Supplementary Information

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1 Computational methods

1.1 Notation

91356 images were obtained, each consisting of 670×510 pixels and comprising 3 color channels each at 12 bit $(0 \ldots 4095)$ intensity resolution. We denote the input data for the three channels as follows: actin $\boldsymbol{a_0}$, tubulin $\boldsymbol{t_0}$ and DNA $\boldsymbol{d_0}$.

1.2 Nucleus segmentation

We computed the nucleus mask $\boldsymbol{N}$, a binary image indicating those pixels that belong to a nucleus. It was defined by

$$\boldsymbol{N} = F\Big(\gamma_{\mathrm{K}}\big(\phi_{\mathrm{K}}(\boldsymbol{d_0} > \boldsymbol{d_0} \bigstar \mathrm{J} + \sigma_d)\big)\Big),$$

where $\bigstar$ is the convolution operator, J is a constant matrix of size 35×35 such that the sum of its elements is equal to 1, σ_d is a parameter, K is a 3×3 matrix of values $(0,1,0;1,1,1;0,1,0)$, ϕ_{K} is the morphological closing operator using K as structuring element, and γ_{K} is the morphological opening operator. The operator F removes internal holes by applying floodfill starting from a point outside the objects and taking the complement. The computation of the nucleus mask $\boldsymbol{N}$ can be seen as an algorithm where the nuclei are first extracted by performing a local adaptive thresholding on the DNA channel $\boldsymbol{d_0}$ using a filter J which is two times bigger than the biggest nuclei we want to detect, followed by two morphological operations to clean the nuclei perimeter and remove artefacts smaller than K and a final step to remove internal holes.

A nucleus N is designated by the set of coordinates (i, j) of its pixels. The set of all nuclei $\{N_i\}_i$ was computed using the watershed segmentation algorithm [2] performed on the distance map of the binary mask $\boldsymbol{N}$, with a height tolerance of 3. Nuclei which were: too faint (`Nint`/`Npxs` < 0.1, too small (`Npxs` < 150) or too large (`Npxs` > 2070) were excluded from the analysis. Here, `Npxs` $= \sum_{i,j \in N} 1$ denotes the nucleus size in pixels and `Nint` $= \sum_{i,j \in N} d_{ij}$ is the nucleus intensity.

1.3 Channel calibration

Let $\boldsymbol{S}$ be the mask defined by $\boldsymbol{S} = \delta_{\mathrm{L}}(\boldsymbol{N})\ \&\ !\varepsilon_{\mathrm{L}}(\boldsymbol{N})$, where δ_{L} and ε_{L} are the morphological dilatation and erosion operators using the structuring element L, which is here a binary disc of diameter 9. The calibrated channels $\boldsymbol{a}$, $\boldsymbol{t}$ and $\boldsymbol{d}$ are then defined by:

$$\begin{aligned}\boldsymbol{a} &= \alpha_a(\boldsymbol{a'}/a'_S)^{\beta_a}\\ \boldsymbol{t} &= \alpha_t(\boldsymbol{t'}/t'_S)^{\beta_t}\\ \boldsymbol{d} &= \alpha_d(\boldsymbol{d'}/d'_N)^{\beta_d}\end{aligned}$$

where $\boldsymbol{a'} = \boldsymbol{a_0} - \bar{a}_0$, with $\bar{a}_0 = \sum_{i,j:a_{0,ij}<q} a_{0ij} / \sum_{i,j:a_{0,ij}<q} 1$, q being the 1% quantile of $\boldsymbol{a_0}$, $\boldsymbol{t'}$ and $\boldsymbol{d'}$ are defined in the same way as $\boldsymbol{a'}$, where $a'_S =$

$\sum_{i,j} a'_{ij} S_{ij} / \sum_{i,j} S_{ij}$, $t'_S = \sum_{i,j} t'_{ij} S_{ij} / \sum_{i,j} S_{ij}$, $d'_N = \sum_{i,j} d'_{ij} N_{ij} / \sum_{i,j} N_{ij}$ and $\alpha_a = 0.3$, $\alpha_t = 0.4$, $\alpha_d = 0.55$, $\beta_a = 1.2$, $\beta_t = 1.4$ and $\beta_d = 1.4$.

1.4 Cell segmentation

To compute the cell mask $\boldsymbol{C}$, a binary image indicating the pixels belonging to any cell, we applied a global thresholding on the mixed channel

$$\boldsymbol{C} = \phi_{\mathrm{K}}(\boldsymbol{m} \bigstar \mathrm{K} > \mu_{\boldsymbol{C}}),$$

where the mixed channel $\boldsymbol{m}$ was defined by $m_{ij} = \sqrt{a_{ij}^2 + t_{ij}^2 + d_{ij}^2}$, $\mu_{\boldsymbol{C}} = 0.12$, and K and ϕ_{K} are as above.

A cell C is designated by the set of coordinates (i, j) of its pixels. The set of all cells $\{C_i\}_i$ was computed using the Voronoi-based cell segmentation algorithm from Jones [6] on the image $\boldsymbol{m}^{0.2}$, with the seeds $\{N_i\}_i$, the cell mask $\boldsymbol{C}$ and the regularization parameter $\lambda = 0.1$. Cells which were mangled because they were too close to the borders (`edg`/`per` > 0.3), too small (`pxs` < 150), too large (`pxs` > 14500) or too long (`per` > 750) were excluded from the analysis. `edg` is the number of pixels that are at the edge of the cell, `per` is the cell perimeter in pixels and `pxs` $= \sum_{i,j \in C} 1$ is the cell size in pixels.

To fuse binucleated cells that were wrongly segmented as two distinct cells, the segmentation was postprocessed with a supervised learning method. Given a pair of cells, the decision of fusing them into one single cell or leaving them unchanged was learned using 17 features: `distp`, `ext`$^{\oplus}$, `ext`$^{\Delta}$, `Next`$^{\oplus}$, `Next`$^{\Delta}$, `NCdist`$^{\oplus}$, `NCdist`$^{\Delta}$, `int`$^{\oplus}$, `int`$^{\Delta}$, `Nint`$^{\oplus}$, `Nint`$^{\Delta}$, `Nt.den`$^{\oplus}$, `Nt.den`$^{\Delta}$, `NtoATint`$^{\Delta}$, `Tz.11`$^{\Delta}$, `Az.11`$^{\Delta}$ and `Nz.33`$^{\Delta}$. The feature `distp` is the Euclidean distance between two cell centers of mass, the superscripted $\oplus$-features are the cell pair mean corresponding features as defined in Section 1.5 and the superscripted Δ-features are the cell pair absolute difference corresponding features. Only the cell pairs with a distance `distp` lower than 70 were considered. The training set consisted of a manually annotated set of 551 cell pairs that had to be fused and 1023 cell pairs that had to be left unchanged. Using a binary support vector machine (SVM) with a radial kernel, the parameters (C, γ) were optimized using grid search through 5-fold cross-validation to maximize the prediction rate. Optimal values $C = 10$ and $\gamma = 0.4$ led to a correct prediction rate of 87.7%.

1.5 Cell feature extraction

Each cell was characterized by a set of 51 morphological descriptors also referred to as features, which were grouped into four categories: 9 geometric features, 26 Haralick textural features, 11 Zernike moments and 5 miscellaneous features. All descriptors are translation and rotation invariant and are commonly used in cell imaging [9, 8] for classification purposes.

Geometric features Geometric features were used to quantify the shape of each cell and of its nucleus. They can be expressed in terms of low-order image moments, computed on the mixed component $\boldsymbol{m}$ over the cell domain C and on the DNA channel d over the nucleus region N. The raw (p, q)-moment μ^c_{pq} of the component $\boldsymbol{m}$ over C is $\mu^c_{pq} = \sum_{i,j \in C} i^p j^q m_{ij}$. The centered (p, q)-moment $\bar{\mu}^c_{pq}$ is $\bar{\mu}^c_{pq} = \sum_{i,j \in C} (i - \mu^c_{10}/\mu^c_{00})^p (j - \mu^c_{01}/\mu^c_{00})^q m_{ij}$. The moments of the DNA component $\boldsymbol{d}$ over the nucleus domain N were defined in the same way and were denoted by μ^n_{pq} and $\bar{\mu}^n_{pq}$.

- `int` - Cell intensity, $\texttt{int} = \mu^c_{00}$.
- `ext` - Cell extension, $\texttt{ext} = (\lambda^c_1 \lambda^c_2)^{1/4}$ where λ^c_1 and λ^c_2 are the eigenvalues of the covariance matrix of the mixed component $\boldsymbol{m}$ computed over the cell C, given by $\lambda_1 = \bar{\mu}^c_{00}(\bar{\mu}^c_{20} + \bar{\mu}^c_{02} + \Delta)/2$ and $\lambda_2 = \bar{\mu}^c_{00}(\bar{\mu}^c_{20} + \bar{\mu}^c_{02} - \Delta)/2$ with $\Delta = \bar{\mu}^c_{00}\sqrt{4{\bar{\mu}^c_{11}}^2 + (\bar{\mu}^c_{20} - \bar{\mu}^c_{02})^2}$. This parameter can also be interpreted as the geometric mean of the lengths of the axes of an ellipse fitted to the cell shape.
- `ecc` - Cell eccentricity, $\texttt{ecc} = \sqrt{1 - \lambda^c_2/\lambda^c_1}$.
- `Nint` - Nucleus intensity, $\texttt{Nint} = \mu^n_{00}$.
- `Next` - Nucleus extension, $\texttt{Next} = (\lambda^n_1 \lambda^n_2)^{1/4}$, where λ^n_1 and λ^n_1 were computed in the same way as λ^c_1 and λ^c_1, but on the DNA channel d over the nucleus domain N.
- `Necc` - Nucleus eccentricity, $\texttt{Necc} = \sqrt{1 - \lambda^n_2/\lambda^n_1}$.
- `NtoATsz` - Nucleus to cell size ratio, $\texttt{NtoATsz} = \texttt{Next}^2/\texttt{ext}^2$.
- `NtoATint` - Nucleus to cell intensity ratio, $\texttt{NtoATint} = \texttt{Nint}/\texttt{int}$.
- `NCdist` - Distance between the nucleus center of mass to the cell center of mass, $\texttt{NCdist} = \sqrt{(\mu^n_{10}/\mu^n_{00} - \mu^c_{10}/\mu^c_{00})^2 + (\mu^n_{01}/\mu^n_{00} - \mu^c_{01}/\mu^c_{00})^2}$.

Haralick textural features Haralick textural features [10] are a set of statistical measures derived from the gray levels co-occurrence matrix (GLCM) f. This matrix represents the frequency f_{ij} that a pixel of intensity i has a right, bottom, right-bottom or left-bottom neighbour of intensity j. When computed over p different gray levels, the GLCM f is by construction a $p \times p$ symmetric matrix which fulfills $\sum_{i,j} f_{ij} = 1$.

- `asm` - Angular second moment, $\texttt{asm} = \sum_{i,j} f^2_{ij}$.
- `con` - Contrast, $\texttt{con} = \sum_{k=0}^{p-1} k^2 \sum_{i,j \,:\, |i-j|=k} f_{ij}$.
- `cor` - Correlation, $\texttt{cor} = \big(\sum_{i,j} ij f_{ij} - \mu_1\mu_2\big)/\sigma_1\sigma_2$, where μ_1, μ_2, σ_1 and σ_2 are the means and standard deviations of the marginal frequencies $f_{i.} = \sum_j f_{ij}$ and $f_{.j} = \sum_i f_{ij}$.

