Supporting Information

Diffusion and Protein Corona Formation of Lipid-based Nanoparticles in Vitreous Humor: Profiling and Pharmacokinetic Considerations

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Supplementary files (Excel):

Supplementary File 1 Protein name Found Min 1 sample
Supplementary File 2 Matrix Filtered Found in Min 3 samples Raw intensities Sample averages
Supplementary File 3 ANOVA significant
Supplementary File 4 ANOVA and T-tests for selected contrasts Relative abundance Sample averages

Supplementary videos (.mp4):

AL3-PEG
AL6
NL7-PEG
CL2
CL7-PEG
CL8
Table S1. Effect of charge, particle size and surface modification (PEG and ICG) on vitreal mobility of lipid-based formulations based on the corresponding $D_v$, $D_w$ and $D_w/D_v$ ratios at a time scale of 1s. A: anionic, N: neutral, C: cationic formulation; L: light-activated liposomes and controls; R: rigid-membrane liposomes; H: hexosomes; and N: nanostructured lipid carriers (NLCs).

| Formulation | Size [nm] | $\zeta$-Potential [mV] | $D_v$ [µm² s⁻¹] | $D_w$ [µm² s⁻¹] | $D_w/D_v$ |
|-------------|-----------|------------------------|-----------------|-----------------|----------|
| **Anionic**< 50 nm | AL1-PEG | 51.0 | -28.1 | 1.02 ± 0.19 | 12.90 | 12.7 |
| | AL2 | 46.7 | -38.0 | 1.01 ± 0.14 | 14.10 | 14.1 |
| | AL3-PEG | 39.2 | -20.9 | 2.9 ± 0.71 | 16.78 | 5.7 |
| | AL4 | 48.7 | -40.8 | 0.91 ± 0.30 | 13.51 | 14.9 |
| 100-200 nm | AL5-PEG | 104.3 | -18.5 | 0.44 ± 0.12 | 6.31 | 14.3 |
| | AL6 | 105.2 | -56.3 | 0.70 ± 0.27 | 6.26 | 8.9 |
| | AL7-PEG | 107.1 | -22.8 | 1.40 ± 0.23 | 5.93 | 4.2 |
| | AL8 | 119.8 | -50.6 | 0.53 ± 0.06 | 5.89 | 11.1 |
| | AR1 | 142.0 | -53.0 | 0.37 | 4.64 | 12.4 |
| | AR2 | 139.0 | -43.0 | 0.60 | 4.74 | 7.8 |
| >200 nm | AL9-PEG | 208.8 | -38.8 | 0.24 ± 0.2 | 3.15 | 13.1 |
| | AL10 | 212.1 | -57.1 | 0.25 ± 0.18 | 3.10 | 12.4 |
| | AL11-PEG | 291.8 | -30.8 | 0.35 ± 0.02 | 2.26 | 6.4 |
| | AL12 | 291.8 | -55.4 | 0.34 ± 0.01 | 2.26 | 6.6 |
| **Neutral**< 50 nm | NL1-PEG | 48.9 | -1.7 | 1.20 ± 0.29 | 13.45 | 11.2 |
| | NL2 | 46.3 | -6.7 | 0.71 ± 0.07 | 14.31 | 20.3 |
| | NL3-PEG | 46.9 | -1.4 | 1.14 ± 0.15 | 14.04 | 12.4 |
| | NL4 | 35.7 | -1.5 | 0.91 ± 0.36 | 18.45 | 20.3 |
| 100-200 nm | NL5-PEG | 107.6 | -3.6 | 0.47 ± 0.25 | 6.12 | 13.0 |
| | NL6 | 125.8 | -7.2 | 0.33 ± 0.17 | 5.27 | 16.0 |
| | NL7-PEG | 110.8 | -1.2 | 0.36 ± 0.01 | 5.94 | 16.3 |
| | NL8 | 110.6 | -7.1 | 0.19 ± 0.002 | 5.95 | 31.4 |
| | NR1 | 180.0 | -10.0 | 0.26 | 3.66 | 14.2 |
| | NN | 152.0 | -11.8 | 0.29 ± 0.22 | 4.33 | 14.8 |
| | NN-PEG | 150.0 | -10.1 | 0.43 ± 0.32 | 4.39 | 10.2 |
| >200 nm | NL9-PEG | 224.4 | -1.4 | 0.15 ± 0.13 | 2.85 | 19.0 |
| | NL10 | 254.4 | -6.8 | 0.09 ± 0.09 | 2.59 | 28.8 |
| | NL11-PEG | 270.6 | -1.2 | 0.13 ± 0.06 | 2.43 | 18.4 |
| | NL12 | 227.3 | -9.6 | 0.09 ± 0.01 | 2.89 | 31.5 |
| | NH | 300.0 | - | 0.25 ± 0.08 | 2.19 | 8.7 |
| **Cationic**< 50 nm | CL1-PEG | 43.0 | 17.7 | 0.121 ± 0.06 | 15.31 | 126.4 |
| | CL2 | 46.5 | 29.4 | 0.008 ± 0.004 | 14.16 | 1770.0 |
| | CL3-PEG | 42.6 | 15.7 | 0.110 ± 0.06 | 15.45 | 140.0 |
| | CL4 | 49.9 | 32.5 | 0.007 ± 0.005 | 13.18 | 1882.0 |
| 100-200 nm | CL5-PEG | 110.8 | 18.2 | 0.042 ± 0.02 | 5.94 | 139.0 |
| | CL6 | 112.6 | 33.1 | 0.002 ± 0.008 | 5.85 | 2923.0 |
|                | L: light-activated liposomes, the formulations are divided based on charge (A: anionic, N: neutral, C: cationic). Based on this nomenclature, for example, AL indicates an Anionic Light-activated liposome formulation. | Track length (μm) | Track length (μm) | Track length (μm) |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------|------------------|------------------|
| CL7-PEG        | 111.6 14.0 0.038 ± 0.01 5.93 156.1                                                                                                                                                    | CL8              | 100.3 31.7 0.003 ± 0.005 6.56 2187.0                                                                                           |
| CR1            | 139 43.0 0.002 4.74 2370.0                                                                                                                                                    | CR2-PEG          | 134 30.0 0.014 4.91 351.0                                                                                                           |
| >200 nm        | CL9-PEG 251.2 18.3 0.015 ± 0.008 2.62 170.2                                                                                                                                                | CL10             | 236.1 41.0 0.0008 ± 0.01 2.79 3486.1                                                                                             |
| ≤50 nm         | CL11-PEG 267.9 14.4 0.013 ± 0.006 2.46 196.8                                                                                                                                                | CL12             | 202.9 33.9 0.002 ± 0.0006 3.26 2037.0                                                                                             |
Vitreal corona protein composition of anionic light-activated liposomes

In total, 535 non-redundant proteins were identified in the porcine vitreous used as source and at least one sample of the liposome corona subsections by nLC-ESI-MS/MS. These included 101 (18.9%) annotations that have not been previously reported in proteomic studies of the human vitreous,[1–4] and 88 (16.4%) previously unknown annotations when reports on dog, rabbit, and mouse vitreal proteomes were included in addition to human (Figure S2 and S4).[5–7] Only 24 common annotations were identified in the corona and human vitreal proteomes, and three when the other species were included (Table S2). Functional analysis with gene sets in the human group identified glycolysis (FDR 1.88E-11) and glucose catabolic process (FDR 5.87E-11) as significantly enriched pathways, while the common genes in the interspecies group were linked by their association with visual perception and sensory perception of light stimulus (both FDR 2.57E-2) (Figure S3).

**Figure S2.** Venn diagram of non-redundant protein identifications in at least one sample of the liposome corona and the human vitreous studies (24 common proteins to all).[1–4]
**Table S2.** Gene names and associated proteins common with liposome corona and human vitreous studies (24 common to all).[1–4]

| Gene   | Name                                                                                                         |
|--------|---------------------------------------------------------------------------------------------------------------|
| ALDOC  | Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)                                         |
| APOE   | Apolipoprotein E (Apo-E)                                                                                     |
| GSTP1  | Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)                                          |
| FAM3C  | Protein FAM3C (Interleukin-like EMT inducer)                                                                  |
| PEBP1  | Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolyptide h3) (Prostatin-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)] |
| CRYAB  | Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component) |
| LDHA   | L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59) |
| PTGDS  | Prostaglandin-H2 D-isomerase (EC 5.3.99.2) (Beta-trace protein) (Cerebrin-28) (Glutathione-independent PGD synthase) (Lipocalin-type prostaglandin-D synthase) (Prostaglandin-D2 synthase) (PGD2 synthase) (PGDS) (PGDS2) |
| A1BG   | Alpha-1B-glycoprotein (Alpha-1-B glycoprotein)                                                               |
| PRDX2  | Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) |
| NRCAM  | Neuronal cell adhesion molecule (Nr-CAM) (Neuronal surface protein Bravo) (hBravo) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) |
| HSPB1  | Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27) |
| HRG    | Histidine-rich glycoprotein (Histidine-proline-rich glycoprotein) (HPRG)                                       |
| LDHB   | L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) |
| PGAM1  | Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B) |
| PARK7  | Protein/nucleic acid dehydrogenase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1) |
| DAG1   | Dystroglycan (Dystrophin-associated glycoprotein 1) [Cleaved into: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta-DG)] |
| DKK3   | Dickkopf-related protein 3 (Dickkopf-3) (Dkk-3) (hDkk-3)                                                   |
| SCG3   | Secretogranin-3 (Secretogranin III) (SgIII)                                                                  |
| PGK1   | Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2) |
| PPIA   | Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed] |
| ALDOA  | Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)             |
| CRYAA  | Alpha-crystallin A2 chain [Cleaved into: Alpha-crystallin A2(1-172); Alpha-crystallin A2(1-168); Alpha-crystallin A2(1-162)] |
| CRYAA  | Alpha-crystallin A chain (Heat shock protein beta-4) (HspB4) [Cleaved into: Alpha-crystallin A(1-172); Alpha-crystallin A(1-168); Alpha-crystallin A(1-162)] |
**Figure S3** Functional analysis of the set of 24 genes common to all common with liposome corona and human vitreous studies shows glycolysis (FDR $1.88 \times 10^{-11}$, red), glucose catabolic process (FDR $5.87 \times 10^{-11}$, blue) and blood microparticle (FDR $6.77 \times 10^{-2}$, purple) as enriched pathways.
Figure S4. Venn diagram of protein identifications in at least one sample of the liposome corona (531) in pig with human and other animal vitreous proteomes with 5496 non-redundant genes (3 common proteins to all) shows 430 in common with humans, 264 with mouse, 58 with rabbit, and 42 with dog (20 nm and 100 nm AuNP and SiNP vitreous corona).

