNL	9	22.6	0.01	85935000	YES	50002000	YES	1585700000	YES	Q60865
KYQHTGAVL	KYQHTGAVL	9	130.3	0.125	100780	NO	209010	YES	3414300	YES	Q9WVA3
KYQIAVTKV	KYQIAVTKV	9	33.9	0.025	7111400	YES	8255600	YES	83978000	YES	Q9CU62
KYQKGFSLW	KYQKGFSLW	9	519.5	0.5	10105000	YES		YES	130820	NO	Q91V04
KYQKTFTVI	KYQKTFTVI	9	9.3	0.01	1930500	YES	5090500	YES	87079000	YES	O35459
KYQRILERL	KYQRILERL	9	43.2	0.04	5444200	NO	1567400	NO	10802000	NO	P58281
KYQRLLHEV	KYQRLLHEV	9	24.3	0.015	15740000	YES		YES	20266000	NO	Q99KJ8
KYQSQNEKL	KYQSQNEKL	9	47.3	0.04	1170000	YES		YES	21778000	YES	Q921T2
KYQTVIDDI	KYQTVIDDI	9	16	0.01	4300500	YES	14042000	YES	30874000	YES	P53798
KYQVSSNGI	KYQVSSNGI	9	15.8	0.01		YES	2063700	YES	43548000	YES	Q3UQN2
KYRHVDGNL	KYRHVDGNL	9	547.4	0.5	211350	NO		YES	4324800	YES	P49962
KYSEVFEAI	KYSEVFEAI	9	53.5	0.05	7639900	YES	34091000	YES	77407000	YES	Q60737:O54833
KYSGVLSSI	KYSGVLSSI	9	18.1	0.01	9785200	YES	38576000	YES	193160000	YES	Q791T5
KYSNVIQLL	KYSNVIQLL	9	327.6	0.3	415640	NO		YES	11216000	YES	Q9Z329
KYSPQRVGL	KYSPQRVGL	9	866.1	0.7	5714400	YES	2222000	YES	33791000	YES	Q9QXB9
KYSSLYENL	KYSSLYENL	9	110.4	0.1	275680	NO	1248500	YES	9424500	YES	Q8K4E0
KYSTSLSWI	KYSTSLSWI	9	13.6	0.01	363830	NO		YES	19394000	YES	Q8K0F1
KYSVLDSPL	KYSVLDSPL	9	49.4	0.04	2082000	YES		YES	765730	YES	P26187
KYTAQNREL	KYTAQNREL	9	74.9	0.07	1526200	NO		YES	1766300	NO	Q61817
KYTEGVQSL	KYTEGVQSL	9	68.4	0.07	1101800	YES		YES	1775000	YES	Q920B9
KYTGNASAL	KYTGNASAL	9	44.5	0.04	37914000	YES		YES		YES	P07759:Q03734:Q91WP6
KYVAVYNLI	KYVAVYNLI	9	23.4	0.01	3822800	YES	37984000	YES	454220000	YES	Q80U87
KYVENFGLI	KYVENFGLI	9	391.8	0.4	2346700	NO	3013100	YES	123840000	YES	Q9CYN2

KYVNSIWDL	KYVNSIWDL	9	60.7	0.06	11665000	YES	19953000	YES	12521000	YES	Q9JLV5	
KYVPLVTGL	KYVPLVTGL	9	61.8	0.06	20549000	YES	28772000	YES	206470000	YES	Q8BMI0	
KYVPQQDAL	KYVPQQDAL	9	105	0.1	179750	NO	440510	YES	4584800	YES	F8VPU2	
KYVYVVTEL	KYVYVVTEL	9	25.9	0.015	4426100	YES	124920000	YES	354330000	YES	P18654	
KYWKGQHVI	KYWKGQHVI	9	41.4	0.03	54139000	YES	1328800	NO	51120000	YES	Q9D1P2	
KYWPDEYAL	KYWPDEYAL	9	480.1	0.4		YES	2985700	YES	5958500	YES	P35235	
KYYVQLEQL	KYYVQLEQL	9	116	0.125	1986400	YES	78528000	YES	70394000	YES	Q9Z131	
LAGNEQVTR	LAGNEQVTR	9	43453.5	99	365890	YES		YES	7393.1	YES	P56183	
LFQPVISQV	LFQPVISQV	9	714.6	0.6	5810700	YES	1923000	YES		YES	O88895	
LLLPGELAK	LLLPGELAK	9	32390.6	39	5723900	YES	3390500	YES	2995200	YES	Q6ZWY9:P10853:Q64525:Q8CGP1:Q8CGP0:Q9D2U9:Q64524	
LYDPVISKL	LYDPVISKL	9	758.6	0.6	31740000	YES	75829000	YES	301920000	YES	Q99L90	
LYEAVREVL	LYEAVREVL	9	183.3	0.175	6988300	YES	10532000	YES	6061600	YES		P53026
LYERLKTEL	LYERLKTEL	9	37.4	0.025	168420000	YES	18590000	YES	199370000	YES	Q9CQF9	
LYHEAGQQL	LYHEAGQQL	9	120.5	0.125	677400	YES	1332700	YES	8388700	YES		Q99JG7
LYIDSRQSL	LYIDSRQSL	9	42.5	0.04		YES		YES	24405000	YES	Q8BUR3	
LYIGHLTAL	LYIGHLTAL	9	113.6	0.125	2436900	NO	4715300	YES	17770000	YES	Q99MI1	
LYIPSVDLL	LYIPSVDLL	9	300.3	0.3	787740	YES		YES		YES	P97432	
LYIQAQNNL	LYIQAQNNL	9	70.5	0.07	77948	NO	1076800	NO	6049600	YES	Q6ZPU9	
LYKDVRNLL	LYKDVRNLL	9	995.1	0.8	4034300	NO		YES	4603000	YES	Q80UU1	
LYKEQLAKL	LYKEQLAKL	9	5054.5	3	318280	NO	725770	YES	1293900	YES	Q8VDD5	
LYKESLTKL	LYKESLTKL	9	181.6	0.175	1921000	NO	1132600	YES	2082000	YES	Q61879	
LYLDNRKEI	LYLDNRKEI	9	226.3	0.2	2470000	YES		YES		YES	Q8BXC6	
LYLPNKAET	LYLPNKAET	9	3577.1	2.5	4492200	YES	515710	YES	4265500	YES	Q8BFQ9	
LYQEVFGRL	LYQEVFGRL	9	281.9	0.25	4065400	YES	39008000	YES	45459000	YES	Q61985	
LYQNQRAVL	LYQNQRAVL	9	387.5	0.4	580370	NO	496710	YES	3739100	YES	Q921M4	
LYQPSAESL	LYQPSAESL	9	24.2	0.015	5001800	NO		YES		YES	Q9QZR0	
LYQPTGGQL	LYQPTGGQL	9	90.4	0.09	29885000	YES	34273000	YES	37939000	YES	P36371	

LYRQSLEII	LYRQSLEII	9	445.1	0.4	53423000	YES	85278000	YES	96446000	YES	P97287
LYSEQKTQL	LYSEQKTQL	9	130.2	0.125	1160400	YES	1332100	YES	13755000	YES	Q8K1N2
LYSPVRSKL	LYSPVRSKL	9	119.2	0.125		YES	617240	YES	4022100	YES	Q9ERA6
LYVPALSAL	LYVPALSAL	9	32.3	0.02		YES	3854600	YES	44526000	YES	P27600
MFIEDLHNL	M(+15.99)FIEDLHNL	9	10516.5	6	2855600	NO	507840	YES	4056700	YES	Q9CPY1
MLPSILNQL	M(+15.99)LPSILNQL	9	28205.5	28	12821000	YES	606170	YES	3272700	YES	Q64152
MFIEDLHNL	MFIEDLHNL	9	10516.5	6	3402200	NO	2370400	YES		YES	Q9CPY1
MLPSILNQL	MLPSILNQL	9	28205.5	28	4195100	YES	394980	YES		YES	Q64152
MYNSVSQRL	MYNSVSQRL	9	94.3	0.09	671790	YES	541010	YES		YES	Q9DBC3
NFIGTKTVI	NFIGTKTVI	9	163.5	0.15	103190000	NO	12253000	NO	70647000	YES	Q9R1J0
NFNPTVNYI	NFNPTVNYI	9	567.2	0.5	25704000	YES	12527000	YES	6265200	YES	Q9DCF9
NLLTTRNYI	NLLTTRNYI	9	391.4	0.4	7307000	NO	1899400	NO	2452600	YES	Q9DCV3
NSIRNLDTI	NSIRNLDTI	9	5225.2	3	2226200	YES	1121900	YES	25661000	YES	P28658
NYARGHYTI	NYARGHYTI	9	23.3	0.01	6186800	YES	1617100	YES	5455700	YES	P68373:P05213:P68368
NYDDIRTEL	NYDDIRTEL	9	290.9	0.3	5010100	NO	3111000	YES	68593000	YES	Q3UMY5
NYFPSKQDI	NYFPSKQDI	9	25.9	0.015	82847000	YES	19257000	YES	362780000	YES	P27600
NYFYDQQRI	NYFYDQQRI	9	788.7	0.6	570230	YES		YES		YES	O70126
NYGDLLQTV	NYGDLLQTV	9	414.4	0.4	7639400	YES		YES	513110	YES	Q6GQT6
NYISGIQTI	NYISGIQTI	9	12.2	0.01	38469000	YES	51459000	YES	118330000	YES	Q921M3
NYITPQTQI	NYITPQTQI	9	14.8	0.01	2996100	NO		YES	2296600	YES	Q5DTW7
NYLDIKGLL	NYLDIKGLL	9	615.9	0.5	104970000	YES	82733000	YES	125160000	YES	Q9WTX5
NYLFSASAI	NYLFSASAI	9	11.8	0.01		YES		YES	6214700	YES	Q68FL6
NYLPAINGI	NYLPAINGI	9	60.4	0.06	101270000	YES	22833000	YES	43986000	YES	Q9CQC9
NYNSVNTRM	NYNSVNTRM(+15.99)	9	32.1	0.02	92792	NO	46245	NO	708110	NO	P70452
NYQEALRYI	NYQEALRYI	9	27.1	0.02	13753000	YES	26366000	YES	47681000	YES	Q91W86
NYQNVVHKL	NYQNVVHKL	9	106.8	0.1	556950	YES	666130	YES	1934300	YES	A2A791
NYQPAGIAV	NYQPAGIAV	9	81	0.08	2361200	NO		YES	3066300	YES	Q6ZQF0

NYTNTPSVI	NYTNTPSVI	9	56.7	0.05	1437000	NO	2224400	YES	6353400	YES	A2A6Q5
NYVDLVSSL	NYVDLVSSL	9	121.5	0.125	2013000	YES		YES		YES	Q9WUR2
NYVNGKTFL	NYVNGKTFL	9	25.5	0.015	100230000	YES	34093000	YES	354240000	YES	P49722
NYVRAGTLI	NYVRAGTLI	9	19.4	0.01	18874000	YES	2486300	YES	36332000	YES	Q924Z4
NYYGSLTQA	NYYGSLTQA	9	219	0.2	934120	NO	278990	NO	2805000	YES	Q9JHU9
NYYPVNTRI	NYYPVNTRI	9	12.4	0.01	8190400	YES	6059700	YES	353920000	YES	O09159
NYYSSRTLL	NYYSSRTLL	9	15.8	0.01		YES	567760	YES	11550000	YES	Q6P8H8
PYFAGISAL	PYFAGISAL	9	40.3	0.03	249430	NO		YES	1503800	YES	Q9CZ42
PYFPIVNFL	PYFPIVNFL	9	220.5	0.2		YES		YES	2414600	NO	Q8C2E7
PYIASGNNL	PYIASGNNL	9	33.4	0.025	30457000	YES	98142	NO		YES	Q61586
PYIESNSKL	PYIESNSKL	9	67.1	0.06		YES		YES		YES	Q9D0V8
PYLPSAHRV	PYLPSAHRV	9	68.2	0.07	7184300	YES		YES		YES	P83887
PYLPSGESL	PYLPSGESL	9	53	0.05	4785800	NO		YES	785550	YES	Q9JKV1
QEKVTYQEL	QEKVTYQEL	9	23825.1	19	1022000	YES		YES	650930	YES	Q8R0W0
QFEKALTQI	QFEKALTQI	9	478.7	0.4	9099700	YES		YES	14132000	YES	Q91VE6
QFISVFSNL	QFISVFSNL	9	484.8	0.4	178640	NO		YES	2993800	YES	Q80ZJ6
QFITSVTAL	QFITSVTAL	9	91.1	0.09	1137700	NO	2566200	YES	26642000	YES	Q8BGA7
QFLPDNINI	QFLPDNINI	9	9574.3	5.5	1175700	NO	763660	NO	1922100	NO	Q6PIP5
QFNSSLHNI	QFNSSLHNI	9	644.9	0.5		YES	2434100	YES	91158000	YES	O35166
QILSDFPKL	QILSDFPKL	9	33951.5	44	585370	YES		YES	9020200	YES	Q99ME9
QWSQLKEQI	QWSQLKEQI	9	10837.8	6	1447000	NO		YES	1543600	NO	P11031
QYASNITSV	QYASNITSV	9	33.1	0.025	4655700	YES		YES	1080500	YES	Q5SWU9:E9Q4Z2
QYHDILHAL	QYHDILHAL	9	231	0.25	4925800	NO	1568600	YES	1037400	NO	Q9D0K0
QYLENLEKL	QYLENLEKL	9	1517.9	1	1954700	NO	2922100	YES	7450300	YES	Q8BKX6
QYLKMLQKL	QYLKMLQKL	9	80.5	0.08	686010	NO	703380	NO	98616	YES	Q8BHG1
QYLKNQTVL	QYLKNQTVL	9	123.9	0.125	13182000	YES	5072100	NO	41298000	NO	Q8BM75
QYNAGGLTV	QYNAGGLTV	9	111.6	0.125	2273000	NO		YES	776120	YES	P97493

QYNKLRNLL	QYNKLRNLL	9	220.1	0.2	2367500	NO	2643500	YES	38004000	NO	Q8C0S1
QYNPSRQTL	QYNPSRQTL	9	24.2	0.015	60095000	YES	9680400	YES	112880000	YES	Q9ESV0
QYNPVKQQL	QYNPVKQQL	9	73.3	0.07	204930000	YES		YES	103070000	YES	Q9DBL7
QYQANASQL	QYQANASQL	9	37.6	0.03	98457	NO		YES	8069000	YES	B1AVY7
QYQNIKNNL	QYQNIKNNL	9	53.4	0.05	808520	NO	1826500	YES	32689000	YES	Q6ZWQ0
QYQQIINRL	QYQQIINRL	9	124.7	0.125	681010	NO	15087000	YES	1746500	YES	Q5I1X5
QYQQSQHNL	QYQQSQHNL	9	67.2	0.06	1757600	YES	52659	YES	4924400	YES	E9Q4N7
QYQSLLRSL	QYQSLLRSL	9	48.6	0.04	173280	NO	15714000	YES	17045000	YES	Q91ZU6
QYRDTQTSI	QYRDTQTSI	9	138.7	0.125	243490	YES	980200	YES	43717000	YES	P47758
QYSKVLNEL	QYSKVLNEL	9	168.5	0.15	17173000	YES	22573000	YES	163590000	YES	Q9EP71
QYSTGKTTF	QYSTGKTTF	9	98.2	0.09	635610	YES		YES	5441800	YES	Q9QXY6:Q9WVK4:Q9EQP2
QYVCQQTGL	QYVC(+119.00)QQTGL	9	346.4	0.3	2121300	NO	468880	NO	12809000	NO	Q8R404
QYVDFYSQL	QYVDFYSQL	9	1235.5	0.9	619310	NO	621140	YES	464230	NO	P35689
QYVSAFSKL	QYVSAFSKL	9	98.8	0.1	9197900	YES	16079000	YES	49982000	YES	Q99JB2
QYWTTVSSL	QYWTTVSSL	9	25.3	0.015	2705800	NO		YES	10164000	YES	P28575
RFFESYHEV	RFFESYHEV	9	1508.5	1	980820	NO		YES	3103500	NO	Q9D8B4
RFKDDITTI	RFKDDITTI	9	2938.2	1.8	2759000	YES		YES	13776000	YES	Q8C147
RFNPSISMI	RFNPSISMI	9	242.1	0.25		YES	4923300	YES		YES	Q9D4H8
RLLASKSLL	RLLASKSLL	9	2952.7	1.8		YES	2327700	YES	10469000	YES	Q9CPW5
RLVPSVNGI	RLVPSVNGI	9	10613	6		YES		YES	535210	YES	Q922D8
RNYEYLIRL	RNYEYLIRL	9	31765.6	37		YES		YES	4510200	NO	Q8R3L2
RSIKNVTEL	RSIKNVTEL	9	6909.6	4		YES	361630	YES	7855200	YES	Q99K95
RSIQNAQFL	RSIQNAQFL	9	11914.5	7		YES		YES	3446500	YES	P24638
RSLLLLAPL	RSLLLLAPL	9	17348.4	11		YES		YES		YES	Q9R0E2
RVTPTRTEI	RVTPTRTEI	9	1494	1	1483800	NO	730240	NO	8617100	NO	P62908
RYAALRELI	RYAALRELI	9	48.8	0.04	4083500	NO	4094600	NO	108460000	YES	Q9DBT3
RYAPSLHEL	RYAPSLHEL	9	34.4	0.025	10022000	YES		YES	750970	NO	Q66JZ4

RYASINTHL	RYASINTHL	9	12	0.01	568360	YES	6489400	YES	130560000	YES	Q9DC28:Q9JMK2
RYFPVFEKI	RYFPVFEKI	9	89.4	0.09	3365400	YES	477960	YES	2091000	NO	P24472
RYHAALAVI	RYHAALAVI	9	63.1	0.06	4402400	YES	3467200	YES	9075800	YES	Q9JJW0
RYIANTVEL	RYIANTVEL	9	268.6	0.25	89638000	YES	25714000	YES	80816000	YES	Q9DBG6
RYIENNSVV	RYIENNSVV	9	84.9	0.08	503980	NO		YES	4579100	YES	O88566
RYIQGILNV	RYIQGILNV	9	180.8	0.175	5557300	NO	506510	YES	563530	YES	Q8C0S1
RYISQTQGL	RYISQTQGL	9	152.3	0.15	136150	NO		YES	1910800	YES	O88904:Q9ERH7
RYKEGRVIL	RYKEGRVIL	9	1260.6	0.9	8817200	NO	3560300	NO	58635000	NO	P62700
RYKGTLSML	RYKGTLSM(+15.99)L	9	122.3	0.125	3079600	YES	2217200	YES	25145000	YES	Q9DB90
RYKGTLSML	RYKGTLSML	9	122.3	0.125	887480	YES	1466800	YES		YES	Q9DB90
RYKQLLTYI	RYKQLLTYI	9	19.7	0.01	16597000	YES	17099000	YES	280570000	YES	P61202
RYLEQLHQL	RYLEQLHQL	9	120.3	0.125	52456000	YES	33871000	YES	131480000	YES	P42227
RYLGLLENV	RYLGLLENV	9	222.8	0.2	9347800	YES	16641000	YES	8504200	YES	P46735
RYLPPATQV	RYLPPATQV	9	27.8	0.02	21702000	YES	4012500	YES	65516000	YES	Q91VC3
RYLQTLTTI	RYLQTLTTI	9	7.2	0.01	32013000	YES	198650000	YES	348490000	YES	P54116
RYLSLKEKL	RYLSLKEKL	9	70.7	0.07	12822000	YES		YES	1291400	NO	Q8CC88
RYMELYTHV	RYMELYTHV	9	17.5	0.01		YES	5275200	YES		YES	Q9WTX6
RYNPGSESI	RYNPGSESI	9	28	0.02	544980	YES		YES	7760800	YES	Q9Z0Y9
RYQAGGLTV	RYQAGGLTV	9	30	0.02	49917000	YES		YES	1224200	YES	Q8R0W0
RYQEALSEL	RYQEALSEL	9	24.8	0.015	3872500	YES	5593300	YES	83003000	YES	Q8R092
RYQEVIQEL	RYQEVIQEL	9	65.4	0.06		YES	2383900	YES	43062000	YES	Q5DU37
RYSGMLETV	RYSGM(+15.99)LETV	9	68.8	0.07	1932900	NO	23121000	YES	54579000	NO	F8VQB6
RYSPAYAHL	RYSPAYAHL	9	254.7	0.25		YES		YES	957370	YES	O09012
RYTESISMV	RYTESISM(+15.99)V	9	56.2	0.05	3012500	YES	262240	YES	17907000	YES	O35657
RYTESISMV	RYTESISMV	9	56.2	0.05	834010	YES	494120	YES		YES	O35657
RYTNSSTEI	RYTNSSTEI	9	11.9	0.01	2896200	YES	110790	YES	3934200	YES	P83940
RYYGAISKL	RYYGAISKL	9	114.6	0.125	10038000	YES	3848700	YES	124160000	YES	Q6KCD5

SAVKNLQQL	SAVKNLQQL	9	14213.6	8.5	713980	YES	101410	YES	4478100	YES	Q8VIJ8
SAVVDKDFL	SAVVDKDFL	9	21369.6	16	1421200	YES		YES	4195300	YES	P55264
SFATSGHLI	SFATSGHLI	9	100.7	0.1	270590	NO		YES		YES	Q9WV76
SFEPVKSHL	SFEPVKSHL	9	98.4	0.09	7365200	YES	2476900	YES	25714000	YES	E9QAT4
SFGVTLHEL	SFGVTLHEL	9	2536.7	1.5	60696000	YES	33964000	YES	31009000	YES	P52332
SFHPSGDFI	SFHPSGDFI	9	251.9	0.25	26202000	YES	15136000	YES	85486000	YES	Q99LC2
SFHPSGNYL	SFHPSGNYL	9	109.5	0.1	3608600	YES	1555100	YES		YES	Q8JZX3
SFHSSFSEI	SFHSSFSEI	9	47.7	0.04	2061300	YES	1709700	YES	31514000	YES	Q8K4J0
SFHSTQTDL	SFHSTQTDL	9	206.1	0.2	746340	YES	2541800	YES	52704000	YES	Q9EP71
SFHVSGTWL	SFHVSGTWL	9	179.5	0.175	627210	NO		YES	18013000	YES	Q5SUQ9
SFIKGKCTV	SFIKGKC(+119.00)TV	9	146.9	0.15	226310	NO	1089500	NO	1765500	NO	E9Q555
SFIPAVNDL	SFIPAVNDL	9	591.6	0.5	4392900	YES	7613000	YES	54993000	YES	Q8BHX1
SFLEDLTKM	SFLEDLTKM(+15.99)	9	4337.1	2.5	1587000	YES	2594200	YES	2986100	NO	Q5U430
SFLESFGRL	SFLESFGRL	9	1731.4	1.1		YES		YES	2504300	YES	Q3V2Q8
SFLETVNQL	SFLETVNQL	9	754.8	0.6	5575500	YES	73794000	YES	338000000	YES	Q9EP52
SFLPAPTQL	SFLPAPTQL	9	104.3	0.1	2931100	YES	8640900	YES	36573000	YES	Q9CSN1
SFLPSGSEI	SFLPSGSEI	9	42.5	0.04		YES		YES	5593100	YES	Q9JKC7
SFMKGLTEL	SFM(+15.99)KGLTEL	9	56.8	0.05	8490500	YES	709040	NO	43896000	NO	O35099
SFNALLREL	SFNALLREL	9	1504.2	1		YES	891090	YES	1224500	YES	Q8C547
SFNNVKQWL	SFNNVKQWL	9	907.9	0.7	20603000	YES	2361500	YES	2893900	YES	P62821
SFNPAISNI	SFNPAISNI	9	131	0.125	1008300	NO		YES	9382600	YES	Q6P3Y5
SFQHLLQTL	SFQHLLQTL	9	280.1	0.25	8777200	YES	2518600	YES	1325400	YES	Q00897:P22599:Q00898:Q00896:P07758
SFQKIFSEL	SFQKIFSEL	9	210.8	0.2	2740600	NO	3181700	YES	10383000	YES	Q80YR4
SFSHSFSAL	SFSHSFSAL	9	803	0.6	2291800	NO	1777500	YES	8594000	YES	Q3UYV9
SFTDVRTAI	SFTDVRTAI	9	72.7	0.07		YES	2123200	YES	2528200	YES	P11276
SFTGTKTSL	SFTGTKTSL	9	108.7	0.1		YES	1599900	YES	97941000	YES	A2A4P0
SFVGTLQYL	SFVGTLQYL	9	805.5	0.6	374550	NO		YES		YES	O88351

SFVGTRSYM	SFVGTRSYM(+15.99)	9	287.2	0.25	11224000	NO	5854900	NO	408150000	NO	P31938:Q63932
SFVNTMTSL	SFVNTM(+15.99)TSL	9	81.4	0.08	5144900	YES	26784000	YES	118000000	YES	P28660
SFVNTMTSL	SFVNTMTSL	9	81.4	0.08	4042500	YES	16995000	YES		YES	P28660
SFVSVLHAL	SFVSVLHAL	9	144.8	0.15	648520	YES	5493100	YES	25028000	YES	Q91V83
SFYNVKTKL	SFYNVKTKL	9	129.2	0.125		YES	142130	YES	666630	NO	Q8K3K7
SFYPSLTVV	SFYPSLTVV	9	128.5	0.125	3711000	NO	4880100	YES	40477000	YES	Q8R316
SGYDFENRL	SGYDFENRL	9	24474.6	20	73167000	YES		YES	84138	NO	Q8VE09
SIAAFIQRL	SIAAFIQRL	9	13280.4	8		YES		YES	1448500	YES	Q9Z1R2
SIINFIERL	SIINFIERL	9	15477.5	9.5		YES	170040	YES		YES	Q9QZ09
SLIGSKTQI	SLIGSKTQI	9	220.7	0.2	23251000	NO	2297400	NO	45963000	NO	Q9R1P4
SMSTTRTYI	SMSTTRTYI	9	78.9	0.08	513670	YES		YES		YES	Q6ZQ38
SQPVNPHSL	SQPVNPHSL	9	16601.8	11		YES	62800	YES		YES	Q3UHH1
STLRLLTTI	STLRLLTTI	9	233.8	0.25	340530	NO	2223900	YES	26576000	YES	Q4VA53
SYADLCSTI	SYADLC(+119.00)STI	9	7.5	0.01	1369500	NO	854610	NO	5568600	NO	P51944
SYADLITRA	SYADLITRA	9	374.3	0.4	747590	NO		YES	614350	YES	Q9WVH4
SYAEQLSML	SYAEQLSM(+15.99)L	9	25.5	0.015	633020	NO	5403800	YES	26060000	YES	E9Q7G0
SYAETPLQL	SYAETPLQL	9	99.7	0.1	3555600	YES	1620200	YES	1022600	YES	Q7TQI7
SYAKNGELL	SYAKNGELL	9	161	0.15	760870	NO		YES	1161200	YES	Q9Z2A0
SYALSRHDV	SYALSRHDV	9	33.5	0.025	2664300	YES	121580	NO	711210	NO	Q8CD26
SYAMANTGI	SYAM(+15.99)ANTGI	9	12.6	0.01	44918000	YES	1493500	YES	17884000	NO	Q8R1S9:Q8CFE6
SYANVKQWL	SYANVKQWL	9	26.6	0.02	17064000	YES		YES	8035600	YES	Q9D1G1
SYAQNAKVI	SYAQNAKVI	9	38.4	0.03		YES	168040	NO	5587000	NO	Q8VDP2
SYASQHSQL	SYASQHSQL	9	13.2	0.01	1308200	YES		YES	5336300	YES	Q68FH0
SYASQQSKL	SYASQQSKL	9	36	0.025	1841000	YES		YES	24726000	YES	Q78T81
SYAVSVNHV	SYAVSVNHV	9	19.8	0.01	7939600	YES	3345100	YES	106950000	YES	Q8K387
SYDPQKQLI	SYDPQKQLI	9	200.6	0.175	5842800	YES		YES	1216600	NO	Q9D358
SYDPVKDVL	SYDPVKDVL	9	204	0.2	3481600	YES	2885500	YES	3564200	YES	Q8CDG3