- `var` - Sum of squares variance `asm` $= \sum_{i,j} (i - \mu_1)^2 f_{ij}$.
- `idm` - Inverse difference moment, `idf` $= \sum_{i,j} f_{ij}/(1 + (i - j)^2)$.
- `sav` - Sum average, `sav` $= \sum_{k=2}^{2p} k f_k^+$, where $f_k^+ = \sum_{i,j \,:\, i+j=k} f_{ij}$.
- `sva` - Sum variance, `sav` $= \sum_{k=2}^{2p} (k - \texttt{sen})^2 f_k^+$ (original Haralick formula), where $f_k^+ = \sum_{i,j \,:\, i+j=k} f_{ij}$.
- `sen` - Sum entropy, `sen` $= -\sum_{k=2}^{2p} f_k^+ \log f_k^+$.
- `ent` - Entropy, `ent` $= -\sum_{ij} f_{ij} \log f_{ij}$.
- `dva` - Difference variance, `dva` $= \sum_{k=0}^{p-1} k^2 f_k^- - \left(\sum_{k=0}^{p-1} k f_k^-\right)^2$, where $f_k^- = \sum_{i,j \,:\, |i-j|=k} f_{ij}$.
- `den` - Difference entropy, `den` $= -\sum_{k=0}^{p-1} f_k^- \log f_k^-$.
- `f12` - Information measure, `f12` $= \left(\sum_{ij} f_{ij} \log f_{ij} - \sum_{ij} f_{ij} \log(f_{i.} f_{.j})\right)/\alpha$ where $\alpha = \max(\sum_i f_{i.} \log f_{i.}, \sum_j f_{.j} \log f_{.j})$.

Actin and tubulin cell textures were captured by the previously defined 12 Haralick features, computed on the actin channel a (prefixed by `At`) and the tubulin channel t (prefixed by `Tt`) on the cell domain C using $p = 32$ gray levels. Nucleus texture was captured by the `ent` and `den` Haralick features, computed on the DNA channel d (prefixed by `Nt`) on the nucleus domain N.

Zernike moments Complex Zernike polynomials are a set of orthogonal polar polynomials over the unit disk. Projection of an image onto them gives rise to Zernike moments [12], which are useful to characterize texture information. Zernike (m, n)-moments Z_{mn} of a centered and scaled to the unit disk image $P_{xy} : x^2 + y^2 \leq 1$ are defined by:

$$Z_{mn} = \frac{m+1}{\pi} \sum_{\substack{x,y \\ x^2+y^2 \leq 1}} P_{xy} [V_{mn}(x, y)]^* S$$

where

$$\begin{aligned}
x &= r\cos\theta \\
y &= r\sin\theta \\
V_{mn}(r, \theta) &= R_{mn}(r)\exp(jn\theta) \\
R_{mn}(r) &= \sum_{s=0}^{\frac{m-|n|}{2}} (-1)^s \quad F(m, n, s, r) \\
F(m, n, s, r) &= \frac{(m-s)!}{s!(\frac{m+|n|}{2} - s)!\,(\frac{m-|n|}{2} - s)!} r^{m-2s}
\end{aligned}$$

The absolute values of the Zernike moments $\mathtt{Z}_{11}$, $\mathtt{Z}_{22}$, $\mathtt{Z}_{31}$, $\mathtt{Z}_{33}$ and Z_{44} were used to describe the texture of the actin channel a (prefixed by `Az`) and the tubulin channel t (prefixed by `Tz`) computed on the cell domain C. The Zernike moment Z_{33} was the only one used to describe the texture of the DNA channel $\boldsymbol{d}$ (prefixed by `Nz`), computed on the nucleus domain N.

Miscellaneous features The following features were also used to further describe the morphology of a cell:

- `AI1` - First translation, rotation and scale-invariant Hu's moment [5] computed on the actin component $\boldsymbol{a}$ over the cell domain C. By definition $\texttt{AI1} = (\bar{\mu}_{20} + \bar{\mu}_{02})/\bar{\mu}_{00}^2$, where $\bar{\mu}_{pq}^a$ is the centered (p, q)-moment of $\boldsymbol{a}$ computed over the support C, i. e. $\bar{\mu}_{pq} = \sum_{i,j \in C} (i - \mu_{10}^a/\mu_{00}^a)^p (j - \mu_{01}^a/\mu_{00}^a)^q a_{ij}$, where $\mu_{pq}^a = \sum_{i,j \in C} i^p j^q a_{ij}$.
- `TI1` - First Hu's moment, computed in the same way as `AI1` on the tubulin component $\boldsymbol{t}$ over the cell domain C.
- `AinNint` - Nucleus actin intensity to cell actin intensity ratio, $\texttt{AinNint} = \sum_{i,j \in N} a_{ij}/\mu_{00}^a$.
- `TinNint` - Nucleus tubulin intensity to cell tubulin intensity ratio, $\texttt{TinNint} = \sum_{i,j \in N} t_{ij}/\mu_{00}^t$.
- `AtoTint` - Cell actin intensity to cell tubulin intensity ratio, $\texttt{AtoTint} = \mu_{00}^a/\mu_{00}^t$.

1.6 Cell classification

Based on their features, cells were classified into the 10 cell classes described in Table SII using the 'one-against-one' multi-class strategy of the SVM algorithm as provided by the `libsvm` [3] library via the R package `e1071`. Cell features were standardized to zero mean and unit variance, computed on all the cells from the screen.

Training set A set of 2545 manually annotated cells distributed according to Table SIII was selected to train the SVM.

Cross-validation performance Using a radial kernel, the SVM parameters (C, γ) were optimized using grid search through 5-fold cross-validation to maximize the mean class prediction rate. Optimal values $C = 200$ and $\gamma = 5.10^{-4}$ led to a mean prediction rate of 83.4%. Class-specific prediction rates are given in Table SIV and the full confusion table is shown in Table SV.

Results Distribution of the predicted cell classes from all the cells of the screen is shown in Table SVI.

Influence of the feature set on classification performance To test the importance of individual features and their redundancy, we conducted a numerical experiment using greedy feature selection: Starting with the original set of $n = 51$ features, we removed independently every feature to produce n sets of $n-1$ features and computed the 5-fold cross-validation classification performances, in the same way as described above, for each of these sets. We iterated the process and removed at each step the feature which least decreased the classification performance. Results are presented in Fig. S2 and show that the classification performance remains almost constant between 51 and 24 features, with a constant and low variability. This suggests that (i) the classification performance is not driven by individual features, but rather depends on the joint behavior of multiple features and (ii) that there is redundancy between features. These properties contribute to the robustness of our method.

1.7 Per well quality control

To discard a small fraction of the data that showed apparent quality problems, for example due to marker stains, sporadic out-of-focus images and plate edge effects, we devised a scheme that detected outliers in the feature value distributions (e. g., too many dead cells, too many cells, too few cells). Data of poor quality was filtered on the *per well* level, and the locations of the filtered wells are shown in Fig. S1.

1.8 Perturbation phenotypic profiles and phenoprints

Each well subject to an RNAi perturbation was summarized by a vector $\boldsymbol{x} \in \mathbb{R}^p$ of $p = 13$ numerical values, corresponding to the rows of Table SVII. $\boldsymbol{x}$ is termed a *phenotypic profile*.

To take into account the experimental variability of the phenotypic profiles $\boldsymbol{x} = (x_1, \ldots, x_{13})$, and to compensate for observed batch effects due to apparent systematic shifts in experimental conditions, we devised a normalisation and data transformation method. The values x_i were transformed to the range $[0, 1]$ using a parameterized sigmoid function. A value of 1 indicated clear presence of the phenotype, a value of 0 clear absence, and values in between were allowed for a range of intermediate, less certain observations. The motivation for this transformation is the assumption that our phenotypes of interest can be modelled, to useful approximation, as being binary (absent or present), and that transformed values are subject to less experimental variability.

Thus, each well subject to an RNAi perturbation was summarized by a *phenoprint* $\boldsymbol{y} \in [0, 1]^{19}$ as described in Table SVII.

For each of the components x_k of $\boldsymbol{x}$, we considered whether its value was significantly elevated, resulting in y_k^+; for 6 of the components, we also considered whether it was significantly decreased, resulting in y_k^-. y_k^+ and y_k^- were obtained from by the following transformations:

$$
y_k^+ \;=\; \frac{1}{1+\exp\big(-\eta^+(x_k-\alpha^+)\big)} \quad \text{with} \begin{cases} \alpha^+ = & F_{a_k^+}(\mathcal{B}_k^{\boldsymbol{x}}) \\ \beta^+ = & F_{b_k^+}(\mathcal{B}_k^{\boldsymbol{x}}) \\ \eta^+ = & \log(3)/\big(\beta^+-\alpha^+\big) \end{cases}
$$

$$
y_k^- \;=\; \frac{1}{1+\exp\big(-\eta^-(x_k-\alpha^-)\big)} \quad \text{with} \begin{cases} \alpha^- = & 1-F_{a_k^-}(\mathcal{B}_k^{\boldsymbol{x}}) \\ \beta^- = & 1-F_{b_k^-}(\mathcal{B}_k^{\boldsymbol{x}}) \\ \eta^- = & \log(3)/\big(\beta^--\alpha^-\big) \end{cases}
$$

Here $k=1,\dots,13$ indexes the perturbation descriptors, $\mathcal{B}_k^{\boldsymbol{x}}$ is the sample of values of the k-th descriptor for all perturbations in the same experimental batch as $\boldsymbol{x}$, and $F_q(\mathcal{B}_k^{\boldsymbol{x}})$ is the q-th quantile of this sample. a_k^+, a_k^-, b_k^+, b_k^- are parameters of the transformation that were obtained as described in Section 1.9. These parameters control the location and slope of the transformation functions and are defined such that their transformed values will be 1/2 and 3/4, respectively. Hence they can be interpreted as follows: a_k^+ (resp. a_k^-) represent the fraction of perturbations in the batch that show a significant increase (resp. decrease) in the values of the descriptor k, b_k^+ (resp. b_k^-) is the fraction of perturbations in the batch that show a significant and particularly strong increase (resp. decrease) in the values of the descriptor k. The transformation functions and the role of the parameters is illustrated in Fig. S3.

1.9 Phenotypic distance metric learning

1.9.1 The distance measure

The phenotypic distance between two phenoprints $\boldsymbol{y_1}$ and $\boldsymbol{y_2}$ is defined by:

$$
d(\boldsymbol{y}_1,\boldsymbol{y}_2)=\sum_k \Big[\big|\max(\tfrac{1}{2},y_{1,k}^+)-\max(\tfrac{1}{2},y_{2,k}^+)\big|+\big|\max(\tfrac{1}{2},y_{1,k}^-)-\max(\tfrac{1}{2},y_{2,k}^-)\big|\Big]/\gamma
$$

with $\gamma=\max(p(\boldsymbol{y}_1),p(\boldsymbol{y}_2))$, where $p(\boldsymbol{y})$ is the number of significant phenotypic traits of the phenoprint $\boldsymbol{y}$, defined by $p(\boldsymbol{y})=\#\left\{k \,|\, y_{1,k}^+>\frac{1}{2} \text{ or } y_{1,k}^->\frac{1}{2}\right\}$. The distance d ranges from 0 (perturbations showing identical phenoprint) to 1 (perturbations showing distinct phenoprints). The phenoprint $\boldsymbol{y}$ of a perturbation is said to show a phenotype (i. e. is a hit) if $p(\boldsymbol{y})>0$.

1.9.2 Parameter optimization

To determine suitable values for the parameters $\{a_k^+,b_k^+,a_k^-,b_k^-\}$, for $k=1,\dots,13$, we used a distance learning approach [13]. For this approach, two training sets were needed: first, a set of pairs of perturbations $\mathcal{S}$ that should be enriched for similar phenotypes, and second, a set of pairs of perturbation that should be unrelated. The enrichment need not be strong or even perfect for the method to be applicable.