Table S3. Common gene sets to liposome corona and all humans,[1–4] and animals,[5–7] associate with visual perception (FDR 2.57e-2) and sensory perception of light (FDR 2.57e-2). Excluding mouse vitreal proteome shows hemoglobin and HC enriched ectonucleotide pyrophosphatase 2 as constitutive to vitreous.

| All common                     |
|--------------------------------|
| CRYAB  | Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component) |
| ACTB   | Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed] |
| CRYAA  | Alpha-crystallin A chain (Heat shock protein beta-4) (HspB4) [Cleaved into: Alpha-crystallin A(1-172); Alpha-crystallin A(1-168); Alpha-crystallin A(1-162)] |

| All except mouse common         |
|--------------------------------|
| HBB    | Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin] |
| ENPP2  | Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 (E-NPP 2) (EC 3.1.4.39) (Autotaxin) (Extracellular lysophospholipase D) (LysoPLD) |
| DKK3   | Dickkopf-related protein 3 (Dickkopf-3) (Dkk-3) (hDkk-3) |

As demonstrated in Figure 3, differential enrichment of 76 vitreous proteins out of 504 was observed after filtering out proteins not present in at least three samples. Two identified proteins were not listed
in the human or animal vitreous proteomes listed above: gamma-synuclein (SNCG) and mitochondrial ATP synthase subunit alpha (ATP5F1A). As these were found enriched in the HC, only 13 out of the 15 HC enriched proteins have been previously reported constitutive to the vitreous. Adipogenesis regulatory factor (ADIRF) has not been previously reported in the vitreous. ATP synthase subunit alpha (ATP5F1A) and vesicle-fusing ATPase (NSF) showed statistically significant differences in enrichment between the liposome formulations within HC, along with endoplasmic reticulum resident protein 29 (ERP29) within SC, all demonstrating a preference for AL2. There were no statistically significant differences in preferential enrichment between the two anionic liposome formulations for HC, and only vesicle-fusing ATPase (NSF) enrichment was significantly less depleted in the SC of AL2 (p<0.05). Since none of the proteins enriched in SC were observed in any of the HC replicates, a functional analysis of related genes was conducted to explore connections between the tightly bound HC and loosely interacting SC proteins (Figure S5). It demonstrated that glyceraldehyde-3-phosphate dehydrogenase (GADPH), one of the most abundant proteins in the liposome corona, had the most connections with other enriched proteins. Its physical interaction partners include D-3-phosphoglycerate dehydrogenase (PHGDH), tubulin beta chain (TUBB), Tubulin alpha-1B chain (TUBA1B) in the HC and 14-3-3 protein epsilon (YWHAE) and zeta/delta (YWHAZ) in the SC. YWHAZ and YWHAE that co-enriched in the SC are physical interaction partners. Interestingly, the keratin contaminants enriched in the HC are also YWHAZ physical interaction partners. Synuclein alpha (SNCA), which belongs to the same family of synucleins with beta and gamma that enriched in the HC, is also a GADPH interaction partner along with enolase 1 (ENO1). The primary enriched function was glucose metabolism, same as the primary function of the overlapping genes between our study and the other human vitreous proteomes. As discussed above, it is possible that protein contaminants influence corona formation through physical interactions with constitutive proteins or limit binding sites on the NPs. Clusterin (CLU), which has been proposed to mediate the stealth activity of polyethylene glycol towards MPS,[8] was enriched in
the source and slightly more enriched on the non-pegylated AL2. Although complement components were present in the vitreous source and are known to bind nanocarriers or corona proteins in serum and plasma,[9] complement components C3 and C4A, the latter of which was the 9th most enriched protein on AuNPs and SiNPs,[5] were relatively enriched in the liposome SC but depleted in the HC. Both C3 and clusterin are components of drusen, which may increase in concentration with age and in AMD.[10] The liposome-associated proteins were compared with earlier studies on protein localization in vitreous substructures,[3] with 15 genes associated with the vitreous cortex and five with core, but most did not localize to any substructure (Table S4). Figure 3 and Table 2 include three keratins that showed uncharacteristic peaks for contaminants and were also contained in one report on the human vitreal proteome.[2] However, these were excluded from further data analysis as probable contaminants from the liposome preparation or analysis steps.

The comparisons with previously published proteomes suggest that the liposomal HC and SC enriched proteins are probable corona constituents in human patients following liposome intravitreal injections. Earlier studies have noted that most vitreal proteins are intracellular but probably carry out specific functions, since they organize into pathways based on biological functions.[3,7] For instance, the enrichment of glucose metabolism pathways confirms that these proteins are highly abundant in all parts of the vitreous and energy metabolism is one of its key biological functions.[3] The overlap between our study and the other proteomes showed a strong association with glucose metabolism. These metabolic proteins are carried by microvesicles,[3] which might contribute to their enrichment on liposomes.
**Figure S5** Functional analysis of HC and SC enriched proteins using GeneMANIA identifies physical interactions (red lines) within HC, between HC and SC, and within SC. Most of them are with the highly enriched HC protein glyceraldehyde-3-phosphate dehydrogenase (GADPH).

**Table S4.** Comparison of liposome corona with human vitreous substructure proteomes by Skeie.[3]

| Vitreous subsection | Number of common | Gene name |
|---------------------|------------------|-----------|
| Anterior hyaloid    | 10               | ILF2, PSMB6, LTBP1, AHCYL2, RBBP4, RPL22, CPPED1, RPS6, HNRNPAB, PEPD |
| Vitreous cortex     | 15               | HSPA4L, SPR, PDC, TPPP3, PHPT1, PDXP, KARS, SH3BGR1L3, NONO, GUK1, UNC119, RPL31, KHDRBS1, GNB3, PCP2 |
| Vitreous base       | 2                | PURB, SH3GL2 |
| Vitreous core       | 5                | MAPT, MAP6, IGF2, TAGLN3, SRSF2 |

501 unique versus 32 common with vitreal substructures.
It has been proposed that some unique proteins such as enolase and catalase are found only in the vitreous as a result of proliferative diabetic retinopathy,[11,12] enolase is one of the most abundant proteins in healthy human vitreous.[3] It was found in the other human vitreous proteomes along with catalase.[1,2,4] Enolase 1 (ENO1) was also abundant in all our samples, including both liposome corona subsections and source vitreous, but no catalases were identified. Instead of reporting unique proteins in the diseased eye, Loukovaara et al.[13] showed that several proteins groups (complement, serpin protease, apolipoprotein, ciliary protein, immunoglobulin, collagen, fibrinogen, interalpha-trypsin protease, and alpha glycoprotein) and notably the coagulation cascade are upregulated in proliferative diabetic retinopathy. In addition to disease-specific changes, aging has been shown to affect the human vitreous proteome.[3] Based on a study comparing the vitreous proteomes of mature (>6 months) and young (8 weeks) New Zealand White Rabbits, the 14-3-3 protein zeta/delta (YWHAZ) was only found in the anterior vitreous of the mature rabbits. Similarly, YWHAZ was found in the vitreous of elderly patients in two studies,[3,6] but not in the other human vitreous studies that used vitrectomy samples from epiretinal gliosis patients[1] or embryonic 14-20 weeks’ gestation and 12-28-year-old young adult vitreous.[4] The review by Semba et al.[2] summarised early human ocular proteome studies on patients with diabetic retinopathies and macular holes, who are probably elderly patients. In our study, both 14-3-3 protein zeta/delta and epsilon (YWHAE) were significantly enriched in the liposome soft corona of both formulations and the HC of AL2, but were not detected in the AL1-PEG HC. Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 (ENPP2) was detected in all SC replicates, but not in any of the HCs. Collagens are the most abundant group of proteins in the vitreous,[14,15] but the heaviest enriched species in the SC is collagen XVIII alpha-1 chain (COL18A1) is not a structural protein but a precursor of the anti-angiogenic endostatin that is ubiquitous in the eye.[16]

While there are no previous reports on liposome vitreal coronas, the HC and SC enriched proteins included 45 annotations contained in the top 60 list of proteins that covered 93% of adsorbed proteins
on 20 nm and 100 nm silica and gold nanoparticle coronas (Table S5).[5] The most abundant protein identified in these vitreal coronas was vitrin (VIT-1), which was not identified by us or in the other studies in human or animal vitreous, despite its potential role in bridging collagen fibrils with hyaluronan.[17]