SYEAAASAL	SYEAAASAL	9	10.7	0.01	589670	NO	267120	YES	10466000	YES	Q61033
SYEEAKNTL	SYEEAKNTL	9	14.3	0.01	1542500	YES	998700	YES	55857000	YES	Q9WV54
SYEKQDTLL	SYEKQDTLL	9	80.1	0.08	8608200	YES		YES	4113000	YES	P46978
SYENMVTEI	SYENM(+15.99)VTEI	9	9.7	0.01	18254000	YES	29515000	YES	205070000	YES	P54728
SYENMVTEI	SYENMVTEI	9	9.7	0.01	23440000	YES	28611000	YES		YES	P54728
SYESTIQSL	SYESTIQSL	9	25	0.015	549550	NO		YES	895180	YES	Q6TXD4
SYFKDRAHI	SYFKDRAHI	9	39.8	0.03	2013200	NO	511080	NO	11298000	NO	O88559
SYFKGASLL	SYFKGASLL	9	19.8	0.01	370730	NO	2846600	YES	19398000	YES	Q8C129
SYFKNNAYL	SYFKNNAYL	9	53.8	0.05	17984000	YES	4467900	YES	58046000	YES	Q922B2
SYFPEITHI	SYFPEITHI	9	21.8	0.01	669520000	YES	1313300000	YES	9931300000	YES	P52332
SYFPTVNDI	SYFPTVNDI	9	23.4	0.01	2598800	NO	3872900	YES	7854100	YES	Q8VHI4
SYGDILHVI	SYGDILHVI	9	193.3	0.175	11318000	YES	5972600	YES	8824000	YES	P70175
SYGDLKNAI	SYGDLKNAI	9	38.5	0.03	123190000	NO	29885000	NO	908840000	YES	O35326
SYGKVKEVL	SYGKVKEVL	9	72.1	0.07	552100	NO	872200	NO	7024600	NO	Q9WTK7
SYGLTPRLL	SYGLTPRLL	9	1078.6	0.8		YES	3584000	YES	15339000	YES	Q8K224
SYGPGRQSL	SYGPGRQSL	9	31.3	0.02		YES	998210	YES	29374000	YES	Q62137
SYGQNKTAF	SYGQNKTAF	9	263.3	0.25	111490	NO	39886	YES	1941700	YES	Q6PFD9
SYGSVFKAI	SYGSVFKAI	9	24.4	0.015	2414600	YES	4834300	YES	4050300	YES	Q9JI10
SYGSVYKAI	SYGSVYKAI	9	21.1	0.01	6326100	NO	2128300	YES	80968000	YES	Q9JI11
SYGTAVTHI	SYGTAVTHI	9	8.1	0.01	8724400	YES	5794600	YES	206830000	YES	P27808
SYGVTVWEL	SYGVTVWEL	9	141	0.125	120120	NO		YES		YES	Q01279:P70424:Q61526
SYHPALNAI	SYHPALNAI	9	9.9	0.01	69395000	YES	22983000	YES	408990000	YES	O88738
SYHPSGLSL	SYHPSGLSL	9	22.3	0.01	8303700	YES	5898500	YES	84080000	YES	Q8BXQ8
SYHSQAVHI	SYHSQAVHI	9	18.7	0.01	295410	NO		YES	4727400	YES	Q8BXQ2
SYHTDINML	SYHTDINM(+15.99)L	9	40.8	0.03	1150400	YES	3028800	YES	18284000	YES	P13864
SYHTDINML	SYHTDINML	9	40.8	0.03		YES	4013700	YES		YES	P13864
SYHVIKGNL	SYHVIKGNL	9	45.9	0.04	1704200	YES	2161800	YES	31336000	YES	B1AZI6
SYIFDINTI	SYIFDINTI	9	31.2	0.02	258120	NO		YES	4468800	YES	Q9QYY0

SYIGANVRL	SYIGANVRL	9	84.7	0.08		YES	2739800	YES	12039000	YES	P40336
SYIGGHEGL	SYIGGHEGL	9	122.8	0.125	33439000	YES	4707400	YES	101260000	YES	P40201
SYIGSPRAV	SYIGSPRAV	9	31.1	0.02	28283000	YES	10988000	YES	184600000	YES	Q8BJS4
SYIKDLSVV	SYIKDLSVV	9	53.9	0.05	6154400	YES	11071000	YES	13454000	NO	Q3TP92
SYIYGAQHL	SYIYGAQHL	9	19.3	0.01	365150	NO	277330	YES		YES	Q9WVG9
SYKAGIYSV	SYKAGIYSV	9	113.4	0.125	6326100	YES	2128300	YES	86673000	YES	Q8K2Z8
SYKDGKMNI	SYKDGKM(+15.99)NI	9	117	0.125	3327500	YES	399100	YES	23918000	YES	Q8R3N1
SYKDGKMNI	SYKDGKMNI	9	117	0.125	2535600	YES	630200	YES		YES	Q8R3N1
SYKENIMRL	SYKENIM(+15.99)RL	9	1059.8	0.8	27755000	YES	209980	YES	470660	NO	Q63886:Q64435:Q62452:Q6ZQM8
SYKNGFLNL	SYKNGFLNL	9	389.9	0.4	12597000	YES	1785100	NO	1430500	YES	Q02053
SYKPHASNL	SYKPHASNL	9	93.8	0.09	1073100	YES	104540	YES	5772200	YES	P70265
SYKSVQTTL	SYKSVQTTL	9	10.1	0.01	257430	YES	1438400	YES	42127000	YES	Q8BFZ9
SYKTIYREL	SYKTIYREL	9	77.7	0.08	11691000	NO	827590	NO	4253800	YES	Q9WVE8
SYLDGKGNL	SYLDGKGNL	9	63.6	0.06	2596500	NO	1757900	YES	63171000	YES	Q8R2K4
SYLDQGTQI	SYLDQGTQI	9	16.6	0.01	5927600	NO		YES		YES	Q9EPL4
SYLDVKQRL	SYLDVKQRL	9	41.6	0.03	82778000	YES	6852400	YES	45632000	YES	P61222
SYLEDKDLV	SYLEDKDLV	9	473.3	0.4	1366300	YES	14867000	YES	83798000	YES	P52332
SYLEDKVYL	SYLEDKVYL	9	158.1	0.15	2075200	NO	1122600	YES	1272400	YES	Q9D1M4
SYLEMGHDI	SYLEMGHDI	9	13.3	0.01		YES	2346000	YES		YES	P08775
SYLESKGLL	SYLESKGLL	9	47.1	0.04	2520200	YES	7724800	YES	83082000	YES	Q99ME2
SYLFSHVPL	SYLFSHVPL	9	44.8	0.04	2905200	YES	43976000	YES	67729000	YES	Q9D7G0:Q9CS42
SYLGGNSTI	SYLGGNSTI	9	8	0.01	1892900	NO	3639200	NO	14089000	NO	P19091
SYLHSLQEV	SYLHSLQEV	9	34.1	0.025	4061600	YES	5307000	YES	179190000	YES	Q5SSZ5
SYLIGRQKI	SYLIGRQKI	9	37	0.025	12728000	YES	6231400	YES	162590000	YES	Q91ZX7
SYLKQLPHF	SYLKQLPHF	9	1488.6	1	1741600	NO	4682800	YES	40511000	YES	Q6P4T2
SYLKSELGL	SYLKSELGL	9	121.1	0.125	488980	NO	2031900	YES		YES	Q922B9
SYLLSIHKV	SYLLSIHKV	9	81.1	0.08	1989200	YES	1019400	YES	3523200	YES	Q8BX17

SYLNSVFQL	SYLNSVFQL	9	64.5	0.06	677420	NO	1007100	YES	1646500	YES	B2RVL6
SYLNSVQQL	SYLNSVQQL	9	29	0.02	8710200	YES		YES	41207000	YES	Q8CIC2
SYLPEKLQI	SYLPEKLQI	9	95	0.09	874490	NO		YES		YES	Q6PD31
SYLPGVREL	SYLPGVREL	9	61	0.06	1610100	YES	5412500	YES		YES	Q9D5E4
SYLPPGTSL	SYLPPGTSL	9	12.1	0.01	166660000	YES	10950000	NO	60470000	YES	Q8VCF0
SYLTSASSL	SYLTSASSL	9	5.6	0.01	1170600	NO	2309600	YES	23258000	YES	Q80TP3
SYLVSKQEL	SYLVSKQEL	9	18.5	0.01	2366300	YES	1946900	YES	102310000	YES	Q3UM18
SYMIPTNDL	SYM(+15.99)IPTNDL	9	99.9	0.1	6227400	YES	2100000	YES	11583000	YES	P00405
SYMPPSTVL	SYM(+15.99)PPSTVL	9	12.6	0.01	13315000	NO	4605000	NO	6171300	NO	Q9DB77
SYMPQQVTV	SYM(+15.99)PQQVTV	9	37.3	0.025	4332500	NO	2654900	YES	19520000	NO	Q5SSH7
SYMPTVSHL	SYM(+15.99)PTVSHL	9	10	0.01	4860700	YES	2574400	YES	86717000	YES	Q9Z2E9
SYMIPTNDL	SYMIPTNDL	9	99.9	0.1	3345900	YES	1513900	YES		YES	P00405
SYMPTVSHL	SYMPTVSHL	9	10	0.01	2927900	YES	5001200	YES		YES	Q9Z2E9
SYNIAITRA	SYNIAITRA	9	272.9	0.25	263550	YES		YES	16355000	YES	E9Q286
SYNKAISYL	SYNKAISYL	9	13.5	0.01	19324000	YES	4738700	YES	32776000	YES	A2ALW5
SYNKVYKSL	SYNKVYKSL	9	23.9	0.015	1474000	YES	125770	YES	3483100	YES	Q6WKZ7
SYNLTVREL	SYNLTVREL	9	177.5	0.175	4703300	YES	7121400	YES	80676000	YES	Q9ESE1
SYNPAENAV	SYNPAENAV	9	26.9	0.02	8908800	YES	564990	YES	5024000	YES	Q8CIE6
SYNPSGQGL	SYNPSGQGL	9	69.3	0.07	17399000	YES		YES	57198000	YES	Q8CI61
SYNPSSQAL	SYNPSSQAL	9	15.1	0.01	3160700	NO	1621100	YES	87359000	YES	Q2NL51
SYNPVTHQL	SYNPVTHQL	9	28.5	0.02	1080500	YES	7308000	YES	83692000	YES	Q6NWV3
SYNTVAQEL	SYNTVAQEL	9	13.7	0.01	10353000	YES	4228300	YES	34171000	YES	Q9QX47
SYNWLQETL	SYNWLQETL	9	83.1	0.08	2300500	YES	1017400	YES	1361500	YES	Q8BM55
SYQDLASQI	SYQDLASQI	9	12.5	0.01	17078000	YES		YES	16264000	YES	P48410
SYQDLRSAL	SYQDLRSAL	9	14.2	0.01	1082200	NO		YES	7215900	YES	Q9CQE2
SYQEGLARL	SYQEGLARL	9	106	0.1	4924400	YES	3194900	YES	29072000	YES	Q9D2V5
SYQEMIANL	SYQEM(+15.99)IANL	9	37	0.025	2757800	YES	8528900	YES	97464000	YES	Q64674
SYQEMIANL	SYQEMIANL	9	37	0.025	3077400	YES	7864600	YES		YES	Q64674

SYQESTKQL	SYQESTKQL	9	29.4	0.02	1495700	YES		YES	369850	YES	Q5DU02:Q8CEG8
SYQGRNEII	SYQGRNEII	9	110	0.1	28055000	YES	343430	YES	1019700	YES	Q9QYF1
SYQPIVDYI	SYQPIVDYI	9	17.3	0.01	2054800	NO	17768000	YES	31441000	YES	Q8C650
SYQQALLRI	SYQQALLRI	9	23.7	0.015		YES	621850	YES	35334000	YES	Q9ERC3
SYQSLVSLP	SYQSLVSLP	9	531.2	0.5	5502900	NO	3752500	NO	5114200	NO	Q9D8Y1
SYQSQINQI	SYQSQINQI	9	12.6	0.01	27692000	YES	15538000	YES	236990000	YES	Q99MJ9
SYSATKETL	SYSATKETL	9	17.9	0.01	19873000	YES	8202500	YES	359450000	YES	P09405
SYSDMKRAL	SYSDM(+15.99)KRAL	9	48.7	0.04	841230	YES	1097200	YES	63545000	YES	Q3TWW8
SYSDMKRAL	SYSDMKRAL	9	48.7	0.04	1068300	YES		YES	201680	YES	Q3TWW8
SYSEVKSDL	SYSEVKSDL	9	40	0.03	141880	NO	1871000	YES	76319000	YES	O35245
SYSGSIQSL	SYSGSIQSL	9	62.6	0.06	36520000	YES		YES	2090400	YES	B2RQE8
SYSKGASVI	SYSKGASVI	9	19.7	0.01	793220	NO		YES	5405800	YES	Q11011
SYSQGRSFA	SYSQGRSFA	9	216.4	0.2	147310	YES		YES	1333000	YES	A2AN08
SYSQLITLV	SYSQLITLV	9	89.4	0.09	1154800	NO		YES	16956000	YES	Q6PAR5
SYSQSKQFL	SYSQSKQFL	9	37	0.025	10402000	YES	1472600	YES	14476000	YES	Q9CR62
SYSSIIREV	SYSSIIREV	9	134.3	0.125	21671000	YES		YES		YES	Q60991
SYSSLIRNL	SYSSLIRNL	9	126.2	0.125	20130000	YES		YES	6686500	YES	Q64324
SYSSSRSDL	SYSSSRSDL	9	17.7	0.01		YES		YES	57247000	YES	Q91VM5;Q9WV02
SYTPSKISV	SYTPSKISV	9	37.9	0.03	387610	YES		YES	7485600	YES	Q8K2H6
SYTSVLSRL	SYTSVLSRL	9	16.8	0.01		YES	1692600	YES	19112000	YES	Q80TA9
SYTVGQSEL	SYTVGQSEL	9	47.4	0.04	2956700	NO	1165300	YES	8399000	YES	Q7TMY8
SYTYPPSSL	SYTYPPSSL	9	51.3	0.04	8541200	NO		YES	13084000	YES	P59326
SYVAIINKS	SYVAIINKS	9	1229.9	0.9	634300	YES	155230	YES		YES	P39054
SYVDIHTGL	SYVDIHTGL	9	77.3	0.07	127960000	YES	26715000	YES	82168000	YES	Q9DCC4
SYVGSHREL	SYVGSHREL	9	53.6	0.05	9450900	YES	2560200	YES	54019000	YES	Q8CHI8
SYVLTRVGL	SYVLTRVGL	9	378.7	0.4	789920	YES		YES	6986100	YES	Q8R3I3
SYVPARSLP	SYVPARSLP	9	371.7	0.4	3499400	NO	6081000	NO	105680000	NO	Q9QZE5
SYVPVNGRL	SYVPVNGRL	9	47	0.04	2495600	YES	1191800	YES	34170000	YES	Q9WUP7

SYVTTSTRT	SYVTTSTRT	9	38	0.03	29213	NO	8155600	YES	33984000	YES	P20152
SYWLVRTEL	SYWLVRTEL	9	15.7	0.01		YES	5702200	YES	66642000	YES	P42859
SYWSVGETI	SYWSVGETI	9	8.4	0.01	1459000	NO	6599800	NO	8664400	NO	Q78IS1
SYYADKHEA	SYYADKHEA	9	352.7	0.3	265480	YES		YES	326700	YES	Q8K1N2
SYYAVAHAV	SYYAVAHAV	9	11.2	0.01		YES	249100	YES	6634300	YES	Q3TKT4
SYYGPLNLL	SYYGPLNLL	9	241	0.25	15221000	YES	36613000	YES	24608000	YES	O09005
SYYTVAHAI	SYYTVAHAI	9	6.3	0.01		YES	7430600	YES	154180000	YES	Q6DIC0
TDPVTIENK	TDPVTIENK	9	38755	70		YES		YES		YES	P01872
TFASTLSHL	TFASTLSHL	9	144.4	0.15	4379500	YES	5374800	YES	30859000	YES	Q8CFI7
TFHPTISGL	TFHPTISGL	9	2069.5	1.3	1701900	YES	1072300	YES	2547500	YES	A2AH22
TFINLMTHI	TFINLM(+15.99)THI	9	69.8	0.07	13991000	YES	36427000	YES	378730000	NO	Q8BVE3
TFINLMTHI	TFINLMTHI	9	69.8	0.07	13480000	YES	49247000	YES	494870	NO	Q8BVE3
TFITSKEDL	TFITSKEDL	9	334.4	0.3	3384100	YES		YES	14686000	YES	Q9Z1D1
TFLPAKALL	TFLPAKALL	9	2987.9	1.8	7521700	YES	5081900	YES	54932000	YES	Q78JE5
TFLPSRGIL	TFLPSRGIL	9	1191.3	0.9	9738400	NO	22953000	NO	28388000	NO	F8VQB6
TFLQTATLI	TFLQTATLI	9	157.3	0.15	579700	NO		YES	15114000	YES	Q9JLV2
TFQEAQSRL	TFQEAQSRL	9	986.9	0.8	60157	NO	2161800	YES	26838000	YES	P26039
TFQPVNNNL	TFQPVNNNL	9	312.6	0.3	4366000	NO	570020	YES	3681800	YES	Q91V09
TFVPVANEL	TFVPVANEL	9	601.4	0.5	2470800	YES	31300000	YES	8875500	YES	Q5SYD0
TGIRNLEWL	TGIRNLEWL	9	17090.2	11		YES		YES	236640	NO	Q8BMD6
TINVGLTSI	TINVGLTSI	9	1704.8	1.1		YES		YES	7078100	YES	O35381
TNQDFIQRL	TNQDFIQRL	9	22944.4	18		YES		YES		YES	Q80TM9
TSPVNEKTL	TSPVNEKTL	9	28217.1	28		YES		YES		YES	P11859
TWNKLLTTI	TWNKLLTTI	9	305.3	0.3	18436000	YES	10438000	YES	76108000	YES	Q9D4H8
TYDEVQTRL	TYDEVQTRL	9	292.1	0.3	625510	YES	420770	YES	1437000	YES	Q80XL1
TYDQMYNDL	TYDQM(+15.99)YNDL	9	235.3	0.25	1650500	NO	222440	YES	1268500	NO	Q9CY97
TYDYAKTIL	TYDYAKTIL	9	166.4	0.15	52832000	YES	7122800	YES	15985000	YES	Q91V92

TYETSLSEI	TYETSLSEI	9	11.9	0.01	16610000	YES		YES	12291000	YES	Q5HZI1
TYFFGATHV	TYFFGATHV	9	20.1	0.01	5533300	YES		YES	7401400	YES	Q7TT23
TYFPTWEGL	TYFPTWEGL	9	476.3	0.4	2166500	YES	1120500	YES	3893800	YES	Q99PV0
TYFSGMVLI	TYFSGM(+15.99)VLI	9	108.3	0.1	1724200	NO	6979800	NO	4548800	NO	O35678
TYGALVTQL	TYGALVTQL	9	69.3	0.07	16552000	YES	41652000	YES	91409000	YES	O55013
TYGITVAEL	TYGITVAEL	9	1878.3	1.2	7720600	NO	5131400	NO	11026000	NO	Q6P4T2
TYHASGTEL	TYHASGTEL	9	12.1	0.01	7531600	YES	3843500	YES	643700000	YES	Q3U1N2
TYHTAASTL	TYHTAASTL	9	7.3	0.01	1949100	YES	1107600	YES	106630000	YES	Q9R0X0
TYIESSTKV	TYIESSTKV	9	20.6	0.01	8565800	YES	1686800	YES	63500000	YES	Q8VBZ3
TYKALNTFI	TYKALNTFI	9	21.2	0.01	1133600	NO	9566200	YES	62959000	YES	Q8VBZ3
TYKDSGVDI	TYKDSGVDI	9	830.1	0.7	439810	NO		YES	2080400	YES	Q64737
TYKPNPNQI	TYKPNPNQI	9	153	0.15	171740	NO		YES	2028500	YES	Q924K8
TYKRQVVEL	TYKRQVVEL	9	1144.4	0.8	218260	NO		YES	1103000	YES	Q8BUK6
TYLAALETL	TYLAALETL	9	19.2	0.01	914380	YES	346240	YES	5872600	YES	P47738
TYLDSKSQL	TYLDSKSQL	9	25.9	0.015	742000	NO	854570	YES	31777000	YES	Q8K389
TYLKDLEVI	TYLKDLEVI	9	212.6	0.2	13803000	YES	16622000	YES	29377000	YES	F8VPU2:Q91VS8
TYLPAGQSV	TYLPAGQSV	9	27.7	0.02	98829000	YES	8522300	YES	39578000	YES	P67778
TYLPGIVGL	TYLPGIVGL	9	772.9	0.6	654170	YES		YES	6942500	YES	Q3TIX9
TYLPQSYLI	TYLPQSYLI	9	154.6	0.15	8195500	YES	6918600	YES	16747000	YES	O89051
TYLVSKESI	TYLVSKESI	9	14.1	0.01	1321300	YES	1446800	YES	130850000	YES	Q6PNC0
TYNHLSSWL	TYNHLSSWL	9	96.9	0.09	3147800	NO		YES	10432000	NO	Q91V41
TYNMVLNLL	TYNM(+15.99)VLNLL	9	173.9	0.175	1510000	NO	11200000	YES	115970000	NO	Q9CZU3
TYNMAPSAL	TYNMAPSAL	9	32.5	0.02		YES	2286900	YES		YES	Q61985
TYNNILTVL	TYNNILTVL	9	55.3	0.05	9060700	YES		YES	45529000	YES	Q9EQH3
TYNPVPGVM	TYNPVPGVM(+15.99)	9	446.6	0.4	9602400	NO	362890	NO	1386400	NO	Q99L13
TYQAMVHEL	TYQAMVHEL	9	17.8	0.01		YES		YES		YES	P97390
TYQDIQNTI	TYQDIQNTI	9	27.9	0.02	34845000	YES	26484000	YES	154470000	YES	P08775
TYQENLTDL	TYQENLTDL	9	72.6	0.07	530820	NO	1345200	YES	12291000	YES	Q9EPW0

TYQLGFHSI	TYQLGFHSI	9	27.4	0.02	4337400	YES	3779400	YES	5434700	YES	Q60692
TYQNTAQTV	TYQNTAQTV	9	16	0.01	2229500	YES		YES	6260600	YES	Q3UA37
TYQQVQQTL	TYQQVQQTL	9	20.1	0.01	20283000	YES	10132000	YES	150790000	YES	Q91V81
TYRELFNSI	TYRELFNSI	9	104.5	0.1	697880	NO	17704000	YES	44182000	YES	P59764
TYRNLINKL	TYRNLINKL	9	929.4	0.7	15999000	NO	7207300	YES	48475000	NO	Q9JI13
TYSPPLNKL	TYSPPLNKL	9	880	0.7	136470000	YES	88076000	YES	1049300000	YES	P02340
TYSPSRVLI	TYSPSRVLI	9	222.7	0.2	34866000	YES	6540700	YES	126060000	YES	Q91XU0
TYSSVYDSI	TYSSVYDSI	9	35.3	0.025	805950	NO	3097400	NO	4782200	YES	Q8R1B4
TYTSARTLL	TYTSARTLL	9	22.1	0.01		YES	8778800	YES	287270000	YES	Q61881
TYTSLKTKL	TYTSLKTKL	9	28.6	0.02	6072300	YES		YES	3707300	YES	Q8K1N1
TYVHSSATI	TYVHSSATI	9	24.3	0.015	3433700	YES	690280	YES	19164000	YES	Q8BGQ7
VAYWRQAGL	VAYWRQAGL	9	38465.9	70		YES		YES		YES	P56382
VFIGNLNTL	VFIGNLNTL	9	1690.7	1.1	7802800	YES	3611900	YES	12274000	YES	Q9Z204
VFIPAGTHV	VFIPAGTHV	9	160.2	0.15	1471800	YES		YES	223380	NO	Q8VCA8
VFVDSLTKV	VFVDSLTKV	9	3673.7	2.5	205500	NO	29854000	YES	15831000	YES	Q8BTM8
VGFDYKERL	VGFDYKERL	9	31254.2	35		YES	1270700	YES	1202400	NO	Q60598
VGVNNPVFL	VGVNNPVFL	9	28002.7	27	344840	YES		YES	781790	YES	Q9DBN5
VQVLVPLPQ	VQVLVPLPQ	9	26981.6	25	163590	YES		YES		YES	Q62419
VSFELFADK	VSFELFADK	9	39546.7	75	4173300	NO		YES	1182200	YES	P17742
VYAGTPTKV	VYAGTPTKV	9	126.5	0.125	219230	NO		YES		YES	P97440
VYAHAGTTL	VYAHAGTTL	9	16.2	0.01	872270	YES	348800	YES	9539100	YES	Q99JN2
VYDLLKTNL	VYDLLKTNL	9	306.3	0.3	8745000	YES	5480700	YES	10263000	YES	Q3TXS7
VYESLISHI	VYESLISHI	9	26.3	0.015	12880000	YES	21960000	YES	111880000	YES	Q61037
VYFPALTSL	VYFPALTSL	9	16	0.01	620160	YES		YES	5965600	YES	Q8VCL5
VYGAMHVEI	VYGAM(+15.99)HVEI	9	98.3	0.09	18325000	YES	1942700	YES	43710000	NO	Q5SW19
VYGSLASVL	VYGSLASVL	9	114.9	0.125	29445000	NO	15442000	NO	14181000	NO	Q8JZK9
VYHNLKNVI	VYHNLKNVI	9	50.1	0.04	9648100	YES		YES	11670000	YES	P17182

VYIITKPEL	VYIITKPEL	9	434.4	0.4	2124200	YES	1007400	YES	1147100	YES	Q9WUE4
VYIPAHGRL	VYIPAHGRL	9	102	0.1	5848500	YES	866430	YES	2709200	YES	Q920I9
VYIPSKTDL	VYIPSKTDL	9	18.6	0.01	13760000	YES	4171000	YES		YES	Q9CRB2
VYISNGQVL	VYISNGQVL	9	137.1	0.125		YES	2127300	YES	2188600	YES	Q9JLJ1
VYKASLNLI	VYKASLNLI	9	108.7	0.1	1160400	NO	6667900	NO	28504000	NO	P52293
VYKELKNLI	VYKELKNLI	9	302.4	0.3	172960	NO	692830	NO	689010	NO	P09055
VYKGQITAI	VYKGQITAI	9	88.6	0.09	8653200	YES		YES	33398000	YES	Q8K442
VYLENKEQV	VYLENKEQV	9	286.6	0.25	440560	NO		YES	6974300	YES	Q9CY66
VYLPNIQSL	VYLPNIQSL	9	148.7	0.15	444610	NO	1096700	YES	14938000	YES	Q62240
VYLTPKTSV	VYLTPKTSV	9	13.4	0.01	397660	NO	987700	NO	8266600	NO	Q8BFX3
VYNASNNEL	VYNASNNEL	9	41.8	0.04	10668000	YES	3778400	YES	208710000	YES	P62242
VYNPMPFEL	VYNPMPFEL	9	186.4	0.175	452940	NO	795920	YES		YES	Q3U0M1
VYNVTQHAV	VYNVTQHAV	9	190.8	0.175	1527200	YES		YES	6468000	YES	O09167
VYQETRERL	VYQETRERL	9	97.2	0.09	3398500	NO	1080700	NO	28503000	NO	Q9CWK3
VYQQTASLL	VYQQTASLL	9	44.6	0.04	2092500	NO	7440600	YES	21786000	YES	Q3U269
VYSNTIQSI	VYSNTIQSI	9	104.4	0.1	4107300	NO	28545000	YES	145670000	YES	P08752:Q9DC51
VYSNTIQSL	VYSNTIQSL	9	253.3	0.25	4107300	NO	28545000	YES	145670000	YES	
VYSRTFTWL	VYSRTFTWL	9	135.6	0.125	864320	NO	58806000	YES	15045000	YES	Q9WTI7
VYTPVINGI	VYTPVINGI	9	164	0.15	2417700	NO	911270	NO	1844300	YES	Q8BYR8
VYTTSYQQI	VYTTSYQQI	9	26.9	0.02	193740	NO		YES	7334000	YES	P63139
VYTTTRSSL	VYTTTRSSL	9	14.3	0.01	1186400	YES	1945100	YES	158170000	YES	Q8BXA5
VYTTTVHWL	VYTTTVHWL	9	151	0.15	2207500	NO		YES	6367000	YES	Q99PV0
VYVAGGQHL	VYVAGGQHL	9	65.3	0.06	79450	NO	58705	NO		YES	Q8BGY4
VYVDGKEEI	VYVDGKEEI	9	144.9	0.15	31211000	YES	5814400	YES	187030000	YES	Q9WUD8
VYWKIYNSI	VYWKIYNSI	9	33.7	0.025	18832000	YES	8523700	YES	59729000	YES	Q99NB9
VYWPTPSAL	VYWPTPSAL	9	42.2	0.04	3229700	NO		YES	14604000	YES	Q8BYH8
VYYFSKGAL	VYYFSKGAL	9	71.8	0.07	559000	NO	1156800	YES	6842400	YES	Q8VEE4
VYYPVRHHL	VYYPVRHHL	9	25.2	0.015	2854400	YES	3167300	YES	75638000	YES	Q80YV3