For $\mathcal{S}$, we used the graph of functionally associated human gene pairs from the STRING database version 7.1 [11] with confidence greater than a threshold of 0.4, subset to the genes for which we had data. For the reference set, we used random graphs which were obtained from $\mathcal{S}$ by node permutation. Denoting by $\mathcal{R}_r$ the r-th random graph ($r = 1, \ldots, W$), with $W = 64$, the parameters $\{a_k^+, a_k^-, b_k^+, b_k^-\}_{1 \leq k \leq p}$ were chosen to maximize the following criterion:

$$J = \frac{1}{W} \sum_{r=1}^{W} \frac{\#\{(i,j) \in \mathcal{S} : p(\boldsymbol{y}_i) > 0, p(\boldsymbol{y}_j) > 0 \text{ and } d(\boldsymbol{y}_i, \boldsymbol{y}_j) \leq \theta\}}{\#\{(i,j) \in \mathcal{R}_r : p(\boldsymbol{y}_i) > 0, p(\boldsymbol{y}_j) > 0 \text{ and } d(\boldsymbol{y}_i, \boldsymbol{y}_j) \leq \theta\}} \qquad (1)$$

with $\theta = 0.2$.

$\mathcal{S}$ contained 131692 edges (pairs of wells) and the phenoprint $\boldsymbol{y} = (\boldsymbol{y}^+, \boldsymbol{y}^-)$ contained 19 elements, requiring the optimization of 38 parameters $\{a_k^+, a_k^-, b_k^+, b_k^-\}$. Maximization of J was performed using a sequence of calls to the Nelder-Mead and BFGS algorithms, under the constraints $0 < \{a_k^+, a_k^-, b_k^+, b_k^-\} < 1$ and using as initial values the parameters $\{a_k^+, a_k^-\} = 3$ % and $\{b_k^+, b_k^-\} = 1$ %, jittered with some random noise for all k. This maximization strategy was chosen in order to cope with the roughness of the criterion J, as illustrated in Fig. S4. Control phenoprints and wells which did not pass the quality control were not considered for the optimization. After optimization, the criterion J had a value of $J = 2.84$, corresponding to the enrichment ratio of gene pairs having a phenotypic distance smaller than θ being in STRING, compared to random graphs. The resulting 38 parameter values are shown in Table SVIII.

The distribution of pairwise distances in $\mathcal{S}$ and $\{\mathcal{R}_k\}_{1 \leq k \leq W}$ is shown in Fig. S5 before and after optimization. The distributions are approximately similar before optimization, while a mixture component of small distances (in the interval [0,0.2]) is clearly enriched in the distribution of $\mathcal{S}$ (red) compared to the random one $\{\mathcal{R}_k\}_{1 \leq k \leq W}$. This peak contains STRING gene pairs that also show similar phenotypes in our screen.

To verify that we were not overfitting, we repeated this procedure with node-permuted random graphs instead of $\mathcal{S}$. This always obtained poor J scores of not more than about 1.1, and the resulting optimized distributions did not show an enrichment for shorter distances of the sort seen in Fig. S5.

However, to confirm that the predicted edges were not overfitting artifacts, we carried out for each of the 9 genes shown in Figure 3B, a jackknife experiment consisting of re-learning the phenotypic distances on the STRING network leaving out the considered gene. We showed that their corresponding 9phenoprints were similar with and without using the gene for learning the parameters that result in the network (Fig. S8). This jackknife analysis indicates that we do not predict individual edges based on their presence in STRING, but rather STRING is used in an agglomerative manner, and all our specific predictions are driven by similarity of the image data.

1.10 Hits

Using the optimized parameters of Table SVIII to compute the phenoprints, 1820 perturbations showed a phenotype, i. e. had $p(\boldsymbol{y}_k) > 0$. This number is excluding control well and wells that were discarded in the quality control step. The spatial distribution of the hits is shown in Fig. S6.

Selected perturbations can be arranged into a heatmap, as in Fig. S7, using the phenotypic distance d for hierarchical clustering. Genes sharing the same function (e.g. COPx) often tend to cluster together.

1.11 Screen quality diagnostics

The Z'-factor [14] is a commonly used tool to quantify the quality of high-throughput screening assays. We used its multivariate generalization

$$\begin{aligned}
Z' &= 1 - 3\frac{\sigma_1 + \sigma_2}{||\boldsymbol{d}||} \\
\boldsymbol{d} &= \boldsymbol{\mu}_1 - \boldsymbol{\mu}_2 \\
\boldsymbol{\mu}_g &= \frac{1}{\#G_g} \sum_{i \in G_g} \boldsymbol{y}_i \qquad g = 1, 2 \\
\sigma_g^2 &= \frac{1}{\#G_g - 1} \sum_{i \in G_g} \left((\boldsymbol{y}_i - \boldsymbol{\mu}_g) \cdot \frac{\boldsymbol{d}}{||\boldsymbol{d}||} \right)^2
\end{aligned}$$

where G_1 and G_2 were sets of positive (PLK1) and negative (*Rluc*) controls. This yielded

$$Z' = 0.39.$$

1.12 Phenotypic map

In order to show a global map of all the phenotypes that occurred in the assay, the phenotypic hits were displayed in a graph to show similarity and dissimilarity relationships between them, using the phenotypic distance previously defined. The `neato` spring-model algorithm from `graphviz` [4] was used to layout the graph. For rendering, 87436 edges with a phenotypic distance < 0.16 were shown, and only the large connected component (comprising 1806 of a total of 1820 nodes) was drawn. The other connected components were of size 5 or smaller. The phenotypic map is available on `http://www.ebi.ac.uk/huber-srv/cellmorph/data.php`.

The comparison between the original distances and the distances in the 2-dimensional embedding induced by the graph layout is shown in the scatter plot of Fig. S9. The Spearman correlation coefficient between them is 0.83, implying that generally the distance relationships are well captured by the 2D embedding.

17 clusters of tightly connected nodes were marked in the phenotypic map, defined by their centers and radii in Table SIX, and rendered with different colors.

1.12.1 Overlap with functional networks

To validate the potential of our measured phenotypic similarities to predict functional relationships, we compared the global overlap between the phenotypic similarity graph and three functional networks of *M. musculus* genes from MouseNet v.1 [7]. After homology mapping to *H. sapiens* using MGI gene annotation, we computed the 2×2 contingency table of gene pairs with respect to (i) being an edge in the MouseNet network and (ii) being an edge in our phenotypic graph, using a two-sided Fisher's test. We only considered the gene pairs that are strongly similar by keeping the edges in the phenotypic graph that have a phenotypic distance smaller than 0.01. This resulted in a graph of 1376 nodes and 18414 edges.

The MouseNet Molecular Function (MF) network, restricted to the 1376 aforementioned nodes, consisted of 486 nodes and 1781 edges. 57 edges were common to the phenotypic graph and the MouseNet MF network. We showed that the MouseNet MF network was significantly enriched with gene pairs with similar phenotypes (odds ratio 1.66, Fisher's test, $\mathrm{P} = 3.93 \times 10^{-4}$). In the MouseNet Biological Process network, which restriction consisted of 503 nodes and 1785 edges, we observed an enrichment ratio of 1.54 (Fisher's test, $\mathrm{P} = 3.37 \times 10^{-4}$). Although modest, these enrichment ratios are highly significant and show that the loss-of-function phenotypic similarities measured in HeLa cells predict functional relationships in mouse genes. The enrichment ratio in the MouseNet Cellular Component Network was 1.45 but only marginally significant (Fisher's test, $P = 1.8 \times 10^{-2}$).

1.13 Data and software availability and performance

The complete data set, including the 91356×3 microscopy images in TIFF format, intermediate image files, and RNAi library annotation are available from `http://www.ebi.ac.uk/huber-srv/cellmorph`.

The complete analysis was conducted using software built on the language and statistical environment R and its add-on packages from the CRAN (`www.r-project.org` and Bioconductor (`www.bioconductor.org`) repositories. Our software is available for download from `http://www.ebi.ac.uk/huber-srv/cellmorph`. Among the main add-on packages used are: `EBImage` for the low-level image processing operations and for Ray Jones' Voronoi segmentation on image manifolds [6] and `e1071` for the SVM classification with `libsvm` [3].

Computing the phenotypic profile of one perturbation from 4 input images took about 49 seconds (i.e. 12.3 seconds per image) on a single 2.6 GHz CPU with 2 GB of RAM, including calibration, cell segmentation, feature extraction and classification. The genome-wide screen (22839 perturbations) was processed in about 313 CPU hours; using a compute cluster of 30 CPUs, this corresponded to about 11 hours wall clock time.

2 References

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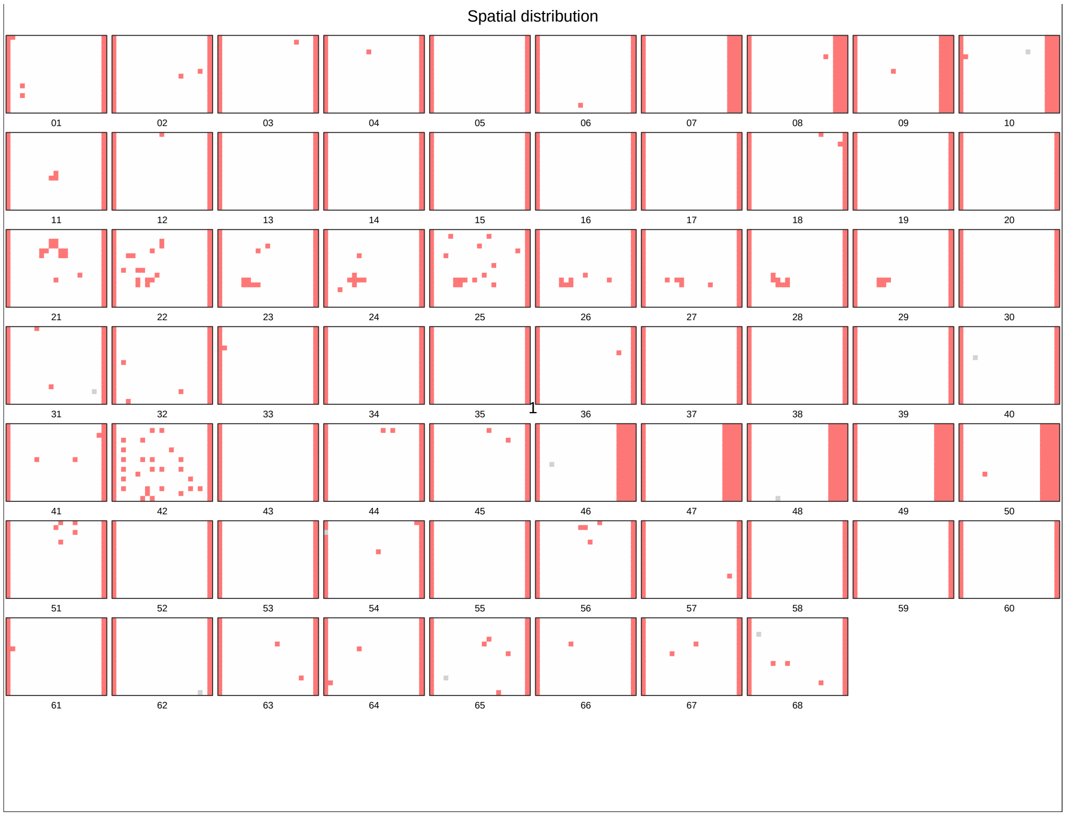


Figure 1: Quality control excluded wells. The figure shows, in red, the locations of all wells excluded from the analysis. Each of the 68 boxes corresponds to one of the 384 well plates, and shown are columns 4 (leftmost, marked in red throughout because it contained controls) to 24 (rightmost, marked in red throughout because it showed a pervasive edge effect), and all rows $1, \ldots, 16$. Further red marks correspond to sporadic wells in columns 5 to 23 that were discarded because of quality defects. In total, 1622 wells (7.1% of all wells) were discarded.