Table S5. Comparison of the liposome corona with the Top 60 proteins in the corona of 20 nm and 100 nm SiNP and AuNP by Jo et al.[5]

| Gene | Name |
|------|------|
| CA3  | Carbonic anhydrase 3 (EC 4.2.1.1) (Carbonate dehydratase III) (Carbonic anhydrase III) (CA-III) |
| ACTB | Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed] |
| LTBP2| Latent-transforming growth factor beta-binding protein 2 |
| ENO1 | Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein) |
| SFRP2| Secreted frizzled-related protein 2 (FRP-2) (sFRP-2) (Secreted apoptosis-related protein 1) (SARP-1) |
| PLG  | Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B] |
| CRYBA2| Beta-crystallin A2 (Beta-A2 crystallin) |
| CRYBA1| Beta-crystallin A3 [Cleaved into: Beta-crystallin A3, isoform A1, Delta4 form; Beta-crystallin A3, isoform A1, Delta7 form; Beta-crystallin A3, isoform A1, Delta8 form] |
| GC   | Vitamin D-binding protein (DBP) (VDB) (Gc protein-derived macrophage activating factor) (Gc-MAF) (GcMAF) (Gc-globulin) (Group-specific component) (Gc) (Vitamin D-binding protein-macrophase activating factor) (DBP-maf) |
| CLSTN1| Calsyntenin-1 (Alcadein-alpha) (Alc-alpha) (Alzheimer-related cadherin-like protein) (Non-classical cadherin XB31alpha) [Cleaved into: Soluble Alc-alpha (SAlc-alpha); CTF1-alpha (C-terminal fragment 1-alpha)] |
| GSN  | Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin) |
| CRYBB3| Beta-crystallin B3 (Beta-B3 crystallin) [Cleaved into: Beta-crystallin B3, N-terminally processed] |
| SPON1| Spondin-1 (F-spondin) (Vascular smooth muscle cell growth-promoting factor) |
| TTR  | Transthyretin (ATTR) (Prealbumin) (TBPA) |
| SERPINF| Pigment epithelium-derived factor (PEDF) (Cell proliferation-inducing gene 35 protein) (EPC-1) (Serpin F1) |
| PTGDS| Prostaglandin-H2 D-isomerase (EC 5.3.99.2) (Beta-trace protein) (Cerebrin-28) (Glutathione-independent PGD synthase) (Lipocalin-type prostaglandin-D synthase) (Prostaglandin-D2 synthase) (PGD2 synthase) (PGDS) (PGDS2) |
| CRYAA| Alpha-crystallin A chain (Heat shock protein beta-4) (HspB4) [Cleaved into: Alpha-crystallin A(1-172); Alpha-crystallin A(1-168); Alpha-crystallin A(1-162)] |
| CRYGC| Gamma-crystallin C (Gamma-C-crystallin) (Gamma-crystallin 2-1) (Gamma-crystallin 3) |
| RBP4 | Retinol-binding protein 4 (Plasma retinol-binding protein) (PRBP) (RBP) [Cleaved into: Plasma retinol-binding protein(1-182); Plasma retinol-binding protein(1-181); Plasma retinol-binding protein(1-179); Plasma retinol-binding protein(1-176)] |
| DKK3 | Dickkopf-related protein 3 (Dickkopf-3) (Dkk-3) (hDkk-3) |
| Protein   | Description                                                                 | Cleavage Products                                                                 |
|-----------|------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|
| OPTC      | Opticin (Oculoglycan)                                                        |                                                                                  |
| HPX       | Hemopexin (Beta-1B-glycoprotein)                                             |                                                                                  |
| RBP3      | Retinol-binding protein 3 (Interphotoreceptor retinoid-binding protein) (IRBP) | (Interstitial retinol-binding protein)                                             |
| ABI3BP    | Target of Nesh-SH3 (Tarsh) (ABI gene family member 3-binding protein) (Nesh-binding protein) (NeshBP) |                                                                                  |
| C3        | Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) | [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2] |
| ALB       | Serum albumin                                                                |                                                                                  |
| CRYAB     | Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component) |                                                                                  |
| APOA1     | Apolipoprotein A-I (Apo-A1) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I-[1-242])] |                                                                                  |
| CLU       | Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytolysis inhibitor) (CL1) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoBeta) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytolysis inhibitor b chain)] |                                                                                  |
| CRYBB2    | Beta-crystallin B2 (Beta-B2 crystallin) (Beta-crystallin Bp)                 |                                                                                  |
| COL2A1    | Collagen alpha-I(II) chain (Alpha-1 type II collagen) [Cleaved into: Collagen alpha-I(II) chain; Chondrocalcin] |                                                                                  |
| ENPP2     | Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 (E-NPP 2) (EC 3.1.4.39) (Autotaxin) (Extracellular lysophospholipase D) (LysoPLD) |                                                                                  |
| CRYBB1    | Beta-crystallin B1 (Beta-B1 crystallin)                                       |                                                                                  |
| FBLN2     | Fibulin-2 (FIBL-2)                                                           |                                                                                  |
| ALDH1A    | Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic) |                                                                                  |
| LDHB      | L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) |                                                                                  |
| AKR1B1    | Aldo-keto reductase family 1 member B1 (EC 1.1.1.300) (EC 1.1.1.372) (EC 1.1.1.54) (Aldehyde reductase) (Aldose reductase) (AR) (EC 1.1.1.21) |                                                                                  |
| CP        | Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)                                     |                                                                                  |
| SERPINA   | Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpin A1) | [Cleaved into: Short peptide from AAT (SPAAAT)]                                    |
| HBB       | Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin] |                                                                                  |
| TUBA1B    | Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain] |                                                                                  |
| FN1       | Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3] |                                                                                  |
| CRYGS     | Gamma-crystallin S (Beta-crystallin S) (Gamma-S-crystallin)                  |                                                                                  |
| EFEMP1    | EGF-containing fibulin-like extracellular matrix protein 1 (Extracellular protein S1-5) (Fibrillin-like protein) (Fibulin-3) (FIBL-3) |                                                                                  |
| HP        | Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain] |                                                                                  |
Figure S6. Venn diagram of protein-encoding genes with ANOVA significant differences between liposomes with at least 1-fold log₂ enrichment (*p<0.05). AL1-PEG SC did not have any proteins with significant differences (Table S4). The gene names are listed in Table S6.

Table S6. Venn diagram of protein-encoding genes with ANOVA significant differences between liposomes with at least 1-fold log₂ enrichment (*p<0.05).

| Liposomes      | Number | Genes                                      |
|----------------|--------|--------------------------------------------|
| AL1-PEG HC*    | 4      | SNCB KRT10 GAPDH KRT2                      |
| AL2HC*         |        |                                            |
| AL2 HC*        | 9      | PCBP3 EFEMP1 RAB11A SFRP2 NSF TUBB TUBA1B ATP5F1A SNCG |
| AL1-PEG HC*    | 2      | PHGDH KRT1                                 |
| AL2 SC*        | 2      | PCP4 ERP29                                  |

Figure S7. Venn diagram of protein-encoding genes in the vitreous union in at least one sample of the liposome hard (HC) and soft coronae (SC). The gene names are listed in Table S7.
Table S7. Venn diagram of protein-encoding genes in the vitreous union in at least one sample of the liposome hard (HC) and soft coronae (SC).