WFTDSNNAI	WFTDSNNAI	9	502.9	0.5	1578500	NO	1147700	YES	1396900	YES	A2AH22
WYDPNASLL	WYDPNASLL	9	502.8	0.5	1421000	NO		YES	4378100	YES	Q9QXL8
WYIGDQNPM	WYIGDQNPM	9	274.2	0.25	1341200000	YES	23636000	YES		YES	P70274
WYIGDQNPM	WYIGDQNPM(+15.99)	9	274.2	0.25	3269900000	YES	69189000	YES	70015000	YES	P70274
WYKSNMNGV	WYKSNM(+15.99)NGV	9	450.9	0.4	8245800	YES	614630	YES	10953000	NO	Q9EQQ9
WYNPILNRV	WYNPILNRV	9	84.2	0.08	4565100	YES	22636000	YES	54569000	YES	Q9Z222
WYQPSFHGV	WYQPSFHGV	9	58.4	0.05	5365700	YES	5918200	YES	1278900	YES	Q9WVG6
YFISSTTRI	YFISSTTRI	9	29.6	0.02	358740	NO		YES	14212000	YES	Q3UMC0
YFKSSLTTI	YFKSSLTTI	9	30.5	0.02	6094400	NO	1553300	YES	54607000	YES	Q9EPT5
YFNWIKTQL	YFNWIKTQL	9	499.3	0.5	637810	NO	655180	YES	323670	NO	Q8BVE3
YFQPAISRL	YFQPAISRL	9	217.9	0.2	7952000	YES	697070	YES	1136700	YES	Q9WU79
YFRQSLSYL	YFRQSLSYL	9	504.5	0.5	13220000	YES	28638000	YES	72366000	YES	Q9Z2X8
YFVPAFSGL	YFVPAFSGL	9	1215.1	0.9	695670	YES		YES	249100	NO	Q64516
YVHVNRDTL	YVHVNRDTL	9	6981.2	4		YES		YES	1114100	YES	Q9JLV6
YYDKAFDRI	YYDKAFDRI	9	231.5	0.25	661030	NO	166900	YES	610480	NO	O70194
YYDPMISKL	YYDPMISKL	9	88.6	0.09	10750000	YES	505480	YES		YES	Q91ZA3
YYFEVVQKL	YYFEVVQKL	9	111.9	0.125	859130	NO	2442100	YES	4273900	YES	Q8BT60
YYFPVKNVI	YYFPVKNVI	9	12.2	0.01	8743000	YES	82641000	YES	1275700000	YES	Q921M3
YYGILQEKI	YYGILQEKI	9	800.1	0.6	28189000	YES	22661000	YES	46171000	YES	P97858
YYHLLAEKI	YYHLLAEKI	9	72.4	0.07	469160	NO	2145500	YES	19897000	YES	P45481:B2RWS6
YYINGKTGL	YYINGKTGL	9	18.7	0.01	22579000	NO	7268400	NO	273280000	YES	Q6ZQ93
YYKASVTRL	YYKASVTRL	9	24.6	0.015	7597600	YES		YES	27561000	YES	Q9QVP9
YYKQGIGHL	YYKQGIGHL	9	137.7	0.125	585950	NO		YES	725700	NO	Q8R1X6
YYLNDLDRI	YYLNDLDRI	9	170.1	0.15	42360000	YES	54185000	YES	23757000	YES	Q9DC51
YYLNDLDRL	YYLNDLDRL	9	439.8	0.4	42360000	YES	54185000	YES	23757000	YES	
YYLNDLERI	YYLNDLERI	9	145.1	0.15	19988000	YES	303410000	YES	412770000	YES	P08752
YYLPLGKTL	YYLPLGKTL	9	20.9	0.01		YES	4972700	YES	24733000	YES	Q8BL99

YYLTDVDRI	YYLTDVDRI	9	76.4	0.07	1221400	NO	3952800	YES	359890	YES	P21278
YYNELETRV	YYNELETRV	9	55.9	0.05	3376500	YES	3580500	YES	44220000	YES	Q8K2T8
YYNMLLKKL	YYNM(+15.99)LLKKL	9	298	0.3	5689000	YES	207870	NO	5311200	YES	Q9DBG3
YYQDTPKQI	YYQDTPKQI	9	49.4	0.04		YES		YES	250170	NO	Q9CPT5
YYQGLYETL	YYQGLYETL	9	30.2	0.02	41368000	YES	37748000	YES	33764000	YES	Q6NZJ6
YYQGNTSRL	YYQGNTSRL	9	62.5	0.06	42020	NO		YES	641000	YES	Q68FH4
YYQGVIQQI	YYQGVIQQI	9	21.8	0.01	2140800	NO	4002900	YES	6643700	YES	Q8K0T4
YYQSGRMLL	YYQSGRM(+15.99)LL	9	43.3	0.04	354030000	YES	7617000	YES	34241000	NO	P55096
YYRNQQQGL	YYRNQQQGL	9	2058.6	1.3	126800	NO	209130	YES	1160400	YES	P23949
YYSGLKHFI	YYSGLKHFI	9	67.4	0.06	144430	NO	270490	NO	6305200	YES	Q8C092
YYSPTKNEI	YYSPTKNEI	9	21.2	0.01	72119000	YES	28448000	NO	41759000	YES	Q4PZA2
YYTNSLEKL	YYTNSLEKL	9	136.8	0.125	673160	YES		YES	646470	YES	Q61329
YYTPQRVDV	YYTPQRVDV	9	348.8	0.3	79815	NO		YES	482530	YES	Q8K1R7
YYVGAAHGL	YYVGAAHGL	9	103.3	0.1	11363000	YES	1856400	YES	13291000	YES	O89112
YYVRILSTI	YYVRILSTI	9	8.5	0.01	5697200	YES	2384600	YES	7239900	YES	P54775

Supplementary Table 3

AA SEQUENCE	Peptide	Length	H-2K^b IC50 (nM)	H-2K^b Rank	Spectral intensity value DDA (hep)	Present in DIA (hep)	Spectral intensity value DDA (skin	Present in DIA (skin)	Spectral intensity value DDA (spleen)	Present in DIA (spleen)	Accession
AAFVFRKL	AAFVFRKL	8	4.9	0.01	294570	YES	6990200	YES	6187400	YES	Q8K0S9
AAILFSERL	AAILFSERL	9	39.3	0.125		YES		YES		YES	Q3KQJ0
AAIRFKDL	AAIRFKDL	8	60.2	0.175	275657.526	NO		YES		YES	Q7TQE6
AALDFKNV	AALDFKNV	8	146.1	0.4	116260	NO	6603200	YES		YES	Q8CG47
AALEFLNRF	AALEFLNRF	9	123.9	0.4	232820	NO	2852800	YES	231350	NO	Q60864
AALIYGKL	AALIYGKL	8	28.4	0.09	53770.4931	NO	6327900	YES	3991800	YES	Q9DC23
AALRFLSQL	AALRFLSQL	9	11.4	0.04	48180.7613	NO	2522300	YES		YES	Q9D2N9
AAPVLVRL	AAPVLVRL	8	399.5	0.9	94546.3206	NO		YES		YES	Q8C0Q3
AAVKFHNL	AAVKFHNL	8	15.8	0.05	182840	YES	4538200	YES	6557300	YES	Q64521
AAVVYHKL	AAVVYHKL	8	94.7	0.3	348390	YES	583970	YES		YES	Q9WTN3
AAYAYSAL	AAYAYSAL	8	2.7	0.01		YES		YES		YES	Q9CQ22
AAYEFTTL	AAYEFTTL	8	3.3	0.01	211837.201	YES	19091000	YES		YES	P32233
AAYGFRNI	AAYGFRNI	8	9.6	0.03	10593612.9	YES	18562000	YES		YES	Q9CYQ7
AAYSFYNV	AAYSFYNV	8	3.3	0.01	438680	YES	9605800	YES	3362200	YES	O70310
AFYKISTL	AFYKISTL	8	187.2	0.5		YES	866640	NO	325800	NO	Q91YW3
AFYQFVNNL	AFYQFVNNL	9	10.8	0.03	224450	NO	11748000	YES	510730	YES	Q9WTV7
AFYYIHNL	AFYYIHNL	8	87.6	0.25	1032800	YES	68357000	YES	13818000	YES	Q9QYC0
AFYYPSRL	AFYYPSRL	8	89	0.25	155445.182	YES	245850	YES		YES	Q6P5C7
AGFDFKQL	AGFDFKQL	8	27.2	0.08	750932.749	NO	501750	YES		YES	Q0VEE6
AGIGFYQHL	AGIGFYQHL	9	7.8	0.02	58087	NO		YES	2049700	YES	Q6ZPY2

AGLSYSKI	AGLSYSKI	8	316	0.8	64494.2085	YES		YES		YES	F8VPZ5
AGPEYKGL	AGPEYKGL	8	249.8	0.6	145500	YES		YES	431740	YES	Q07113
AGPWYRNL	AGPWYRNL	8	16.7	0.05	112300	YES	6784700	YES	2133200	YES	P98195
AGYMYTQL	AGYM(+15.99)YTQL	8	3.1	0.01	956440	NO	11525000	YES	26600000	NO	A2AN08
AGYSFEKL	AGYSFEKL	8	10.7	0.03		YES		YES	1421300	YES	Q91Y86
AIFNFQSL	AIFNFQSL	8	4	0.01		YES	44311000	YES		YES	Q9CR64
AIHEFQETL	AIHEFQETL	9	296	0.7	110937.673	NO	2561500	YES		YES	Q64282
AILERFPTI	AILERFPTI	9	147.7	0.4	50915.2503	NO	3915500	YES		YES	P50652
AIRVFANI	AIRVFANI	8	11.5	0.04	454774.346	NO		YES	512020	NO	Q8QZY1
AIVNFVSKV	AIVNFVSKV	9	183.2	0.5	172350.713	NO	4391300	YES	7011900	YES	Q5SSZ5
AIVSFAHV	AIVSFAHV	8	10.5	0.03	792690.188	YES		YES		YES	P43247
AIVTFITKV	AIVTFITKV	9	441.4	1		YES	16513000	YES	8339500	YES	Q8CGB6
AIYAFSHL	AIYAFSHL	8	2.2	0.01	400084.566	YES	1908100	YES		YES	Q9JJ59
AIYEFIHNF	AIYEFIHNF	9	46.3	0.15	1540000	NO	4882700	YES		YES	Q9WVL1
ALVRFVNL	ALVRFVNL	8	39.5	0.125	1723468.17	NO	6226700	YES		YES	A2BE28
AMYIFLHTV	AM(+15.99)YIFLHTV	9	31.7	0.09	5706700	YES	25153000	YES	15170000	YES	Q9CQZ0
AMYIFLHTV	AMYIFLHTV	9	31.7	0.09	3655400	YES	59652000	YES	1244300	YES	Q9CQZ0
ANFSFAPVTKL	ANFSFAPVTKL	11	315.4	0.8	50350.4342	NO		YES	1055800	YES	Q8BJ34
ANIDFYAQV	ANIDFYAQV	9	7.5	0.02	172820	YES	20108000	YES	867440	YES	P16882
ANILFTREL	ANILFTREL	9	55.1	0.175	208191.216	NO	507260	YES	111340	YES	Q9ERI6
ANIQFRTI	ANIQFRTI	8	128.1	0.4	190432.619	YES	490680	YES	2203400	YES	F8VPQ2
ANLIYYSL	ANLIYYSL	8	9.2	0.025	1624200	YES	7724900	YES	5338000	YES	Q91VR2
ANLKYLSL	ANLKYLSL	8	25.3	0.08	1446318.76	NO	2597200	YES	1559700	YES	Q8R1T4
ANLLFTREL	ANLLFTREL	9	56	0.175	208191.216	NO	507260	YES	111340	YES	
ANRYFTTV	ANRYFTTV	8	130.1	0.4		YES	1687100	NO		YES	Q6PAR5
ANVVFTQL	ANVVFTQL	8	13.4	0.04		YES	9351100	YES	1901700	YES	Q8VHH5
ANYQRDGPM	ANYQRDGPM	9	214.7	0.6	139990	YES	375930	YES	27928	YES	P24270
ANYQRDGPM	ANYQRDGPM(+15.99)	9	214.7	0.6	17986000	YES	143040	YES	265360	YES	P24270

AQFEHTILL	AQFEHTILL	9	206.7	0.5	286751.293	NO	2350100	YES		YES	O08663
AQFEHTLL	AQFEHTLL	8	132.4	0.4		YES	4416500	YES		YES	Q8BP48
AQFKFTVL	AQFKFTVL	8	25.6	0.08	3074500	NO	25223000	NO	431260	YES	P50580
AQFNFQNV	AQFNFQNV	8	13.1	0.04	1019863.12	NO		YES		YES	Q91YI6
AQQLFQKL	AQQLFQKL	8	435.6	1	605015.43	NO		YES		YES	Q8R420
AQYHFPKL	AQYHFPKL	8	14.5	0.05	597970	YES	6229000	NO	143760	NO	P39061
AQYKFIYV	AQYKFIYV	8	18.9	0.06	2079700	NO	28620000	NO	1191600000	YES	P29351
AQYNFILV	AQYNFILV	8	25.3	0.08		YES		YES		YES	Q9D0R2
AQYRFIYM	AQYRFIYM	8	8.7	0.025	3406503.31	YES	32786000	YES	4627700	YES	P35235
AQYRFIYM	AQYRFIYM(+15.99)	8	8.7	0.025	2208900	YES	15790000	YES	44105000	YES	P35235
AQYSFDKL	AQYSFDKL	8	36.3	0.125	125810	YES	16345000	YES	5552400	YES	Q8C547
ASITFEHM	ASITFEHM(+15.99)	8	22	0.07	847980	NO	9001500	YES	1327000	NO	Q91WK2
ASLRYLGL	ASLRYLGL	8	5.5	0.015	1118998.08	YES	6380400	YES	6640200	YES	Q8VC16
ASPEFTKL	ASPEFTKL	8	20.9	0.06	17233000	YES	84586000	YES	70477000	YES	Q3TJZ6
ASPIFTHV	ASPIFTHV	8	17.1	0.05	1096800	YES	35247000	YES	120870000	YES	Q8C5N3
ASVKFHVL	ASVKFHVL	8	64	0.2	1058738.05	YES	4419800	YES		YES	Q6PDQ2
ASVRLAALL	ASVRLAALL	9	122.9	0.4	651850	YES	4436600	YES		YES	Q91ZU9
ASYEFTTL	ASYEFTTL	8	2.6	0.01	8478500	YES	16574000	YES	10134000	YES	Q9QXB9
ASYEFVQRL	ASYEFVQRL	9	4.2	0.01	21688000	YES	865700000	YES	154000000	YES	Q9JHU4
ASYEVKEL	ASYEVKEL	8	215.3	0.6	287588.779	NO	2098400	YES	380350	NO	Q60967
ASYLFRGL	ASYLFRGL	8	2.1	0.01	1195890.98	YES	15684000	YES	21413000	YES	Q7TN60
ASYLLAAL	ASYLLAAL	8	3.4	0.01	749490	NO	3658600	YES		YES	P99027
ASYNHPVL	ASYNHPVL	8	28.9	0.09	26479.358	NO	1582600	YES	1912800	YES	Q6NZM9
ATIFFTRL	ATIFFTRL	8	9.5	0.03	182270	YES	9519200	YES		YES	Q61194
ATIRVTNL	ATIRVTNL	8	84	0.25	1400600	YES	13367000	YES	6405500	YES	Q9Z1D1
ATLAYTKL	ATLAYTKL	8	22.2	0.07		YES	6899700	YES		YES	Q8BUR4
ATLEFEERL	ATLEFEERL	9	107.1	0.3	61720.7667	NO	665310	YES	377830	YES	Q5SW75
ATLVFHNL	ATLVFHNL	8	6.9	0.02	37932000	YES	1110600000	YES	1629400000	YES	P42227

ATPIFSKM	ATPIFSKM(+15.99)	8	103.3	0.3	2370100	YES	2628300	NO	4524800	NO	P10649
ATQVYPKL	ATQVYPKL	8	118.9	0.4	14029000	YES	67874000	YES	122660000	YES	Q8K3W0
ATRSFPQL	ATRSFPQL	8	37.4	0.125	513200	YES	245240000	YES	159290000	YES	Q07076
ATYIFLQTF	ATYIFLQTF	9	39	0.125		YES	8473900	YES	718510	YES	Q8K1A5
ATYIFNGL	ATYIFNGL	8	3.1	0.01	468950	NO	7482700	YES	988130	YES	Q9QXK3
ATYSYKEAL	ATYSYKEAL	9	27.7	0.08	601050	YES	19085000	YES	2846800	YES	Q8R349
ATYTFIQQL	ATYTFIQQL	9	7.6	0.02	9016900	YES	57050000	YES	17251000	YES	Q9R0N0
AVDRFQTL	AVDRFQTL	8	481.1	1	352490	YES	5790900	YES	1288200	YES	Q9WVJ2
AVFTWTNL	AVFTWTNL	8	12	0.04	76152	NO	5669100	YES		YES	Q3UH60:Q8BWT5
AVIDFSEAHL	AVIDFSEAHL	10	199.7	0.5	206991.469	NO	2303100	YES	2062800	NO	P0CB42
AVIHFAGL	AVIHFAGL	8	5.9	0.015		YES	6541500	YES	4090200	YES	Q8R059
AVIKFLEL	AVIKFLEL	8	70.5	0.2		YES	50551000	YES		YES	P43247
AVIQFLERI	AVIQFLERI	9	236.9	0.6		YES	8257900	YES		YES	Q571H0
AVLKFAAA	AVLKFAAA	8	212.1	0.6	42594.9248	NO	727220	YES	271940	YES	P14206
AVLKYYKV	AVLKYYKV	8	177	0.5	600613.759	YES	2701700	YES	2032500	YES	P62983
AVLRYTKL	AVLRYTKL	8	14	0.04	1539416.03	YES	13493000	YES	22335000	YES	Q9WUK4
AVLSFSTRL	AVLSFSTRL	9	20.1	0.06	2384400	YES	90025000	YES	151070000	YES	P46978
AVPEFQGL	AVPEFQGL	8	40	0.125	3529477.41	YES	13494000	YES		YES	Q9QZE5
AVPVFKTL	AVPVFKTL	8	76.1	0.25	58943	NO	1792700	YES	620180	YES	Q8K2G4
AVVAFVMKM	AVVAFVM(+15.99)KM	9	339.2	0.8	372850	YES	421170000	YES	40534000	YES	P01902:P01901:P04223
AVVAFVMKM	AVVAFVM(+15.99)KM(+15.99)	9	339.2	0.8	13066000	YES	568050000	YES	633310000	YES	P01902:P01901:P04223
AVVAFVMKM	AVVAFVMKM	9	339.2	0.8	13818000	YES	1161900000	YES		YES	P01902:P01901:P04223
AVVAFVMKM	AVVAFVMKM(+15.99)	9	339.2	0.8	7300000	YES	645460000	YES	74529000	YES	P01902:P01901:P04223
AVVRFINRF	AVVRFINRF	9	216.3	0.6	1122815.46	NO	2212800	NO	759340	NO	Q6ZPE2
AVVSFKEL	AVVSFKEL	8	178.9	0.5		YES		YES		YES	Q8K394
AVYQFGSAL	AVYQFGSAL	9	10.4	0.03		YES		YES		YES	Q80ZE4
AVYSFEAL	AVYSFEAL	8	4.4	0.01	2395400	NO		YES		YES	Q99KC8
AVYTYLRL	AVYTYLRL	8	3.7	0.01	167070	YES	2234200	YES	3955300	YES	Q7TPD0

AWYQKQELL	AWYQKQELL	9	259.4	0.7	203715.535	NO	369610	YES	40471	NO	Q6NXY1
AYFTHSNL	AYFTHSNL	8	44.4	0.15	4911562.94	YES	14987000	YES	5398100	YES	Q8CIE6
EALSFVSL	EALSFVSL	8	474.8	1	405490	NO		YES		YES	P52332:Q62120
EIISFQHL	EIISFQHL	8	146.9	0.4	1037200	YES	38617000	YES		YES	Q8BGR2:Q5DU41:Q80WG5
EQYKFYSV	EQYKFYSV	8	269.9	0.7	12983758.9	NO	6982900	NO	4638800	NO	Q62425
ESFKFVRL	ESFKFVRL	8	13.9	0.04	727911.623	NO	1760800	NO	616150	NO	Q99LC8
ESFQFYDRL	ESFQFYDRL	9	13.2	0.04	204175.179	NO	899810	YES	144360	NO	Q8K284
ETPVYANL	ETPVYANL	8	42.8	0.125	2748700	YES	12346000	NO	33253000	YES	P15066
ETYKYFSL	ETYKYFSL	8	23.6	0.07	984532.899	NO	7780800	NO	5289000	NO	Q9ET30
EVYLFERI	EVYLFERI	8	288.1	0.7	847925.307	YES	7195400	YES		YES	P97390
FAPIYADL	FAPIYADL	8	34.3	0.1	670080	YES	5140300	YES		YES	Q9D710
FAYRFSNL	FAYRFSNL	8	2	0.01	1584800	NO	29455000	NO	67624000	NO	Q8BU03
FQFTFKHL	FQFTFKHL	8	15.8	0.05	964790	NO	8642600	YES	1155300	NO	Q9QYJ0
FSPSFINHI	FSPSFINHI	9	161.1	0.5	258200	NO	4297100	YES	663560	NO	Q9JIX9
FSQEYINL	FSQEYINL	8	15.7	0.05	493376.605	YES	7226600	YES	1486900	YES	Q9D8V0
FSVRPFAL	FSVRPFAL	8	147.3	0.4		YES		YES		YES	O08852
FTFEYRYL	FTFEYRYL	8	5.8	0.015	142540	NO	12504000	YES		YES	Q8K0V4
FTFQFNNL	FTFQFNNL	8	3.6	0.01	197767.437	NO	4755500	NO		YES	Q8R5H1
FTYDYHTL	FTYDYHTL	8	12.9	0.04	7739600	YES	8368700	YES	1324000	YES	Q9Z239
FVYIFQEV	FVYIFQEV	8	19.9	0.06		YES	110510000	YES	1307900	YES	Q99K51
GAVDFSHL	GAVDFSHL	8	328.3	0.8		YES		YES		YES	O88487
GLYLHALL	GLYLHALL	8	167.4	0.5	65471.9247	NO		YES		YES	Q5IXF8
GMYIFLHTV	GMYIFLHTV	9	172.6	0.5	124271.229	YES	5013700	YES		YES	Q9CPZ6
GNYLFHYI	GNYLFHYI	8	69.4	0.2	38380	NO	1249800	YES		YES	P70280
GQLEFRALL	GQLEFRALL	9	352.8	0.8	142123.313	NO	2037100	YES		YES	P11499:P07901
GQYEFHSL	GQYEFHSL	8	91.9	0.25	1430700	YES	16506000	YES	561140	YES	Q61805
GTYDYTQL	GTYDYTQL	8	31.7	0.09	765630	NO		YES	996050	YES	Q8K2A8
GTYEFLYTV	GTYEFLYTV	9	170.8	0.5	401690	NO	2134200	YES		YES	Q9ESN6

GVLKFARL	GVLKFARL	8	15.5	0.05		YES		YES		YES	O35127
GVLRFVNL	GVLRFVNL	8	30.8	0.09	2488200	YES	34288000	YES		YES	Q3UGP8
HAVVFAQL	HAVVFAQL	8	20.2	0.06	325969.007	NO	743660	YES	1101400	YES	Q9EPL9
HAYIISSL	HAYIISSL	8	303.5	0.8		YES	2198200	YES	1986100	YES	Q9QXY6
HAYIISYL	HAYIISYL	8	160.8	0.4		YES	8362800	YES		YES	Q8BH64
HGVSYVSL	HGVSYVSL	8	451.6	1		YES		YES	515100	YES	Q99L04
HGYIFSSL	HGYIFSSL	8	6.4	0.015	1757707.72	YES	26834000	YES	19580000	YES	Q9DAA6
HGYTFANL	HGYTFANL	8	3	0.01	1415800	YES	72188000	YES	125310000	YES	Q9R1T2
HIYEFPQL	HIYEFPQL	8	7.9	0.02	40560000	YES	276940000	YES	343060000	YES	Q8C4B4
HIYQFEYM	HIYQFEYM	8	33.8	0.1	487533.68	NO	3111100	YES		YES	Q8C079
HIYQFEYM	HIYQFEYM(+15.99)	8	33.8	0.1	368489.922	NO	3152900	YES	1809900	YES	Q8C079
HSALIYSNL	HSALIYSNL	9	107.8	0.3	405320	YES	28194000	YES	3452300	YES	O55013
HSIRFVTL	HSIRFVTL	8	20.3	0.06	1343483.27	NO	1184500	NO	361920	NO	Q91XU0
HSPAFVQL	HSPAFVQL	8	52.2	0.175	802973.736	NO		YES		YES	Q61191
HSYLYGLL	HSYLYGLL	8	4.2	0.01	740220.719	YES		YES		YES	Q9QYC7
HTFTYTGL	HTFTYTGL	8	10.7	0.03	429377.098	NO	6812100	YES		YES	A2AGH6
HTYDFEKL	HTYDFEKL	8	90.4	0.25	2210534.42	YES	39527000	YES	3549200	YES	P07742
HTYVHATL	HTYVHATL	8	15	0.05		YES	773030	YES	691870	YES	Q9EQJ0
HVYYFAHL	HVYYFAHL	8	2.7	0.01		YES	31254000	YES	1038200	YES	Q80SU7
IAAVFHTL	IAAVFHTL	8	32.3	0.1	163547.372	NO	3174600	YES	875050	YES	Q9JHZ2
IAFGFHQL	IAFGFHQL	8	5.4	0.015	2926136.95	YES	4662900	YES	1004200	YES	Q9R0A0
IAFSYELSKL	IAFSYELSKL	10	54	0.175	138855.17	NO		YES		YES	Q9D1P2
IAGPYNRL	IAGPYNRL	8	95.3	0.3	755540	YES	9045100	YES	2444000	YES	Q8VDJ3
IALRYVAL	IALRYVAL	8	4.2	0.01	3105600	YES	28335000	YES	69440000	YES	Q9JIF7
IAPEYFEKL	IAPEYFEKL	9	17.2	0.05	1792648.41	YES	280820	NO	451760	NO	Q9D9V7
IAPSFVKGF	IAPSFVKGF	9	193.5	0.5	602930	YES	7042200	YES	1899200	YES	O88967
IAVIFKQL	IAVIFKQL	8	13.3	0.04	189010	NO		YES		YES	Q6PGC1
IAVSFREL	IAVSFREL	8	10.8	0.03	4228600	YES	50840000	YES	67920000	YES	Q8BJW5

IAYAFFHL	IAYAFFHL	8	2	0.01		YES	12616000	YES	1095200	YES	Q8K4P7
IAYKFGKTV	IAYKFGKTV	9	30.1	0.09	4634997.81	YES	4537100	YES	1444400	YES	Q8R3Q0
IAYKFGKTVV	IAYKFGKTVV	10	276	0.7	272650.367	NO	266690	NO	116460	NO	Q8R3Q0
IAYLYDRL	IAYLYDRL	8	2.7	0.01	98394	NO	2716300	YES	1267700	YES	Q9CZ15
IDFDFTHL	IDFDFTHL	8	48.1	0.15	422209.776	NO		YES		YES	O70566
IDYQYQLL	IDYQYQLL	8	26.2	0.08	126990	YES	10378000	YES	3196500	YES	Q9D8X5
IDYSFPSL	IDYSFPSL	8	21.7	0.07	307740	YES		YES		YES	Q91VE6
IFYFVNKL	IFYFVNKL	8	79.5	0.25	67271.5457	NO	3859900	YES		YES	Q8BH24
IFYYVQKL	IFYYVQKL	8	52.7	0.175	3267207.97	YES	31918000	YES	21433000	YES	Q69ZR2
IGFDEYMNL	IGFDEYMNL	9	10.7	0.03	39394	NO	3296000	YES		YES	P62305
IGIAYNRL	IGIAYNRL	8	6.1	0.015	1069100	YES	10650000	YES		YES	Q8CIB5
IGIVKQAGL	IGIVKQAGL	9	76.6	0.25	439738.552	YES	6112800	YES	5997900	YES	Q9Z2X1
IGPEYKSM	IGPEYKSM	8	212.5	0.6	418236.587	YES	1554500	NO	84240	NO	Q99K01
IGPEYKSM	IGPEYKSM(+15.99)	8	212.5	0.6	5935100	YES	688020	NO	1546300	NO	Q99K01
IGPRFKLL	IGPRFKLL	8	14	0.04	1431900	YES		YES	1862300	YES	E9Q3L2
IGPRFSNL	IGPRFSNL	8	4.2	0.01	2796501.91	NO	7480700	NO	2699400	NO	P46460
IGPTYYQRL	IGPTYYQRL	9	3.9	0.01	467700	YES	41366000	YES	208580	YES	Q8CFI7
IGYEHEVL	IGYEHEVL	8	64	0.2	322550	YES		YES	1912900	YES	Q3U4G0
IHYDRITSL	IHYDRITSL	9	80.6	0.25	364668.649	NO	772650	YES		YES	Q8CFQ3
IIFETPLRV	IIFETPLRV	9	417.4	0.9	352207.637	NO	2833700	YES		YES	Q6NZJ6
IIHKYPSL	IIHKYPSL	8	10.6	0.03	863000.054	NO	9896600	YES	1128000	YES	Q3TEA8
IILKNFEKL	IILKNFEKL	9	115.1	0.3	758645.41	NO	1786900	NO	2466900	YES	P97371
IILKYIGM	IILKYIGM	8	15.3	0.05	3091608.59	NO		YES		YES	Q9JKW0
IILKYIGM	IILKYIGM(+15.99)	8	15.3	0.05	1668700	NO	12168000	YES	68646000	YES	Q9JKW0
IITRFYQL	IITRFYQL	8	9.1	0.025	105440	NO	476280	NO	1018700	NO	Q69ZT1
IIVQFRYI	IIVQFRYI	8	23	0.07	48989	NO	10144000	YES		YES	Q8BHK1
IIWVKTNQL	IIWVKTNQL	9	130.8	0.4	1036184.36	NO	2659500	YES	1389900	YES	Q8C3P7
IIYDRKFLM	IIYDRKFLM(+15.99)	9	84.1	0.25	183534.072	NO	6929900	YES	9705500	NO	Q60876