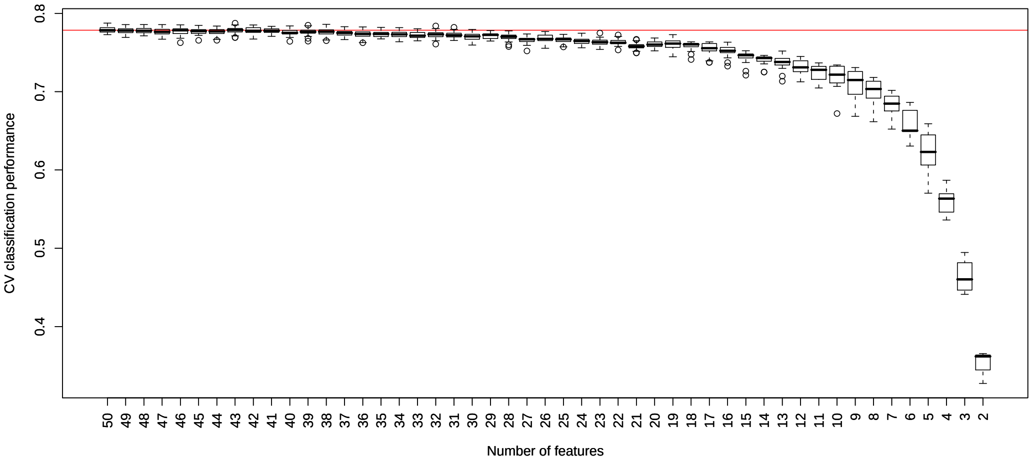


Figure 2: Influence of feature selection on cell classification performance. A greedy feature selection algorithm was applied, based on the estimated influence of features on the classification performance (see Section 1.6). The classification performance remained almost constant between 51 and 24 features with a constant and low variability.

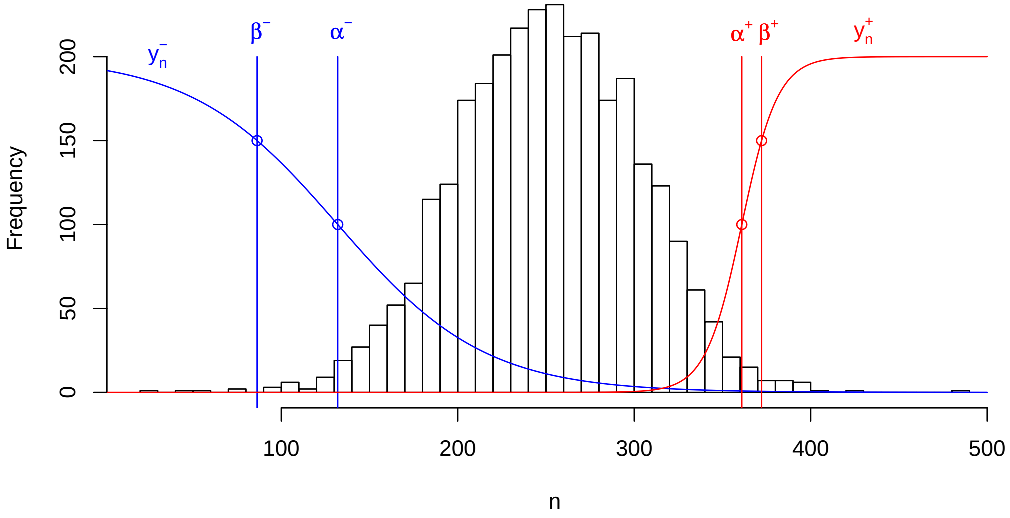


Figure 3: Sigmoid transformation. The histogram shows the 'number of cells' perturbation descriptor n from the plates of the second batch. The increase (red) and decrease (blue) transformation functions are shown, with their parameters (α^+, β^+) and (α^-, β^-).

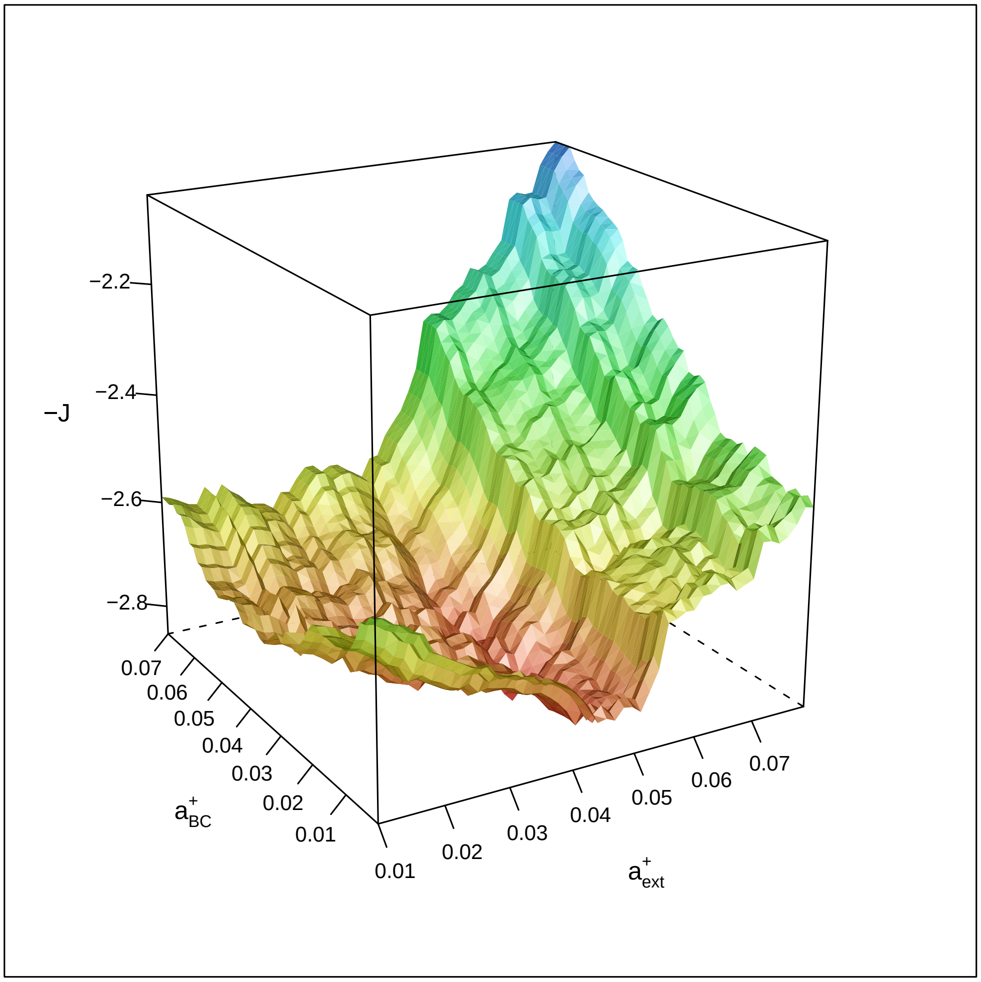


Figure 4: Distance metric learning optimization surface. The surface shows the criterion $-J$ as a function of the two variables a^+_{ext} and a^+_{BC}, illustrating the roughness of the maximization surface. The maximum of J is located in the reddish bottom part of the surface.

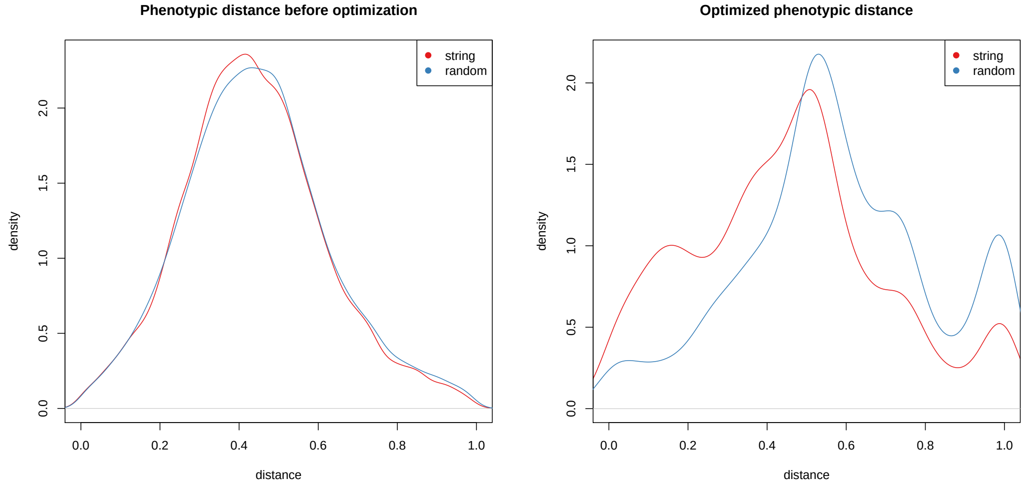


Figure 5: Distance distributions (STRING $\mathcal{S}$ (red) and random $\{\mathcal{R}_k\}_{1 \leq k \leq W}$ (blue)) before optimization (left), using the initial parameter values and after optimization (right), using the parameters of Table SVIII.

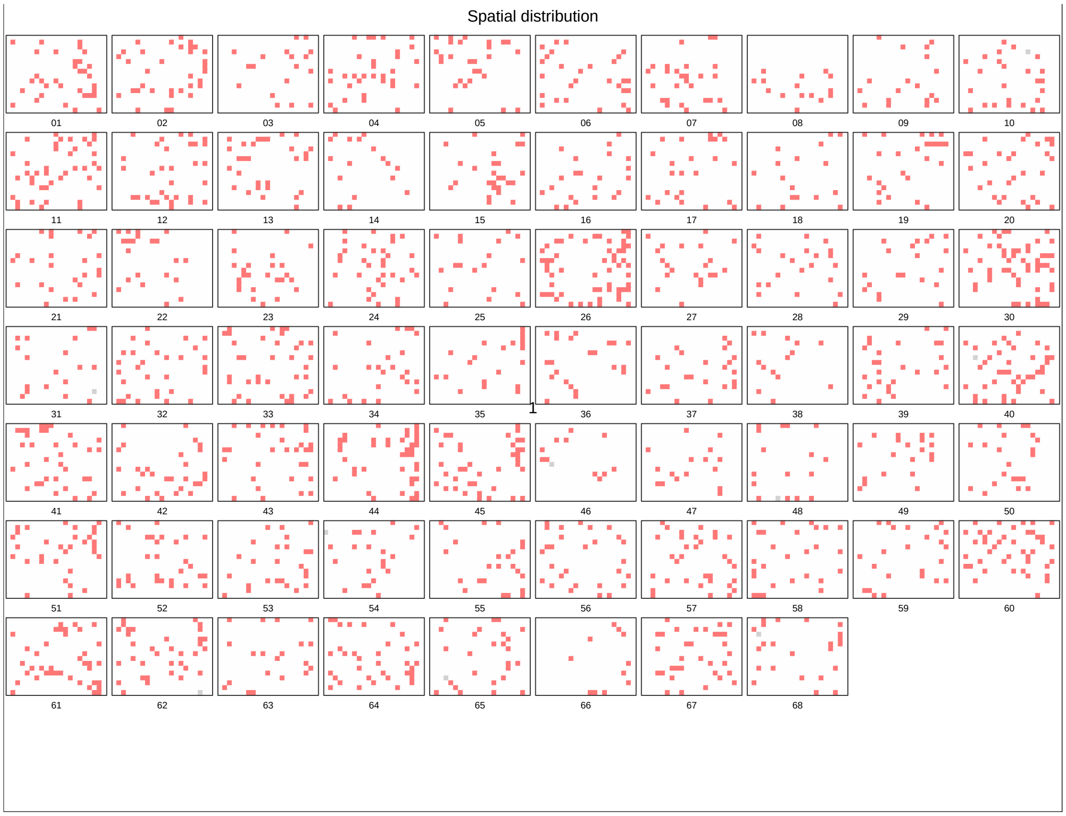


Figure 6: Distribution of hits (wells showing a non-wildtype phenoprint) over the 68 plates.