| Liposomes | Number | Genes |
|-----------|--------|-------|
| AL1-PEG   | 124    | MAP4  |
| AL1-PEG   |         | HSPB1 | |
| AL1-PEG   |         | RTN4  | |
| AL1-PEG   |         | CHGB  | |
| AL1-PEG   |         | UBE2NL| |
| AL1-PEG   |         | RLBP1 | |
| AL1-PEG   |         | MATR3 | |
| AL1-PEG   |         | HRG   | |
| AL1-PEG   |         | YWHAG | |
| AL1-PEG   |         | DPYSL2| |
| AL2 SC    | 124    | GOT1  | |
| AL2 SC    |         | CRABP2| |
| AL2 SC    |         | ATP6V1B2| |
| AL2 SC    |         | NSF   | |
| AL2 SC    |         | TTR   | |
| AL2 SC    |         | PTGDS | |
| AL2 SC    |         | CRYAA | |
| AL2 SC    |         | SAG   | |
| AL2 SC    |         | EPB41L2| |
| AL2 SC    |         | ALDOC | |
| AL2 SC    |         | MDH1  | |
| AL2 SC    |         | SOD1  | |
| AL2 SC    |         | LGALS1| |
| AL2 SC    |         | TPI1  | |
| AL2 SC    |         | APOE  | |
| AL2 SC    |         | C3    | |
| AL2 SC    |         | HSPA5 | |
| AL2 SC    |         | TUBB  | |
| AL2 SC    |         | CFL1  | |
| AL2 SC    |         | CRYAB | |
| AL2 SC    |         | CKB   | |
| AL2 SC    |         | HBZ   | |
| AL2 SC    |         | GNAT1 | |
| AL2 SC    |         | CLU   | |
| AL2 SC    |         | COL18A1| |
| AL2 SC    |         | HNRNPM| |
| AL2 SC    |         | CRYBB1| |
| AL2 SC    |         | FBLN2 | |
| AL2 SC    |         | LDHB  | |
| AL2 SC    |         | GDI1  | |
| AL2 SC    |         | HSP90AB1| |
| AL2 SC    |         | C4A   | |
| AL2 SC    |         | CST3  | |
| AL2 SC    |         | SNCG  | |
| AL2 SC    |         | CHGA  | |
| AL2 SC    |         | HSPA8 | |
| AL2 SC    |         | MAP2  | |
| AL2 SC    |         | KHSRP | |
| AL2 SC    |         | ALDH1A2| |
| AL2 SC    |         | HBB   | |
| AL2 SC    |         | TUBA1B| |
| AL2 SC    |         | FN1   | |
| AL2 SC    |         | CRMP1 | |
| AL2 SC    |         | PRPH  | |
| AL2 SC    |         | YWHAZ | |
| AL2 SC    |         | DDX17 | |
| AL2 SC    |         | GFAP  | |
| AL2 SC    |         | ACTB  | |
| AL2 SC    |         | GOT2  | |
| AL2 SC    |         | ENO1  | |
| AL2 SC    |         | SFRP2 | |
| AL2 SC    |         | BFSP1 | |
| AL2 SC    |         | ETFA  | |
| AL2 SC    |         | VCAN  | |
| AL2 SC    |         | GC    | |
| AL2 SC    |         | YWHAH | |
| AL2 SC    |         | LOC100739163| |
| AL2 SC    |         | BFSP2 | |
| AL2 SC    |         | PCBP1 | |
| AL2 SC    |         | GSN   | |
| AL2 SC    |         | CNRIP1| |
| AL2 SC    |         | SPON1 | |
| AL2 SC    |         | PKM   | |
| AL2 SC    |         | HSPA1B| |
| AL2 SC    |         | ELAVL1| |
| AL2 SC    |         | NRCAM | |
| AL2 SC    |         | LDHA  | |
| AL2 SC    |         | CFB   | |
| AL2 SC    |         | GDI1  | |
| AL2 SC    |         | LTF   | |
| AL2 SC    |         | HSP90AA1| |
| AL2 SC    |         | C4A   | |
| AL2 SC    |         | CST3  | |
| AL2 SC    |         | SNCG  | |
| AL2 SC    |         | CHGA  | |
| AL2 SC    |         | HSPA8 | |
| AL2 SC    |         | MAP2  | |
| AL2 SC    |         | KHSRP | |
| AL2 SC    |         | ALDH1A2| |
| AL2 SC    |         | HBB   | |
| AL2 SC    |         | TUBA1B| |
| AL2 SC    |         | FN1   | |
| AL2 SC    |         | CRMP1 | |
| AL2 SC    |         | PRPH  | |
| AL2 SC    |         | YWHAZ | |
| AL2 SC    |         | DDX17 | |
| AL2 SC    |         | GFAP  | |
| AL2 SC    |         | ACTB  | |
| AL2 SC    |         | GOT2  | |
| AL2 SC    |         | ENO1  | |
| AL2 SC    |         | SFRP2 | |
| AL2 SC    |         | BFSP1 | |
| AL2 SC    |         | ETFA  | |
| AL2 SC    |         | VCAN  | |
| AL2 SC    |         | GC    | |
| AL2 SC    |         | YWHAH | |
| AL2 SC    |         | LOC100739163| |
| AL2 SC    |         | BFSP2 | |
| AL2 SC    |         | PCBP1 | |
| AL2 SC    |         | GSN   | |
| AL2 SC    |         | CNRIP1| |
| AL2 SC    |         | SPON1 | |
| AL2 SC    |         | PKM   | |
| AL2 SC    |         | HSPA1B| |
| AL2 SC    |         | ELAVL1| |
| AL2 SC    |         | NRCAM | |
| AL2 SC    |         | LDHA  | |
| AL2 SC    |         | CFB   | |
| AL2 SC    |         | GDI1  | |
| AL2 SC    |         | LTF   | |
| AL2 SC    |         | HSP90AA1| |
| AL2 SC    |         | C4A   | |
| AL2 SC    |         | CST3  | |
| AL2 SC    |         | SNCG  | |
| AL2 SC    |         | CHGA  | |
| AL2 SC    |         | HSPA8 | |
| AL2 SC    |         | MAP2  | |
| AL2 SC    |         | KHSRP | |
| AL2 SC    |         | ALDH1A2| |
| AL2 SC    |         | HBB   | |
| AL2 SC    |         | TUBA1B| |
| AL2 SC    |         | FN1   | |
| AL2 SC    |         | CRMP1 | |
| AL2 SC    |         | PRPH  | |
| AL2 SC    |         | YWHAZ | |
| AL2 SC    |         | DDX17 | |
| AL2 SC    |         | GFAP  | |
| AL2 SC    |         | ACTB  | |
| AL2 SC    |         | GOT2  | |
| AL2 SC    |         | ENO1  | |
| AL2 SC    |         | SFRP2 | |
| AL2 SC    |         | BFSP1 | |
| AL2 SC    |         | ETFA  | |
| AL2 SC    |         | VCAN  | |
| AL2 SC    |         | GC    | |
| AL2 SC    |         | YWHAH | |
| AL2 SC    |         | LOC100739163| |
| AL2 SC    |         | BFSP2 | |
| AL2 SC    |         | PCBP1 | |
| AL2 SC    |         | GSN   | |
| AL2 SC    |         | CNRIP1| |
| AL2 SC    |         | SPON1 | |
| AL2 SC    |         | PKM   | |
| AL2 SC    |         | HSPA1B| |
| AL2 SC    |         | ELAVL1| |
| AL2 SC    |         | NRCAM | |
| AL2 SC    |         | LDHA  | |
| AL2 SC    |         | CFB   | |
| AL2 SC    |         | GDI1  | |
| AL2 SC    |         | LTF   | |
| AL2 SC    |         | HSP90AA1| |
| AL2 SC    |         | C4A   | |
| AL2 SC    |         | CST3  | |
| AL2 SC    |         | SNCG  | |
| AL2 SC    |         | CHGA  | |
| AL2 SC    |         | HSPA8 | |
| AL2 SC    |         | MAP2  | |
| AL2 SC    |         | KHSRP | |
| AL2 SC    |         | ALDH1A2| |
| AL2 SC    |         | HBB   | |
| AL2 SC    |         | TUBA1B| |
| AL2 SC    |         | FN1   | |
| AL2 SC    |         | CRMP1 | |
| AL2 SC    |         | PRPH  | |
| AL2 SC    |         | YWHAZ | |
| AL2 SC    |         | DDX17 | |
| AL2 SC    |         | GFAP  | |
| AL2 SC    |         | ACTB  | |
| AL2 SC    |         | GOT2  | |
| AL2 SC    |         | ENO1  | |
| AL2 SC    |         | SFRP2 | |
| AL2 SC    |         | BFSP1 | |
| AL2 SC    |         | ETFA  | |
| AL2 SC    |         | VCAN  | |
| AL2 SC    |         | GC    | |
| AL2 SC    |         | YWHAH | |
Table S8. Protein-encoding genes with ANOVA significant differences between liposome hard (HC) and soft coronae (SC) with at least 1-fold log2 enrichment in ascending order from higher to the lowest fold-change (*p<0.05).

| AL1-PEG HC | AL1-PEG SC | AL2 HC | AL2 SC |
|------------|------------|--------|--------|
| PHGDH      | TUBA1B     | ERP29  | PCP4   |
| KRT1       | NSF        |        |        |
| KRT10      | ATP5F1A    |        |        |
| KRT2       | SNCG       |        |        |
| GAPDH      | TUBB       |        |        |
| SNCB       | PCBP3      |        |        |
| GAPDH      |            |        |        |
| EEFEMP1    |            |        |        |
| RAB11A     |            |        |        |
| KRT10      | SFRP2      |        |        |
| KRT2       |            |        |        |

Table S9. Protein-encoding genes in at least one sample of the liposome hard (HC) and soft coronae (SC) in alphabetical order.