IIYEFESSTQM	IIYEFESSTQM(+15.99)	11	101.2	0.3	125410	NO	8198900	YES	45969000	YES	Q9DB00
IIYNPKNL	IIYNPKNL	8	25.5	0.08	1628800	YES	21285000	YES	4971000	YES	Q9D554
ILSSFESRL	ILSSFESRL	9	244.7	0.6	304490.414	NO		YES		YES	O35250
INAEFVTQL	INAEFVTQL	9	40.7	0.125	331270.488	NO	8932700	YES	4395100	YES	Q8CFQ3
INAIFERL	INAIFERL	8	25.9	0.08	41399.0728	NO	527920	NO	472550	YES	Q8C5N3
INFDFNTI	INFDFNTI	8	19.8	0.06	1897500	YES		YES		YES	Q8CDD8
INFDFPKL	INFDFPKL	8	6.2	0.015	286070000	YES	1772900000	YES	277580000	YES	P54823
INFSHDSSFL	INFSHDSSFL	10	187.8	0.5	366748.73	NO	404440	NO	66207	NO	Q91VM3
ININSLRL	ININSLRL	8	159.7	0.4	88960.4841	YES	12526000	YES	2967400	YES	P16460
INLEFVKV	INLEFVKV	8	37	0.125	235270	NO		YES		YES	A2AAE1
INLEHSVPM	INLEHSVPM	9	84.3	0.25		YES		YES		YES	Q80TY5
INLNYKDL	INLNYKDL	8	38.1	0.125	778010	YES	15517000	YES		YES	Q9CY50
INQRFEEL	INQRFEEL	8	40.2	0.125	520293.014	YES	3531700	NO	1393000	NO	P42230
INYDYVHEL	INYDYVHEL	9	21.2	0.06	162160	NO	14779000	YES		YES	E9Q784
INYQPPTV	INYQPPTV	8	237	0.6	46852	NO	511000	YES	338810	YES	P68373:P05213:P68368:Q9JJZ2
INYSFPAKGKL	INYSFPAKGKL	11	35.6	0.125	343077.092	NO	50256	NO		YES	Q8K4L0
INYVIKQL	INYVIKQL	8	33.2	0.1	409783.822	YES		YES		YES	P98192
INYVVPRV	INYVVPRV	8	24.6	0.07	44916.5138	NO		YES	289900	YES	Q80U59
IPPEYRHL	IPPEYRHL	8	132.1	0.4	1278899.47	YES	9571700	YES	6949400	YES	P51125
IQLEFREL	IQLEFREL	8	25.1	0.08	3984095.94	NO		YES	1736900	YES	A2AJ15
IQQQYAQV	IQQQYAQV	8	53.6	0.175		YES		YES	3182500	YES	Q6Y7W8
IRYFPTQAL	IRYFPTQAL	9	437.1	1	366530	YES	29716000	YES	10250000	YES	P51881:P48962
ISARFVQL	ISARFVQL	8	6.4	0.015	1912800	NO	19232000	NO	14575000	NO	Q7TN98:Q812E0:Q7TN99
ISATFKML	ISATFKM(+15.99)L	8	16.8	0.05	297973.605	NO	3271200	YES	4595400	NO	Q9CZX9
ISATFKML	ISATFKML	8	16.8	0.05	631737.074	NO	6350500	YES	207500	NO	Q9CZX9
ISFEFRSL	ISFEFRSL	8	2.2	0.01	18539212.2	YES	38297000	YES		YES	Q3THF9
ISFEFRSLL	ISFEFRSLL	9	4.3	0.01		YES	9432300	YES		YES	Q3THF9

ISFKFDHL	ISFKFDHL	8	2.7	0.01	4034500	YES	120960000	YES	473140000	YES	P47753
ISILYHQL	ISILYHQL	8	3.7	0.01	341950	NO	75767000	NO	4447000	NO	Q9D2V5
ISLDYHQL	ISLDYHQL	8	7.9	0.02		YES		YES		YES	Q7TPV2
ISLDYQHL	ISLDYQHL	8	4.4	0.01	247110	YES	11531000	YES		YES	Q5SYL3
ISLEFRNL	ISLEFRNL	8	2.5	0.01	16607000	YES	12365000	YES	6056600	YES	P53798
ISLRFTHL	ISLRFTHL	8	2.1	0.01	307341.762	NO		YES	1943200	NO	Q6P549
ISPEWKQQL	ISPEWKQQL	9	83.6	0.25	45855.2771	NO	1387300	YES	59327	NO	Q9WTI7
ISPFFPNGV	ISPFFPNGV	9	53.6	0.175	120660	YES	5108300	YES	399880	YES	Q640L3
ISPNFNFM	ISPNFNFM(+15.99)	8	16.2	0.05	302106.501	NO	7797500	YES	4367300	YES	Q9DBB1:Q91Z46
ISPPIPHL	ISPPIPHL	8	270.5	0.7	50042	NO	4546500	YES	3900200	YES	Q5SVR0
ISPRFDVQL	ISPRFDVQL	9	17.4	0.05	32432130.2	YES	329740000	YES	62385000	YES	P62245
ISSRFQNL	ISSRFQNL	8	5.1	0.015	1166987.98	NO	8631600	NO	4834000	NO	Q9QXZ0
ISTIFKSL	ISTIFKSL	8	17	0.05	445520	YES	3015400	YES		YES	Q9ES00
ISVRFHNL	ISVRFHNL	8	2.9	0.01		YES	3825300	YES		YES	Q8CFL8
ISVSFYHV	ISVSFYHV	8	6	0.015	660140	YES	44932000	YES	37833000	YES	Q8JZQ9
ISYAWKEL	ISYAWKEL	8	9.4	0.03	1266707.23	YES		YES	494690	YES	Q9JIK5
ISYLYNKL	ISYLYNKL	8	2.1	0.01	1060400	YES		YES	3008400	YES	Q61471:Q9JM55
ITALHIKL	ITALHIKL	8	422.1	0.9	173032.387	NO	28797000	YES	1863900	NO	P62264
ITFIFKSL	ITFIFKSL	8	3.7	0.01		YES	44803000	YES	681380	YES	Q9JLN9
ITFSYVNNM	ITFSYVNNM(+15.99)	9	9.4	0.03	343879.521	NO	2516100	YES	6404800	YES	Q8C172
ITPPGYSHV	ITPPGYSHV	9	197.3	0.5	765000	NO	20186000	NO	14664000	NO	Q8BLB7
ITYVHNEL	ITYVHNEL	8	8.1	0.025		YES	5421600	YES		YES	Q80YA7
ITYYFDNV	ITYYFDNV	8	3.4	0.01	865921.517	NO		YES		YES	Q6ZQ58
IVELFRNL	IVELFRNL	8	17.8	0.05	738273.077	YES	9835200	YES		YES	P42227
IVLTFRQL	IVLTFRQL	8	4.6	0.01	431180	YES		YES		YES	Q8BGF9
IVWEFEQL	IVWEFEQL	8	9.6	0.03		YES	13599000	YES		YES	Q62158
IWIRVASL	IWIRVASL	8	44.9	0.15	4903100	YES	37280000	YES	2278600	YES	Q8BRG6
IYFKVTHV	IYFKVTHV	8	308.1	0.8	116624.787	NO		YES		YES	Q80SY5

KAFASLRM	KAFASLRM	8	497.1	1.1	295784.456	YES	1938000	YES	601580	NO	P47963
KAFASLRM	KAFASLRM(+15.99)	8	497.1	1.1	978884.738	YES	738210	YES	3830700	NO	P47963
KAFDYPSRL	KAFDYPSRL	9	32.4	0.1	3783177.22	YES	5843200	YES	5456200	YES	Q6P5C7
KAFEHLQQL	KAFEHLQQL	9	61.4	0.175	385364.29	NO	854210	YES	145090	NO	O88708
KAFGFNVL	KAFGFNVL	8	59.5	0.175	171750.839	NO		YES		YES	O88712
KAFHFPSL	KAFHFPSL	8	9.8	0.03	417496.483	YES	1614500	YES	678590	NO	Q6P5C7
KAFTYINL	KAFTYINL	8	4.2	0.01	305580	YES	5796100	YES	20891000	YES	Q62351
KALEYLKL	KALEYLKL	8	88.9	0.25	160064.989	NO	2212400	YES	1107600	YES	A2AGT5
KALLFVNTL	KALLFVNTL	9	64	0.2	106072.464	NO	639890	YES		YES	Q9D0R4
KALQFKQV	KALQFKQV	8	236	0.6	222557.021	YES	94649	NO		YES	Q8R164
KALQFLEQV	KALQFLEQV	9	353	0.8	285570	YES	18801000	YES	5818300	YES	P80317
KALTLSNL	KALTLSNL	8	93.2	0.25	195001.786	YES		YES		YES	Q8VI47
KALTYEKL	KALTYEKL	8	119.7	0.4	267629.347	NO	2129400	YES	3160500	YES	O08800
KAPGFAHL	KAPGFAHL	8	13	0.04	235956.797	YES		YES	40184	NO	Q91WD5
KAPVFMEKL	KAPVFM(+15.99)EKL	9	135.3	0.4	1804412.17	YES	2654900	NO	1457500	NO	Q9ET54
KAPVFMEKL	KAPVFMEKL	9	135.3	0.4	3241187.48	YES	5452100	NO	447130	NO	Q9ET54
KAVTFIDL	KAVTFIDL	8	205.6	0.5	964280	YES		YES		YES	Q91YP3
KAYSFKEQI	KAYSFKEQI	9	64.5	0.2	5602975.75	YES	2653200	YES	430200	YES	E9PVA8
KEFIFPNM	KEFIFPNM	8	277.2	0.7	2920021.35	YES	1033800	NO		YES	Q61471
KGFEFTLM	KGFEFTLM	8	20.2	0.06	1129086.87	YES	115880000	YES		YES	P42208
KGFGFIKL	KGFGFIKL	8	52.9	0.175	206610	YES	1292000	YES		YES	Q8VIJ6
KGFTFSAL	KGFTFSAL	8	4.2	0.01		YES		YES		YES	Q9CYV5
KGFYFAKL	KGFYFAKL	8	3.8	0.01	1273700	YES	6887100	YES	22488000	NO	Q9ERU9
KGIIYRDL	KGIIYRDL	8	152.1	0.4		YES	3719800	YES		YES	P28867
KGLDFALL	KGLDFALL	8	15.2	0.05		YES	24567000	YES	6028200	YES	Q9Z1M8
KGPQYGTL	KGPQYGTL	8	148.3	0.4	1976100	YES		YES		YES	Q99JB8
KGVAYVYL	KGVAYVYL	8	65	0.2	1614049.66	NO		YES		YES	Q8K1H1
KGYAYTFI	KGYAYTFI	8	27.4	0.08	196380	YES	5100200	YES	18883000	YES	Q569Z5

KGYGFAEYM	KGYGFAEYM	9	106.5	0.3	309507.539	NO		YES		YES	Q9CW46
KGYGYQAL	KGYGYQAL	8	9.7	0.03		YES		YES		YES	Q99LI9
KGYIFLTL	KGYIFLTL	8	7.6	0.02		YES	23538000	YES	10935000	YES	Q80VI1
KIFEFKETL	KIFEFKETL	9	63.4	0.2	895720.436	NO	23426000	YES	212030000	YES	Q8BW96
KIFTASNV	KIFTASNV	8	171.6	0.5	230164.51	NO		YES	956870	YES	Q80X50
KIIPFNRL	KIIPFNRL	8	17.3	0.05		YES		YES		YES	Q8VCM7
KIITYRNL	KIITYRNL	8	7.5	0.02		YES		YES		YES	Q8BFV2
KILTFDQL	KILTFDQL	8	66.5	0.2	3864400	YES	55083000	YES	35815000	NO	P35980
KIQSFINRM	KIQSFINRM	9	202.8	0.5	2194719.57	YES	14078000	YES		YES	Q8C1Y8
KIVPFFKL	KIVPFFKL	8	139.2	0.4	1664143.01	YES	21855000	YES	177590	YES	Q9JHU4
KIYQWINEL	KIYQWINEL	9	89.5	0.25	2946700	YES	80391000	YES		YES	Q9JKY0
KNFAFLEF	KNFAFLEF	8	247.3	0.6		YES	5128900	YES	498150	NO	P26369
KNFAFTLV	KNFAFTLV	8	14.6	0.05		YES	22810000	YES		YES	A3FIN4;Q148W0
KNFDKLSFL	KNFDKLSFL	9	146.9	0.4	876220	NO	3378800	YES	628630	YES	Q8CIE6
KNFPFERL	KNFPFERL	8	11.2	0.04	1317400	YES	29532000	YES	6481900	YES	Q6P4T2
KNFVYRTL	KNFVYRTL	8	5.9	0.015	993725.768	YES		YES		YES	A2RSX7
KNHEFIATF	KNHEFIATF	9	233.3	0.6	570736.935	NO	5348400	YES	16647000	YES	P28867
KNIDRFIPV	KNIDRFIPV	9	82.8	0.25	183553.548	NO	470870	YES	201630	NO	Q9CX30
KNIIYRFL	KNIIYRFL	8	25.2	0.08	1012300	YES	4915500	YES		YES	Q9D4H2
KNIRFPLM	KNIRFPLM	8	35.4	0.125	830840	NO	25938000	YES	3992100	YES	Q6ZPT1
KNIRFPLM	KNIRFPLM(+15.99)	8	35.4	0.125	514910	NO	21403000	YES	47522000	YES	Q6ZPT1
KNIRYVAL	KNIRYVAL	8	10.9	0.03	3511909.68	YES	1677900	YES	9440700	YES	P22892
KNLNYLHL	KNLNYLHL	8	14.7	0.05	4629154.88	YES	6068500	YES	1621800	YES	Q99PV0
KNLVFVVGL	KNLVFVVGL	9	42.5	0.125		YES	6228700	YES	1592400	YES	Q8BT14
KNNQFQAL	KNNQFQAL	8	149.7	0.4	82680	YES	336060	YES	527540	NO	P17225:Q8BHD7
KNNQFQALL	KNNQFQALL	9	78.7	0.25	1133371.68	NO	1785100	YES	1219900	YES	P17225:Q8BHD7
KNPGYIKL	KNPGYIKL	8	416.9	0.9	1776327.17	YES	540580	YES	159330	NO	O35129
KNVLFSHL	KNVLFSHL	8	7.9	0.02	2590519.32	YES	24861000	YES	25310000	YES	P12849;Q9DBC7

KNVTFEHV	KNVTFEHV	8	302.9	0.7	760410	YES	4106700	YES	4897800	YES	O88967
KNVVYERV	KNVVYERV	8	337.2	0.8	173680	YES	6426700	YES		YES	Q8K4L4
KNVVYRDL	KNVVYRDL	8	172.5	0.5	1482233.27	YES	6426700	YES	10218000	YES	P31750
KNWEFMTI	KNWEFMTI	8	83	0.25	351210.444	NO	2357400	YES		YES	Q04592
KNYDFAQV	KNYDFAQV	8	5.5	0.015	547730	YES	1174400	YES	1235900	YES	Q8BGF7
KNYDFAQVL	KNYDFAQVL	9	29.5	0.09	4638300	YES	26337000	YES	25694000	YES	Q8BGF7
KNYGFVHI	KNYGFVHI	8	23.9	0.07		YES	11400000	YES		YES	Q8VE92
KNYGYVRV	KNYGYVRV	8	19.7	0.06	380680	YES	421160	YES	582900	YES	Q61586
KNYLLPIL	KNYLLPIL	8	132.1	0.4		YES	5267500	YES	2686000	YES	P50172
KNYSFPLNNL	KNYSFPLNNL	10	25	0.08	176680	YES	15035000	YES	29275000	YES	Q8CDG3
KQFAFVHM	KQFAFVHM	8	32.1	0.1	387167.806	NO	153870	NO	57969	NO	Q8C2Q3
KQFEYIEV	KQFEYIEV	8	309.5	0.8	63090	YES		YES		YES	P42859
KQFSYTHI	KQFSYTHI	8	49.5	0.15	707889.866	YES		YES	243110	NO	Q99LC5
KSFDYGNL	KSFDYGNL	8	4.3	0.01	219027.895	NO		YES	9577200	YES	Q3UHF7
KSFEWLSQM	KSFEWLSQM	9	38.9	0.125	2019626.58	YES	43332000	YES		YES	Q9JHU4
KSFEWLSQM	KSFEWLSQM(+15.99)	9	38.9	0.125	1101600	YES	24455000	YES	459290	YES	Q9JHU4
KSFLFSAL	KSFLFSAL	8	2.4	0.01		YES	66535000	YES	1457600	YES	Q920L5
KSIAFPSI	KSIAFPSI	8	68.3	0.2		YES		YES	2635400	YES	Q9QZQ8
KSITFSKL	KSITFSKL	8	7.5	0.02	13769437.6	YES	9271700	YES	7622800	YES	O35459
KSLAFQKL	KSLAFQKL	8	13.2	0.04	3467776.12	YES		YES	1125400	YES	Q8BIL5
KSLERATQL	KSLERATQL	9	327.8	0.8		YES		YES		YES	Q63829
KSLSFPKL	KSLSFPKL	8	13.4	0.04	373873.203	NO		YES	3151300	YES	Q8BH48
KSPEYESL	KSPEYESL	8	99.2	0.3	2194485.85	YES	2308100	YES	9309200	YES	Q3V1L4
KSYLMNKL	KSYLM(+15.99)NKL	8	29.4	0.09	243350.045	NO	94214000	YES	6447900	NO	Q9Z0E6:Q8CFB4:Q01514
KSYLMNKL	KSYLMNKL	8	29.4	0.09	254591.833	NO	199660000	YES	1684400	NO	Q9Z0E6:Q8CFB4:Q01514
KSYLMNRL	KSYLMNRL	8	9.9	0.03	829929.098	YES	56274000	YES	2711700	NO	Q61107
KSYSFDEV	KSYSFDEV	8	26.2	0.08	729510	YES	9297900	YES	1468200	YES	Q99KQ4
KSYSFIARM	KSYSFIARM	9	4.4	0.01	3179875.71	YES	12133000	YES	130240	NO	Q8CGZ0

KSYSFIARM	KSYSFIARM(+15.99)	9	4.4	0.01	1361362.62	YES	5948400	YES	1743900	NO	Q8CGZ0
KTFDFKGL	KTFDFKGL	8	19.5	0.06	531978.865	NO	3453100	YES	2483500	YES	Q924W7
KTFLFSATM	KTFLFSATM	9	17.4	0.05	230550.143	NO		YES	1120300	YES	Q9CWX9
KTFLFSATM	KTFLFSATM(+15.99)	9	17.4	0.05	322560	NO	4847700	YES	24311000	YES	Q9CWX9
KTFSYAGF	KTFSYAGF	8	16.7	0.05	667028.343	NO	3334400	YES		YES	P80313
KTLVLSNL	KTLVLSNL	8	71.3	0.2	1051843.4	YES	2703600	YES		YES	P09405
KTVCFQNL	KTVC(+119.00)FQNL	8	21.2	0.06	516943.07	NO	17106000	NO	1960800	NO	Q7TMB8
KTVEYTRL	KTVEYTRL	8	24.6	0.07	139891.316	YES	491770	YES		YES	A8C756
KTVIFENL	KTVIFENL	8	33.4	0.1	1172869.86	NO	5900500	YES	5046500	YES	Q99KZ6
KTWRFSNM	KTWRFSNM	8	6.1	0.015	5095420.32	YES	7395700	YES	1389300	YES	Q8CIB5
KTWRFSNM	KTWRFSNM(+15.99)	8	6.1	0.015	5972248.63	YES	4587600	YES	7300200	YES	Q8CIB5:Q8K1B8
KTYEHFNAM	KTYEHFNAM	9	16.8	0.05	4290265.22	YES	2736100	YES	505990	YES	P37040
KTYEHFNAM	KTYEHFNAM(+15.99)	9	16.8	0.05	4691300	YES	1624100	YES	12153000	YES	P37040
KTYQFLNDI	KTYQFLNDI	9	89.3	0.25	792620	YES	15599000	YES	18020000	YES	Q3UFY0
KTYSFLITL	KTYSFLITL	9	15.3	0.05		YES		YES		YES	P27656
KVFEYHNV	KVFEYHNV	8	18.2	0.06		YES	9587700	YES	15290000	YES	Q9DAX9
KVFQFLNA	KVFQFLNA	8	143.9	0.4	775550	YES	6631400	YES	4279000	NO	Q8BP67
KVIEFKKL	KVIEFKKL	8	122.5	0.4	438219.391	YES	487110	YES	1507900	NO	Q8R4D1
KVITFIDL	KVITFIDL	8	135.5	0.4	820930.993	YES	38822000	YES	14261000	YES	O08582
KVLEFERV	KVLEFERV	8	211.9	0.6	5696462.56	YES	12869000	YES	8690800	YES	Q8CEC6
KVLIFSQM	KVLIFSQM(+15.99)	8	42.8	0.125	29475	NO	766590	YES	8739700	YES	Q09XV5:Q8BYH8
KVLRFIAEV	KVLRFIAEV	9	107.3	0.3	506542.663	NO	15107000	YES	5355900	NO	Q9QYH6
KVQEFQRL	KVQEFQRL	8	59.9	0.175		YES	1583700	YES	610770	YES	Q62172
KVQEFVLL	KVQEFVLL	8	198.9	0.5	844630	YES		YES		YES	Q3UHQ6
KVVDHFGRL	KVVDHFGRL	9	53.1	0.175	653706.473	YES		YES	488000	NO	Q8VCC1
KVVEFSEL	KVVEFSEL	8	65.2	0.2		YES	4187700	YES		YES	Q3UFM5
KVYLYTHL	KVYLYTHL	8	2.7	0.01		YES	8677600	YES		YES	Q8R0A7
KVYNYNHL	KVYNYNHL	8	4	0.01	122070	YES	11420000	YES	46183000	YES	P61358

KVYTFNSV	KVYTFNSV	8	10.5	0.03	350154.822	NO	1761700	YES	2781200	YES	G5E829:Q9R0K7:Q6Q477
LAPHFNSL	LAPHFNSL	8	87.3	0.25	163330	YES	1633500	YES		YES	Q6P6J9
LAPVFQRV	LAPVFQRV	8	64.3	0.2	248310	YES		YES		YES	Q9JJA2
LAPVYQRL	LAPVYQRL	8	17.7	0.05	3609900	YES	98327000	YES		YES	P82198
LGYKYVGM	LGYKYVGM	8	10.2	0.03	446672.156	NO	4696300	YES	773390	YES	Q9CX30
LGYKYVGM	LGYKYVGM(+15.99)	8	10.2	0.03	367700	NO	4401900	YES	6116600	YES	Q9CX30
LGYQYPSL	LGYQYPSL	8	5.3	0.015	6405600	YES	3584700	YES	2941100	YES	Q9QYG0
LIYKFLNV	LIYKFLNV	8	5.8	0.015	6060300	YES	37941000	YES	871200	YES	Q6P5F9
LQYEFTKL	LQYEFTKL	8	10.8	0.03	1714119.49	YES	168370000	YES	273580000	YES	A2APV2;Q6ZPF4
LQYIFAHV	LQYIFAHV	8	4.7	0.01		YES		YES	9228300	YES	Q99PV0
LSLPFEARL	LSLPFEARL	9	10.9	0.03	1331914.28	YES	8527400	YES		YES	Q9JL15
LSPKYIKM	LSPKYIKM(+15.99)	8	152.1	0.4	320140	YES	1832800	YES	1747400	NO	P60843
LSPPSYSKL	LSPPSYSKL	9	148.2	0.4	2030260.7	NO	7906600	NO	5303000	NO	P98195
LSPSHYALL	LSPSHYALL	9	5.4	0.015	6995929.13	YES	7231100	YES	9300300	YES	Q8C7X2
LSYDYSGRFL	LSYDYSGRFL	10	91.5	0.25	108265.509	NO		YES	155860	YES	Q80UJ9
LSYSYQSRF	LSYSYQSRF	9	28.8	0.09	648330.982	YES	4388600	YES	3918200	YES	Q921M3
LTQQYHQL	LTQQYHQL	8	206.2	0.5	103110	NO		YES	608060	YES	P10404:P11370
LVAIFTHL	LVAIFTHL	8	58.8	0.175		YES	37825000	YES	2915000	YES	Q9JHU4
LVYKNFPQL	LVYKNFPQL	9	17.5	0.05	386380.959	NO	7943600	YES	2906300	YES	Q8K1A5
LVYQFKEM	LVYQFKEM	8	27	0.08	356161.349	NO	7286300	YES	1157800	NO	Q60775
LVYQFKEM	LVYQFKEM(+15.99)	8	27	0.08	159426.162	NO	3676000	YES	25991000	NO	Q60775
MSFQFAHL	M(+15.99)SFQFAHL	8	1.8	0.01	1345800	YES	7670100	YES	2189500	YES	Q80TY5
MAYLFRNI	MAYLFRNI	8	3.1	0.01	598210	YES		YES		YES	Q9D0M1
MSFQFAHL	MSFQFAHL	8	1.8	0.01	1312200	YES	20512000	YES		YES	Q80TY5
MSYLFRNI	MSYLFRNI	8	2.4	0.01	39090	YES	3542300	YES		YES	Q8R574
NIFMFSKV	NIFMFSKV	8	55.6	0.175	299120	YES	2348400	YES		YES	Q9D710
NMVPFPRL	NMVPFPRL	8	315	0.8		YES		YES		YES	P68372
NNPIFRYL	NNPIFRYL	8	160.9	0.5	2092818.95	YES	1952300	YES		YES	Q8VCH6

NNYVFKNAL	NNYVFKNAL	9	27.4	0.08	98714.2739	NO	1492600	YES		YES	Q9JJJ7
NNYVYAGL	NNYVYAGL	8	3.9	0.01	400870	YES	5269200	YES	4679900	YES	Q8CIK8
NSFRYNGL	NSFRYNGL	8	9.3	0.025	495930	YES	29392000	YES	5432100	YES	P41105
NSPEFQKL	NSPEFQKL	8	386.5	0.9	307090	YES	2015800	YES	559980	YES	P42859
NSPEYQRL	NSPEYQRL	8	126.3	0.4	2523300	YES	2664600	YES	5966800	YES	Q9CVD2
NTHEFVNL	NTHEFVNL	8	116.6	0.4	479790	YES	16164000	YES		YES	P40336
NTPKYAKL	NTPKYAKL	8	171.4	0.5	257790	NO	148120	NO		YES	Q9R020
NTYKYAKI	NTYKYAKI	8	37.2	0.125	638610	YES	579670	YES		YES	Q7TQI7
NTYSYQKV	NTYSYQKV	8	134.4	0.4	1247300	YES		YES	2852700	YES	Q3TA59
QAFDFEFTHV	QAFDFEFTHV	10	101.1	0.3	1175207.03	NO	11974000	YES		YES	Q8C0E2
QAIDYHEL	QAIDYHEL	8	442.9	1	728418.01	NO		YES	488040	NO	O35648
QALKYFNL	QALKYFNL	8	11.4	0.04	19960000	YES	100420000	YES	70000000	YES	Q9Z2G6
QALSRFPVM	QALSRFPVM	9	235.4	0.6	97775.5106	NO	2015900	YES	66467	YES	Q91VH2
QGQIYVHL	QGQIYVHL	8	99.7	0.3		YES		YES		YES	Q922H4
QGYTVARI	QGYTVARI	8	157.2	0.4		YES		YES		YES	Q9Z2G6
QIIPFKTL	QIIPFKTL	8	139.6	0.4	37205410.6	YES	137410000	YES	50332000	YES	Q8BVY0
QIVSFYRV	QIVSFYRV	8	98.7	0.3	499725.917	NO	3389100	NO	714870	YES	Q8BUR4
QIYARQYYM	QIYARQYYM	9	162.3	0.5	594069.683	NO	426660	YES		YES	Q9JJK5
QIYDIFQKL	QIYDIFQKL	9	76.4	0.25	212811.022	YES	95679000	YES	136110	NO	P60843
QIYYYHNV	QIYYYHNV	8	7	0.02		YES		YES		YES	Q6WKZ8
QNAVYINL	QNAVYINL	8	52.3	0.175		YES	6268600	YES	422970	YES	Q3U0M1
QNHVFPLL	QNHVFPLL	8	48.9	0.15	3090907.44	YES	51268000	YES	10677000	YES	Q7TMY7
QNPNYYNL	QNPNYYNL	8	16.9	0.05	1875500	YES	2084800	YES	2953300	YES	Q6P4T2
QNPRFSKL	QNPRFSKL	8	28	0.08		YES		YES		YES	Q8BFT2
QNYEMPNL	QNYEM(+15.99)PNL	8	34.5	0.1	5676400	YES	23478000	YES	75330000	YES	P0DP99
QNYEMPNL	QNYEMPNL	8	34.5	0.1	483130	YES	64019000	YES	15229000	YES	P0DP99
QNYLFGCEL	QNYLFGC(+119.00)EL	9	36.3	0.125	142247.962	NO	9810500	NO	1933000	NO	Q61937
QQFIYEKL	QQFIYEKL	8	114.5	0.3	5746711.71	YES	25431000	YES		YES	Q8K2V6