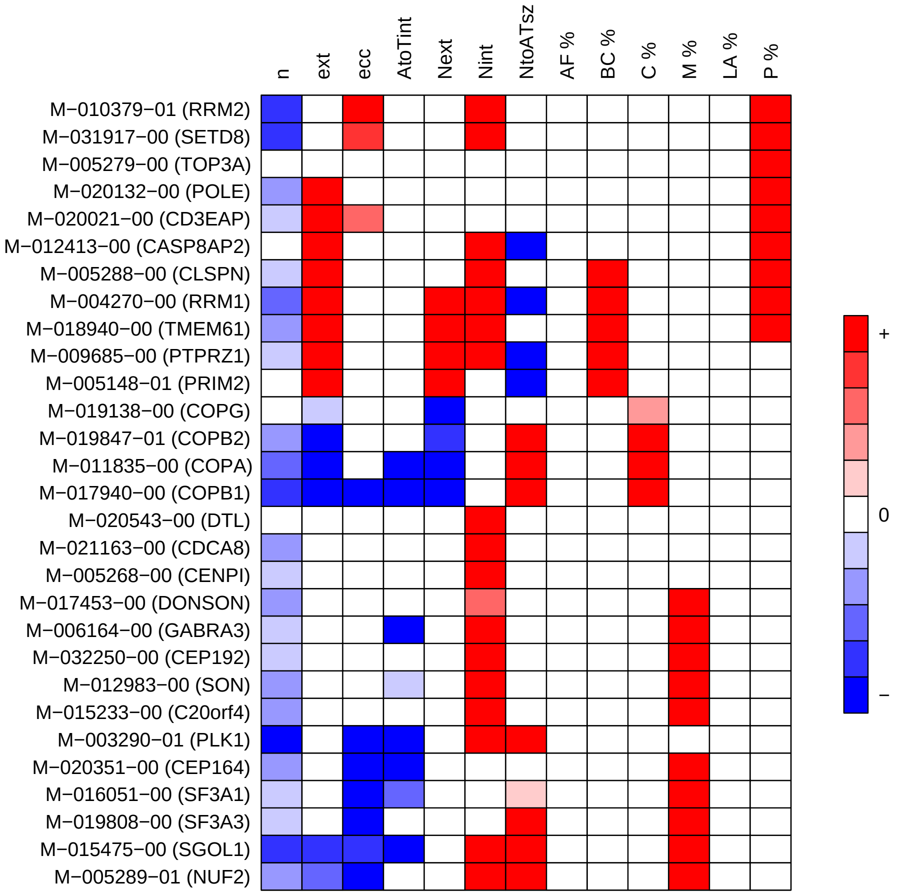


Figure 7: Heatmap of selected phenoprints. Shown are the values of phenoprints $\boldsymbol{y}_i$, using the gene descriptors of Table SVII and the color code indicated on the right hand side (right: increase, blue: decrease).

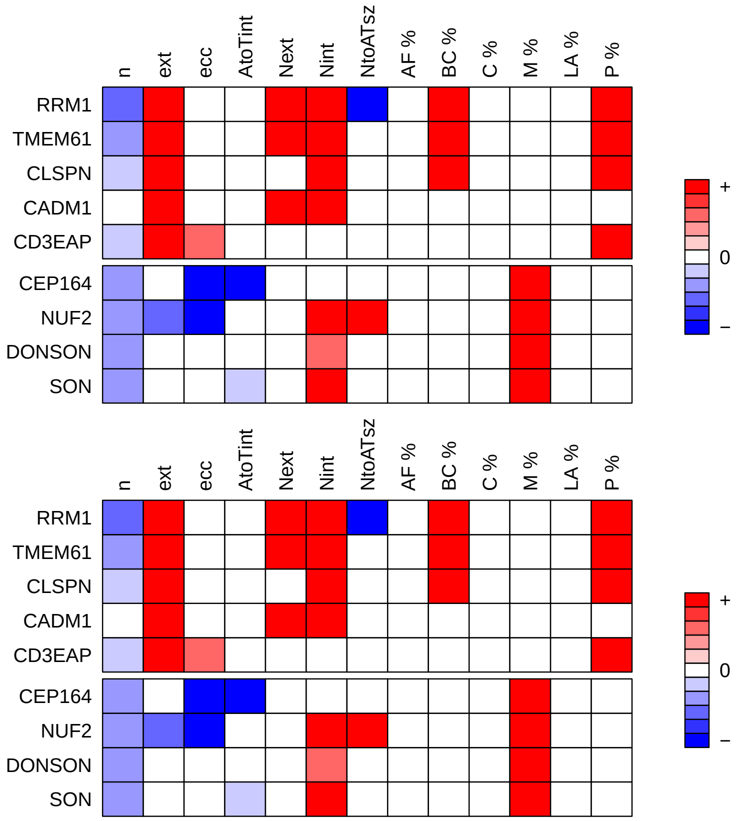


Figure 8: Leave-one-out experiment. Comparison of the original phenoprints (top) learned from STRING to phenoprints which have been learned, for each of them, from STRING where the corresponding gene has been removed (bottom). The phenoprints are similar with and without using the gene for learning the parameters.

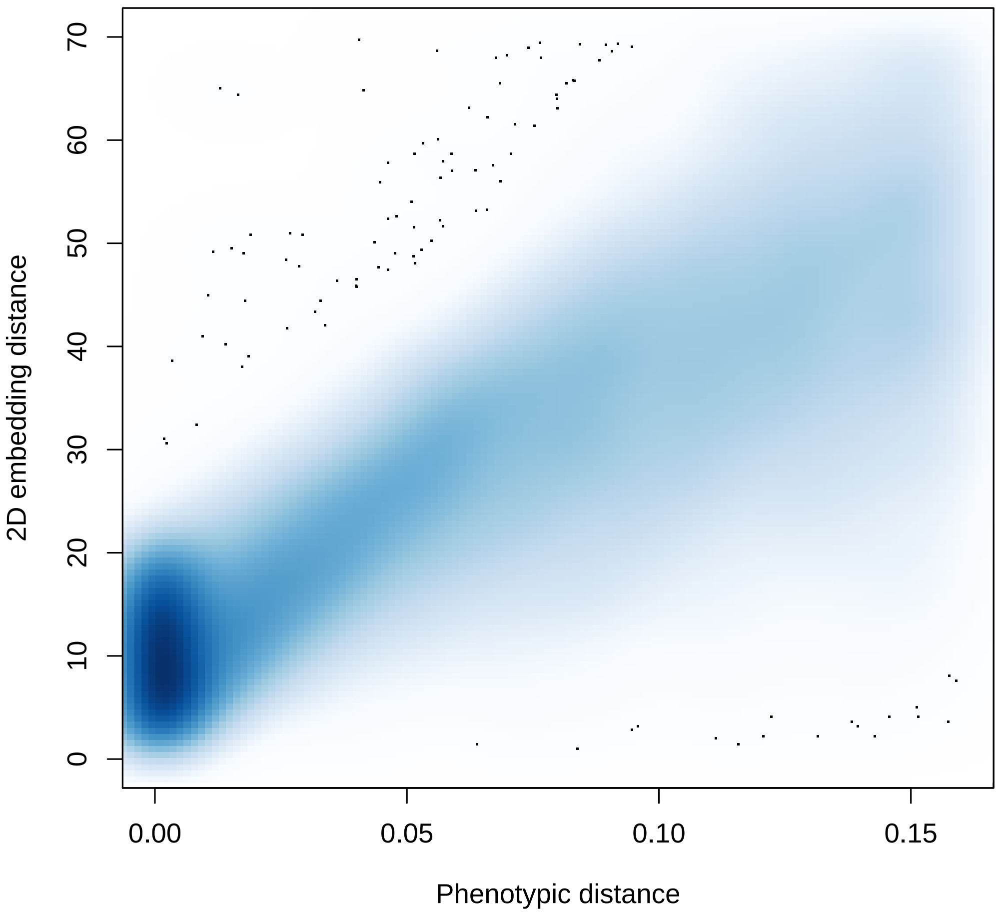


Figure 9: Scatter plot of the phenotypic distances, on the x-axis, against the distances in the 2D embedding.

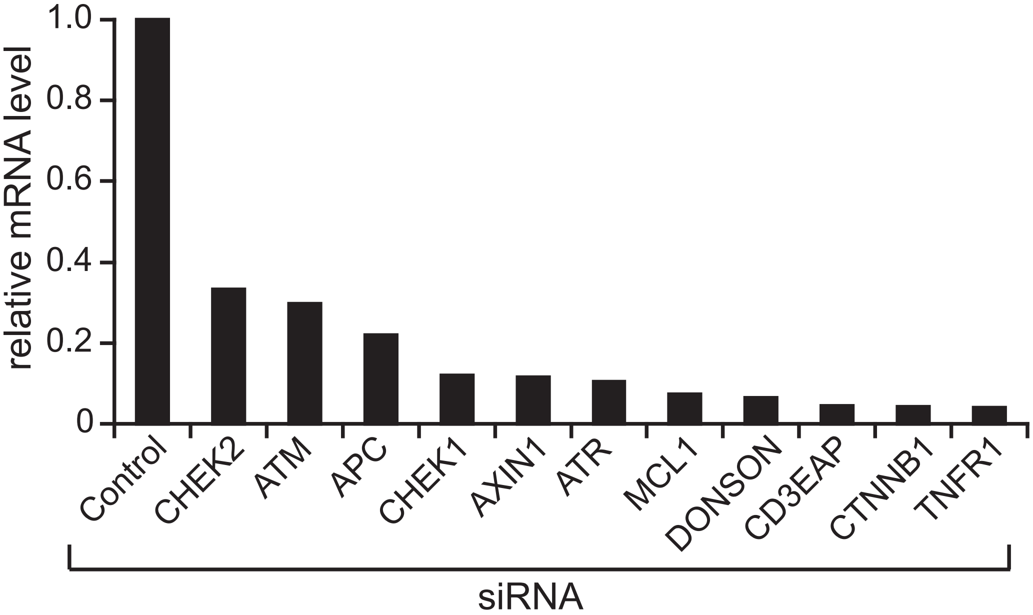


Figure 10: mRNA levels of exemplary genes are reduced under standard assay conditions to at least 65%. HeLa cells were transfected in 96-well format with indicated siRNA pools (Dharmacon, 20 nM final concentration) according to the standard high-throughput reverse transfection protocol described in the Methods section. Quantitative RT-PCR analysis was performed 48 h after siRNA transfection. GAPDH was used as internal negative control. Shown are representative knockdown efficiencies of perturbations yielding 95 to 65% decrease in mRNA levels.

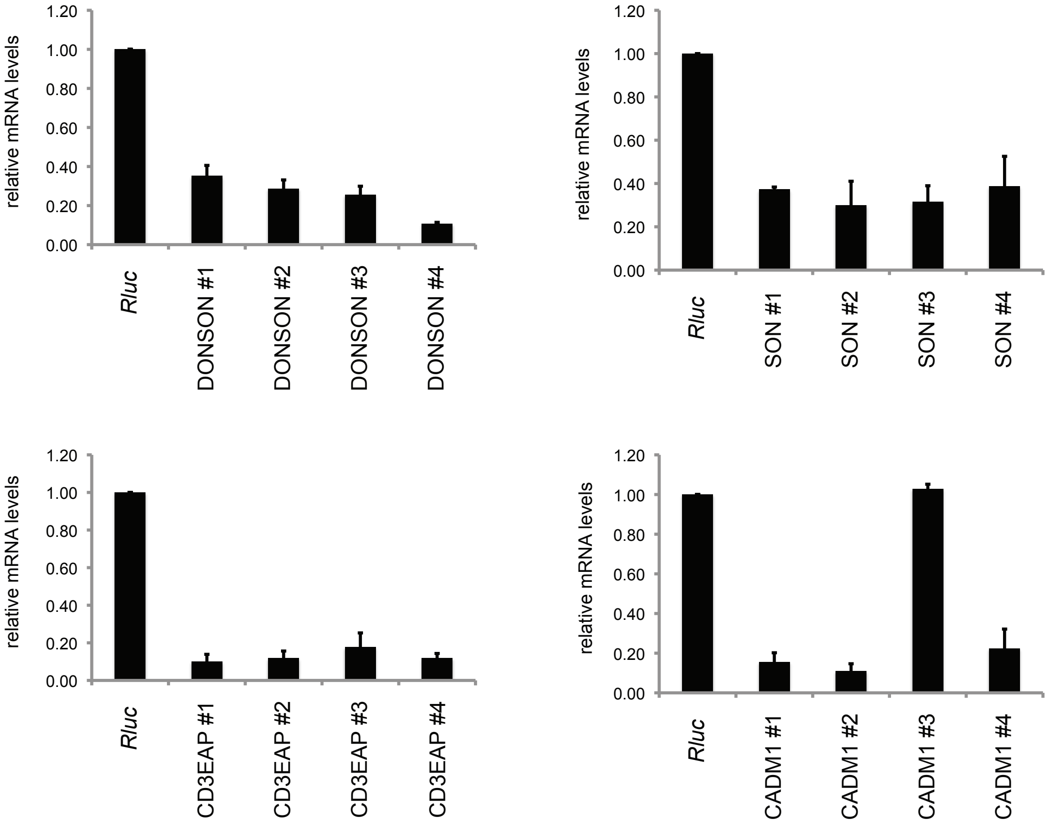


Figure 11: mRNA levels of candidate genes are reduced by single siRNAs. Quantitative RT-PCR analysis of mRNA levels 48 h after transfection with siRNAs. U2OS cells were transfected with the indicated single siRNAs (Dharmacon, 20 nM final concentration). GAPDH was used as internal control. Values are shown as mean +/- s.d. of three independent biological replicates.