| AL1-PEG HC | AL1-PEG SC | AL2 HC | AL2 SC | AL1-PEG ALL | AL2 ALL |
|------------|------------|--------|--------|-------------|---------|
| ACTB       | A1BG       | A1BG   | A1BG   | A1BG        | A1BG    |
| AHSG       | A2M        | A2M    | A2M    | A2M         | A2M     |
| ALB        | AAK1       | AB13BP | AAK1   | AAK1        | AAK1    |
| ALDH1A2    | AB13BP     | ACOT7  | AB13BP | AB13BP      | AB13BP  |
| ALDOC      | ACAT2      | ACTB   | ACAT2  | ACAT2       | ACAT2   |
| APOA1      | ACLY       | AHCY   | ACLY   | ACLY        | ACLY    |
| APOD       | ACO2       | AHSG   | ACO2   | ACO2        | ACO2    |
| APOE       | ACOT7      | AKR1A1 | ACTB   | ACOT7       | ACOT7   |
| APP        | ACTB       | AKR1B1 | ACTG2  | ACTB        | ACTB    |
| ARR3       | ACTG1      | ALB    | ACTN4  | ACTG1       | ACTG2   |
| ATP5F1A    | ACTG2      | ALDH1A2| ACYP1  | ACYP1       | ACYP1   |
| ATP6V1B2   | ACTN4      | ALDOC  | ADD1   | ACTN4       | ACYP1   |
| BFSP1      | ACYP1      | APLP1  | ADH5   | ACYP1       | ADD1    |
| BFSP2      | ADD1       | APOA1  | AGA    | ADD1        | ADH5    |
| Gene  | Gene  | Gene  | Gene  | Gene  | Gene  |
|-------|-------|-------|-------|-------|-------|
| C3    | ADH5  | APOD  | AGT   | ADH5  | AGA   |
| C4A   | ADPGK | APOE  | AHCY  | ADFPGK| AGT   |
| CFB   | AGA   | APP   | AHCYL2| AGA   | AHCY  |
| CFL1  | AGT   | ARR3  | AHSG  | AGT   | AHCYL2|
| CHGA  | AHCY  | ASRGL1| AK1   | AHCY  | AHSG  |
| CHGB  | AHCYL2| ATP4A | AKR1A1| AHCYL2| AK1   |
| CKB   | AHSG  | ATP5F1A| AKR1B1| AHSG  | AKR1A1|
| CLU   | AK1   | ATP5F1B| AKR7A2| AK1   | AKR1B1|
| CNRIP1| AKR1A1| ATP6V1A| ALB   | AKR1A1| AKR7A2|
| COL18A1| AKR1B1| ATP6V1B2| ALDH1A2| AKR1B1| ALB   |
| COL9A2| AKR7A2| BFP1  | ALDH3A1| AKR7A2| ALDH1A2|
| CP    | ALB   | BFP2  | ALDH9A1| ALB   | ALDH3A1|
| CRYBP2| ALDH1A2| BIN1  | ALDOC | ALDH1A2| ALDH9A1|
| CRMP1 | ALDH3A1| C3    | APLP1 | ALDH3A1| ALDOC |
| CRYAA | ALDH9A1| C4A   | APOE  | ALDH9A1| APLP1 |
| CRYAB | ALDOC | CA2   | APP   | ALDOC  | APOA1 |
| CRYBB1| APLP1 | CAPS  | ASRGL1| APLP1  | APOD  |
| CRYBB2| APOA1 | CCT4  | ATP4A | APOA1  | APOE  |
| CRYBB3| APOE  | CDH2  | ATP5F1A| APOD   | APP   |
| CST3  | APP   | CFB   | ATP5F1B| APOE   | ARR3  |
| CTSD  | ARL3  | CFH   | ATP6AP2| APP    | ASRGL1|
| DDAH1 | ASRGL1| CFL1  | ATP6V1A| ARL3   | ATP4A |
| DDX17 | ATP4A | CHGA  | ATP6V1B2| ARR3  | ATP5F1A|
| DHX9  | ATP5F1A| CHGB  | ATP6V1G2| ASRGL1| ATP5F1B|
| DYSPL2| ATP5F1B| CKB   | B4GAT1 | ATP4A  | ATP6AP2|
| DYSPL3| ATP6AP2| CLSTN1| BCAM   | ATP5F1A| ATP6V1A|
| DYSPL4| ATP6V1A| CLTC  | BDH2   | ATP5F1B| ATP6V1B2|
| DSTN  | ATP6V1B2| CLU   | BFP1   | ATP6AP2| ATP6V1G2|
| EEF1G | ATP6V1G2| CNRIP1| BFP2   | ATP6V1A| B4GAT1|
| EFEMP1| B4GAT1| COL18A1| BLMH   | ATP6V1B2| BCAM |
| EFEMP2| BCAM  | CP    | BLVRB  | ATP6V1G2| BDH2 |
| ELAVL1| BDH2  | CRABP2| C2    | B4GAT1 | BFSP1 |
| ELN   | BFP1  | CRMP1 | C3    | BCAM   | BFSP2 |
| ENO1  | BFP2  | CRYAA | C4A   | BDH2   | BIN1  |
| ENO2  | BIN1  | CRYAB | CA2   | BFSP1  | BLMH  |
| EPB41L2| BLMH  | CRYBA4| CA3   | BFSP2  | BLVRB |
| ETLFA | BLVRB | CRYBB1| CADM1 | BIN1   | C2    |
| ETFB  | C2    | CRYBB2| CADM2 | BLMH   | C3    |
| FBN2  | C3    | CRYBB3| CADPS2| BLVRB  | C4A   |
| FN1   | C4A   | CRYM  | CALR  | C2    | CA2   |
| GAPDH | CA2   | CST3  | CAMK2A| C3    | CA3   |
| GC    | CA3   | CSTB  | CANX  | C4A   | CADM1 |
| GDHI  | CADM1 | CTSN  | CAP1  | CA2   | CADM2 |
| GFAP  | CADM2 | DCTN2 | CARHSP1| CA3   | CADPS2|
| GNAT1 | CADM3 | DDX17 | CCT3  | CADM1 | CALR  |
| Gene1 | Gene2 | Gene3 | Gene4 | Gene5 | Gene6 |
|-------|-------|-------|-------|-------|-------|
| GNAT2 | CADM4 | DHX9  | CCT5  | CADM2 | CAMK2A |
| GNB1  | CADPS2| DPYS12| CCT6B | CADM3 | CANX   |
| GOT1  | CALR  | DPYS14| CCT8  | CADM4 | CAP1   |
| GOT2  | CAMK2A| DSN   | CD44  | CADPS2| CAPS   |
| GPX4  | CANX  | EEF1G | CDC37 | CALR  | CARHSP1|
| GRIFIN| CAP1  | EFEMP1| CDH2  | CAMK2A| CCT3   |
| GRK1  | CARHSP1| EFEMP2| CDH7  | CANX  | CCT4   |
| GSN   | CCT3  | ELAVL1| CDHR1 | CAP1  | CCT5   |
| GYG1  | CCT5  | ELN   | CFB   | CARHSP1| CCT6B  |
| HBB   | CCT6B | ENO1  | CFH   | CCT3  | CCT8   |
| HBZ   | CCT8  | ENO2  | CFI   | CCT5  | CD44   |
| HNRNPK| CDC37 | ENPP2 | CFL1  | CCT6B | CDC37  |
| HNRNPM| CDH2  | EPB41L2| CFL2  | CCT8  | CDH2   |
| HNRNPU| CDH7  | ESD   | CHGA  | CDC37 | CDH7   |
| HPX   | CDHR1 | ETFA  | CHGB  | CDH2  | CDHR1  |
| HRG   | CEND1 | ETFB  | CHRLD1| CDH7  | CFB    |
| HSP90AA1| CFB  | F2    | CKAP1 | CDHR1 | CFH    |
| HSP90AB1| CFH  | FBLN2 | CKB   | CEND1 | CF1    |
| HSPA12A| CF1   | FBN2  | CKM   | CFB   | CFL1   |
| HSPA1B| CFL1  | FN1   | CKMT1A| CFH   | CFL2   |
| HSPA5 | CFL2  | FSCN1 | CLEC3B| CF1   | CHGA   |
| HSPA8 | CHGA  | GAPDH | CLSTN1| CFL1  | CHGB   |
| HSPB1 | CHGB  | GAPDHS| CLSTN3| CFL2  | CHRLD1 |
| ILF3  | CHRLD1| GC    | CLTC  | CHGA  | CKAP1  |
| KHSRP | CKAP1 | GDH1  | CLU   | CHGB  | CKB    |
| KIF5B | CKB   | GFAP  | CMPK1 | CHRD1 | CKM    |
| KPNB1 | CKM   | GNAT1 | CNDP2 | CKAP1 | CKMT1A |
| LAP3  | CKMT1A| GNAT2 | CNRIP1| CKB   | CLEC3B |
| LDHA  | CLEC3B| GB1   | CNTN1 | CKM   | CLSTN1 |
| LDHB  | CLSTN1| GNB3  | COL11A1| CKMT1A| CLSTN3 |
| LGALS1| CLSTN3| GNGT1 | COL18A1| CLEC3B| CLTC   |
| LOC100739163| CLTC | GOT1 | COL1A2 | CLSTN1 | CLU |
| LOC110259374| CLU  | GOT2 | COL5A1 | CLSTN3 | CMPK1 |
| LTF   | CMPK1 | GPX4  | COL9A2| CLTC  | CNRD2  |
| MAP2  | CNDP2 | GRIFIN| COMT  | CLU   | CNRIP1 |
| MAP4  | CNRIP1| GRK1  | CORO1B| CMPK1 | CNTN1  |
| MATR3 | CNTN1 | GSN   | CP    | CNDP2 | COL11A1|
| MDH1  | COL11A1| GUK1  | CRABP2| CNRIP1| COL18A1|
| MDH2  | COL18A1| GYG1  | CRMP1 | CNTN1 | COL1A2 |
| MSI2  | COL1A2 | HAPLN1| CRTAC1| COL11A1| COL5A1 |
| MYEF2 | COL5A1| HBB   | CRYAA | COL18A1| COL9A2 |
| NOVA1 | COL9A2| HBJ   | CRYAB | COL1A2| COMT   |
| NRCAM | COMT   | HDGF  | CRYBA4| COL5A1| CORO1B |
| NSF   | CORO1B | HMG2  | CRYBB1| COL9A2| CP     |