QQIAFKNL	QQIAFKNL	8	82.2	0.25	202285.966	NO	1261100	NO	949770	NO	Q08639:Q64163
QQYLFDRL	QQYLFDRL	8	13.1	0.04	393189.914	NO	3615700	YES	3796800	NO	Q8BHG1
QQYRFSVI	QQYRFSVI	8	59.4	0.175	1704615	NO	10986000	NO	6041400	NO	Q0GNC1
QQYRFSVIM	QQYRFSVIM(+15.99)	9	181.2	0.5	359200	NO	2008800	NO	2414200	NO	Q0GNC1
QQYVFINQM	QQYVFINQM	9	58.4	0.175	1778469.58	NO	1481400	NO		YES	Q8BGR2
QRVEFAAL	QRVEFAAL	8	381	0.9		YES		YES		YES	E9Q7G0
QSIAFISRL	QSIAFISRL	9	13.5	0.04	18119690.2	YES	73708000	YES	66159000	YES	Q9CR67
QSIEFSRL	QSIEFSRL	8	5.5	0.015	5254200	YES	188430000	YES	22150000	YES	P23116
QSLAFHTL	QSLAFHTL	8	19.7	0.06	507360	YES	21435000	YES		YES	Q91WG4
QSPAFTRQL	QSPAFTRQL	9	69	0.2		YES	536170	YES	208770	YES	Q6ZQ93
QSPEFQSL	QSPEFQSL	8	32.7	0.1	944420	YES		YES	7284600	YES	Q8K1J6
QSPGFYRNV	QSPGFYRNV	9	10.7	0.03	523097.618	YES	5525900	YES	1784200	YES	P32921
QSYEFFHL	QSYEFFHL	8	2.6	0.01	463850	YES	63805000	YES		YES	Q8BHB0
QTFVFHVV	QTFVFHVV	8	139.8	0.4	770430	NO		YES	1294100	NO	A2AAE1
QTLKYLAV	QTLKYLAV	8	287.6	0.7	957499.632	NO	5258500	YES		YES	Q9DBG6
QTYDYRNI	QTYDYRNI	8	20.8	0.06	330510	NO	14079000	NO	41363000	NO	Q9JHI7
QVVEFKKL	QVVEFKKL	8	449.9	1	1110233.7	YES	1734000	YES	433180	NO	Q62559
QVVQFNRL	QVVQFNRL	8	36.9	0.125	2988071.96	YES	26351000	YES		YES	O88653
QVYGFLEV	QVYGFLEV	8	191.7	0.5	768960	NO	36730000	YES		YES	Q9CQE7
RAFDYFNL	RAFDYFNL	8	5.8	0.015	3266312.05	YES	23216000	YES		YES	Q9Z2G6
RAFEFTYV	RAFEFTYV	8	10.4	0.03		YES	30650000	YES	29351000	NO	Q8VDR7
RAFSFRTV	RAFSFRTV	8	15.3	0.05	1576400	YES	45215000	YES	3954900	NO	P46735
RAFVFDVL	RAFVFDVL	8	52.6	0.175		YES	2349400	YES		YES	Q9DC50
RAIAFQHL	RAIAFQHL	8	11.2	0.04	2728918.75	YES	19771000	YES	19342000	YES	Q7TPV4
RALNYTHL	RALNYTHL	8	8.8	0.025		YES	6634100	YES	3045500	YES	Q6PFD9
RAPAFHQL	RAPAFHQL	8	65	0.2	1423687.16	YES	11701000	YES	3290100	YES	Q3UHH1
RAPSYRTL	RAPSYRTL	8	60.3	0.175	1515654.8	YES	3742000	YES		YES	Q924W7
RAPVYARI	RAPVYARI	8	25	0.08	32588720.6	YES	4311100	YES	3352300	YES	P52840

RAVEYNTL	RAVEYNTL	8	140.1	0.4	42497.5427	NO		YES		YES	
RAVLFVGL	RAVLFVGL	8	31.2	0.09	20940	YES	3377300	YES		YES	P47758
RAYFFVEV	RAYFFVEV	8	40.5	0.125	96190.1302	NO		YES		YES	
RAYLFAHV	RAYLFAHV	8	2.5	0.01	2292900	YES	58967000	YES	13272000	YES	Q5SWD9
RAYLFNSV	RAYLFNSV	8	7	0.02	763340	YES	34049000	YES	31992000	YES	Q65Z95:Q65Z93
RGFEFTLM	RGFEFTLM	8	18.5	0.06		YES	54087000	YES		YES	O55131
RGLDYFSSL	RGLDYFSSL	9	14.6	0.05	309920	YES		YES		YES	B1AZA5
RGLDYYTGV	RGLDYYTGV	9	32.3	0.1	208160.054	NO		YES	107980	YES	Q61035:Q99KK9
RGPTYVNM	RGPTYVNM	8	78.8	0.25	514527.995	YES	7860700	YES	3316600	YES	Q8K2K6
RGYAFVTF	RGYAFVTF	8	99.6	0.3	572020	YES		YES		YES	Q5YD48:Q7TMK9
RGYDFAAV	RGYDFAAV	8	6.8	0.02		YES	2320700	YES		YES	Q9QXY6
RGYEFIVRL	RGYEFIVRL	9	14.8	0.05	316510	NO	8938600	YES		YES	Q9JKK8
RGYEFLGV	RGYEFLGV	8	15.9	0.05		YES	29871000	YES	6673800	YES	Q8K3B1
RGYIFSLV	RGYIFSLV	8	7.5	0.02		YES		YES		YES	Q8VDR9
RGYSFTTT	RGYSFTTT	8	277.1	0.7	1137000	YES	13746000	YES	14272000	YES	P60710:P63260
RGYSFTTTA	RGYSFTTTA	9	360.9	0.8	335450	YES		YES	14615000	YES	P60710:P63260
RGYSYDLKV	RGYSYDLKV	9	330.6	0.8		YES	1653900	YES		YES	O55234
RIFDFQGL	RIFDFQGL	8	7.2	0.02	1180426.7	YES	2014700	YES		YES	Q9DBL1
RIILFDRL	RIILFDRL	8	29	0.09	520430	NO	8262800	YES		YES	Q8BM85
RIYDITNV	RIYDITNV	8	379.5	0.9	34625.5644	NO		YES		YES	Q61502:Q8R0K9
RIYGFTAV	RIYGFTAV	8	13.3	0.04	2799300	YES		YES		YES	Q69ZR2
RIYGKFLGL	RIYGKFLGL	9	19.2	0.06	13972000	NO	45415000	NO	2017800	YES	Q60996:Q61151:Q6PD03
RNFIFSRL	RNFIFSRL	8	2.9	0.01	376720	NO	40867000	YES	6231000	YES	Q60848
RNIHYNSV	RNIHYNSV	8	386.2	0.9		YES	336660	YES	482900	YES	Q3U2S4
RNLEFHEL	RNLEFHEL	8	79.3	0.25	8936559.35	YES	31724000	YES	8032400	YES	Q8CCN5
RNLQFVGV	RNLQFVGV	8	66.8	0.2	105890	YES	5556900	YES		YES	Q8BX02
RNPQFQKL	RNPQFQKL	8	93.2	0.25	1537468.39	YES	2131900	YES		YES	P06745
RNPTFKVL	RNPTFKVL	8	415.2	0.9		YES		YES		YES	Q08288

RNPTFMGL	RNPTFM(+15.99)GL	8	12.1	0.04	6459300	YES	12637000	YES	18217000	NO	P17427
RNQVYTQL	RNQVYTQL	8	49	0.15	9031200	YES	4265100	YES	22223000	YES	Q91ZV0
RNVESYTKL	RNVESYTKL	9	327.9	0.8	101370	YES	6159700	YES	3649200	YES	Q91YQ5
RNYEYLIRL	RNYEYLIRL	9	11.9	0.04	18009000	YES	144190000	YES	12631000	YES	Q8R3L2
RNYLHYSL	RNYLHYSL	8	6.6	0.02	523175.524	NO	7273400	YES		YES	P14685
RNYQFDFL	RNYQFDFL	8	11.1	0.04	7670600	YES	245290000	YES	2347000	YES	Q8K4Z5
RNYSYEKL	RNYSYEKL	8	11.6	0.04	2583200	YES	232040000	YES	156990000	YES	Q02257
RQYIFSKL	RQYIFSKL	8	6.8	0.02	1073400	YES	185760000	YES	13740000	YES	Q80SU7
RQYMFSSL	RQYMFSSL	8	4	0.01	8404074.1	YES	9799300	YES	3452900	NO	P27641
RSFDFIHL	RSFDFIHL	8	4	0.01	4750687.73	YES	26675000	YES		YES	A2RSY6
RSIDQFANL	RSIDQFANL	9	10.9	0.03	348980	YES	7410300	YES		YES	Q8VC85
RSISFSNM	RSISFSNM(+15.99)	8	6.2	0.015	39677	NO	334580	YES	7228800	YES	O35242
RSIWFQQL	RSIWFQQL	8	7.2	0.02	197520	YES	4651600	YES		YES	Q9CWP6
RSLKFYSL	RSLKFYSL	8	5.7	0.015	4659700	NO	59177000	NO	25266000	NO	Q99KP6
RSLQFPEL	RSLQFPEL	8	15.3	0.05		YES		YES		YES	Q8CHI8
RSPAFTSRL	RSPAFTSRL	9	19	0.06	1022044.48	NO	6719300	YES	3207300	NO	Q7TMY8
RSPEYLSL	RSPEYLSL	8	28.5	0.09	12999729.5	YES	60241000	YES	19620000	YES	Q9JLV5
RSPKYLEL	RSPKYLEL	8	58	0.175	4948957.66	YES		YES		YES	Q7TPV4
RSPWFTTL	RSPWFTTL	8	11	0.03	5107106.17	YES	13490000	YES		YES	P10404
RSTIFYYV	RSTIFYYV	8	160.4	0.4	578722.266	NO	3427500	YES		YES	Q69ZR2
RSYDFEFM	RSYDFEFM	8	21.5	0.07	12712000	YES	164560000	YES	9099500	YES	P40336
RSYDFEFM	RSYDFEFM(+15.99)	8	21.5	0.07	9694000	YES	108350000	YES	4269300	YES	P40336
RSYLFLGGI	RSYLFLGGI	9	9.4	0.025		YES	24464000	YES	681470	YES	Q9D2C7
RSYNMPSL	RSYNMPSL	8	23	0.07	1023875.26	YES	2064200	YES		YES	Q91ZV0
RSYQQALL	RSYQQALL	8	13.6	0.04		YES	6597600	YES	2410500	YES	Q9ERC3
RSYSFLNSSL	RSYSFLNSSL	10	18.3	0.06	180990.451	NO	7783200	YES	9934300	YES	Q9D7J6
RSYSFQKV	RSYSFQKV	8	6.4	0.015		YES	1321500	YES	5133000	YES	Q8CI75
RSYVFSSL	RSYVFSSL	8	2.2	0.01		YES	3773300	YES		YES	Q91VM4

RTFEFQLM	RTFEFQLM	8	16.3	0.05	240327.305	NO	8332600	YES		YES	Q8C5N5
RTGTYRQL	RTGTYRQL	8	371.7	0.9	444310	YES	1043600	YES		YES	P68373:P05213
RTLIYITL	RTLIYITL	8	61.4	0.175	11658000	YES		YES		YES	Q9JM76
RTTEFTNL	RTTEFTNL	8	37.5	0.125	109050	YES	1858700	YES		YES	O35231
RTYSFLNL	RTYSFLNL	8	2.9	0.01	1877700	YES	18415000	YES		YES	Q810L4
RTYTYEKL	RTYTYEKL	8	9.4	0.03	15970000	YES	857150000	YES	1299800000	YES	Q02248
RVAEFTTNL	RVAEFTTNL	9	132.4	0.4	173640	YES	101240000	YES	119620000	YES	Q8VDD5
RVDVFTNL	RVDVFTNL	8	115.5	0.3	2554098.42	YES	16254000	YES	5811000	YES	Q5U4D9
RVFNYNTL	RVFNYNTL	8	10.5	0.03	286096.886	NO		YES		YES	O55029
RVIDFFTV	RVIDFFTV	8	373.1	0.9		YES	38810000	YES	1509700	YES	Q80Y17
RVIDFTVL	RVIDFTVL	8	246.4	0.6	9923000	YES		YES		YES	Q3TJ91
RVIDFVAQV	RVIDFVAQV	9	107.5	0.3	169390.297	NO	3963600	YES	3535200	YES	E9PYK3
RVLEYLAV	RVLEYLAV	8	359.9	0.8	359420	YES	628370	YES		YES	Q9DBN5
RVLIFSQM	RVLIFSQM	8	42.3	0.125		YES	56619000	YES	22278000	YES	Q6PDQ2
RVLIFSQM	RVLIFSQM(+15.99)	8	42.3	0.125	1802100	YES	26779000	YES	128460000	YES	Q6PDQ2:Q91ZW3:Q6PGB8:A2AJK6:P40201
RVLLFSQM	RVLLFSQM	8	31.8	0.09		YES	56619000	YES	22278000	YES	Q9CXF7
RVLLFSQM	RVLLFSQM(+15.99)	8	31.8	0.09	1802100	YES	26779000	YES	128460000	YES	Q9CXF7
RVMEYINRL	RVMEYINRL	9	78.4	0.25	418950	YES	74227000	YES		YES	Q68FD5
RVYEFLDKL	RVYEFLDKL	9	34.9	0.125	14797000	YES	99013000	YES	1817000	YES	P14685
SAARFALL	SAARFALL	8	5.9	0.015	414870	NO		YES	67638000	YES	Q924N4
SAFEFNEL	SAFEFNEL	8	5.6	0.015		YES		YES		YES	Q9Z2C4
SAFIFRVL	SAFIFRVL	8	5.5	0.015		YES	10932000	YES		YES	Q9R0A1
SAFRFAVQL	SAFRFAVQL	9	8.5	0.025	516397.731	NO	19095000	YES		YES	Q9Z2W9
SAFSFRTL	SAFSFRTL	8	3.3	0.01	5522200	YES	42711000	YES	209650000	YES	Q8BMI0
SAHIFSNL	SAHIFSNL	8	4.3	0.01	1432700	YES		YES		YES	Q9DBB9
SAIHAVNL	SAIHAVNL	8	214.4	0.6	204770	YES	3539100	YES	1732900	YES	Q9JJ28
SALAFGQGL	SALAFGQGL	9	30.4	0.09	73527.3709	NO	788180	NO		YES	Q80U78

SALFFHYL	SALFFHYL	8	10.4	0.03		YES	14824000	YES	826850	YES	Q6WKZ8
SALKYYQL	SALKYYQL	8	6.4	0.015	760870	YES	20860000	YES	4017300	YES	Q6ZPU9
SALPFVKL	SALPFVKL	8	19.3	0.06	95329.2725	NO		YES		YES	Q0VGY8
SALRFLNL	SALRFLNL	8	3.3	0.01	347710	YES	36995000	YES	36290000	YES	Q3TAA7
SALTFAGL	SALTFAGL	8	2.8	0.01	2855600	YES	3855700	YES	447120	YES	Q9CXV1
SALVFTRL	SALVFTRL	8	3.6	0.01	4060833.03	YES		YES	109510000	YES	Q9JHJ3
SAMVFSAM	SAM(+15.99)VFSAM(+15.99)	8	8.4	0.025	1023500	NO	13695000	NO	61537000	NO	P63082
SANIFRTL	SANIFRTL	8	52.8	0.175		YES		YES	2409800	YES	Q6PD03
SAPIYKRI	SAPIYKRI	8	197.1	0.5		YES	1088800	YES		YES	Q9CSH3
SAPKFPSSGL	SAPKFPSSGL	10	272	0.7	552351.197	YES		YES		YES	P70295
SAPLYTNL	SAPLYTNL	8	4.6	0.01	1435700	NO	2188100	NO	12994000	YES	Q8K4S1
SAPRFLTAF	SAPRFLTAF	9	56.3	0.175	476782.698	YES	8143600	YES		YES	Q3TQR0
SAPTFINF	SAPTFINF	8	67.5	0.2		YES	8805500	YES		YES	Q9CQY5
SAPVFDRL	SAPVFDRL	8	22.3	0.07		YES	2263300	YES		YES	A2AIV2
SAPVFKEKL	SAPVFKEKL	9	118.3	0.4	776407.903	YES	1985900	YES	2081900	YES	Q6PDN3
SAPWYLNRV	SAPWYLNRV	9	53.6	0.175	18719	NO	2089200	YES	598660	YES	P29416
SASHFSQL	SASHFSQL	8	56.7	0.175	79561.165	NO		YES		YES	Q3TLH4
SATAFQRI	SATAFQRI	8	245.8	0.6	1050000	YES		YES		YES	Q91VS7
SATTFRLL	SATTFRLL	8	31.7	0.09	789350	YES	5742100	YES		YES	P01027
SATVFRTV	SATVFRTV	8	178	0.5	440244.939	YES	4323100	YES	3979600	YES	Q8CDD8
SAVIFRTL	SAVIFRTL	8	13.2	0.04	5686600	YES	66144000	YES	147100000	YES	A2AT37
SAVSFHSL	SAVSFHSL	8	17.6	0.05		YES		YES	2834100	YES	Q8BZT9
SAYEFYHA	SAYEFYHA	8	13	0.04	3024142.28	YES	39530000	YES	31735000	YES	P97481
SAYEFYHAL	SAYEFYHAL	9	2.8	0.01	1093200	YES	596940000	YES	304430000	YES	P97481
SAYEVIKL	SAYEVIKL	8	56.8	0.175	4865800	YES	45863000	YES	2072600	YES	P06151:P16125
SAYLFVKL	SAYLFVKL	8	3	0.01	1378462.92	YES	18493000	YES		YES	B9EJ80
SAYLYKQGF	SAYLYKQGF	9	26.3	0.08	29469	YES	622800	YES		YES	Q9D8U2
SAYNAFNRF	SAYNAFNRF	9	43.1	0.15	399071.792	YES	121840	YES		YES	Q9D1C8

SAYNYAEQTM	SAYNYAEQTM	10	123.5	0.4		YES	1025900	YES		YES	Q8VE92
SAYNYAEQTM	SAYNYAEQTM(+15.99)	10	123.5	0.4	1831500	YES	1909700	YES	3082000	YES	Q8VE92
SAYQRGESL	SAYQRGESL	9	233.2	0.6	290970	YES	1419000	YES	4757600	YES	O35382
SAYRFSGV	SAYRFSGV	8	2.5	0.01	1681515.97	NO	1449100	NO	2430800	NO	Q8CJF7
SDYVYPSL	SDYVYPSL	8	39.5	0.125	6086.5	NO		YES	11981000	YES	Q9WTU0
SFYEHIITV	SFYEHIITV	9	141.5	0.4	488000	NO	29851000	YES	4511200	YES	Q8BGZ3
SFYNELRV	SFYNELRV	8	464.1	1		YES	6560700	YES	536460	YES	P63268
SGFSFRGV	SGFSFRGV	8	6.9	0.02	596562.665	YES		YES		YES	P23188
SGFVFTRL	SGFVFTRL	8	2.5	0.01	6137300	YES	38898000	YES	2912400	YES	Q6PCN7
SGIDFKQL	SGIDFKQL	8	68.8	0.2	6127900	YES	115270000	YES	11335000	YES	O55222
SGLIFNKV	SGLIFNKV	8	97.9	0.3	94128	YES	2912400	YES	724800	YES	P70279
SGLIFTKI	SGLIFTKI	8	97.7	0.3		YES	5732000	YES		YES	P55284
SGLKYVAV	SGLKYVAV	8	39.3	0.125	2102600	YES	7001900	NO	42053000	YES	Q923D2
SGLKYVNV	SGLKYVNV	8	14.6	0.05	14281000	YES	75444000	YES	65593000	YES	Q8VCP8
SGLLFRSL	SGLLFRSL	8	6.5	0.02	7230300	YES		YES		YES	Q9R1S7
SGLLFTHL	SGLLFTHL	8	4.1	0.01	1609647.99	YES	6220800	YES		YES	P58158
SGLTYIKI	SGLTYIKI	8	186.5	0.5	5041665.4	YES	15119000	YES	6071100	YES	O88738
SGLVFVQV	SGLVFVQV	8	32.7	0.1		YES		YES		YES	O35604
SGPEYLKRL	SGPEYLKRL	9	121.3	0.4	71186.3055	NO	537930	NO	222540	NO	Q02395
SGPTYIKL	SGPTYIKL	8	33.3	0.1	1526300	YES		YES	23130000	YES	Q6NSR3
SGVDYRGV	SGVDYRGV	8	431.9	1	1967600	YES	698820	NO	1520400	NO	P62313
SGVEYTRL	SGVEYTRL	8	14.1	0.04	366880	YES	1422400	YES	2921000	YES	Q62178
SGVVYSVGM	SGVVYSVGM(+15.99)	9	137.1	0.4	385360	NO	101610	NO	92725	NO	P11276
SGYDFENRL	SGYDFENRL	9	14.2	0.04	59060000	YES	65547000	YES	15536000	YES	Q8VE09
SGYDFSRL	SGYDFSRL	8	3.6	0.01	6539700	YES	26764000	YES	45159000	YES	Q6GQT6
SGYDYYHV	SGYDYYHV	8	6.9	0.02	995946.079	YES		YES	450710	YES	O08785
SGYFHPLL	SGYFHPLL	8	12.1	0.04	5902912.58	YES	4343800	YES	4480500	YES	P10518
SGYHYGLL	SGYHYGLL	8	3.7	0.01	4264556.35	YES	4061800	YES	18907000	YES	P45448

SGYHYNAL	SGYHYNAL	8	4.2	0.01	30537000	YES		YES		YES	Q60641
SGYIYHKL	SGYIYHKL	8	4.8	0.01	684360	YES	53924000	YES	134540000	YES	Q9EPU0
SGYKFFSL	SGYKFFSL	8	2.6	0.01	48314000	YES	105830000	YES	2688800	YES	Q80W47
SGYKFGVL	SGYKFGVL	8	4.6	0.01	2956800	NO	140980000	NO	148490000	YES	Q9D902
SGYKYVGM	SGYKYVGM	8	4.8	0.01	796140	YES	20298000	YES	1583400	YES	Q91XB7
SGYKYVGM	SGYKYVGM(+15.99)	8	4.8	0.01	5634600	YES	9435100	YES	57970000	YES	Q91XB7
SGYQFIHA	SGYQFIHA	8	25.9	0.08	1033535.57	YES	1586700	YES		YES	P30561
SGYQYKRL	SGYQYKRL	8	4.4	0.01	216060	YES	1117200	YES	204340	YES	O88974
SGYSFTHI	SGYSFTHI	8	4.5	0.01	708570	YES	7118300	YES	2177000	YES	Q9D864
SHYDFGLRAL	SHYDFGLRAL	10	147.1	0.4	1339821.7	YES	30271000	YES	11295000	NO	Q9JHU4
SIAAFIQRL	SIAAFIQRL	9	47.7	0.15		YES	253990000	YES	24752000	YES	Q9Z1R2
SIANFTNV	SIANFTNV	8	31.2	0.09	13411000	YES	15193000	YES	5616400	YES	Q91V92
SIFEFVHA	SIFEFVHA	8	36.6	0.125	169980	NO		YES		YES	Q91YE6
SIIALVRTL	SIIALVRTL	9	448.5	1		YES	594990	YES		YES	Q9CYV5
SIIKATNL	SIIKATNL	8	83.5	0.25	2365021.36	YES	8149900	YES	10832000	YES	Q80X82
SIINFIERL	SIINFIERL	9	21.3	0.06	680440	YES	33760000	YES		YES	Q9QZ09
SILALTHL	SILALTHL	8	47.9	0.15	183990	NO		YES		YES	Q6P5B0
SILQYSNV	SILQYSNV	8	6.8	0.02	288520	NO	646740	NO	1596300	YES	Q9WUE4
SILTYSRI	SILTYSRI	8	12.8	0.04		YES		YES		YES	Q8VD65
SIMAFHKL	SIMAFHKL	8	14.8	0.05	66006	YES	4815200	YES		YES	Q7TPM9
SITKFLNRI	SITKFLNRI	9	195.8	0.5	332719.534	YES	3509900	YES	4012700	NO	Q7TNB8
SITSFPRL	SITSFPRL	8	15.6	0.05		YES		YES	4986200	YES	Q99JP7
SIVQFYYM	SIVQFYYM	8	20.1	0.06	523840	YES	17244000	YES		YES	Q9R190
SIVQFYYM	SIVQFYYM(+15.99)	8	20.1	0.06	1600400	YES	29424000	YES	23029000	YES	Q9R190
SIVSYNHL	SIVSYNHL	8	10.2	0.03	2361400	YES	23392000	YES	64640000	YES	Q9JHU9
SIYAPARL	SIYAPARL	8	7.8	0.02		YES		YES	5800200	YES	P51944
SIYAREALI	SIYAREALI	9	53.6	0.175	998906.495	NO	14465000	YES		YES	Q9CU62
SIYEKLIQF	SIYEKLIQF	9	89.8	0.25	6771171.27	YES	28208000	YES		YES	Q02614

SIYEYYHAL	SIYEYYHAL	9	3.2	0.01	42700.0975	NO	6213200	YES	453050	YES	Q61221
SIYIPRGV	SIYIPRGV	8	224.8	0.6	1345625.68	YES	10569000	YES		YES	P50516
SIYLPQKL	SIYLPQKL	8	67.2	0.2	64955	NO		YES		YES	Q8CFG9:Q8CG16
SIYPAPQV	SIYPAPQV	8	333.3	0.8	1482400	YES		YES	215330	NO	P68373:P05213:P68368
SLILFSTRL	SLILFSTRL	9	47	0.15		YES	8325200	YES	14659000	YES	Q9QUK4
SLNERFTNM	SLNERFTNM	9	311.4	0.8	1302699.65	NO	1036000	NO		YES	Q9CY57
SLVEFVHV	SLVEFVHV	8	356.1	0.8	541870	YES		YES	117170	YES	Q9D665
SLVIFMQL	SLVIFM(+15.99)QL	8	46.8	0.15	853480	YES	2818700	YES	113460	YES	Q9R049
SLVIFMQL	SLVIFMQL	8	46.8	0.15		YES		YES		YES	Q9R049
SLVTFRTL	SLVTFRTL	8	85.4	0.25	680340	YES	59377000	YES	8219400	YES	Q9QXS1
SLYSLPKL	SLYSLPKL	8	202.4	0.5	377526.979	NO		YES	1673300	YES	Q8C726
SMYVPGKL	SM(+15.99)YVPGKL	8	85.4	0.25	3819700	YES	46563000	YES	498200	YES	Q9WU28
SMFEFSEKL	SMFEFSEKL	9	22	0.07	254821.655	NO	1793400	YES		YES	Q60674
SMVSLRAL	SMVSLRAL	8	280.7	0.7	1229974.71	YES		YES		YES	P48758
SMYVPGKL	SMYVPGKL	8	85.4	0.25	4934155.58	YES	43835000	YES	4375000	YES	Q9WU28
SNFHFAVL	SNFHFAVL	8	3.4	0.01	600020	NO	14741000	YES		YES	Q80TY5
SNFNYERSL	SNFNYERSL	9	20	0.06		YES		YES	959480	YES	O35841
SNFQPPKL	SNFQPPKL	8	415.5	0.9	335566.986	NO	3280400	YES	391730	NO	Q8BPM2:Q99JP0
SNHVFNAL	SNHVFNAL	8	11	0.04	1783900	YES	48367000	YES	19966000	YES	Q9DBU3
SNIHYHTL	SNIHYHTL	8	23.9	0.07	25335.3133	NO	1614300	YES	192770	YES	Q9D0N7
SNIQYITRF	SNIQYITRF	9	115	0.3	909431.833	YES	3853100	YES	3129000	YES	Q9JM13
SNIRAGNL	SNIRAGNL	8	70.7	0.2	167230	YES		YES		YES	Q78PY7
SNLELHSL	SNLELHSL	8	485	1.1	376170	YES	10935000	NO	1782800	NO	P70195
SNLKYILV	SNLKYILV	8	44.9	0.15	714940.329	YES	32359000	YES	46739000	YES	A2AWL7
SNLRYLSL	SNLRYLSL	8	6.4	0.015	48725	NO	11804000	YES	4033300	NO	Q99MB1
SNLYYKYL	SNLYYKYL	8	9.4	0.03	319884.574	NO	6849800	YES	3354200	YES	O88845
SNPEFAFL	SNPEFAFL	8	6.3	0.015	494233.568	YES	125970000	YES		YES	Q62077
SNPEFRQL	SNPEFRQL	8	17.3	0.05	2551900	YES	29116000	YES	60359000	YES	Q3UWM4

SNPEFSSV	SNPEFSSV	8	44.6	0.15	1656000	NO	2817500	YES	5802900	YES	P26039
SNPEYAKI	SNPEYAKI	8	69.8	0.2		YES		YES		YES	Q99PP2
SNTMYARL	SNTMYARL	8	5.3	0.015		YES		YES	155670	YES	Q8JZN5
SNTQYARL	SNTQYARL	8	7.7	0.02	2148900	YES	980380	YES	1472100	YES	P50544
SNVAREAAL	SNVAREAAL	9	201.8	0.5	39291.7244	NO		YES	261870	YES	Q99JY0
SNVDFLLRL	SNVDFLLRL	9	32.9	0.1		YES	2292800	YES	25806	YES	Q99MR8
SNVKHVINF	SNVKHVINF	9	436.4	1	9959850.32	YES	9310000	YES	1473600	YES	Q62167
SNVKYVML	SNVKYVM(+15.99)L	8	16.8	0.05	5565970.56	NO	9099000	YES	22452000	YES	Q61115
SNVKYVML	SNVKYVML	8	16.8	0.05	697450.507	NO	3204700	YES		YES	Q61115
SNVLYQHNL	SNVLYQHNL	9	35.7	0.125	65885	YES	4445500	YES	1143800	YES	P42227
SNYDHAYL	SNYDHAYL	8	5.3	0.015	227293.686	NO	1753300	YES		YES	Q9QXN0
SNYERLESL	SNYERLESL	9	64.4	0.2	304930	YES	17591000	YES	869350	YES	P43883
SNYHFYSSI	SNYHFYSSI	9	3.9	0.01	3121900	YES	163830000	YES	4199100	YES	Q60795
SNYLFTKL	SNYLFTKL	8	2.4	0.01	556550000	YES	3308400000	YES	4708700000	YES	P97481
SNYLHRVV	SNYLHRVV	8	57.5	0.175	119980	YES	2430200	YES	5207700	YES	Q78JE5
SNYLYREV	SNYLYREV	8	5.5	0.015	745050.871	YES		YES	1470500	YES	Q9EPL0
SNYNFEKPF	SNYNFEKPF	9	33.6	0.1	191632.366	NO	1135700	YES		YES	P62827
SNYQHITNF	SNYQHITNF	9	98.7	0.3	913490	YES	20981000	YES		YES	O54774
SNYQMHLL	SNYQMHLL	8	20.2	0.06	584721.003	NO	2884900	YES	699330	NO	Q3TEA8
SNYRFEGL	SNYRFEGL	8	2.9	0.01	646910	NO	8535700	NO	2296500	YES	F8VPZ5
SNYSYPQV	SNYSYPQV	8	5.6	0.015	4328200	YES	7480300	YES	50569000	YES	Q61545
SNYVFVFL	SNYVFVFL	8	2.6	0.01	5415600	YES		YES		YES	Q9Z0S9
SQFKYALV	SQFKYALV	8	6.4	0.015	2603607.48	NO	12248000	NO	5488900	YES	Q9QXB9
SQHNFNNL	SQHNFNNL	8	28.6	0.09	147120	YES	590980	YES		YES	Q69ZB8
SQLEFRQNL	SQLEFRQNL	9	23.5	0.07	30034.9728	NO		YES		YES	Q80UK0
SQQLYRHI	SQQLYRHI	8	459.7	1	463149.205	YES	1532800	YES	3223600	YES	Q6ZQ18
SQQLYRHL	SQQLYRHL	8	36.4	0.125	463149.205	YES	1532800	YES	3223600	YES	Q8BM75
SQQTYYRV	SQQTYYRV	8	234.3	0.6		YES	564190	YES		YES	P48410