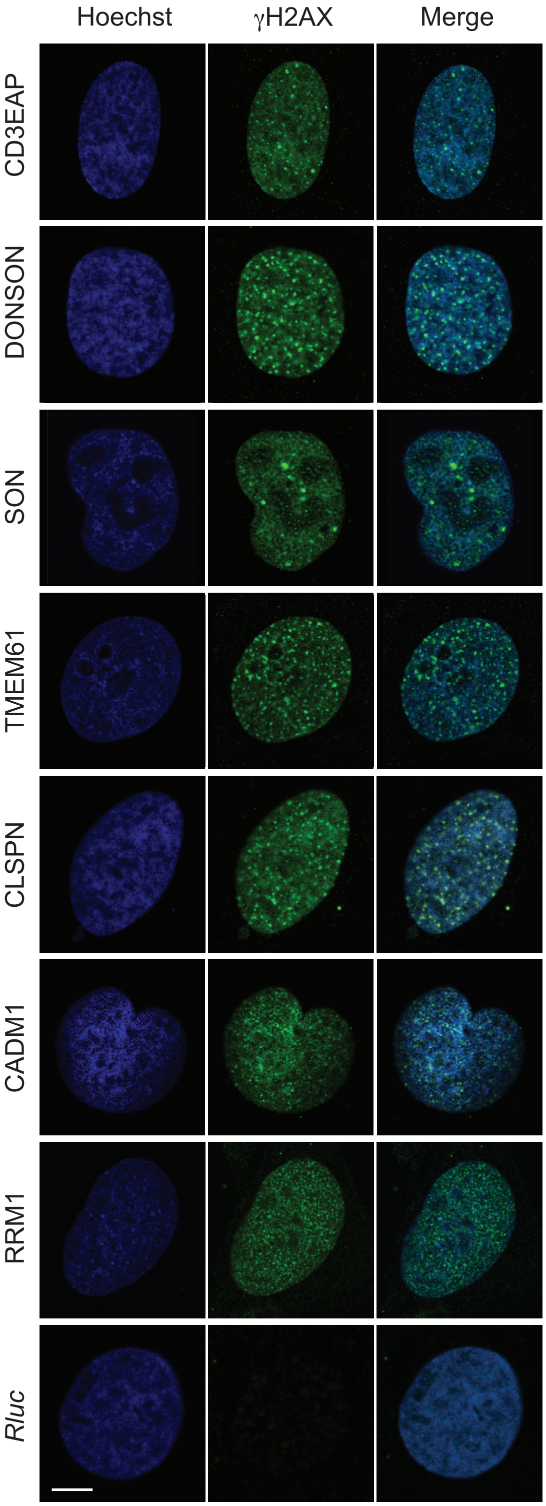
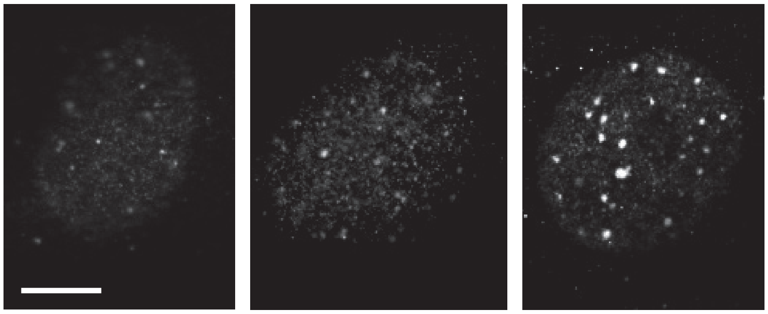


Figure 12: Knockdown of RRM1, CLSPN, CD3EAP, CADM1, TMEM61, DONSON and SON induces γH2AX foci formation. U2OS cells were fixed with PFA, permeabilized and stained with primary mouse anti-γH2AX antibody and goat secondary anti-mouse Alexa 488 secondary antibody (green) 72 h after siRNA transfection. DNA is counterstained with Hoechst (blue). Scale bar represents 2.5 μm.



DONSON #1 DONSON #2 DONSON #4

Figure 13: γH2AX foci formation after DONSON knockdown correlates with the knockdown efficiency of the siRNA. U2OS cells were transfected with indicated siRNAs (Dharmacon, 20 nM final concentration). 72 h after siRNA transfection cells were fixed, permeabilized and immunostained with primary mouse anti-γH2AX antibody and goat secondary anti-mouse Alexa 488 secondary antibody. The results reflect a strong correlation between the silencing efficiency of the siRNA (Fig. S10) and the induced foci formation. The scale bar represents 2.5 μm.

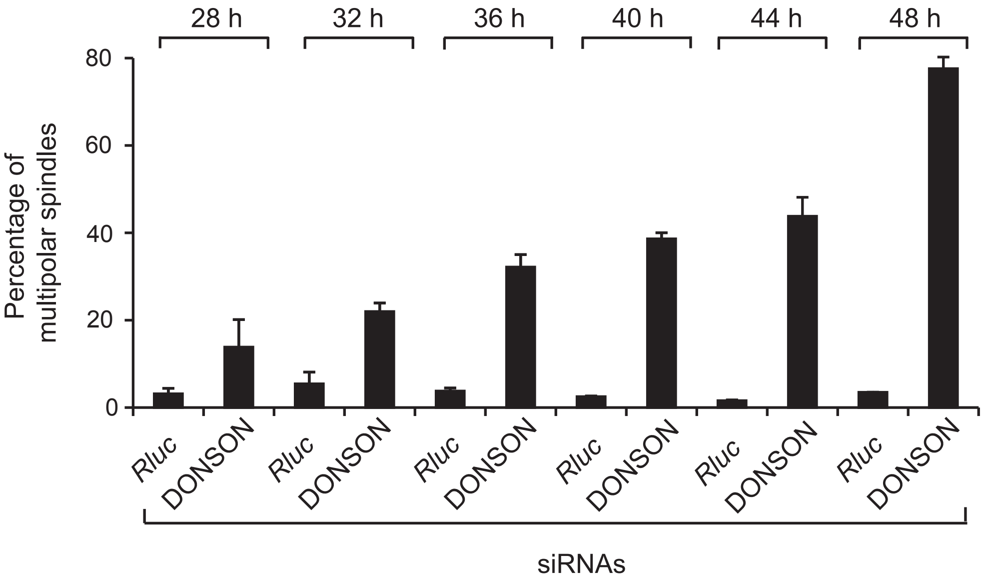


Figure 14: Prolonged DONSON knockdown in HeLa cells increases the amount of multipolar spindles. HeLa cells were transfected with a siRNA pool (Dharmacon, 20 nM final concentration) targeting DONSON. A pool targeting Renilla luciferase (*Rluc*) was used as internal negative control. Cells were fixed, permeabilized and immunostained at indicated time points. Cells were immunostained as described in Fig. 4d and metaphase spindles were analyzed. A total of 500 mitotic spindles were counted in each independent experiment in order to calculate the percentage of multipolar spindles within the total number of metaphase spindles. The results shown represent mean +/- s.d. from two independent experiments. In comparison to control conditions, prolonged DONSON depletion led to a 15 fold increase in the percentage of multipolar spindles.

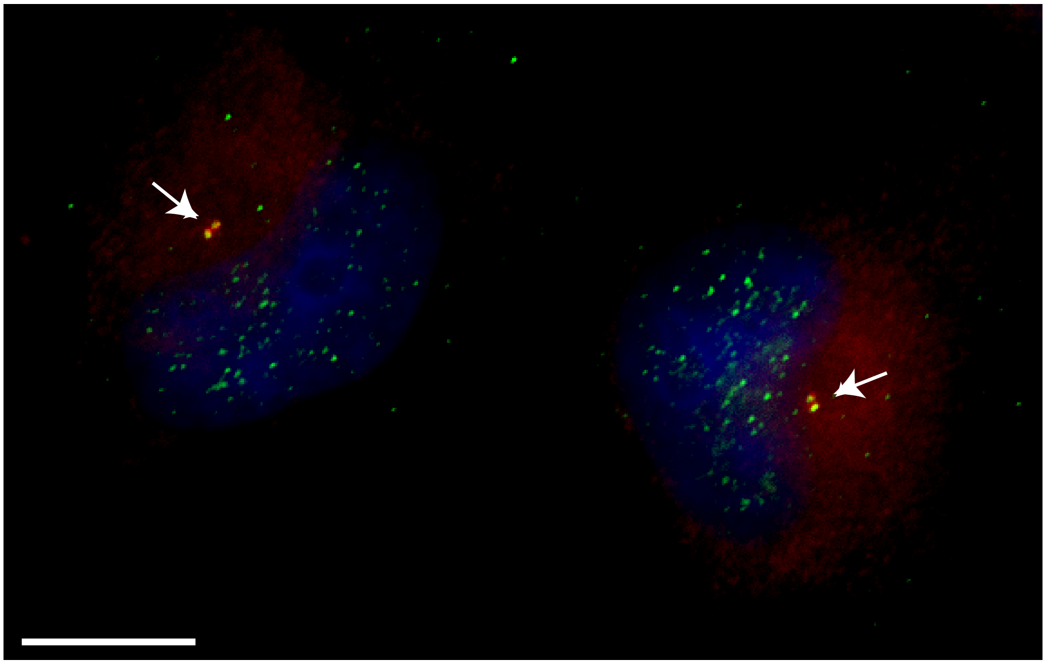


Figure 15: DONSON-HA partially overlaps with γ-Tubulin foci at centrosomes. HeLa cells were transfected with HA-tagged DONSON, fixed with methanol/acetone 24 h after transfection and immunostained. Immunostaining was performed using rabbit anti-γ-Tubulin and mouse anti HA-tag, and goat anti-mouse Alexa 488 or goat anti-rabbit Alexa 594 secondary antibody, respectively. DONSON-HA staining (green) showed a prominent centrosomal staining as seen in Fig. 4e. DNA is counterstained with Hoechst (blue). Interestingly, colocalization analysis using γ-Tubulin specific antibody (red) revealed that a substantial amount of cells showed a colocalization pattern in which only one of the two centrioles, colocalizes with DONSON-HA staining. A similar localization pattern has been described for other centrosomal proteins such as cyclin G2 [1]. Scale bar represents 10 μm.