| PCBPI | CP     | HRNRPH1| CRYBB2| COMT  | CRABP2 |
| Gene 1 | Gene 2 | Gene 3 | Gene 4 | Gene 5 | Gene 6 |
|--------|--------|--------|--------|--------|--------|
| PCSK1N | CRABP2 | HNRNPM | CRYBB3 | CORO1B | CRMP1  |
| PEBP1  | CRMP1  | HNRNPU | CRYM   | CP     | CRTAC1 |
| PKM    | CRATC1 | HP     | CRYZ   | CRABP2 | CRYAB  |
| PGK1   | CRYAA  | HPX    | CS     | CRMP1  | CRYBA4 |
| PGHDH  | CRYAB  | HRG    | CST3   | CRTAC1 | CRYBB1 |
| PKM    | CRYBA4 | HSP90A1| CSTB   | CRYAA  | CRYBB2 |
| PLD3   | CRYBB1 | HSP90A1| CTS1   | CRYAB  | CRYBB3 |
| PPA1   | CRYBB2 | HSPA12A| CTS1   | CRYBA4 | CRYGD  |
| PPIA   | CRYBB3 | HSPA1B | CUTA   | CRYBB1 | CRYM   |
| PRELP  | CRYGD  | HSPA5  | CZIB   | CRYBB2 | CRYZ   |
| PROS1  | CRYM   | HSPA8  | DAG1   | CRYBB3 | CS     |
| PRPH   | CRYZ   | HSPB1  | DAZAP1 | CRYGD  | CST3   |
| PTGDS  | CS     | HSPG2  | DBI    | CRYM   | CSTB   |
| QSOX1  | CST3   | ILF2   | DBNL   | CRYZ   | CTS1   |
| RAB11B | CSTB   | IMPDH1 | DCTN2  | CS     | CTS1   |
| RAB1A  | CTSD   | IMPG1  | DDAH1  | CST3   | CUTA   |
| RAB3A  | CTSL   | ITIH4  | DDX17  | CSTB   | CZIB   |
| RAB6A  | CUTA   | KHSRP  | DDX39B | CTS1   | DAG1   |
| RAB7A  | CZIB   | KIAA0513| DLG2  | CTS1   | DAZAP1 |
| RALY   | DAG1   | KIF5B  | DPP3   | CUTA   | DBI    |
| RAN    | DAZAP1 | LAP3   | DYS1L2 | CZIB   | DBNL   |
| RBP3   | DB1    | LCN2   | DYS1L3 | DAG1   | DCTN2  |
| RLPB1  | DBNL   | LDHA   | DYS1L4 | DAZAP1 | DDAH1  |
| RPL31  | DCTN2  | LDHB   | DYS1L5 | DBI    | DDX17  |
| RPS13  | DDAH1  | LGALS1 | DSC2   | DBNL   | DDX39B |
| RPS18  | DDX17  | LMAN1  | DUSP3  | DCTN2  | DHX9   |
| RPS3   | DDX39B | LOC100739163| DYNC1I2| DDAH1  | DLG2   |
| RPS3A  | DLG2   | LOC110259374| ECE2  | DDX17  | DPP3   |
| RTN4   | DNM2   | LTF    | EEF1B2 | DDX39B | DYS1L2 |
| SAG    | DPP3   | MAP1B  | EEF1D  | DHX9   | DYS1L3 |
| SERPIN3-2| DPYSL2 | MAP2   | EEF1G  | DLG2   | DYS1L4 |
| SERPIND1| DPYSL3 | MAP4   | EEF2   | DNM2   | DYS1L5 |
| SFRP2  | DPYSL4 | MAP6   | EFEMP1 | DPP3   | DSC2   |
| SH3GL1 | DPYSL5 | MAPK1  | EIF4H  | DYS1L2 | DSTN   |
| SIRT2  | DSC2   | MATR3  | ELAVL1 | DYS1L3 | DUSP3  |
| SNCA   | DUSP3  | MDH1   | ELOC   | DYS1L4 | DYNC1I2|
| SNCG   | DYNC1I2| MDH2   | ENOD1  | DYS1L5 | ECE2   |
| SOD1   | ECE2   | MIF    | ENO1   | DSC2   | EEF1B2 |
| SPON1  | EEF1B2 | MS12   | ENO2   | DSTN   | EEF1D  |
| SPP1   | EEF1D  | NCL    | ENO3   | DUSP3  | EEF1G  |
| STPG4  | EEF1G  | NME2   | ENPP2  | DYNC1I2| EEF2   |
| STXB1P | EEF2   | NOVA1  | EPB41L2| ECE2   | EFEMP1 |
| SUCLA2 | EFEMP1 | NRCA   | EPB41L3| EEF1B2 | EFEMP2 |
| TMSB4  | EIF4A1 | NSF    | EPHX1  | EEF1D  | EIF4H  |
| TPI1 | EIF4H | NSFL1C | ERH | EEF1G | ELAVL1 |
|------|-------|-------|-----|-------|--------|
| TTR  | ELAVL1 | ORM1  | ERP29 | EEF2   | ELN    |
| TUBA1B | ELN  | OXR1  | ESD  | EFEMP1 | ELOC   |
| TUBB  | ELOC  | PCBP1 | ETFA | EFEMP2 | ENDOD1 |
| TUBB1 | ENDOD1 | PCSK1N | EZR  | EIF4A1 | EN01   |
| TUBB4A | EN01 | PEPB1 | F2   | EIF4H  | EN02   |
| TUFM  | EN02  | PFKL  | FABP3 | ELAVL1 | EN03   |
| UBE2NL | EN03 | PFKM  | FAM3C | ELN    | ENPP2  |
| VAT1  | ENPP2 | PFN1  | FARS A | ELOC | EPB41L2 |
| VCAN  | EPB41L2 | PFN2  | FARS B | ENDOD1 | EPB41L3 |
| YWHAB | EPB41L3 | PGK1  | FASN | EN01  | EPHX1  |
| YWHAG | EPHX1 | PHGDH | FBLN2 | EN02  | ERH    |
| YWHAH | ERH  | PKM   | FBN2 | EN03  | ERP29  |
| YWHAZ | ERP29 | PLK4  | FETUB | ENPP2 | ESD    |
| ZNF385A | ESD | PPA1  | FGA  | EPB41L2 | ETFA  |
| ETPA  | PHX H1 | FGB   | EPB41L3 | ETFB |
| ETPB  | PRDX1 | FKB P3 | EPHX1 | EZR   |
| EZR   | PRDX2 | FKB P4 | ERH  | F2    |
| F2    | PRDX6 | FMO D | ERP29 | FABP3 |
| FABP3 | PRELP | FN1   | ESD  | FAM3C |
| FAM3C | PROS1 | FSCN1  | ETFA | FARS A |
| FARS A | PRPH | FUBP3  | ETFB | FARS B |
| FARS B | PTGDS | GALM | EZR  | FASN  |
| FASN  | QSOX1 | GANAB | F2   | FBLN2 |
| FBLN2 | RAB11B | GAPD H | FABP3 | FBN2  |
| FBN2  | RAB14 | GARS  | FAM3C | FETUB |
| FETUB | RAB1A | GBE1  | FARS A | FGA  |
| FGA   | RAB3A | GC    | FARS B | FGB  |
| FGB   | RAB6A | GDI1  | FASN | FKB P3 |
| FKB P3 | RAB7A | GDI2 | FBLN2 | FKB P4 |
| FMOD  | RALY  | GFAP  | FBN2 | FMOD  |
| FN1   | RAN  | GLO1  | FETUB | FN1   |
| FSCN1 | RBP3  | GLUD1 | FGA  | FSCN1 |
| FUBP3 | RBP4  | GNAO1 | FGB  | FUBP3 |
| GALM  | RLBP1 | GNAT1 | FKB P3 | GALM |
| GANAB | RPL31 | GNB1  | FMOD | GANAB |
| GAPDH | RPS13 | GNGT1 | FN1  | GAPDH |
| GARS  | RPS18 | GOLM1 | FSCN1 | GAPD H |
| GBE1  | RPS3  | GOT1  | FUBP3 | GARS |
| GC    | RPS3A | GOT2  | GALM | GBE1  |
| GD11  | RTN4  | GPR37 | GANAB | GC   |
| GD12  | SAG   | GPX1  | GAPDH | GD1I |
| GFAP  | SELE NP1 | GRIF IN | GARS | GD1I |
| GLO1  | SERPINA1 | GSN | GBE1 | GFAP |
| GLUD1 | SERPINA3-2 | GSS | GC  | GLO1 |
| GLUL | SERPIND1 | GUK1 | GDI1 | GLUD1 |
|------|----------|------|------|-------|
| GNAO1 | SFRP2 | GYG1 | GDI2 | GNAO1 |
| GNAT1 | SH3GL1 | HAGH | GFAP | GNAT1 |
| GB1 | SIRT2 | HAPLN1 | GLO1 | GNAT2 |
| GNGT1 | SNCA | HBB | GLUD1 | GNB1 |
| GOLM1 | SNCG | HBZ | GLUL | GNB3 |
| GOT1 | SOD1 | HDGF | GNAO1 | GNGT1 |
| GOT2 | SPARC1 | HINT1 | GNAT1 | GOLM1 |
| GPHN | SPON1 | HMGB2 | GNAO1 | GOT1 |
| GPR37 | SPP1 | HNRNPA3 | GNB1 | GOT2 |
| GPX1 | SRSF3 | HNRNPB | GNGT1 | GPR37 |
| GRFIN | STPG4 | HNRNPC | GOLM1 | GPX1 |
| GRK1 | STXB1 | HNRNPD | GOT1 | GPX4 |
| GSN | SUC2 | HNRNPH1 | GOT2 | GRFIN |
| GSS | TFC | HNRNPK | GPHN | GRK1 |
| GUK1 | TMSB4 | HNRNPM | GPR37 | GSN |
| GYGI | TPI1 | HNRNPU | GPX1 | GSS |
| HAGH | TPM3 | HNRNPU2 | GPX4 | GUK1 |
| HAPLN1 | TTR | HP | GRFIN | GYG1 |
| HBB | TUBA1A | HPRT1 | GRK1 | HAGH |
| HBB | TUBA1B | HPX | GSN | HAPLN1 |
| HDGF | TUBB | HRG | GSS | HBB |
| HINT1 | TUBB1 | HSP90AA1 | GUK1 | HBZ |
| HIST1H1T | TUBB4A | HSP90AB1 | GYG1 | HDGF |
| HMGB2 | TUFM | HSP90B1 | HAGH | HINT1 |
| HNRNPA3 | UBB | HSPA1B | HAPLN1 | HMGB2 |
| HNRNPAB | UBE2NL | HSPA4 | HBB | HNRNPA3 |
| HNRNPC | UBE2V1 | HSPA5 | HBZ | HNRNPAB |
| HNRNPD | UCHL1 | HSPA6 | HDGF | HNRNPC |