SQQYYHSL	SQQYYHSL	8	180	0.5	30400	NO	2005100	YES	1197000	YES	Q69Z38
SQYLFPKL	SQYLFPKL	8	4.5	0.01	1910519.69	YES	13704000	YES	4180300	YES	P35396
SQYQRFTYL	SQYQRFTYL	9	5.6	0.015	260508.768	NO	1743000	YES	277170	YES	O88942
SQYRFEHL	SQYRFEHL	8	3.8	0.01	1241855.33	NO	12725000	YES	8898200	NO	Q3UJK4
SQYVFTEM	SQYVFTEM(+15.99)	8	7.8	0.02	2131600	NO	21620000	NO	96687000	NO	Q5SYH2
SRIVFRHL	SRIVFRHL	8	44.5	0.15	2009498.84	YES	7202800	YES	9002700	NO	Q9CR88
SRYQFRNL	SRYQFRNL	8	6.2	0.015	1914687.64	YES	3104300	YES	264880	NO	Q8R035
SSATTFRL	SSATTFRL	8	309.9	0.8	143290	YES	1611600	NO		YES	P01027
SSFAHAQV	SSFAHAQV	8	7.1	0.02	419132.502	YES		YES		YES	Q9EQQ9
SSFEPRSL	SSFEPRSL	8	100.8	0.3	959018.792	YES		YES		YES	Q99MJ9
SSFSHYSGL	SSFSHYSGL	9	2.9	0.01		YES		YES		YES	Q9CY58
SSFSRVTNF	SSFSRVTNF	9	66.3	0.2	249169.598	NO		YES	201360	NO	Q8BYH7
SSFSSPHM	SSFSSPHM(+15.99)	8	88.2	0.25	507360.673	NO	487160	YES	12962000	NO	O88291
SSFVFSTV	SSFVFSTV	8	2.9	0.01	12189000	YES	35991000	YES		YES	Q01237
SSHSFPQL	SSHSFPQL	8	8.5	0.025	6365672.26	YES		YES	39601000	YES	Q8K371
SSHSFVNV	SSHSFVNV	8	8	0.025	229360	YES	3747400	YES	5198900	YES	E9Q5F9
SSIFFREL	SSIFFREL	8	6.5	0.02	29841766.7	YES	21128000	YES		YES	P45448
SSINFLTRV	SSINFLTRV	9	10	0.03	506425.805	NO	2470200	YES	4395200	YES	Q8K409
SSIRQPSL	SSIRQPSL	8	238.9	0.6		YES		YES	1930700	YES	Q9R190
SSIRYFEI	SSIRYFEI	8	20.7	0.06	642760.727	NO		YES	1844300	YES	Q9WUM4:Q9WUM3:O8905 3
SSISHSVL	SSISHSVL	8	77.1	0.25		YES	483270	YES		YES	Q99K28
SSIVFAEL	SSIVFAEL	8	2.7	0.01	1979400	YES	2774200	YES		YES	Q9Z2R9
SSLHFSFL	SSLHFSFL	8	4.4	0.01		YES		YES		YES	Q80TN4
SSLHPMGGL	SSLHPM(+15.99)GGL	9	369	0.9	1168200	NO	3524900	YES	5266600	NO	P28659
SSLHPMGGL	SSLHPMGGL	9	369	0.9	70476	NO	4683000	YES	484870	NO	P28659
SSLLFVKL	SSLLFVKL	8	5.6	0.015	714784.518	YES	28252000	YES	25985000	YES	Q80ZV0
SSLPKRLAL	SSLPKRLAL	9	287.6	0.7	87791.899	NO	1396500	NO	469880	NO	Q8R1F0

SSLSFNTRL	SSLSFNTRL	9	10.9	0.03	210060	YES	5006300	YES		YES	Q5SSN7
SSLVKVNL	SSLVKVNL	8	85.4	0.25	356640.469	NO	1547400	YES	578280	YES	Q9QYC0
SSLYFRDL	SSLYFRDL	8	7	0.02	1679139.85	YES		YES	1659100	YES	Q9DCM7
SSMAYPNL	SSM(+15.99)AYPNL	8	3.8	0.01	665390	NO	586060	NO	2868500	NO	Q61249
SSPAFSKV	SSPAFSKV	8	26.3	0.08	396440	YES	193390	YES	422310	YES	Q99M02
SSPEYEAL	SSPEYEAL	8	20.8	0.06		YES		YES		YES	Q8R242
SSPHYTTL	SSPHYTTL	8	12.2	0.04	18334000	YES	11403000	YES	33812000	YES	P27046
SSPKFSEI	SSPKFSEI	8	53.5	0.175	11409000	NO	151370000	NO	51956000	NO	Q91VM3
SSPKFSEL	SSPKFSEL	8	9.3	0.025	11409000	NO	151370000	NO	51956000	NO	A2AGT5
SSPKYDYL	SSPKYDYL	8	27.6	0.08	2941133.79	YES		YES	4066700	YES	Q7TQG1
SSPVFKAM	SSPVFKAM	8	22.9	0.07	53924	NO	1125000	YES	225100	NO	Q9Z2X8
SSPVFKAM	SSPVFKAM(+15.99)	8	22.9	0.07	559910	NO	500250	YES	1487500	NO	Q9Z2X8
SSPVFKAMF	SSPVFKAM(+15.99)F	9	37.9	0.125	907940	NO	7465000	YES	10939000	NO	Q9Z2X8
SSPVFKAMF	SSPVFKAMF	9	37.9	0.125	202210	NO	13474000	YES	1651300	NO	Q9Z2X8
SSPVYIDL	SSPVYIDL	8	15.2	0.05		YES	3301900	YES		YES	P13439
SSTHFATL	SSTHFATL	8	7.4	0.02	147550	NO	1736300	YES	1616300	YES	Q6S5J6
SSTYFHQL	SSTYFHQL	8	15.4	0.05	337580	YES	4094100	YES	560340	YES	Q8BN78
SSVEYIHRI	SSVEYIHRI	9	182.6	0.5	294440.583	NO	183490	YES	53238	NO	Q8K301
SSVEYNHRL	SSVEYNHRL	9	119.5	0.4	25896	NO		YES	137400	NO	P49935
SSVKYSKI	SSVKYSKI	8	63.6	0.2	112300	NO	87328	NO	456110	NO	Q64511
SSVLYSRV	SSVLYSRV	8	7	0.02	1623700	YES	4247300	YES		YES	Q8CGC7
SSVRFSYM	SSVRFSYM	8	5.1	0.015	378738.413	NO		YES	1179300	YES	Q8R5K4
SSVRPVNL	SSVRPVNL	8	95.8	0.3	62326	YES		YES	179580	YES	Q8CDG3
SSVSFKERL	SSVSFKERL	9	28.3	0.09	165078.218	NO		YES	181650	NO	Q8BTJ4
SSVYFRSV	SSVYFRSV	8	14.4	0.04	1068900	YES	16084000	YES	3159900	YES	Q9D6Y4
SSYAYTKV	SSYAYTKV	8	3.7	0.01	76713.7128	NO		YES	2014600	YES	Q8BG87
SSYFFGKV	SSYFFGKV	8	4	0.01	1481700	YES	6839600	YES	754810	YES	Q7TMS5
SSYKFNHL	SSYKFNHL	8	2.3	0.01	2775584.24	YES	18568000	YES	17621000	YES	Q8K2I1

SSYLHSLL	SSYLHSLL	8	3.2	0.01	64357.8736	NO	1735100	YES	2890500	NO	Q8BWZ3
SSYNTFRL	SSYNTFRL	8	8.6	0.025		YES		YES		YES	Q9EPZ6
SSYNYIRV	SSYNYIRV	8	2.7	0.01	551500	YES	47041000	YES	5415000	YES	Q5SYD0
SSYNYRVV	SSYNYRVV	8	5.4	0.015	638710	YES	8930000	YES		YES	P11881
SSYQHTSV	SSYQHTSV	8	11.8	0.04	565100	YES	93776	YES	429620	YES	Q9CRT8
SSYRFVQNV	SSYRFVQNV	9	3.1	0.01	694256.374	NO	2285200	NO	3669800	NO	P42128
SSYSFRHL	SSYSFRHL	8	2.1	0.01	11488749.1	YES	7244900	YES	5886900	YES	O35448
SSYSFRHLL	SSYSFRHLL	9	4.5	0.01	204062.216	NO	1069900	YES	404220	NO	O35448
SSYTFPKM	SSYTFPKM	8	3.4	0.01	1337600	YES	43571000	YES	6079500	YES	Q9WUR2
SSYTFPKM	SSYTFPKM(+15.99)	8	3.4	0.01	17705000	YES	39878000	YES	81483000	YES	Q9WUR2
SSYTFPKMM	SSYTFPKM(+15.99)M(+15.99)	9	13.7	0.04	675170	YES	2123600	YES	4546800	YES	Q9WUR2
SSYTFPKMM	SSYTFPKMM	9	13.7	0.04	4857808.02	YES	4715300	YES	58298	YES	Q9WUR2
SSYTFPKMM	SSYTFPKMM(+15.99)	9	13.7	0.04	4362717.49	YES	1066600	YES	951970	YES	Q9WUR2
SSYVHSNL	SSYVHSNL	8	3.2	0.01	995460	YES	1668900	YES	13793000	YES	Q6P4T1
SSYVVKKV	SSYVVKKV	8	193.7	0.5	21685.8222	NO	51785	YES	154110	YES	Q4U2R1
STFEFHSI	STFEFHSI	8	16.8	0.05		YES		YES	42125000	YES	O70481
STFFYPKL	STFFYPKL	8	6.9	0.02	673611.372	YES		YES	929860	YES	Q91ZX6
STFSFTKV	STFSFTKV	8	7.7	0.02	171330	YES	30304000	YES	9882700	YES	Q3TZZ7
STFSHKTV	STFSHKTV	8	278.5	0.7	32656.4986	NO	58292	NO	54070	YES	Q78IS1
STFTFADL	STFTFADL	8	2.7	0.01	961620	YES	1780300	YES		YES	Q9ERU9
STFVYNSM	STFVYNSM	8	7	0.02		YES	93050000	YES	1482100	YES	Q61107
STFVYNSM	STFVYNSM(+15.99)	8	7	0.02	3258600	YES	114800000	YES	63565000	YES	Q61107
STIEFKNM	STIEFKNM(+15.99)	8	20.7	0.06	851710	NO	2471900	YES	4413300	YES	Q6NXI6
STIVYYKL	STIVYYKL	8	8.2	0.025	116280	YES	5397200	YES	197140	YES	Q8R3W5
STLIYRNM	STLIYRNM	8	8.3	0.025		YES	4143400	NO	1361200	NO	Q9D8N6
STLIYRNM	STLIYRNM(+15.99)	8	8.3	0.025	1349200	YES	2357700	NO	8092200	NO	Q9D8N6
STLSYRSL	STLSYRSL	8	8.3	0.025	1980206.31	YES		YES		YES	Q80W22
STLTYSRM	STLTYSRM	8	8.3	0.025		YES	35731000	YES	2924300	YES	Q9WVC6

STLTYSRM	STLTYSRM(+15.99)	8	8.3	0.025	857975.139	YES	20508000	YES	55938000	YES	Q9WVC6
STPEFYQV	STPEFYQV	8	40.3	0.125	1347300	NO	26781000	NO	10381000	YES	Q99JY9
STPKYQRL	STPKYQRL	8	13.3	0.04		YES		YES	824260	YES	Q6PGC1
STRLFAVL	STRLFAVL	8	9.8	0.03	5883825.69	YES	27109000	YES		YES	P46978
STTVFHSL	STTVFHSL	8	44.2	0.15	5173325.99	YES		YES		YES	P19096
STVEFTNL	STVEFTNL	8	5.4	0.015		YES	9748800	YES		YES	O54692
STVLLQRL	STVLLQRL	8	164.7	0.5	488624.359	YES		YES	455990	YES	O88907
STVQFHIL	STVQFHIL	8	68.1	0.2	157710	YES		YES	284380	NO	Q9CR50
STYEYVRFI	STYEYVRFI	9	31.4	0.09	54463.8536	NO	2380100	YES	387580	YES	O08785
STYFPHTAI	STYFPHTAI	9	111.7	0.3	3909306.5	YES	6559500	YES		YES	P70255
STYIKFVNL	STYIKFVNL	9	4.1	0.01	120520.071	NO	824830	YES	148640	NO	P17427
STYKFFEV	STYKFFEV	8	6.5	0.02	58662969.2	YES	451740000	YES	189500000	YES	Q9CZM2
STYSHSAL	STYSHSAL	8	6.1	0.015	337919.737	YES	252820	YES	9890900	YES	Q61687
STYSVAKM	STYSVAKM(+15.99)	8	33.1	0.1	375390	NO	369240	YES	16475000	YES	O09159
SVFAFGENKM	SVFAFGENKM	10	377.8	0.9	782874.073	NO	10787000	YES	1785500	NO	Q8BK67
SVFAFGENKM	SVFAFGENKM(+15.99)	10	377.8	0.9	73913	NO	5453600	YES	11256000	NO	Q8BK67
SVIKFENL	SVIKFENL	8	7.1	0.02	30541000	YES	71650000	YES	103480000	YES	Q9CPV7
SVISVIHL	SVISVIHL	8	187.5	0.5	41921.0408	NO		YES		YES	Q8VDP6
SVITVKNL	SVITVKNL	8	319.1	0.8	131550	YES		YES		YES	Q8BGQ4
SVLLFMQL	SVLLFMQL	8	5	0.01		YES		YES		YES	Q9Z0E8
SVLQFLGL	SVLQFLGL	8	8.6	0.025	3989200	YES	2064500	YES		YES	Q9CQC9
SVNIFRTL	SVNIFRTL	8	62.6	0.2	388176.684	NO	6813600	YES		YES	Q6PD28
SVPKFKHL	SVPKFKHL	8	19.3	0.06	1750267.72	YES	190830	YES	361930	YES	Q9QZW0
SVRLAALL	SVRLAALL	8	270.7	0.7		YES		YES	391860	YES	Q91ZU9
SVVAFHNL	SVVAFHNL	8	8.7	0.025	6466700	YES	60109000	YES	29296000	YES	Q71B07
SVVALHNL	SVVALHNL	8	299	0.7	17220.6587	NO		YES		YES	P26516
SVVAYNNL	SVVAYNNL	8	11	0.03	1735800	NO	3440200	NO	2624900	NO	Q99LM9
SVVDYCNRL	SVVDYC(+119.00)NRL	9	67.6	0.2	298495.573	NO	2642800	NO	426500	NO	Q8BU14

SVVEYSRL	SVVEYSRL	8	8.7	0.025	342399.313	NO		YES		YES	G5E8F4
SVVRYVQL	SVVRYVQL	8	11	0.03	851860	YES	30668000	YES	15728	YES	O35900
SVYLVRQL	SVYLVRQL	8	16.2	0.05	59777	YES		YES		YES	Q8C5D8:O54714
SVYQPAQL	SVYQPAQL	8	13.6	0.04	2847300	YES	10213000	YES		YES	B2RVL6
SVYTHSYL	SVYTHSYL	8	4.6	0.01	918450	YES	17020000	YES	14553000	YES	Q8K0L2:Q3TZX8
SVYVYKVL	SVYVYKVL	8	6.7	0.02	16062000	YES	910460000	YES	855000000	YES	Q6ZWY9:P10853:Q64525:Q8CGP1
SYFKGASL	SYFKGASL	8	270.1	0.7	173215.466	NO	1756100	YES	1300000	YES	Q8C129
TAFGYKGL	TAFGYKGL	8	23.5	0.07	378411.209	NO	581840	YES		YES	Q8BY71
TAFKFKAL	TAFKFKAL	8	6.5	0.02		YES	9336800	YES	4782800	YES	Q04690
TAFRFSEL	TAFRFSEL	8	3.3	0.01	14826000	YES	48645000	NO	33178000	NO	A3KGB4
TAHAFVNV	TAHAFVNV	8	41.4	0.125	108250	YES	362360	YES	94368	YES	P19096
TAILFQRI	TAILFQRI	8	33.8	0.1	1480800	YES		YES		YES	E9Q414
TALAFRTL	TALAFRTL	8	13.3	0.04	675481.108	NO	7635900	YES	4884700	YES	Q8CIP4
TALDHYSEL	TALDHYSEL	9	36.8	0.125	592862.145	NO	3513200	YES	1507400	YES	Q6ZWQ0
TALRFLEL	TALRFLEL	8	21.7	0.07		YES	28940000	YES	2125400	YES	Q8VD65
TALRYIQSL	TALRYIQSL	9	32.6	0.1	115522.422	NO	1123600	YES	627840	YES	O08789
TAPHYQLL	TAPHYQLL	8	72	0.2	384150	YES	6562000	YES	1033300	YES	Q9D5R2
TAPQYYRL	TAPQYYRL	8	11.9	0.04	5644400	YES	28696000	YES	43130000	YES	Q6PJN8
TAYAFHFL	TAYAFHFL	8	4.5	0.01		YES	39382000	YES	2128800	YES	Q9R0H0
TAYEFAKL	TAYEFAKL	8	2.4	0.01	15600000	YES	22428000	YES	27740000	YES	Q9EQ06
TAYHFSLV	TAYHFSLV	8	6.3	0.015	821910	YES	6521300	YES		YES	Q8R0L1
TAYLFSRF	TAYLFSRF	8	8.1	0.025	1188600	YES		YES		YES	Q9CRT8
TEYVFTHL	TEYVFTHL	8	15.1	0.05	1134900	YES	128070000	YES	25324000	YES	Q6NWW9
TGATYPHL	TGATYPHL	8	111.7	0.3	135890	YES	379150	YES		YES	Q9DBA6
TGIKFVVL	TGIKFVVL	8	107.1	0.3	2039531.48	YES		YES		YES	Q9ES56
TGPKYIHL	TGPKYIHL	8	26.7	0.08	5749438.41	YES	11527000	YES	130220000	YES	Q60805
TGYNFQRV	TGYNFQRV	8	6.8	0.02	1416300	YES		YES	119030	YES	Q922V4

THFQPAQL	THFQPAQL	8	345.9	0.8	363605.236	NO	1538900	YES	66558	NO	P54822
THYSFLATL	THYSFLATL	9	7.1	0.02	294290	NO	1102900	YES		YES	Q5U419
TIIIFHSL	TIIIFHSL	8	18.4	0.06	4184313.51	YES		YES		YES	O08575;P97480
TIILFTKV	TIILFTKV	8	58.7	0.175	1239300	YES		YES		YES	Q8K2V6
TILEFSQNM	TILEFSQNM	9	34.2	0.1	1127918.28	NO	20337000	YES	3643900	YES	Q6P5F9
TILEFSQNM	TILEFSQNM(+15.99)	9	34.2	0.1	735920	NO	17792000	YES	59154000	YES	Q6P5F9
TITSFPRL	TITSFPRL	8	32.3	0.1		YES		YES		YES	P97494
TIYERFVLV	TIYERFVLV	9	24.9	0.08	40382.4038	NO		YES		YES	P63154
TIYRFLKL	TIYRFLKL	8	3.7	0.01	1936700	YES	10735000	YES		YES	Q8CEF1
TNIDFAFKRL	TNIDFAFKRL	10	136.9	0.4	186946.34	NO	9278900	YES	4783900	NO	P29416
TNINFPNL	TNINFPNL	8	6.2	0.015	496414.926	NO	5379500	YES	4129800	YES	Q8BRH4
TNISFTNM	TNISFTNM(+15.99)	8	10.5	0.03	839680	NO	7431100	NO	16721000	NO	Q9CYY7
TNLIYQQV	TNLIYQQV	8	63.8	0.2	1322300	YES	16126000	YES	7374200	YES	P97479
TNLQRVSYL	TNLQRVSYL	9	162.2	0.5	189513.332	NO	377600	YES	262690	YES	Q810A7
TNLRYLAL	TNLRYLAL	8	9.1	0.025	260120	YES	15581000	YES	28988000	YES	P17427:P17426
TNLVPYPRI	TNLVPYPRI	9	121	0.4	785110	YES	50228000	YES	24822000	YES	P68373:P05213:P68368:Q9JJZ2
TNLVYPAL	TNLVYPAL	8	10.4	0.03		YES		YES	6421600	YES	Q8BLR9
TNPSFDGRL	TNPSFDGRL	9	88.6	0.25	4145700	YES	16339000	YES		YES	Q6PA06
TNQDFIQRL	TNQDFIQRL	9	149.4	0.4	1766900	YES	231070000	YES	4415800	YES	Q80TM9
TNVEYAHL	TNVEYAHL	8	6.6	0.02		YES	310790	YES	402950	YES	Q8K370
TNVKFLAI	TNVKFLAI	8	284.6	0.7		YES		YES	2471900	YES	Q02248
TNVLFNHL	TNVLFNHL	8	11.1	0.04	782010	YES	68713000	YES	14588000	YES	Q9D706
TNVQYSNL	TNVQYSNL	8	9.8	0.03	1048000	NO		YES	3082200	YES	Q45VK7
TNVTFSKV	TNVTFSKV	8	111.7	0.3	1067200	YES	1094100	YES		YES	Q6P5B0
TNYIFDSL	TNYIFDSL	8	6.3	0.015	1429500	YES	12847000	YES	2465400	YES	Q9CXF4
TNYNFQYI	TNYNFQYI	8	7	0.02	2145300	YES	28333000	YES	21076000	YES	Q8K2C8
TNYNFQYISL	TNYNFQYISL	10	9.9	0.03	423430	YES	3189300	YES		YES	Q8K2C8

TNYTFENV	TNYTFENV	8	5.6	0.015	176787.441	NO	2045600	YES	1362000	YES	Q61493
TQFLYPKV	TQFLYPKV	8	68.3	0.2	454969.11	YES	6723200	YES		YES	P15066
TQQLYPSL	TQQLYPSL	8	248.3	0.6		YES	12020000	YES	9969800	YES	P69566
TQYIFNNM	TQYIFNNM	8	6.4	0.015	86678	YES	5618300	NO	8366.5	NO	P27046
TQYIFNNM	TQYIFNNM(+15.99)	8	6.4	0.015	774970	YES	4094200	NO	7762500	NO	P27046
TQYSFYQQL	TQYSFYQQL	9	3.8	0.01	705046.309	NO		YES	1428100	NO	Q9Z329
TSFMFQRV	TSFMFQRV	8	3.3	0.01	4558650.25	YES	9173400	YES	552770	YES	P97429
TSFRYSSL	TSFRYSSL	8	2.3	0.01	805630	NO	13743000	NO	21160000	NO	Q8BX90
TSFTFRKV	TSFTFRKV	8	7.3	0.02		YES	1292600	YES	855270	YES	Q80Y20
TSIAFKNI	TSIAFKNI	8	30.6	0.09	251210	YES	5640100	YES	5274600	YES	Q8VHJ5:Q03141
TSIQFNLRNL	TSIQFNLRNL	10	81.8	0.25	131808.602	NO	4166200	YES		YES	Q8BJ56
TSLKYLEM	TSLKYLEM	8	70.9	0.2	717472.264	NO	1380700	YES		YES	Q9CWG9
TSPEYQKL	TSPEYQKL	8	40.9	0.125	26719000	YES	1862700	YES	7601600	YES	Q920R0
TSPLFLHF	TSPLFLHF	8	110.4	0.3		YES	21702000	YES	6210600	YES	Q5SSZ5
TSVRFTQL	TSVRFTQL	8	5.3	0.015	8610400	YES	134680000	YES	290030000	YES	Q9D6T0
TSVVFNKL	TSVVFNKL	8	16.7	0.05	282890	YES	13397000	YES	9304700	YES	Q791N7
TSYIFVSV	TSYIFVSV	8	4.2	0.01	110960	NO	3372200	NO		YES	P42337
TSYRFLAL	TSYRFLAL	8	2.1	0.01	4515300	NO	48499000	NO	730320	YES	Q8QZX2
TSYSYIRL	TSYSYIRL	8	2.3	0.01		YES	1072100	YES		YES	F8VPZ5
TTFEHAHNM	TTFEHAHNM	9	268.3	0.7	229989.222	YES	571140	YES		YES	P58252
TTFEHAHNM	TTFEHAHNM(+15.99)	9	268.3	0.7	107010	YES	334450	YES	2947900	YES	P58252
TTLIFQKL	TTLIFQKL	8	18.8	0.06	420370	YES	11678000	YES	77775000	YES	P15307
TTLLYKPI	TTLLYKPI	8	89.8	0.25	44701	YES		YES	402240	NO	Q9R078
TTVAFTQV	TTVAFTQV	8	95.5	0.3	5370000	YES	13987000	YES	1149600	YES	P12970
TTYKYEMI	TTYKYEM(+15.99)I	8	28.6	0.09	1389700	YES	34702000	YES	23347000	NO	Q8QZY1
TTYKYFAL	TTYKYFAL	8	2.7	0.01	3912300	YES		YES	115940000	YES	Q5BLK4
TTYVHKGL	TTYVHKGL	8	26.3	0.08	136760	YES		YES		YES	Q9CZW5
TTYVHKGLL	TTYVHKGLL	9	41.6	0.125	105277.827	YES	126810	NO	126130	NO	Q9CZW5

TVQSFHHL	TVQSFHHL	8	41.8	0.125	68927.0411	NO		YES	84697	NO	Q9R1J0
TVRFFNSV	TVRFFNSV	8	298.8	0.7		YES		YES		YES	Q9ERV1
TVTEFKQL	TVTEFKQL	8	368	0.9	89607	NO		YES		YES	Q8BY87
VAALFKNL	VAALFKNL	8	9.7	0.03	348210	YES	3538100	YES	1208000	YES	Q5U464
VAASFKGL	VAASFKGL	8	36.5	0.125	1284313.92	YES	2843300	YES	605700	YES	Q6P5B0
VADKFSEL	VADKFSEL	8	100.9	0.3	1715755.51	NO	16091000	YES	7016600	YES	Q7TNP2
VADKFTEL	VADKFTEL	8	140.9	0.4	2136700	YES	90223000	YES	58585000	YES	Q76MZ3
VAFAFKKL	VAFAFKKL	8	4.6	0.01	816030	YES	4007500	YES	5848600	YES	Q8CFA1
VAFAYKNV	VAFAYKNV	8	4.4	0.01	3911700	NO	59748000	NO	30798000	NO	Q9DCF9
VAFDFTKV	VAFDFTKV	8	10.6	0.03	6244100	YES	304680000	YES	323470000	YES	Q7M6Y3
VAFIFNQKF	VAFIFNQKF	9	53.7	0.175	85914.3724	NO	2216400	YES		YES	Q8CJ19:Q8BML1
VAFNHQNL	VAFNHQNL	8	5.5	0.015	1351390.7	YES	3213200	YES	923520	YES	Q8BX90
VAHTFVIGV	VAHTFVIGV	9	72.7	0.2	139060	YES	8479300	YES	12603000	YES	P50580
VAIGFKTKL	VAIGFKTKL	9	40.9	0.125	1021109.61	NO		YES		YES	Q64310
VAIRFDSGL	VAIRFDSGL	9	9.5	0.03	1269122.31	NO	7503700	YES	8532100	YES	Q9ERU3
VAITYKEL	VAITYKEL	8	15.3	0.05	1452200.63	YES	14976000	YES		YES	Q03963
VALDFEQEM	VALDFEQEM	9	87.5	0.25	352363.448	NO	30764000	YES	5250600	YES	P60710:P63260:Q8BFZ3
VALDFEQEM	VALDFEQEM(+15.99)	9	87.5	0.25	505240	NO	30454000	YES	99404000	YES	P60710:P63260:Q8BFZ3
VALLFRQL	VALLFRQL	8	3.6	0.01	2950365.61	YES	24914000	YES		YES	Q6ZPE2
VAMVFKTL	VAMVFKTL	8	8.3	0.025	273117.801	YES	3321900	YES	809390	YES	Q65Z40
VAPDRFPTL	VAPDRFPTL	9	24.2	0.07	2309279.86	NO	20794000	YES	23681000	YES	Q9DBS8
VAPFFKSYI	VAPFFKSYI	9	52	0.15	152140	NO	11649000	YES		YES	Q9JHU4
VAPHHLFL	VAPHHLFL	8	242.8	0.6	228415.528	NO	4538500	NO	2948700	YES	B2RQC6
VAPQYQEL	VAPQYQEL	8	17.2	0.05	6267900.64	YES		YES	2697600	YES	Q9D711
VAPRYVALL	VAPRYVALL	9	5.9	0.015	1492700	YES	2346500	NO	1665700	NO	Q8CGC7
VAPSAVNL	VAPSAVNL	8	108.9	0.3		YES		YES		YES	Q8BTI8
VAQKFNHL	VAQKFNHL	8	10.2	0.03	106259.438	NO	112870	YES		YES	Q80ZE4
VAVIHQSL	VAVIHQSL	8	98.9	0.3		YES	215020	YES		YES	Q8K158