RT-PCR primers

Name	Sequence
q-APC-for	5-acgcgcttactgtgaaacct-3
q-APC-rev	5-ttcaacaggagctggcatt-3
q-ATM1-for	5-ccaggcaggaatcattcag-3
q-ATM1-rev	5-caatccttttaaatagacggaaagaa-3
q-ATR-for	5-cgctgaactgtacgtggaaa-3
q-ATR-rev	5-caattagtgcctggtgaacatc-3
q-AXIN1-for	5-ggagctctccgagacagagac-3
q-AXIN1-rev	5-acaacgatgctgtcacacg-3
q-CD3EAP-for	5-gcagactttgccccagaat-3
q-CD3EAP-rev	5-tgccaatttgcccttgac-3
q-CHEK1-for	5-caggagagaaggcaatatccaa-3
q-CHEK1-rev	5-gcatgcctatgtctggctct-3
q-CHEK2-for	5-gccagagaatgttttactgtcatc-3
q-CHEK2-rev	5-cttggagtgcccaaaatcag-3
q-CTNNB1-for	5-agctgaccagctctctcttca-3
q-CTNNB1-rev	5-ccaatatcaagtccaagatcagc-3
q-DONSON-for	5-gtccagcattgtagggcaac-3
q-DONSON-rev	5-ggctctgctggaaggtacaa-3
q-MCL1-for	5-aagccaatgggcaggtct-3
q-MCL1-rev	5-tgtccagtttccgaagcat-3
q-TNFR1-for	5-gagaggccatagctgtctgg-3
q-TNFR1-rev	5-gaggggtatattcccaccaac-3

DONSON-HA PCR primers

Name	Sequence
DonHA-forw	5-ccgctagcgccaccatggccctttcggtgc-3
DonHA-rev	5-ccgaattcctaagcatagtctgggacatcataagggtatccgccggatctccaattataaatgtagtctctc-3

Table I: RT-PCR primers and DONSON-HA PCR primers.

Class	Description
AF	Actin fibres
BC	Big (large) cells
C	Condensed cells
D	Debris
LA	Lamellipodia
M	Metaphase
MB	Membrane blebbing
N	Normal cells
P	Cells with protrusions and elongations
Z	Telophase

Table II: 10 cell classes were considered during the screen analysis. AF: actin fibers/stress fibers, BC: cells with increased nuclear and cytoplasmic size or flat/adherent cells with increased cell body, C: small and condensed cells, D: cellular debris, LA: lamellipodia or increased cortical actin, M: mitotic cells in proto metaphase, MB: apoptotic cells with membrane blebbing, N: wildtype cells, P: elongated cells or cells with protrusions, Z: telophase cells.

AF	BC	C	D	LA	M	MB	N	P	Z
170	310	338	219	258	186	110	542	315	97

Table III: Training set sizes. Number of cells in the training set in each of the cell phenotype classes.

AF	BC	C	D	LA	M	MB	N	P	Z
0.79	0.82	0.83	0.93	0.79	0.85	0.82	0.87	0.77	0.86

Table IV: Classification accuracy. Class-specific prediction rates computed on the training set (in %).

	AF	BC	C	D	LA	M	MB	N	P	Z
AF	135	10	2	0	2	4	0	2	4	0
BC	20	255	11	1	1	5	0	9	16	0
C	0	3	279	8	2	5	9	9	6	12
D	0	1	3	203	0	0	0	1	1	0
LA	1	0	2	1	205	0	0	31	7	0
M	0	5	6	1	0	159	0	3	6	0
MB	0	0	6	1	0	0	90	3	1	0
N	10	23	15	2	46	3	7	469	27	0
P	4	12	6	2	2	6	3	14	244	2
Z	0	1	8	0	0	4	1	1	3	83

Table V: Confusion matrix of the predicted cell classes computed on the training set. Columns represent the real classes while rows are the predicted ones.

AF	BC	C	D	LA	M	MB	N	P	Z
6.62	5.57	15.11	4.25	3.93	1.87	1.66	53.99	5.28	1.74

Table VI: Distribution of the size of predicted cell classes (in %).

Name	Description	$\boldsymbol{y}$
n	Number of live cells	+/-
ext	Median cell extension	+/-
ecc	Median cell eccentricity	+/-
AtoTint	Median cell actin-to-tubulin ratio	+/-
Next	Median nucleus extension	+/-
Nint	Median nucleus intensity	+
NtoATsz	Median nucleus-to-cell size ratio	+/-
AF %	Fraction of Actin Fiber cells	+
BC %	Fraction of Big Cells	+
C %	Fraction of Condensed cells	+
LA %	Fraction of Lamellipodia cells	+
M %	Fraction of Metaphase cells	+
P %	Fraction of Protusions cells	+

Table VII: The perturbation phenotype descriptors and phenoprints. Each row corresponds to an element of the descriptor vector $\boldsymbol{x}$. The column $\boldsymbol{y}$ describes whether the increase (+), the decrease (-) or both (+/-) of the descriptor value was considered in the phenoprint $\boldsymbol{y}$.

Descriptor k	a_k^-	b_k^-	a_k^+	b_k^+
n	2.00	0.19	0.54	0.51
ext	0.62	0.20	0.73	0.70
ecc	0.68	0.57	0.86	0.68
AtoTint	0.46	0.31	0.72	0.71
Next	0.71	0.40	0.61	0.59
Nint			0.73	0.66
NtoATsz	0.54	0.54	0.88	0.69
AF			0.62	0.50
BC			0.69	0.69
M			0.65	0.60
LA			0.58	0.52
P			0.55	0.52
C			0.37	0.33

Table VIII: Optimized parameters of the distance metric / sigmoid transformation (in %).

ID	color	label	center	radius	size
1	●	BL phenotype	51F06	2	49
2	●	Bright nuclei	42E06	1	33
3	●	Large nuclei	49D13	1	36
4	●	Cells with protrusions	06G09	1	44
5	●	Elongated cells	24O13	1	91
6	●	Elongated cells with protrusions	12N20	1	42
7	●	SM phenotype	19A10	3	36
8	●	Small cells	64F17	1	58
9	●	Low eccentricity cells	68C05	1	60
10	●	High actin ratio cells	26P23	1	91
11	●	Metaphase cells	68H13	1	81
12	●	Actin fiber cells	35H12	1	59
13	●	Big cells	43L11	1	51
14	●	Large cells	35G13	1	35
15	●	Lamellipodia cells	02L08	1	67
16	●	Lamellipodia + high actin ratio cells	01J11	1	31
17	●	Proliferating cells	38B05	1	100

Table IX: Cluster definition. Each cluster is defined by its center (well ID) and radius (k-th neighboring degree). The field 'size' indicates how many nodes are present in each cluster. Each cluster is rendered with a different color and is labelled according to its most representative phenoprint. The 'BL phenotype' is characterized by a decrease in the number of cells and increase of metaphase cells. The 'SM phenotype' shows an abundance of large cells with protrusions and bright nuclei.

HGNC	HeLa phenotype	U2OS phenotype	HeLa reproducibility	Qiagen reproducibility
AADACL1	P,LA	P,LA		X
ABCB10	BC,Z,M	BC,Z,M	X	X
ACRC	N,C,M	N,C,M		X
ADAMTS18	BC,P	BC,P	X	X
ADIPOR2	N	N		X
AFAP1	P,C	P,C		X
AGR2	P,BC	P,BC		X
AGXT2	LA	LA	X	X
AMTN	BC,C,M	BC,C,M		X
ANAPC7	N	N	X	X
ANLN	BC,P,M	BC,P,M	X	X
AP4E1	BC,LA	BC,LA		X
APBB1IP	C	C	X	X
ARCN1	C	C	X	X
ARFGEF1	P	P	X	X
ARHGAP1	N,C	N,C		X
ARHGAP20	N	N		X
ARHGEF4	P	BC	X	
ARIH2	C,LA	N		
ASF1B	P,M	BC		
ASNSD1	P,LA	P,LA	X	X
ASPH	N,BC	N,BC	X	X
ATP1B3	LA	LA		X
ATP5G2	BC,AF	BC,AF		X
ATP7A	BC,AF	BC,AF	X	X
B3GALNT1	P,M	P,M		X
BCAR3	P,C	P,C	X	X
BCKDHA	C,AF,P	C,AF,P		X
BCL2L1	N,BC,P	N,BC,P	X	X
BEX2	BC,LA	BC,LA		X
BIN3	N	N		X
BIRC5	BC,AF	BC,AF		X
BLR1	P	P		X
BRCC3	N,M	N,M		X
BRD9	BC,P	BC,P	X	X
C10ORF116	BC,AF,C	BC,AF,C		X
C11ORF48	AF,P	AF,P		X
C11ORF61	P,LA	P,LA		X
C12ORF24	P	P		X
C12ORF59	P,C,M	P,C,M		X
C13ORF3	C,M	C,M	X	X
C15ORF42	BC,P	BC,P		X
C16ORF68	BC,AF	BC,AF	X	X
C1ORF177	C	C		X
C1QA	BC,LA	BC,LA	X	X
C20ORF20	BC,P	BC,P	X	X
C20ORF4	C,M	C,M		X
C2ORF60	BC,C	BC,C	X	X
C4ORF18	AF,C	AF,C		X
C6ORF142	C	C		X
C6ORF182	BC,P	BC,P	X	X
C6ORF204	BC,P	BC,P		X
C6ORF64	P	P		X
C9ORF90	BC,C	BC,C		X
CA14	LA	LA		X
CABLES1	BC,AF	BC,AF		X
CACNA1A	P,C,M	M	X	
CACNA1F	BC,P	BC,P		X
CADM1	BC,AF	BC,AF	X	X
CAPRIN1	BC,AF	BC,AF	X	X
CARS	N,BC	N,BC	X	X
CASP8AP2	BC,P,AF	BC,P,AF	X	X
CBLC	BC,AF	C		
CCBE1	P	P		X
CCDC114	AF	AF		X
CCDC132	BC,P,C	BC,P,C		X
CCDC142	BC	BC		X
CCDC98	BC,AF	BC,AF		X
CD33	P,M	P,M		X
CD3EAP	BC,P,AF,M	BC,P,AF,M	X	X
CDC37L1	LA	LA	X	X

CDC42	P,C,D	P,C,D	X	X
CDC6	BC	BC		X
CDCA5	M,BC	M,BC	X	X
CDCA8	BC,P,M	BC,P,M	X	X
CDH10	AF	AF		X
CDKL1	LA,BC,P	LA,BC,P		X
CDKN2A	C,M	C,M	X	X
CEBPD	BC,LA	BC,LA		X
CECR6	BC,C	BC,C		X
CENPE	BC,M	BC,M	X	X
CENPH	N,M	C		
CENPI	BC,M,P	BC,M,P	X	X
CEP164	AF	P		
CEP192	BC,M	BC,M	X	X
CFL1	N	N	X	X
CGRRF1	P,C,M	P,C,M	X	X
CHD4	N	P		
CHEK1	M,BC	M,BC	X	X
CHIT1	AF,C,M	AF,C,M		X
CHN1	C,LA	C,LA	X	X
CHST12	C,M	C,M	X	X
CHST5	P,AF	P,AF	X	X
CKAP5	M,P	M,P	X	X
CLDN11	N,C	N,C	X	X
CLDN4	LA,C	LA,C		X
CLIC2	P,AF	P,AF		X
CLN8	BC,AF	BC,AF	X	X
CLPS	BC,LA	BC,LA		X
CLSPN	BC,P,M,D	BC,P,M,D	X	X
CLTC	N,C	N,C	X	X
CLU	N,AF	N,AF		X
CLUAP1	P,C,M	P,C,M	X	X
CNTFR	P,C	P,C	X	X
COL20A1	P,C	BC	X	
COL9A3	AF,C	AF,C	X	X
COPA	C,M	C,M	X	X
COPB1	M,D	M,D	X	X
COPB2	C,M	C,M	X	X
COPE	BC,P,C	BC,P,C		X
COPG	C,D,P	C,D,P	X	X
COPZ1	P,C	P,C	X	X
COPZ2	P,C	P,C		X
CORO7	BC,AF	BC,AF		X
COX6A2	LA	LA	X	X
CPNE5	AF,C	AF,C		X
CR2	C,LA,P	C,LA,P	X	X
CRNKL1	M,BC,LA	M,BC,LA	X	X
CSAD	N,M	P		
CSDC2	BC,AF	BC,AF		X
CST5	C	N		
CTDSP1	M,P	M,P		X
CTF1	BC,AF	BC,AF		X
CTRC	BC,AF	BC,AF		X
CUTA	BC,AF	BC,AF		X
CXXC4	BC,LA,P	BC,LA,P	X	X
CYBRD1	BC,AF	BC,AF	X	X
CYP2B6	BC,LA,M	BC,LA,M		X
CYR61	C,N	C,N		X
DAB2	N	N		X
DAND5	C,M,P	C,M,P		X
DDX5	P,C	P,C		X
DERL2	N	N		X
DHX58	LA	LA		X
DLG4	N	N		X
DLG5	P,LA,C	P,LA,C		X
DLL4	P,AF	BC		
DNAJB9	LA	LA	X	X
DNASE1	P,C	BC		
DNMT1	BC,AF	BC,AF		X
DONSON	BC,C,M,P	BC,C,M,P	X	X
DQX1	P,C	P,C		X
DSCAML1	AF,M	AF,M		X
DSCR3	BC,P	BC,P		X