| HNRNPH1 | VAMP1 | HSPA8 | HINT1 | HNRNPD |
| HNRNPK | VAT1 | HSPB1 | HIST1H1T | HNRNPH1 |
| HNRNPM | VCAN | HSPE1 | HMGB2 | HNRNPK |
| HNRNPUS | YWHAH | HSPG2 | HNRNPA3 | HNRNPM |
| HNRNPUS2 | YWAH | HSPH1 | HNRNPA4 | HNRNPU |
| HP | YWHAZ | IGFBP5 | HNRNPC | HNRNPUS2 |
| HPRT1 | ZNF385A | IGFBP7 | HNRNPD | HP |
| HPX | ILF2 | HNRNPH1 | HPRT1 |
| HRG | ILF3 | HNRNPK | HPX |
| HSP90AA1 | IMPA1 | HNRNPM | HRG |
| HSP90AB1 | IMPD1 | HNRNPU | HSP90AA1 |
| HSP90B1 | IMG1 | HNRNPL2 | HSP90AB1 |
| HSPA1B | ITH4 | HP | HSP90B1 |
| HSPA4 | KHSRP | HPRT1 | HSPA12A |
| HSPA5 | KIAA0513 | HPX | HSPA1B |
| HSPA6 | KTN1 | HRG | HSPA4 |
| Gene1 | Gene2 | Gene3 | Gene4 | Gene5 |
|-------|-------|-------|-------|-------|
| HSPA8 | KYAT3 | HSP90AA1 | HSPA5 |       |
| HSPB1 | LAP3  | HSP90AB1 | HSPA6 |       |
| HSPE1 | LCN2  | HSP90B1  | HSPA8 |       |
| HSPG2 | LDHA  | HSPA12A  | HSPB1 |       |
| HSPH1 | LDHB  | HSPA1B  | HSPE1 |       |
| IDH1  | LGALS1 | HSPA4  | HSPG2 |       |
| IGFBP5 | LIN7B | HSPA5  | HSPH1 |       |
| IGFBP7 | LMNA  | HSPA6  | IGFBP5 |       |
| ILF2  | LMNB2 | HSPA8  | IGFBP7 |       |
| ILF3  | LOC100736623 | HSPB1 | ILF2 |       |
| IMPA1 | LOC100739163 | HSPE1 | ILF3 |       |
| IMPDH1 | LOC106504545 | HSPG2 | IMPA1 |       |
| IMPG1 | LOC110256000 | HSPH1 | IMPDH1 |       |
| ITIH4 | LSAMP | IDH1  | IMPG1 |       |
| KHSRP | LTBP1 | IGFBP5 | ITIH4 |       |
| KIAA0513 | LTBP2 | IGFBP7 | KHSRP |       |
| KTN1  | LTF   | ILF2  | KIAA0513 |       |
| KYAT3 | MAGOH | ILF3  | KIF5B |       |
| LAP3  | MAN2B1 | IMPA1 | KTN1 |       |
| LCN2  | MAP1A | IMPDH1 | KYAT3 |       |
| LDHA  | MAP1B | IMPG1 | LAP3 |       |
| LDHB  | MAP1LC3B | ITIH4 | LCN2 |       |
| LGALS1 | MAP2  | KHSRP | LDHA |       |
| LIN7B | MAP4  | KIAA0513 | LDHB |       |
| LMAN1 | MAP6  | KIF5B | LGALS1 |       |
| LMNA  | MAPK1 | KPNB1 | LIN7B |       |
| LMNB2 | MAPT  | KTN1  | LMAN1 |       |
| LOC100514912 | MATA2 | KYAT3 | LMNA |       |
| LOC100736623 | MATR3 | LAP3 | LMNB2 |       |
| LOC100739163 | MDH1 | LCN2 | LOC100736623 |       |
| LOC106504545 | MDH2 | LDHA | LOC100739163 |       |
| LOC110256000 | MIA3 | LDHB | LOC106504545 |       |
| LSAMP | MIF   | LGALS1 | LOC110256000 |       |
| LTBPI | MPI   | LIN7B | LOC110259374 |       |
| LTBP2 | MYH10 | LMAN1 | LSAMP |       |
| LTF   | MYL6  | LMNA  | LTBPI |       |
| MAGOH | NCAM1 | LMNB2 | LTBP2 |       |
| MAN2B1 | NCAM2 | LOC100514912 | LTF |       |
| MAP1A | NCL   | LOC100736623 | MAGOH |       |
| MAP1B | NEFL  | LOC100739163 | MAN2B1 |       |
| MAP1LC3B | NEFM | LOC106504545 | MAP1A |       |
| MAP2  | NEGR1 | LOC110256000 | MAP1B |       |
| MAP4  | NFASC | LOC110259374 | MAP1LC3B |       |
| MAP6  | NIT2  | LSAMP | MAP2 |       |
| MAPK1 | NME2  | LTBPI | MAP4 |       |
| Gene1 | Gene2 | Gene3 | Gene4 |
|-------|-------|-------|-------|
| MAPT  | NONO  | LTBP2 | MAP6  |
| MATA2 | NOVA1 | LTF   | MAPK1 |
| MATR3 | NPEPPS| MAGOH | MAPT  |
| MDH1  | NPM1  | MAN2B1| MATA2 |
| MDH2  | NPTX2 | MAP1A | MATR3 |
| MIA3  | NQO2  | MAP1B | MDH1  |
| MIF   | NRCAM | MAP1LC3B| MDH2 |
| MPI   | NSF   | MAP2  | MIA3  |
| MSN   | NSFL1C| MAP4  | MIF   |
| MYH10 | NUCB1 | MAP6  | MPI   |
| MYL6  | NUCKS1| MAPK1 | MSI2  |
| NCAM1 | NUDT5 | MAPT  | MYH10 |
| NCAM2 | OPTC  | MATA2 | MYL6  |
| NCL   | ORM1  | MATR3 | NCAM1 |
| NEFL  | OTUB1 | MDH1  | NCAM2 |
| NEFM  | OXR1  | MDH2  | NCL   |
| NEGR1 | PA2G4 | MIA3  | NEFL  |
| NFASC | PAFAH1B3| MIF | NEFM  |
| NIT2  | PAICS | MPI   | NEGR1 |
| NME2  | PAK2  | MSI2  | NFASC |
| NONO  | PCBP1 | MSN   | NIT2  |
| NOVA1 | PCBP3 | MYEF2 | NME2  |
| NPEPPS| PCMT1 | MYH10 | NONO  |
| NPTX2 | PCSK1N| MYL6  | NOVA1 |
| NQO2  | PDC   | NCAM1 | NPEPPS|
| NRCAM | PDCD5 | NCAM2 | NPM1  |
| NSF   | PDCD6IP| NCL | NPTX2 |
| NSFL1C| PDHB  | NEFL  | NQO2  |
| NUCB1 | PDLA4 | NEFM  | NRCAM |
| NUCKS1| PDXK  | NEGR1 | NSF   |
| NUDT5 | PEBP1 | NFASC | NSFL1C|
| OPTC  | PEPD  | NIT2  | NUCB1 |
| ORM1  | PFKP  | NME2  | NUCKS1|
| OTUB1 | PFN1  | NONO  | NUDT5 |
| OXR1  | PFN2  | NOVA1 | OPTC  |
| PA2G4 | PGK1  | NPEPPS| ORM1  |
| PABPC1 | PGM1 | NPTX2 | OTUB1 |
| PAFAH1B3| PGM3 | NQO2  | OXR1  |
| PAICS | PGRMC1| NRCAM | PA2G4 |
| PAK2  | PHGDH | NSF   | PAFAH1B3|
| PALM  | PHPT1 | NSFL1C| PAICS |
| PAM   | PIN1  | NUCB1 | PAK2  |
| PCBPI | PKM   | NUCKS1| PCBPI |
| PCBPI | PLD3  | NUDT5 | PCBPI |
| PCMT1 | PLG   | OPTC  | PCMT1 |
| PCSK1N | PLK4 | ORM1 | PCSK1N |
|--------|------|------|--------|
| PDC    | PNPO | OTUB1| PDC    |
| PDCD5  | POLDIP3 | OXR1 | PDCD5  |
| PDCD6IP| PPA1  | PA2G4| PDCD6IP|
| PDHB   | PPIA  | PABPC1| PDHB   |
| PDLA4  | PPM1A | PAFAH1B3| PDLA4 |
| PDXK   | PPME1 | PAICS | PDXK   |
| PEBP1  | PPP2R1A | PAK2 | PEBP1  |
| PEPD   | PPP5C | PALM | PEPD   |
| PFKL   | PRDX1 | PAM  | PFKL   |
| PFKP   | PRDX2 | PCBP1| PFKM   |
| PFN1   | PRDX4 | PCBP3| PFKP   |
| PFN2   | PRDX5 | PCMT1| PFN1   |
| PGAM2  | PRDX6 | PCSK1N| PFN2   |
| PGK1   | PRKAR1A| PDC  | PGK1   |
| PGM1   | PRKAR2A| PDCD5| PGM1   |
| PGM3   | PRKCSH| PDCD6IP| PGM3   |
| PGRMC1 | PROS1| PDHB  | PGRMC1 |
| PHGDH  | PRPH  | PDI4  | PHGDH  |
| PHPT1  | PRPS2 | PDXK  | PHPT1  |
| PIN1   | PSAT1 | PEBP1 | PIN1   |
| PKM    | PSIP1 | PEPD  | PKM    |
| PLD3   | PSMA1 | PFKL  | PLD3   |
| PLG    | PSMA2 | PFKM  | PLG    |
| PLK4   | PSMA3 | PFKP  | PLK4   |
| PNPO   | PSMA5 | PFN1  | PNPO   |
| POLDIP3| PSMA6 | PFN2  | POLDIP3|
| PPA1   | PSMA8 | PGAM2 | PPA1   |
| PPIA   | PSMB1 | PGK1  | PPIA   |
| PPM1A  | PSMC3 | PGM1  | PPM1A  |
| PPME1  | PTGDS | PGM3  | PPME1  |
| PPP1R7 | PTPN11| PGRMC1| PPP2R1A|
| PPP2R1A| PTPRD | PHGDH | PPP5C  |
| PPP5C  | PTRG  | PHPT1 | PRDX1  |
| PRDX1  | PYGB  | PIN1  | PRDX2  |
| PRDX2  | QSOX1 | PKM   | PRDX4  |
| PRDX4  | RAB11B| PLD3  | PRDX5  |
| PRDX5  | RAB6A | PLG   | PRDX6  |
| PRDX6  | RAB7A | PLK4  | PRELP  |
| PRKAR1A| RALY  | PNPO  | PRKAR1A|
| PRKAR2A| RAN   | POLDIP3| PRKAR2A|