VAYGFRNI	VAYGFRNI	8	3.8	0.01	1082200	YES		YES	15263000	YES	Q7TMW6
VAYKFPEL	VAYKFPEL	8	2.6	0.01	3324936.07	YES	40786000	YES	114680000	YES	Q6WKZ8
VAYKFPELL	VAYKFPELL	9	9.5	0.03	3719200	YES	16675000	YES	110820	YES	Q6WKZ8
VAYRHLVGV	VAYRHLVGV	9	12.3	0.04	175018.982	YES	1768900	NO	386090	NO	Q9D0M3
VAYRYEVL	VAYRYEVL	8	3.4	0.01	2236515.96	NO	2496900	NO		YES	Q5U4C9
VAYSHDGAFL	VAYSHDGAFL	10	89.7	0.25	504945.597	NO	8629000	YES	1187400	YES	O88342
VAYWRQAGL	VAYWRQAGL	9	6.3	0.015	2112900	YES	59981000	YES		YES	P56382
VEYDFHLL	VEYDFHLL	8	67.5	0.2	2727243.77	YES	13793000	YES		YES	P46664
VFIDKQTNL	VFIDKQTNL	9	267.2	0.7	433130	YES	7778400	YES	5870600	YES	P28659:Q9Z0H4
VFRLLPQL	VFRLLPQL	8	299.9	0.7		YES	49991000	YES	30905000	YES	Q9EST5
VFTEVANL	VFTEVANL	8	195.2	0.5	532560	YES		YES		YES	Q62141
VFVKVINL	VFVKVINL	8	239.3	0.6	59712	NO	20249000	YES	12375000	YES	Q69Z37
VFYQVQSL	VFYQVQSL	8	32.5	0.1	47380	NO		YES		YES	B1AY13
VGFDYKERL	VGFDYKERL	9	37.1	0.125	16326301.6	YES	668150000	YES	46848000	YES	Q60598
VGFTFPNRL	VGFTFPNRL	9	7.8	0.02	2852243.42	YES	42465000	YES	10415000	YES	Q9Z0E0
VGIGFSNL	VGIGFSNL	8	4.6	0.01		YES		YES		YES	Q9JJT0
VGITYQHI	VGITYQHI	8	19.6	0.06	1683100	YES	79695000	YES	70998000	YES	Q9DBZ5
VGLKFPGL	VGLKFPGL	8	5.6	0.015	1436775.31	YES	2401200	YES		YES	Q62086
VGLRYEKI	VGLRYEKI	8	124.7	0.4		YES	6228900	YES	9261500	YES	Q9WUN2
VGLYYINKI	VGLYYINKI	9	200.2	0.5	194170	YES		YES	865020	YES	Q5RL79
VGMKYRNL	VGMKYRNL	8	4.5	0.01		YES	92171	YES		YES	Q91YP2
VGNEFSHL	VGNEFSHL	8	15	0.05	460461.46	NO		YES	502140	YES	Q99ML9
VGNNFHNL	VGNNFHNL	8	18.9	0.06	100591.801	NO	557820	YES		YES	Q8K2H6
VGPKFRGV	VGPKFRGV	8	43.4	0.15	70001	YES	5180300	YES	7039400	YES	Q9D2V5
VGPRYTNL	VGPRYTNL	8	4.6	0.01	194610000	YES	645770000	NO	1217400000	YES	P63085
VGPRYTQL	VGPRYTQL	8	6.8	0.02	8149500	YES	88811000	NO	47054000	NO	Q63844
VGPYTYREL	VGPYTYREL	9	30.7	0.09	567776.52	YES	424210	YES	217010	YES	O35114
VGQEYLERL	VGQEYLERL	9	123.6	0.4	315658.192	NO		YES		YES	Q3URE1

VGTAFSRL	VGTAFSRL	8	10.4	0.03	59138.1938	NO		YES		YES	Q9CZ42
VGVKYVNKL	VGVKYVNKL	9	97.9	0.3		YES	2269700	NO	1390200	YES	Q9WVL3
VGVTYRTL	VGVTYRTL	8	12.2	0.04		YES	6915400	YES	6355100	YES	B1AUR6
VGYLHEGL	VGYLHEGL	8	9.3	0.025	7129926.88	YES	16219000	YES	2568000	YES	Q6P4T2
VGYNPYSHL	VGYNPYSHL	9	4.2	0.01	164349.8	NO	4113000	YES	8202800	YES	O54941
VGYRFVTAI	VGYRFVTAI	9	6.8	0.02	259655.701	NO	189760000	NO	168190000	YES	Q80TM9
VGYRTQPM	VGYRTQPM	8	20.8	0.06	211541.16	NO	739700	NO		YES	Q8C2Q3
VGYRYETL	VGYRYETL	8	2.9	0.01	1133600	NO	61989000	NO	113300000	NO	Q9DBT5
VHYVFDTTI	VHYVFDTTI	9	45.1	0.15	725574.453	NO	2164900	YES	1138900	NO	Q9CYQ7
VIAGFNRL	VIAGFNRL	8	34.7	0.125	11570550	YES		YES		YES	O70591
VIASFKVL	VIASFKVL	8	173.6	0.5	2183501.15	NO	23296000	YES	10493000	YES	P57780
VIEEFRHL	VIEEFRHL	8	34.6	0.125		YES	2790500	YES	945650	YES	P52633
VIFKPALL	VIFKPALL	8	14.3	0.04	290202.514	NO		YES		YES	A3KG59
VIFNYKGKNV	VIFNYKGKNV	10	122.2	0.4	3172357.82	NO	9450900	NO	1464000	NO	P14211
VIFQPHIL	VIFQPHIL	8	271.4	0.7	1674100	YES	8919500	YES		YES	Q2EMV9
VILEYFTRL	VILEYFTRL	9	4.6	0.01		YES	10700000	YES		YES	Q9CR08
VILSFRSL	VILSFRSL	8	4	0.01	21148000	YES		YES		YES	P28660
VIMKLFPQL	VIM(+15.99)KLFPQL	9	27.8	0.08	96680.9359	YES	5808500	YES	6332300	YES	Q64FW2
VIMKLFPQL	VIMKLFPQL	9	27.8	0.08		YES	17881000	YES	406810	YES	Q64FW2
VINELIGNL	VINELIGNL	9	477.2	1		YES	9735200	YES		YES	Q99J56
VINPYKNL	VINPYKNL	8	34.5	0.1	1788869.98	YES	13419000	YES	3004300	YES	Q8VDD5
VINSFVHV	VINSFVHV	8	47.4	0.15	1576800	YES	15507000	YES	3914700	YES	Q9D4H8
VINVFHHL	VINVFHHL	8	11.3	0.04	137840	YES	10331000	YES	14264000	YES	Q52KE7
VIQDFQASVL	VIQDFQASVL	10	324.3	0.8	397241.009	NO	3140400	YES	523550	YES	Q9Z2N8
VIQDFVKM	VIQDFVKM	8	189.8	0.5	6404625.09	NO	23903000	YES	764290	NO	Q8BHG9
VIQDFVKM	VIQDFVKM(+15.99)	8	189.8	0.5	3131963.73	NO	21591000	YES	14070000	NO	Q8BHG9
VIQKFLYL	VIQKFLYL	8	13.7	0.04	443945.458	NO	21942000	YES		YES	Q9R111
VIQVFQQL	VIQVFQQL	8	7.5	0.02	3871989.68	YES	143810000	YES	30172000	YES	Q8BHC4

VISDFITRL	VISDFITRL	9	68.6	0.2	322270000	YES		YES	1318000	YES	Q9DBG1
VITEFARI	VITEFARI	8	13.9	0.04		YES		YES	19962000	YES	Q3TX08
VITNFSARI	VITNFSARI	9	31.1	0.09	128300	YES	8624500	YES		YES	Q3UVL4
VIVDTFHGL	VIVDTFHGL	9	79.1	0.25	321828.321	NO	641430	YES	272730	YES	P35123:Q99K46
VIVEFRDL	VIVEFRDL	8	18.4	0.06	1364100	YES		YES	6583800	NO	Q922X9
VIVKFAQL	VIVKFAQL	8	3	0.01	89171	YES		YES	9241200	YES	Q6NS46
VIVPHIVNL	VIVPHIVNL	9	91	0.25	242384.014	NO		YES	9020400	YES	Q8BW70
VIVRFLTV	VIVRFLTV	8	40	0.125	13656000	YES	112680000	YES	7495700	YES	P62245
VIVRFLTVM	VIVRFLTVM	9	96.4	0.3		YES	27445000	YES		YES	P62245
VIWGKYAQV	VIWGKYAQV	9	16.2	0.05	119290	YES	3688300	YES		YES	Q9CR47
VIYDVSHNI	VIYDVSHNI	9	293.1	0.7	143829.447	NO		YES	508770	YES	Q99LF4
VIYNPRNL	VIYNPRNL	8	11	0.04	4286100	YES	225420000	YES	31169000	YES	P97481
VIYPFMQGL	VIYPFMQGL	9	3.5	0.01		YES	10682000	YES	3130900	YES	Q91VV4
VLIPKLPQL	VLIPKLPQL	9	430.2	1	586720	YES	6630800	YES		YES	Q9CPZ6
VLLRYQQL	VLLRYQQL	8	12	0.04	416240	YES	2071900	YES		YES	Q9EQ20
VMYKFLTV	VM(+15.99)YKFLTV	8	6.1	0.015	254680	NO	62765000	YES	206300	NO	Q9WVC3
VMYRVIQV	VM(+15.99)YRVIQV	8	34.4	0.1	1513785.06	NO	7405800	YES	15807000	NO	Q61069
VMYRVIQV	VMYRVIQV	8	34.4	0.1	41132	NO		YES	271150	NO	Q61069
VNAQFPRF	VNAQFPRF	8	322.2	0.8		YES		YES	792860	YES	P58742
VNFAFNQI	VNFAFNQI	8	7.1	0.02	842260	NO	3289700	YES	3455800	YES	Q9JLF7
VNFEFPEF	VNFEFPEF	8	43.3	0.15		YES	216020000	YES	4050400	YES	P62082
VNFGRQGLNL	VNFGRQGLNL	10	270.9	0.7	309367.309	NO	5085300	YES		YES	Q99KK1
VNFIKENLL	VNFIKENLL	9	55.6	0.175	44333	NO	4352000	YES	2934200	YES	Q61687
VNFKHEVSV	VNFKHEVSV	9	65.8	0.2		YES		YES	458810	YES	Q9CQT2
VNFLHSNKL	VNFLHSNKL	9	34.1	0.1	314622.046	YES		YES	1008400	YES	P22518
VNFPFLVKL	VNFPFLVKL	9	15.1	0.05	194760	NO	48739000	YES	281020	YES	P05132
VNFTYQFL	VNFTYQFL	8	2.9	0.01		YES	10012000	YES		YES	Q3UMB9
VNFVHTNL	VNFVHTNL	8	3.6	0.01	1515537.94	YES	18761000	YES	45280000	YES	Q9D8E6

VNIKLNQL	VNIKLNQL	8	136	0.4		YES		YES		YES	Q9DBC3
VNIPFVRL	VNIPFVRL	8	5	0.015	1587500	YES	75922000	YES		YES	Q8R151
VNIVINNL	VNIVINNL	8	64.5	0.2	943476.611	YES	1014200	YES		YES	Q80TY5
VNLQYSEV	VNLQYSEV	8	16.7	0.05		YES	3769400	YES		YES	P62700
VNLTFRTV	VNLTFRTV	8	11	0.04	728885.444	YES		YES		YES	Q8K1E6
VNLVFEKI	VNLVFEKI	8	74.7	0.25	3389325.11	YES	17730000	YES	12673000	YES	Q6AW69
VNMVPFPRL	VNM(+15.99)VPFPRL	9	14.9	0.05	2087400	YES	31147000	YES	12370000	YES	P99024:P68372:Q9CWF2:Q922F4:Q9ERD7:A2AQ07
VNMVPFPRL	VNMVPFPRL	9	14.9	0.05	1052800	YES	66374000	YES		YES	P99024:P68372:Q9CWF2:Q922F4:Q9ERD7:A2AQ07
VNNIFQLTV	VNNIFQLTV	9	316.5	0.8	76592.959	NO		YES		YES	Q9JKY5
VNNLFVQL	VNNLFVQL	8	19.2	0.06	472225.216	YES		YES	603820	YES	P97393
VNRKYEYL	VNRKYEYL	8	20.6	0.06		YES	342350	YES	956300	YES	Q505B7
VNRVFDKL	VNRVFDKL	8	49.7	0.15		YES	137320000	YES	145780000	YES	P28076
VNSIFQHL	VNSIFQHL	8	13.7	0.04	3323500	NO	137350000	YES	32646000	YES	Q80SU7
VNSNFYLRM	VNSNFYLRM	9	19.3	0.06	1023953.17	NO	2740300	YES	413830	NO	Q9CQJ2
VNSNFYLRM	VNSNFYLRM(+15.99)	9	19.3	0.06	425793.437	NO	1605500	YES	3586500	NO	Q9CQJ2
VNVAKLRYM	VNVAKLRYM	9	256.1	0.7	474874.009	NO	1830400	NO	377100	NO	Q9CQS5
VNVAKLRYM	VNVAKLRYM(+15.99)	9	256.1	0.7	281730.273	NO	988290	NO	7248300	NO	Q9CQS5
VNVCYKEL	VNVC(+119.00)YKEL	8	66.9	0.2	1670920.8	NO	2033700	NO	1774300	NO	Q8BKT7
VNVDHPINL	VNVDHPINL	9	178.5	0.5	4120041.33	YES	17227000	YES	3182600	YES	Q3UIW5
VNVDYSKL	VNVDYSKL	8	26	0.08	152950000	YES	230980000	YES	626740000	YES	Q62425
VNVEFVRV	VNVEFVRV	8	17.9	0.05	406290	YES	10933000	YES		YES	Q8BML1
VNVERVLNV	VNVERVLNV	9	239.5	0.6	1890692.69	YES	13378000	YES	3734400	YES	Q6DFV5
VNVPFHLAL	VNVPFHLAL	9	15.8	0.05	49018.2473	NO	7272000	YES	866010	YES	Q8BMG7
VNVQKISNL	VNVQKISNL	9	124.3	0.4	353839.761	NO		YES	375550	YES	Q8CFI7
VNVRFTGV	VNVRFTGV	8	8.5	0.025	9266100.34	YES	12450000	YES	9581000	YES	Q6PDI6;Q76LS9
VNVVFIGHV	VNVVFIGHV	9	28.6	0.09	320983.044	YES	5655200	YES	6154700	YES	Q149F3;Q8R050
VNWDFVEQV	VNWDFVEQV	9	101.4	0.3	1257787.03	YES	13764000	YES	257840	YES	Q3UIW5

VNWEKHVLI	VNWEKHVLI	9	97.3	0.3	716576.348	NO	7715300	YES	2005300	NO	O09117
VNYDFGHM	VNYDFGHM(+15.99)	8	3.9	0.01	30730	NO	630870	NO	3974700	NO	P58283
VNYDYSTLIL	VNYDYSTLIL	10	36.8	0.125	98677	NO	5810400	YES		YES	D2EAC2
VNYEPLGL	VNYEPLGL	8	37	0.125	142250	NO	8613600	YES	811920	YES	Q80YE7
VNYRHLAL	VNYRHLAL	8	3.3	0.01	1033340.8	YES	5841000	YES	17383000	YES	P08775
VNYRHLALL	VNYRHLALL	9	3.7	0.01	260890	YES	13170000	YES	61216000	NO	P08775
VNYRVPNM	VNYRVPNM(+15.99)	8	9.3	0.025	156340	NO	4680000	NO	9607400	YES	Q62077
VNYYFERNM	VNYYFERNM(+15.99)	9	5	0.01	5242.4	NO	374050	YES	3394900	NO	Q9D4H9
VQEEFLQRL	VQEEFLQRL	9	367.5	0.9	19873	NO	468860	YES	567510	YES	Q9JK81
VQFLYREL	VQFLYREL	8	5.5	0.015	1332420.67	YES	5220100	YES	3740900	NO	B9EJR8
VQQYYRVL	VQQYYRVL	8	168.9	0.5	1297207.3	YES	2458300	YES		YES	E9PVA8
VQRSFSQV	VQRSFSQV	8	70.6	0.2	359700	NO	403260	YES	310730	YES	Q3U1N2
VQWEYGRL	VQWEYGRL	8	8.9	0.025		YES		YES	844860	YES	Q8BML9
VQYEMRTL	VQYEMRTL	8	36.7	0.125	553714.546	NO	2878700	YES	621270	NO	Q80ZK0
VQYEPAHL	VQYEPAHL	8	15.5	0.05	261346.254	NO		YES	1839400	YES	Q9WUK6
VQYKFSHL	VQYKFSHL	8	2.3	0.01	6963987.8	YES	20528000	YES	45164000	YES	Q9JHD1;Q9JHD2
VQYLYRVF	VQYLYRVF	8	54.4	0.175	134087.343	NO	4096700	YES	699490	YES	Q80Y44
VQYVLPRL	VQYVLPRL	8	12.3	0.04		YES	9579900	YES	13573000	YES	Q62245
VRVFFSGL	VRVFFSGL	8	49	0.15		YES		YES		YES	Q66JV4;Q80YR9
VSAPYGRI	VSAPYGRI	8	94.8	0.3	287908.192	YES		YES		YES	Q5SQX6;Q7TMB8
VSDAFQKL	VSDAFQKL	8	65.8	0.2		YES		YES	69105	YES	Q9CQK3
VSFPFGKI	VSFPFGKI	8	7.5	0.02	222697.252	YES	2848300	YES		YES	Q6NS46
VSFTYRYL	VSFTYRYL	8	1.9	0.01	6218700	YES	186290000	YES	623610000	YES	Q920Q4
VSIIFCEAV	VSIIFC(+119.00)EAV	9	31.1	0.09	61857.1016	NO	2759500	NO	163030	NO	Q91V37
VSIQFYHL	VSIQFYHL	8	2.5	0.01		YES	26313000	YES	36751000	YES	Q5H8C4
VSISFKSL	VSISFKSL	8	4.4	0.01	1055582.87	YES	1602200	YES	3360500	YES	Q3UHA3
VSLDGYFHL	VSLDGYFHL	9	35.9	0.125	225182.443	NO	3580500	YES		YES	Q8BGZ3
VSLKYAHM	VSLKYAHM(+15.99)	8	2.5	0.01	122190	NO	410630	YES	2438000	YES	P46664

VSMDFVQRF	VSMDFVQRF	9	49.8	0.15	183179.601	NO		YES		YES	Q921L5
VSNAFVRL	VSNAFVRL	8	7	0.02		YES		YES		YES	Q9D483
VSPEFHTL	VSPEFHTL	8	7.2	0.02	423962.654	YES	457930	NO		YES	Q7TMK6
VSPLFQKL	VSPLFQKL	8	4.7	0.01	14781000	YES	50370000	YES	81709000	YES	Q68FL6
VSPRLTFL	VSPRLTFL	8	30	0.09	2920371.93	YES	81597000	YES	16639000	YES	P36371
VSPTLYKQL	VSPTLYKQL	9	15.8	0.05	110770	YES		YES		YES	Q3TCH7
VSQKFTSI	VSQKFTSI	8	26.9	0.08	449710.477	NO		YES	1396200	YES	Q3UCV8
VSQYYPKL	VSQYYPKL	8	10.1	0.03	901060	YES	198170000	YES	61723000	YES	Q3TEA8
VSRSPSLL	VSRSPSLL	8	409	0.9	111432.374	NO		YES		YES	Q7TPV4
VSTKFEHL	VSTKFEHL	8	13.1	0.04	1105754.12	YES	4105400	YES	8420600	YES	B2RXC1
VSVEYTEKM	VSVEYTEKM	9	225.2	0.6	215977.888	YES	8288800	YES	1585500	YES	O35130
VSVEYTEKM	VSVEYTEKM(+15.99)	9	225.2	0.6	2140200	YES	3635600	YES	21084000	YES	O35130
VSVSFPHF	VSVSFPHF	8	26.2	0.08	216270.034	NO	6365000	YES		YES	Q3U1V6
VSVSFRVL	VSVSFRVL	8	7.8	0.02	292037.193	NO		YES		YES	Q8BG28
VSYKNPSL	VSYKNPSL	8	34.3	0.1	129837.589	NO	4433500	YES	1540800	YES	Q920B9
VSYKVDNL	VSYKVDNL	8	10.1	0.03	389185.563	NO	1072100	YES		YES	Q8K284
VSYKYSKV	VSYKYSKV	8	2.7	0.01	389460	YES	392460	NO	2141500	YES	Q07113
VSYLFSHV	VSYLFSHV	8	1.8	0.01	6238600	YES	72119000	YES	57394000	YES	Q9D7G0:Q9CS42
VSYQFPKL	VSYQFPKL	8	2.1	0.01		YES		YES		YES	Q924W7
VSYQHAFL	VSYQHAFL	8	2.3	0.01	488858.076	NO	2562900	YES		YES	Q9WV70
VSYWFDQRF	VSYWFDQRF	9	12.4	0.04	4160552.28	NO	12934000	YES		YES	P54751
VTFERVEQM	VTFERVEQM	9	169.8	0.5	96236.8736	NO		YES		YES	Q923J1
VTFIYQKL	VTFIYQKL	8	3.2	0.01	311520	YES		YES	1571800	YES	Q8C963
VTIHYNKL	VTIHYNKL	8	14.6	0.05	358973.744	YES	911080	YES	911290	NO	Q62083
VTIKYSKL	VTIKYSKL	8	5.5	0.015	95111.1367	YES	557520	NO		YES	Q8BGF7
VTNEFVHI	VTNEFVHI	8	123.1	0.4	398331.688	NO	1464500	YES		YES	Q9CQR6
VTPEGYAHL	VTPEGYAHL	9	12	0.04		YES		YES		YES	Q9Z2V5
VTVDFSKL	VTVDFSKL	8	15.3	0.05	179060	YES	5524900	YES	2485700	YES	Q6NVF4

VTVNFRKL	VTVNFRKL	8	9.4	0.03		YES	1145400	YES	323300	YES	Q6NZJ6
VTWRVTNL	VTWRVTNL	8	11	0.03	551300	YES	17765000	YES	5214500	YES	P10404
VTYESRKL	VTYESRKL	8	52.3	0.175		YES		YES		YES	Q9CY00
VTYHGFPNL	VTYHGFPNL	9	7.1	0.02	1450564.61	YES	17522000	YES	23925000	YES	O08760
VTYSFRQSF	VTYSFRQSF	9	15	0.05	218920	YES	11649000	YES		YES	Q8R0S2:Q5DU25
VTYSKPRL	VTYSKPRL	8	32.9	0.1	122440	YES	1344900	YES		YES	Q9CPQ8
VVAEFGRI	VVAEFGRI	8	114.7	0.3	756050	YES		YES		YES	Q8BXC6
VVDIFRKL	VVDIFRKL	8	142.8	0.4	3052460.99	YES		YES		YES	P51791;Q61418;Q9WVD4
VVVDYGTRL	VVVDYGTRL	9	69.6	0.2	48278.1434	YES		YES	211140	YES	P27046
VVYAVRNL	VVYAVRNL	8	5.5	0.015		YES	3012500	YES		YES	P28658
VVYIYHSL	VVYIYHSL	8	2.6	0.01	738520	YES	14886000	YES	11521000	YES	Q8CD15
VVYIYKEHF	VVYIYKEHF	9	39.8	0.125	320480	YES	11815000	YES		YES	Q5XG71
VVYIYRQI	VVYIYRQI	8	4.4	0.01	1625151.22	YES	1835600	YES		YES	Q62417
VVYSYHYL	VVYSYHYL	8	2.3	0.01	307478.097	NO	6055000	YES		YES	O08811
VVYTPWSNL	VVYTPWSNL	9	10.4	0.03	1218300	YES	11204000	YES	399990	YES	Q78PG9
VWIRNIQL	VWIRNIQL	8	441.2	1	106270	NO		YES		YES	Q8R1T4
VWIYNSQL	VWIYNSQL	8	283.7	0.7	73188.4813	NO	2340600	YES	1708200	YES	Q8BRG6
VWLEAARL	VWLEAARL	8	61.9	0.175	6873617.22	YES	17261000	YES		YES	Q91YR7
VWYRVIQI	VWYRVIQI	8	155.6	0.4	4804832.17	YES	23428000	YES		YES	P17427
VWYRVLQI	VWYRVLQI	8	209.6	0.6	4804832.17	YES	23428000	YES		YES	P17426
VYYRKPLL	VYYRKPLL	8	95.2	0.3	38638.0959	NO	647450	NO	861790	NO	Q02053
YAMIYRNL	YAM(+15.99)IYRNL	8	8.9	0.025	1935371.6	YES	1009700	YES	95412	YES	P23804
YAMIYRNL	YAMIYRNL	8	8.9	0.025	1504007.9	YES	2494400	YES		YES	P23804
YAYSFKYL	YAYSFKYL	8	4.6	0.01	232902.894	NO	4247800	YES	6003600	NO	Q62383
YGYEHILTL	YGYEHILTL	9	127.1	0.4	221563.724	NO	1725900	YES		YES	Q9D2N9
YGYHFPEL	YGYHFPEL	8	10.8	0.03	2092200	YES	44736000	YES	3081300	YES	Q9D6Z1
YNFQYISL	YNFQYISL	8	7.8	0.02	1744400	YES	8064300	YES	195380	YES	Q8K2C8
YNWRYKNL	YNWRYKNL	8	9.2	0.025	528473.109	NO	4153100	NO	897640	YES	Q8CFQ3

YQFVYQNL	YQFVYQNL	8	6.3	0.015	438764.731	NO	2842200	NO	1895500	NO	Q5NCI0
YSLVYQAL	YSLVYQAL	8	7.3	0.02	130382.929	NO	5381600	YES		YES	Q8BSP2
YSPAYAHL	YSPAYAHL	8	5.6	0.015	3701493.12	YES	5109700	YES	7457600	YES	O09012
YSPEFKGQI	YSPEFKGQI	9	498.2	1.1	1354467.97	YES	6545500	YES	1048500	YES	Q8CIE6
YTFVYRVL	YTFVYRVL	8	14.1	0.04	428130.607	YES	2060000	YES		YES	Q62136