| PRKCSH | RANBP1| PPA1  | PRKCSH |
| PROS1  | RBMX  | PPIA  | PROS1  |
| PRPH   | RBP3  | PPM1A | PRPH   |
| PRPS2  | RBP4  | PPME1 | PRPS2  |
| PRSS35 | RELN | PPP1R7 | PSAT1 |
|--------|------|--------|-------|
| PSAT1  | RLBP1| PPP2R1A| PSIP1 |
| PSIP1  | RNH1 | PPP5C  | PSMA1 |
| PSMA1  | RPH3A| PRDX1  | PSMA2 |
| PSMA2  | RPL13| PRDX2  | PSMA3 |
| PSMA3  | RPL24| PRDX4  | PSMA5 |
| PSMA5  | RPL26| PRDX5  | PSMA6 |
| PSMA6  | RPL29| PRDX6  | PSMA8 |
| PSMA8  | RPL31| PRELP  | PSMB1 |
| PSMB1  | RPL8 | PRKAR1A| PSMC3 |
| PSMC2  | RPS11| PRKAR2A| PTGDS |
| PSMC3  | RPS20| PRKCSH | PTPN11|
| PTGDS  | RPSA | PROS1  | PTPRD |
| PTPN11 | RTCB | PRPH   | PTPRG |
| PTPRD  | RTN1 | PRPS2  | PYGB  |
| PTPRG  | RTN4 | PRSS35 | QSOX1 |
| PYGB   | RUVBL2| PSAT1 | RAB11B|
| QSOX1  | SAG  | PSIP1  | RAB14 |
| RAB11B | SARS | PSMA1  | RAB1A |
| RAB14  | SCG2 | PSMA2  | RAB3A |
| RAB3A  | SCG3 | PSMA3  | RAB6A |
| RAB7A  | SLY  | PSMA5  | RAB7A |
| RAN    | SCRN1| PSMA6  | RALY  |
| RANBP1 | SEC22B| PSMA8 | RAN   |
| RBMX   | SELENBP1| PSMB1 | RANBP1|
| RBP3   | SEMA7A| PSMC2  | RBMX  |
| RBP4   | SEPTIN2| PSMC3  | RBP3  |
| RELN   | SEPTIN7| PTGDS  | RBP4  |
| RLBP1  | SERPINA1| PTPN11| RELN  |
| RNH1   | SERPINA3-2| PTPRD | RLBP1 |
| RPH3A  | SERPINB1| PTPRG | RNH1  |
| RPL13  | SERPINII| PYGB  | RPH3A |
| RPL26  | SEZ6L | QSOX1  | RPL13 |
| RPL29  | SEZ6L2| RAB11B | RPL24 |
| RPL31  | SF3B2 | RAB14  | RPL26 |
| RPL8   | SFRP2 | RAB1A  | RPL29 |
| RPS11  | SH3GL1| RAB3A  | RPL31 |
| RPS20  | SMOC1 | RAB6A  | RPL8  |
| RPSA   | SNAP25| RAB7A  | RPS11 |
| RTCB   | SNAP91| RALY   | RPS13 |
| RTN1   | SNCG | RAN    | RPS18 |
| RTN4   | SOD1 | RANBP1 | RPS20 |
| RUVBL2 | SPARC| RBMX  | RPS3  |
| SAG    | SPARC1| RBP3  | RPS3A |
| SARS   | SPON1 | RBP4  | RPSA  |
| SCG2  | SPP1   | RELN  | RTCB  |
|-------|--------|-------|-------|
| SCG3  | SPR    | RLBP1 | RTN1  |
| SCLY  | SPTAN1 | RNH1  | RTN4  |
| SCRN1 | SRSF2  | RPH3A | RUVE2L|
| SEC22B| SRSF3  | RPL13 | SAG   |
| SELENBP1 | ST13 | RPL26 | SARS  |
| SEMA7A| STIP1  | RPL29 | SCG2  |
| SEPTIN2| STMN2 | RPL31 | SCG3  |
| SEPTIN7| STPG4 | RPL8  | SCLY  |
| SERPINA1| STX1B | RPS11 | SCRN1 |
| SERPINA3-2| STXB1 | RPS13 | SEC22B|
| SERPINB1| SUMO4 | RPS18 | SELENBP1|
| SERPINI1| SYN1   | RPS20 | SEMA7A|
| SEZ6L | SYNCRIP| RPS3  | SEPTIN2|
| SEZ6L2| TALDO1 | RPS3  | SEPTIN7|
| SF3B2 | TARS   | RPSA  | SERPINA1|
| SFRP2 | TCEA1  | RTCB  | SERPINA3-2|
| SH3GL1| TCEAL3 | RTN1  | SERPINB1|
| SMOC1 | TF     | RTN4  | SERPIND1|
| SNAP25| TIMP-2 | RUVE2L| SERPIN1|
| SNAP91| TFC    | SAG   | SEZ6L2|
| SNCG  | TMSB4  | SARS  | SEZ6L2|
| SOD1  | TNR    | SCG2  | SF3B2 |
| SPARC | TPI1   | SCG3  | SFRP2 |
| SPARCL1| TPM3  | SCLY  | SH3GL1|
| SPON1 | TPT1   | SCRN1 | SIRT2 |
| SPP1  | TRMT112| SEC22B| SMOC1 |
| SPR   | TTR    | SELENBP1| SNAP25|
| SPTAN1| TUBA1B | SEMA2A  | SNAP91|
| SRSF2 | TUBA4A | SEPTIN2 | SNCA |
| SRSF3 | TUBB   | SEPTIN7| SNCG  |
| STIP1 | TUBB1  | SERPINA1| SOD1 |
| STMN2 | TUBB4A | SERPINA3-2| SPARC|
| STPG4 | TXN    | SERPINB1| SPARCL1|
| STX1B | UBB    | SERPIN1D| SPON1 |
| STXB1 | UBE2NL | SERPINI1| SPP1  |
| SUMO4 | UBE2V1 | SEZ6L  | SPR   |
| SYN1  | UBE2V2 | SEZ6L2 | SPTAN1|
| SYNCRIP| UCHL1 | SF3B2  | SRSF2 |
| TALDO1| UCHL3  | SFRP2  | SRSF3 |
| TARS  | UNC119 | SH3GL1 | ST13  |
| TCEA1 | USO1   | SIRT2  | STIP1 |
| TCEAL3| VAMP1  | SMOC1  | STMN2  |
| TF    | VAT1   | SNAP25 | STPG4 |
| TIMP-2| VATIL  | SNAP91 | STX1B |
| TKFC   | VCAN | SNCA   | STXBP1 |
|--------|------|--------|--------|
| TMSB4  | VCP  | SNCG   | SUCLA2 |
| TNC    | VSIG10L | SOD1 | SUMO4  |
| TNR    | VSTM2A | SPARC  | SYN1   |
| TPII   | VSTM2B | SPARCL1| SYNCRIP |
| TPM3   | VTN  | SPON1  | TALDO1 |
| TPM4   | WARS | SPP1   | TARS   |
| TPT1   | WFIKKN2 | SPR  | TCEA1  |
| TRMT112| XYLTI| SPTAN1 | TCEAL3 |
| TTR    | YWHAB| SRSF2  | TF     |
| TUBA1B | YWHAG| SRSF3  | TIMP-2 |
| TUBA4A | YWHAH| STIP1  | TKFC   |
| TUBB   | YWHAQ| STMN2  | TMSB4  |
| TUBB1  | YWHAZ| STPG4  | TNR    |
| TUBB4A | ZFYVE19 | STX1B | TPII   |
| TXN    | ZNF207| STXBPI| TPM3   |
| TXNL1  | SUCLA2| TPT1   |        |
| UBB    | SUMO4 | TRMT112|        |
| UBE2NL | SYN1 | TTR    |        |
| UBE2V1 | SYNCRIP| TUBA1A |        |
| UBE2V2 | TALDO1| TUBA1B |        |
| UCHL1  | TARS  | TUBA4A |        |
| UCHL3  | TCEA1 | TUBB   |        |
| UNC119 | TCEAL3| TUBB1  |        |
| USO1   | TF    | TUBB4A |        |
| VAMP1  | TIMP-2| TUFM   |        |
| VAT1   | TKFC  | TXN    |        |
| VAT1L  | TMSB4 | UBB    |        |
| VCAN   | TNC   | UBE2NL |        |
| VCL    | TNR   | UBE2V1 |        |
| VCP    | TPII  | UBE2V2 |        |
| VSIG10L| TPM3  | UCHL1  |        |
| VSTM2A | TPM4  | UCHL3  |        |
| VSTM2B | TPT1  | UNC119 |        |
| VTN    | TRMT112| USO1  |        |
| WARS   | TTR   | VAMP1  |        |
| WFIKKN2| TUBA1B| VAT1   |        |
| XYLTI  | TUBA4A| VAT1L  |        |
| YWHAB  | TUBB  | VCAN   |        |
| YWHAG  | TUBB1 | VCP    |        |
| YWHAH  | TUBB4A| VSIG10L|        |
| YWHAQ  | TUFM  | VSTM2A |        |
| YWHAZ  | TXN   | VSTM2B |        |
| ZFYVE19| TXNL1 | VTN    |        |
| ZNF207 | UBB   | WARS   |        |
| UBE2NL    | WFIKKN2   |
|----------|-----------|
| UBE2V1   | XYLT1     |
| UBE2V2   | YWHAB     |
| UCHL1    | YWHAG     |
| UCHL3    | YWHAH     |
| UNC119   | YWHAQ     |
| USO1     | YWHAZ     |
| VAMP1    | ZFYVE19    |
| VAT1     | ZNF207    |
| VAT1L    | ZNF385A   |
| UCAN     |            |
| VCL      |            |
| VCP      |            |
| VSIG10L  |            |
| VSTM2A   |            |
| VSTM2B   |            |
| VTN      |            |
| WARS     |            |
| WFIKKN2  |            |
| XYLT1    |            |
| YWHAB    |            |
| YWHAG    |            |
| YWHAH    |            |
| YWHAQ    |            |
| YWHAZ    |            |
| ZFYVE19  |            |
| ZNF207   |            |
| ZNF385A  |            |

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