Supplementary Table 4

PEPTIDE NUMBER	Sequence	Length	H-2K^b IC50 (nM)	Product of Spectral Intensity Values	Found in DIA	CD44$^+$ PD-1^{hi} Male B10.BR	CD44$^+$ PD-1$^-$ Male B10.BR	CD44$^+$ PD-1^{hi} Female B10.BR	CD44$^+$ PD-1$^-$ Female B10.BR	CD44$^+$ PD-1^{hi} Male BALB/c	CD44$^+$ PD-1$^-$ Male BALB/c
PEPTIDE 1	SNYLFTKL	8	2.4	8.67E+27	YES	19.5 (18.1-22.1)	0.5 (0.2-1.1)	14.6 (10.3-17)	0.1 (0.1-0.2)	20.7 (17.3-26.2)	1.1 (0.6-1.7)
PEPTIDE 2	ATLVFHNL	8	6.9	6.86E+25	YES	7.1 (2.6-11.6)	0.2 (0.1-0.2)	4.6 (4-5.6)	0.1 (0-0.1)	17.8 (14.4-22.9)	2.3 (1.9-2.9)
PEPTIDE 3	VGPRYTNL	8	4.6	1.53E+26	NO	12.2 (10.8-14.5)	0.2 (0.1-0.3)	8.1 (6.7-9.7)	0.1 (0.1-0.1)	6.7 (5.8-8.1)	1.2 (1-1.6)
PEPTIDE 4	RTYTYEKL	8	9.4	1.78E+25	YES	8.4 (7.7-9)	0.2 (0.1-0.3)	8 (7.1-8.6)	0.1 (0.1-0.1)	16.2 (13.2-17.7)	0.6 (0.4-0.8)
PEPTIDE 5	INFDFPKL	8	6.2	1.41E+26	YES	9.1 (5.2-15.1)	0.1 (0-0.1)	2.8 (1.5-4.3)	0.1 (0.1-0.1)	5.4 (2.9-9)	0.8 (0.3-1)
PEPTIDE 6	SVYVYKVL	8	6.7	1.25E+25	YES	11.9 (9.8-13.3)	0.3 (0.2-0.4)	10.1 (8.3-12)	0.1 (0-0.1)	13.9 (10.1-21.4)	0.7 (0.2-0.9)
PEPTIDE 7	VNVDYSKL	8	26	2.21E+25	YES	2.9 (1.3-3.7)	0.2 (0-0.4)	2.7 (1.7-3.9)	0.1 (0.1-0.1)	4.3 (2.1-7.2)	2.2 (0.5-3.4)
PEPTIDE 8	ASYEFVQRL	9	4.2	2.89E+24	YES	0.6 (0.5-0.9)	0.2 (0.1-0.2)	1 (0.8-1.3)	0.1 (0.1-0.1)	1 (0.5-1.6)	1.4 (0.4-2.1)
PEPTIDE 9	HIYEFPQL	8	7.9	3.85E+24	YES	7.9 (5.6-9.5)	0.2 (0.1-0.2)	6.9 (2.7-9.9)	0.1 (0-0.1)	5.2 (1.8-8.6)	0.6 (0.4-0.8)
PEPTIDE 10	VAFDFTKV	8	10.6	6.15E+23	YES	6.1 (3.1-10.7)	0.2 (0.1-0.2)	2.2 (1.4-2.9)	0.1 (0-0.1)	4.1 (1-8.9)	1.7 (1-2.3)
PEPTIDE 11	TSVRFTQL	8	5.3	3.36E+23	YES	2.2 (1.2-3.6)	0.1 (0.1-0.2)	1.7 (1.4-1.9)	0 (0-0.1)	3.6 (2.7-4.6)	1.5 (0.9-2)
PEPTIDE 12	AVVAFVMKM	9	339.2	2.74E+23	YES	0.4 (0.2-0.5)	0.3 (0.2-0.5)	0.6 (0.5-0.6)	0.4 (0.3-0.5)	0.6 (0.5-0.7)	0.2 (0.1-0.3)
PEPTIDE 13	SAYEFYHAL	9	2.8	1.99E+23	YES	2.8 (1.4-5.5)	0.2 (0.2-0.2)	1 (0.6-1.7)	0.1 (0-0.1)	2.2 (0.2-6)	0.9 (0.5-1.4)
PEPTIDE 14	SVIKFENL	8	7.1	2.26E+23	YES	2.6 (1-5.7)	0.1 (0.1-0.1)	1 (0.4-1.6)	0.1 (0-0.2)	1.3 (0.5-1.9)	1.4 (1.1-1.7)
PEPTIDE 15	SGYDFENRL	9	14.2	6.01E+22	YES	0.6 (0.6-0.6)	0.1 (0.1-0.2)	0.5 (0.3-1)	0 (0-0)	0.4 (0.1-0.6)	1 (0.3-1.5)
PEPTIDE 16	VSFTYRYL	8	1.9	7.22E+23	YES	5.4 (2.9-9.7)	0.4 (0.3-0.5)	10 (7.9-13.5)	0.1 (0.1-0.2)	11.2 (7.8-16.6)	2.2 (1.5-3)
PEPTIDE 17	ISFKFDHL	8	2.7	2.31E+23	YES	1.6 (1.3-1.9)	0.1 (0-0.1)	1.6 (0.8-2.6)	0.1 (0-0.1)	2.3 (2.1-2.5)	0.9 (0.6-1.1)
PEPTIDE 18	RNYSYEKL	8	11.6	9.41E+22	YES	6.7 (6.2-7)	0.1 (0.1-0.1)	7.6 (6-8.6)	0.1 (0.1-0.2)	17.5 (12.4-23)	0.6 (0.3-0.8)
PEPTIDE 19	SGYKFGVL	8	4.6	6.19E+22	NO	0.5 (0.4-0.7)	0.1 (0.1-0.2)	1.2 (0.9-1.8)	0.1 (0-0.1)	3.3 (2.3-3.9)	0.3 (0.1-0.4)
PEPTIDE 20	VGFDYKERL	9	37.1	5.11E+23	YES	2.1 (1.1-3.4)	0.1 (0.1-0.2)	5.1 (1.9-6.8)	0.1 (0.1-0.1)	0.9 (0.2-2)	0.7 (0.5-1.2)
PEPTIDE 21	SSPKFSEL	8	9.3	8.97E+22	NO	2 (0.7-4.3)	0.1 (0-0.1)	0.7 (0.4-1.1)	0.1 (0-0.1)	1.1 (0.7-1.8)	0.9 (0.7-1.3)

PEPTIDE 22	ASPEFTKL	8	20.9	1.03E+23	YES	1.1 (1-1.4)	0.1 (0-0.2)	1 (0.6-1.2)	0.1 (0.1-0.3)	2.9 (2.3-4)	1.4 (1.1-1.9)
PEPTIDE 23	ATQVYPKL	8	118.9	1.17E+23	YES	3.1 (1.7-4.2)	0.2 (0.2-0.2)	4.1 (3.2-5.3)	0.1 (0-0.2)	7.1 (6.3-7.7)	0.7 (0.2-1.2)
PEPTIDE 24	SGLKYVNV	8	14.6	7.07E+22	YES	3.1 (1.8-5.1)	0.2 (0.2-0.3)	2 (1.4-3.1)	0.1 (0.1-0.2)	3.7 (3.2-4)	2.2 (1.7-2.4)
PEPTIDE 25	QIIPFKTL	8	139.6	2.57E+23	YES	1.9 (0.8-2.5)	0.2 (0.1-0.3)	2.5 (1.5-3.5)	0.2 (0.1-0.3)	1.9 (1.8-2)	0.8 (0.5-1.1)
PEPTIDE 26	ATRSFPQL	8	37.4	2.00E+22	YES	1.8 (0.6-3.5)	0.1 (0-0.1)	1.1 (0.5-1.7)	0 (0-0.1)	11.3 (5.7-18.1)	0.1 (0-0.2)
PEPTIDE 27	SGYIYHKL	8	4.8	4.96E+21	YES	13.5 (9.7-16.8)	0.4 (0.3-0.5)	8.1 (5.8-11.1)	0.1 (0.1-0.2)	23.5 (14.4-29.5)	0.5 (0.2-0.9)
PEPTIDE 28	VSPLFQKL	8	4.7	6.08E+22	YES	3.1 (1.3-5.3)	0.2 (0.1-0.2)	3 (2.3-4)	0.1 (0-0.1)	15.4 (6.5-23.7)	0.5 (0.3-0.8)
PEPTIDE 29	QSIAFISRL	9	13.5	8.84E+22	YES	2.6 (1.2-4.8)	0.5 (0.4-0.5)	3 (2.4-3.9)	0.3 (0.1-0.4)	0.8 (0.4-1.3)	0.8 (0.5-1.1)
PEPTIDE 30	SSYTFPKM	8	3.4	4.75E+21	YES	5.4 (3.3-8.2)	0.2 (0.2-0.3)	3.1 (2-5)	0.1 (0-0.1)	9.6 (7.1-12.4)	0.2 (0.1-0.3)
PEPTIDE 31	VSQYYPKL	8	10.1	1.10E+22	YES	2.3 (2-2.5)	0.1 (0.1-0.1)	6.3 (4.5-7.5)	0 (0-0)	12.5 (3.8-21.8)	0.2 (0.2-0.3)
PEPTIDE 32	QSIEFSRL	8	5.5	2.19E+22	YES	1.7 (1.1-2.1)	0.1 (0.1-0.1)	2.9 (1.3-5.6)	0.1 (0-0.1)	0.7 (0.5-1)	0.4 (0.3-0.6)
PEPTIDE 33	SGIDFKQL	8	68.8	8.01E+21	YES	1 (0.8-1.2)	0 (0-0.1)	2.9 (0.4-7.1)	0 (0-0)	0.2 (0.2-0.3)	0.2 (0.1-0.4)
PEPTIDE 34	AVLSFSTRL	9	20.1	3.24E+22	YES	4.8 (3.3-5.6)	0.7 (0.6-0.9)	6.5 (4.1-10.5)	0.2 (0.1-0.3)	0.7 (0.4-1.2)	0.8 (0.6-1.2)
PEPTIDE 35	VGPRYTQL	8	6.8	3.41E+22	NO	3.9 (1.9-5.8)	0.1 (0-0.1)	8.5 (4.6-12.5)	0 (0-0)	3.1 (1.4-4)	0.1 (0-0.1)
PEPTIDE 36	RNYEYLIRL	9	11.9	3.28E+22	YES	2 (1.6-2.2)	0.2 (0.1-0.3)	2.8 (1.2-5.4)	0 (0-0.1)	0.3 (0.2-0.4)	0.3 (0.2-0.6)
PEPTIDE 37	VAYKFPEL	8	2.6	1.56E+22	YES	0.9 (0.6-1.3)	0.1 (0-0.1)	3.7 (2.5-5.4)	0 (0-0)	1.9 (0.6-3.5)	0.6 (0.2-0.9)
PEPTIDE 38	LQYEFTKL	8	10.8	7.90E+22	YES	1 (0.6-1.8)	0 (0-0.1)	2.8 (0.9-6)	0 (0-0)	6.1 (1.1-8.6)	0.3 (0.2-0.4)
PEPTIDE 39	VSYLFSHV	8	1.8	2.58E+22	YES	4.4 (4-5.1)	0.1 (0.1-0.1)	7.3 (4.1-13.5)	0 (0-0)	8.5 (3.9-13.6)	1.8 (1.1-2.6)
PEPTIDE 40	SAFSFRTL	8	3.3	4.94E+22	YES	5.2 (4.5-6.4)	0.4 (0.3-0.5)	6.1 (4.6-9.1)	0.1 (0.1-0.2)	19.4 (13.3-22.9)	3.1 (2.8-3.2)
PEPTIDE 41	SNYHFYSSI	9	3.9	2.15E+21	YES	1.2 (0.9-1.4)	0.4 (0.3-0.4)	2.5 (1-5.3)	0.1 (0.1-0.1)	0.6 (0.4-0.8)	0.6 (0.5-0.7)
PEPTIDE 42	HGYTFANL	8	3	1.28E+22	YES	1.1 (0.8-1.4)	0.1 (0-0.1)	2.8 (1.1-5.8)	0 (0-0)	15 (13.2-17)	1.1 (0.6-2)
PEPTIDE 43	SGYDFSRL	8	3.6	7.90E+21	YES	1.9 (1.9-2.1)	0.1 (0.1-0.1)	2.4 (2-2.9)	0.1 (0-0.2)	4.3 (1-7.4)	0.7 (0.7-0.8)
PEPTIDE 44	TAYEFAKL	8	2.4	9.71E+21	YES	1.6 (1.4-1.8)	0.1 (0-0.1)	2.9 (2.2-3.6)	0.1 (0-0.1)	7.5 (0.7-18)	0.7 (0.2-0.9)
PEPTIDE 45	VADKFTEL	8	140.9	1.13E+22	YES	0.3 (0.2-0.5)	0 (0-0)	0.7 (0.4-1.2)	0 (0-0.1)	0.5 (0.5-0.5)	0.2 (0.1-0.2)
PEPTIDE 46	TAFRFSEL	8	3.3	2.39E+22	NO	0.9 (0.6-1.2)	0 (0-0)	1.8 (1.6-2.1)	0.1 (0-0.1)	5.2 (1.4-9.2)	0.7 (0.4-1)
PEPTIDE 47	KILTFDQL	8	66.5	7.62E+21	NO	2.3 (1.2-4.2)	0.1 (0-0.1)	3.2 (2.8-3.8)	0.1 (0.1-0.1)	9.3 (6.2-11.1)	1.8 (1-2.4)
PEPTIDE 48	VGYRYETL	8	2.9	7.96E+21	NO	7.8 (2.7-16.1)	0.1 (0-0.1)	3.9 (2.6-6.7)	0.1 (0.1-0.1)	4.4 (2.7-6.7)	1.4 (0.9-1.9)
PEPTIDE 49	RVAEFTTNL	9	132.4	2.10E+21	YES	1.5 (0.7-2)	0.1 (0.1-0.1)	1.2 (1.1-1.3)	0.1 (0.1-0.1)	0.2 (0.2-0.4)	1.2 (1-1.5)

PEPTIDE 50	RSLKFYSL	8	5.7	6.97E+21	NO	3 (2.1-4.5)	0.3 (0.3-0.3)	2.3 (1.9-2.7)	0.3 (0.2-0.3)	2.2 (1.4-3.4)	2 (1.5-2.5)
PEPTIDE 51	TNQDFIQRL	9	149.4	1.80E+21	YES	2.5 (1.7-3.7)	0.2 (0.2-0.2)	1.8 (1.4-2.3)	0 (0-0.1)	0.6 (0.5-0.9)	2 (1.8-2.3)
PEPTIDE 52	TTYKYFAL	8	2.7	#N/A	YES	1.6 (1.2-2.1)	0.1 (0-0.1)	1.6 (0.9-2)	0 (0-0)	2 (1.7-2.3)	0.5 (0.3-0.7)
PEPTIDE 53	VGITYQHI	8	19.6	9.52E+21	YES	4.3 (3.5-4.7)	0.3 (0.2-0.4)	4.8 (2.8-8.5)	0.2 (0.1-0.3)	5.3 (3.1-7.5)	2.3 (2.1-2.5)
PEPTIDE 54	TAPQYYRL	8	11.9	6.99E+21	YES	4.3 (3.4-5)	0.6 (0.5-0.7)	3.6 (2.3-5.8)	0.2 (0.2-0.3)	1.6 (1.2-2.1)	2.7 (2.6-2.9)
PEPTIDE 55	KNYDFAQVL	9	29.5	3.14E+21	YES	0.3 (0.2-0.6)	0.1 (0-0.1)	0.4 (0.3-0.5)	0 (0-0)	0.5 (0.1-1.2)	0.5 (0.3-0.8)
PEPTIDE 56	FAYRFSNL	8	2	3.16E+21	NO	4.8 (1.7-7.7)	0.1 (0.1-0.2)	2 (1.8-2.3)	0 (0-0.1)	3.6 (3.1-4.2)	0.5 (0.4-0.8)
PEPTIDE 57	ATYTFIQQL	9	7.6	8.87E+21	YES	1 (0.7-1.7)	0.2 (0-0.5)	4.4 (2.8-6.4)	1.8 (0-4.2)	1.3 (0.2-2.7)	2.7 (0.4-5.6)
PEPTIDE 58	SGYKFFSL	8	2.6	1.37E+22	YES	1 (0.7-1.3)	0.1 (0.1-0.2)	1.7 (0.8-2.7)	0 (0-0.1)	1.8 (1.5-2.2)	0.4 (0.3-0.6)
PEPTIDE 59	RAYLFAHV	8	2.5	1.79E+21	YES	4.9 (4.1-6.4)	0.5 (0.4-0.7)	6.7 (5.5-7.6)	0.2 (0.2-0.3)	12.6 (9.1-16.3)	1.9 (1.8-2)
PEPTIDE 60	VIVRFLTV	8	40	1.15E+22	YES	7.3 (6.3-9.1)	3.3 (3-3.4)	9.3 (8.9-10.1)	0.9 (0.6-1.1)	7.5 (4.4-10.2)	1.2 (0.8-1.5)
PEPTIDE 61	SGYKYVGM	8	4.8	6.63E+21	YES	2 (1.7-2.4)	0.2 (0.1-0.3)	2.6 (2.1-3)	0.1 (0-0.1)	7.1 (4-10.2)	0.1 (0.1-0.2)
PEPTIDE 62	RNYQFDFL	8	11.1	4.42E+21	YES	4.1 (2.5-7)	0.2 (0.2-0.3)	12.9 (10.9-16.9)	0.1 (0-0.1)	5.9 (3.5-7.8)	0.1 (0-0.3)
PEPTIDE 63	ISILYHQL	8	3.7	1.15E+20	NO	1.3 (1-1.6)	0.3 (0.2-0.3)	2.4 (2.2-2.7)	0.1 (0-0.1)	4.2 (2-8.2)	0.2 (0.1-0.3)
PEPTIDE 64	VNSIFQHL	8	13.7	1.49E+22	NO	1.3 (1.1-1.8)	0.2 (0.1-0.3)	3.4 (2.9-4.3)	0 (0-0)	7.8 (3.7-12.1)	0.3 (0.2-0.4)
PEPTIDE 65	SSPHYTTL	8	12.2	7.07E+21	YES	3.6 (1.6-6.8)	0.1 (0.1-0.1)	5.5 (4.9-6.1)	0.1 (0.1-0.2)	7.7 (5.3-11.1)	0.9 (0.7-1)
PEPTIDE 66	VGYRFVTAI	9	6.8	8.29E+21	NO	2.5 (0.4-3.6)	0.1 (0-0.1)	5.8 (5.2-6.5)	0.1 (0.1-0.2)	3.9 (1-6.7)	0.2 (0-0.3)
PEPTIDE 67	TGPKYIHL	8	26.7	8.63E+21	YES	3.4 (0.5-8.9)	0 (0-0.1)	2.1 (1.9-2.4)	0.1 (0.1-0.2)	2.8 (1.8-4)	0.4 (0.1-0.8)
PEPTIDE 68	VQYKFSHL	8	2.3	6.46E+21	YES	3.6 (0.9-8.8)	0 (0-0)	2.8 (1.7-3.9)	0.1 (0-0.1)	4.7 (3.4-5.4)	0 (0-0.1)
PEPTIDE 69	RVLLFSQM	8	31.8	1.31E+22	YES	0.8 (0.5-1.3)	0.3 (0.2-0.3)	0.2 (0.1-0.3)	0.2 (0.1-0.3)	0.6 (0.4-1)	0 (0-0)
PEPTIDE 70	RVLIFSQM	8	42.3	1.31E+22	YES	1.1 (1-1.3)	0.3 (0.2-0.4)	0.8 (0.3-1.3)	0.4 (0.2-0.6)	0.2 (0.1-0.3)	0 (0-0.1)
PEPTIDE 71	KIFEFKETL	9	63.4	4.45E+21	NO	0.5 (0.1-0.9)	0 (0-0)	0.9 (0.6-1.3)	0 (0-0)	0.2 (0.1-0.3)	0.1 (0.1-0.2)
PEPTIDE 72	TTYKYEMI	8	28.6	6.70E+21	NO	3.6 (0.4-9.6)	0 (0-0.1)	2.2 (1.7-2.6)	0.1 (0.1-0.1)	13.3 (5.4-19.8)	0.4 (0.2-0.5)
PEPTIDE 73	ISVSFYHV	8	6	1.12E+21	YES	2.7 (2-3.8)	0.1 (0-0.2)	2.9 (2.5-3.1)	0.1 (0.1-0.1)	4.4 (2-8)	0.9 (0.4-1.7)
PEPTIDE 74	KNFPFERL	8	11.2	2.52E+20	YES	4.9 (2.2-6.3)	0.1 (0-0.1)	6.3 (5-9)	0.1 (0.1-0.1)	16.3 (7.6-22.9)	0.6 (0.4-0.7)
PEPTIDE 75	RVYEFLDKL	9	34.9	2.66E+21	YES	0.6 (0.1-1.2)	0 (0-0)	1.3 (1-1.6)	0 (0-0.1)	0.3 (0.2-0.5)	0.2 (0.1-0.3)
PEPTIDE 76	AFYYIHNL	8	87.6	9.76E+20	YES	0.7 (0.2-1.6)	0 (0-0)	2 (1.9-2)	0.1 (0.1-0.1)	0.8 (0.4-1.6)	0.5 (0.2-0.9)

PEPTIDE 77	TNYNFQYI	8	7	1.28E+21	YES	4.1 (2.8-6.6)	0.1 (0.1-0.1)	3.9 (3.4-4.5)	0 (0-0)	8.4 (4.6-16)	0.4 (0.2-0.8)
PEPTIDE 78	RAYLFNSV	8	7	8.32E+20	YES	5.1 (4.2-6)	0.1 (0.1-0.2)	6 (3.5-7.4)	0.1 (0.1-0.1)	18 (13.6-21.1)	1 (0.8-1.2)
PEPTIDE 79	ISARFVQL	8	6.4	5.36E+20	NO	0.9 (0.6-1.1)	0.1 (0-0.1)	2.3 (2.1-2.8)	0 (0-0)	5.5 (5-6)	0.5 (0.3-0.8)
PEPTIDE 80	SAYEVIKL	8	56.8	4.63E+20	YES	1 (0.6-1.2)	0.1 (0-0.1)	2.5 (1.7-3.3)	0.1 (0-0.2)	3.9 (1.7-5.6)	0.2 (0.1-0.3)
PEPTIDE 81	LAPVYQRL	8	17.7	#N/A	YES	1.1 (1-1.3)	0.1 (0.1-0.1)	2.1 (1.9-2.2)	0.2 (0.1-0.3)	11 (7.7-16.7)	0.5 (0.2-1)
PEPTIDE 82	KGFTFSAL	8	4.2	#N/A	YES	2.3 (0.8-5)	0 (0-0)	2.4 (1.2-4.3)	0 (0-0.1)	10.3 (3.9-16)	0.2 (0.1-0.3)
PEPTIDE 83	VSPRLTFL	8	30	3.96E+21	YES	1.4 (1.1-2)	0.1 (0.1-0.2)	3.2 (1.3-6)	0.1 (0.1-0.1)	5.8 (5.3-6.6)	0.6 (0.2-0.8)
PEPTIDE 84	VNMVPFPRL	9	14.9	8.64E+20	YES	2.8 (1.6-4.6)	0.6 (0.3-0.9)	1.6 (1.3-2.1)	0.1 (0.1-0.2)	2.2 (1-4.1)	1.1 (0.9-1.4)
PEPTIDE 85	TNVLFNHL	8	11.1	7.84E+20	YES	0.4 (0.3-0.5)	0.1 (0-0.1)	0.9 (0.6-1.5)	0.2 (0.2-0.3)	0.3 (0.1-0.6)	0.3 (0.3-0.4)
PEPTIDE 86	IGPTYYQRL	9	3.9	4.04E+18	YES	2.1 (1.4-3)	0.1 (0-0.1)	2.8 (2.3-3)	0.1 (0-0.1)	7.4 (4.1-10.4)	0.5 (0.4-0.8)
PEPTIDE 87	SVYTHSYL	8	4.6	2.27E+20	YES	5.9 (2.8-11.1)	0 (0-0.1)	6.9 (4.6-9.6)	0 (0-0.1)	15 (8.4-26.4)	0.2 (0.1-0.3)
PEPTIDE 88	KTYQFLNDI	9	89.3	2.23E+20	YES	0.9 (0.5-1.5)	0 (0-0.1)	0.9 (0.5-1.4)	0 (0-0)	2.2 (0.6-4.3)	0 (0-0.1)
PEPTIDE 89	TSFRYSSL	8	2.3	2.34E+20	NO	1.9 (1-3.4)	0.1 (0-0.2)	1.2 (0.6-1.8)	0.1 (0-0.1)	6.3 (3.9-7.5)	0.1 (0-0.3)
PEPTIDE 90	AMYIFLHTV	9	31.7	3.31E+21	YES	0.7 (0.7-0.8)	1.7 (1.2-2.1)	0.6 (0.4-0.7)	0.3 (0.1-0.3)	0.8 (0.1-1.2)	0.3 (0.1-0.7)
PEPTIDE 91	SGLKYVAV	8	39.3	6.19E+20	NO	2.5 (2-2.7)	0.1 (0.1-0.1)	1.1 (0.5-1.6)	0.1 (0.1-0.2)	3.1 (0.7-5.5)	0.9 (0.6-1.1)
PEPTIDE 92	VNFVHTNL	8	3.6	1.29E+21	YES	3.5 (2.1-5.2)	0.2 (0.1-0.3)	3.8 (2.8-4.5)	0 (0-0)	9.6 (7.6-11)	0.3 (0-0.5)
PEPTIDE 93	IFYYVQKL	8	52.7	2.24E+21	YES	1.7 (0.9-2.9)	0.2 (0.1-0.3)	2.1 (1.9-2.3)	0.1 (0-0.1)	5.7 (2.6-7.6)	0.1 (0-0.4)
PEPTIDE 94	IRYFPTQAL	9	437.1	1.12E+20	YES	0.4 (0.3-0.5)	0.1 (0.1-0.1)	0.5 (0.3-0.7)	0.1 (0-0.1)	0.5 (0.1-1.3)	0.1 (0-0.2)
PEPTIDE 95	KNVLFSHL	8	7.9	1.63E+21	YES	1.2 (0.6-2.1)	0.1 (0-0.1)	1.4 (1.1-1.7)	0 (0-0)	5.3 (2.6-7.9)	0.3 (0.1-0.5)
PEPTIDE 96	SSPKFSEI	8	53.5	8.97E+22	NO	0.8 (0.3-1.8)	0.1 (0-0.1)	0.8 (0.7-0.9)	0 (0-0.1)	4.1 (2.3-6.1)	0.2 (0-0.4)
PEPTIDE 97	INFDFNTI	8	19.8	#N/A	YES	3.7 (1-6.4)	2.4 (1.6-4)	3.2 (2.3-4.1)	0.4 (0.3-0.5)	3.4 (2.7-4.8)	0.1 (0-0.2)
PEPTIDE 98	KIITYRNL	8	7.5	#N/A	YES	2.2 (1.7-2.8)	0.4 (0.2-0.5)	3.7 (2.9-5.1)	0.2 (0.1-0.2)	2.1 (1.7-2.4)	1.1 (1-1.2)
PEPTIDE 99	KVLHFYNV	8	52.8	#N/A	NO	3.5 (2.9-4.2)	0.3 (0.2-0.4)	4.2 (3.1-4.8)	0.2 (0.1-0.2)	3.4 (1.9-4.3)	1 (0.6-1.4)
PEPTIDE 100	KVITFIDL	8	135.5	4.55E+20	YES	2.7 (0.4-6)	1.4 (0-4.1)	1.5 (0.7-2.9)	0.1 (0-0.1)	3.5 (1.6-7)	0.2 (0-0.3)

Supplementary Table 5

Antibodies used for IHC				
Antibody Target	Clone	Format	Supplier	Catalogue #
H-2K^b	AF6-88.5	FITC	BD Biosciences	553569
H-2K^d	SF1-1.1	FITC	BD Biosciences	553564
H-2D^b/H-2K^b	28-8-6	FITC	BioLegend	114605
CD4	GK1.5	FITC	BD Biosciences	553729
CD8a	53-6.7	FITC	BioLegend	100706
F4/80	BM8	FITC	BioLegend	123108
CD19	6D5	FITC	BioLegend	115506
CD11c	N418	FITC	BioLegend	117306
FITC	polyclonal	HRP	Bio-Rad	4510-7864

Antibodies used for hepatocyte/RMA-S staining (flow)				
Antibody Target	Clone	Format	Supplier	Catalogue #
H-2K^b	AF6-88.5	biotin	BD Biosciences	553568
H-2K^b	Y-3	purified	WEHI*	N/A
H-2K^d	SF1-1.1	biotin	BioLegend	116604
H-2K^b-SIINFEKL	25D-1.16	APC	BioLegend	141606
Mouse IgG2b	RMG2b-1	PE	BioLegend	406708
biotin	streptavidin	PE	BioLegend	405204

Antibodies used for Des-RAG Adoptive Transfer/Screening experiment				
Antibody Target	Clone	Format	Supplier	Catalogue #
CD4	GK1.5	FITC	BD Biosciences	553729
CD8a	53-6.7	PE	BD Biosciences	553033
CD90.2	53-2.1	PerCPCy5.5	BioLegend	140322
CD44	IM7	APC	BD Biosciences	559250
PD-1	29F.1A12	BV421	BioLegend	104530
Vbeta2	B20.6	PE	BioLegend	127908
CD45.1	A20	BV711	BioLegend	110730
CD45.2	104	PerCPCy5.5	BioLegend	109828

Antibodies used for multimer staining				
Antibody Target	Clone	Format	Supplier	Catalogue #
CD8a	KT-15	FITC	Biorad	MCA609FB
CD90.2	53-2.1	PerCPCy5.5	BioLegend	140322
CD44	IM7	APC	BD Biosciences	559250
PD-1	29F.1A12	BV421	BioLegend	104530
CD19	6D5	BV605	BioLegend	115540
CD14	rmC5-3	BV605	BD Biosciences	740357

Antibodies used for confocal imaging				
Antibody Target	Clone	Format	Supplier	Catalogue #
CD31	PECAM-1	AF488	BioLegend	102414
CD45	30-F11	AF647	BioLegend	103124
CK19	EPNCIR127B	purified	Abcam	Ab133496
H-2K^b	Y-3	purified	WEHI*	N/A
Rabbit IgG	Polyclonal	AF750	Invitrogen	A21039
Mouse IgG2b	RMG2b-1	PE	BioLegend	406708

Antibodies used for immunoaffinity purification				
Antibody Target	Clone	Format	Supplier	Catalogue #
H-2K^b	K9-178	purified	In-house	In-house
H-2K$^{b/k}$	Y-3	purified	In-house	In-house
H-2K^d	SF1-1.1.10	purified	In-house	In-house
H-2D^b	28-14-8	purified	In-house	In-house

*Antibody core, Walter & Eliza Hall Institute, Melbourne, Australia

Supplementary Table 6: Variable Window widths used for DIA acquisition

	Start	End	Width
MS1	375	1000	
DIA	375	386.1	11.1
DIA	385.1	398.7	13.6
DIA	397.7	412	14.3
DIA	411	425.4	14.4
DIA	424.4	441	16.6
DIA	440	457	17
DIA	456	474.7	18.7
DIA	473.7	493.7	20
DIA	492.7	510.7	18
DIA	509.7	528.8	19.1
DIA	527.8	545.8	18
DIA	544.8	565.7	20.9
DIA	564.7	591.3	26.6
DIA	590.3	616.3	26
DIA	615.3	643.3	28
DIA	642.3	668.3	26
DIA	667.3	693.3	26
DIA	692.3	851.3	159
DIA	850	1000	150