DTL	P	BC	X	
DUX1	BC,AF	BC,AF	X	X
DYNC1I2	P,M	P,M	X	X
DYSF	AF,M	AF,M		X
ECOP	BC,C	BC,C		X
EDC3	LA	LA		X
EFEMP2	P,LA	AF	X	
EFHA2	BC,LA	BC,LA		X
EI24	BC,AF,C	BC,AF,C		X
EIF2B5	P,BC	P,BC		X
EIF2S1	AF	AF		X
EIF3C	M,P	M,P	X	X
EIF3I	AF,C	AF,C	X	X
EIF4A3	M,C	M,C	X	X
ELAC2	C,LA	C,LA	X	X
ELAVL4	N,C	N,C		X
ELF3	BC,AF	BC,AF		X
ELL3	N,LA	N,LA	X	X
ELMO2	P	P	X	X
ELMO3	BC	BC		X
ENOSF1	C	C		X
EPSTI1	C,M,D	C,M,D	X	X
ERAF	P,AF,C	P,AF,C	X	X
ESF1	LA	LA	X	X
EXOSC8	P,C	P,C		X
EZH1	P,M	P,M		X
FAM107A	P	P		X
FAM113A	LA	LA		X
FAM12B	BC	BC	X	X
FAM195B	BC,LA	BC,LA	X	X
FAM69B	P,LA,C	P,LA,C	X	X
FAM89B	BC,LA	C		
FANCB	P,BC	P,BC		X
FASLG	BC,AF	BC,AF		X
FBXL6	BC,AF,C	BC,AF,C	X	X
FBXL7	P,LA	P,LA		X
FBXO5	BC,P	BC,P		X
FBXW8	P,C	P,C		X
FGF22	BC	BC	X	X
FGFRL1	AF,BC	AF,BC	X	X
FIBIN	BC	BC	X	X
FKBP1A	BC,M	BC,M		X
FKBP2	N,C	P		
FLJ21075	N	N		X
FMO5	P,LA	P,LA		X
FNTB	C,P	N	X	
FOSL1	BC,AF	BC,AF	X	X
FOSL2	BC,AF	BC,AF	X	X
FUCA2	N,C	N,C		X
FXYD1	BC	BC		X
FZD2	BC,P	BC,P	X	X
GABBR1	C,LA	AF		
GABRA3	C,M	C,M	X	X
GABRG3	P,M	P,M		X
GALNT4	P,C	P,C		X
GAPDH	C	C		X
GBA	C,M,AF	C,M,AF		X
GCNT1	AF	AF	X	X
GDF3	AF,M	AF,M	X	X
GFM1	LA,P	LA,P	X	X
GGTL3	BC,C	BC,C		X
GIMAP5	P,C	P,C	X	X
GLIS1	C	C		X
GMEB1	C,AF	C,AF		X
GNA12	P,C,D	P,C,D	X	X
GNAI1	BC,BC,AF	BC,BC,AF	X	X
GOLPH3L	BC,P	BC,P	X	X
GORASP2	BC,AF	BC,AF		X
GOSR1	BC,LA	BC,LA		X
GOSR2	C,M,LA	C,M,LA		X
GPR37	P,C	P,C		X
GPR89A	BC,LA	BC,LA	X	X
GRIA4	C,M	C,M		X

GRINL1A	N,LA	N,LA		X
GSPT1	BC,AF	BC,AF		X
GTF3A	C,LA	C,LA	X	X
GTF3C6	N,LA	N,LA		X
GUCA2A	BC,AF	BC,AF	X	X
GZMM	N,LA	N,LA	X	X
HDAC1	P,C,M	P,C,M	X	X
HEBP1	P	P	X	X
HHIPL2	N,C	N,C		X
HIPK2	P	P	X	X
HIST1H2AE	N,C	N,C	X	X
HIST1H2BO	BC,AF	BC,AF	X	X
HLA-DQB2	P,M	P,M	X	X
HN1	P,C	P,C	X	X
HOXC5	P	P		X
HP	N,P	N,P		X
HSD17B10	C	C		X
HSPA6	BC,P	BC,P		X
HTRA2	BC,C	BC,C	X	X
IER3IP1	N,P	N,P		X
IGSF6	BC,LA	BC,LA		X
IGSF9	AF	AF		X
IL12A	BC,C	BC,C		X
IL2RG	AF	AF		X
INF2	N,C,LA	N,C,LA	X	X
INPP4A	BC,C	BC,C		X
INSIG1	LA	LA		X
IRX4	C,M	C,M		X
JMJD6	BC	BC	X	X
KATNAL1	BC,AF	BC,AF		X
KCND1	P,M	P,M		X
KCNIP1	P,M	P,M	X	X
KCNK10	P,C	P,C		X
KCNK16	N,LA	N,LA	X	X
KCNN3	N,AF,M	N,AF,M	X	X
KCNT2	P,C	P,C	X	X
KEAP1	AF,C,M	AF,C,M	X	X
KERA	BC,LA	BC,LA	X	X
KIAA0090	C	C		X
KIAA0157	C	C		X
KIAA1026	BC,P,AF	BC,P,AF	X	X
KIAA1407	P,C	P,C	X	X
KIAA1468	LA	LA		X
KIAA1529	BC,P	BC,P	X	X
KIAA1604	M,C	M,C	X	X
KIAA1622	P,C	P,C	X	X
KIAA1737	N	N		X
KIAA1946	P,AF	P,AF		X
KIF11	M	M	X	X
KIF12	BC,LA	BC,LA	X	X
KIF13A	N,BC	N,BC	X	X
KIF15	P,LA	P,LA	X	X
KIF20A	LA	LA	X	X
KIF23	BC,BC	BC,BC	X	X
KIF3A	C	C		X
KLHDC2	BC	BC		X
KLK1	N,LA	N,LA	X	X
KPNB1	P,M	P,M		X
KRIT1	P,C	P,C		X
KSR1	AF,LA	AF,LA		X
KY	BC,P,AF	BC,P,AF		X
LEPROT	BC,C	BC,C	X	X
LGI2	C,M	C,M		X
LIF	P	P		X
LIG4	P,M	N	X	
LILRB1	BC,LA	BC,LA	X	X
LILRB2	AF,BC	AF,BC		X
LIN7C	N,C	N,C		X
LSR	C,LA	C,LA		X
MAGEB1	BC,AF	BC,AF		X
MAGED1	N	N	X	X
MAGEE1	BC,AF	BC,AF	X	X
MAGEE2	P,LA	P,LA	X	X

MAGEH1	LA	LA	X	X
MAGI1	BC,AF	BC,AF	X	X
MARCH7	N,P	N,P		X
MAST1	P	P	X	X
MAX	BC,LA	BC,LA	X	X
MC1R	BC,LA	BC,LA	X	X
MCM10	P,M	N		
METTL1	BC,AF	BC,AF		X
MFAP1	BC,M,D	BC,M,D	X	X
MFAP3	LA,P	LA,P		X
MFSD4	BC,AF	BC,AF		X
MGAT2	BC,AF	BC,AF		X
MGAT5	BC	BC	X	X
MGC29891	C,P	C,P	X	X
MIA	BC,AF,C	BC,AF,C		X
MID1IP1	P,LA	P,LA	X	X
MLN	BC,AF	BC,AF	X	X
MSL3L1	BC,AF	BC,AF	X	X
MSN	AF,M	AF,M		X
MSTN	BC,AF	BC,AF	X	X
MT3	BC,AF	BC,AF	X	X
MYH9	P,BC	P,BC	X	X
NACA	BC	C		
NAGA	N	N		X
NANOG	LA,C	LA,C		X
NANS	AF,C	AF,C	X	X
NCOA5	C,M	AF	X	
NCR1	C,LA,P	C,LA,P	X	X
NCR3	BC,AF	BC,AF		X
NDC80	M,BC	M,BC	X	X
NDE1	P,C	P,C		X
NDOR1	P,C	P,C		X
NDUFA7	P,BC	P,BC	X	X
NEDD4	M,AF	M,AF	X	X
NEDD8	BC,AF	BC,AF	X	X
NFIA	C,P	C,P	X	X
NGFR	P,C,LA	P,C,LA	X	X
NHP2L1	BC,D	BC,D	X	X
NINJ2	N,P	N,P	X	X
NKD2	P,LA	P,LA	X	X
NLRP9	BC	BC		X
NNT	LA,C	LA,C		X
NOL1	C,BC	C,BC		X
NONO	BC,LA	BC,LA		X
NOS3	P,C	P,C	X	X
NOTUM	C,BC	C,BC		X
NOX4	P	P	X	X
NPFFR2	P,C	C		
NPHS1	C,LA	C,LA		X
NR2F6	P	P	X	X
NR3C1	BC,M	BC,M		X
NR4A3	BC,AF	BC,AF		X
NRN1	LA	LA		X
NSUN4	P,LA	P,LA	X	X
NUAK2	N,BC	N,BC		X
NUCB1	P,C	P,C	X	X
NUF2	M	M	X	X
NUMA1	BC,P	BC,P		X
NUMBL	BC,AF	BC,AF	X	X
NUP205	P	BC	X	
NXF1	BC,LA,D	BC,LA,D	X	X
NXF5	P,M	P,M		X
OFCC1	P,C	P,C		X
OPCML	P,AF,C	BC	X	
OPTN	N,P	N,P		X
OR2F1	P,D	P,D		X
OR5B3	BC,AF	BC,AF		X
OR8K1	C,LA	C,LA		X
ORC4L	BC,P	BC,P	X	X
OVOL1	N,BC,AF	N,BC,AF		X
PAX2	P,LA	P,LA	X	X
PCBD1	N	N		X
PCDH24	BC,AF,C	BC,AF,C		X

PCDHB10	BC	BC	X	X
PCDHB7	C	C	X	X
PCDHB9	LA,C	LA,C	X	X
PDCD1LG2	P	N	X	
PDE4DIP	BC,AF	BC,AF	X	X
PDYN	P,C	P,C		X
PEG3	BC,AF	BC,AF	X	X
PEX11A	BC,LA	BC,LA	X	X
PEX13	BC,AF	BC,AF	X	X
PEX26	BC,LA,P	BC,LA,P	X	X
PGLYRP2	N,C	N,C	X	X
PGLYRP3	P,C	C		X
PHCA	BC,AF	BC,AF	X	X
PHF11	BC,LA	BC,LA		X
PIK3R4	P,C	P,C	X	X
PIP5K1C	BC,LA	BC,LA		X
PKIB	C,M	C,M	X	X
PLAUR	N,P	N,P		X
PLEK	P,C	C	X	
PLK1	M	M	X	X
PLXNA2	BC,P	BC,P		X
PLXNB1	P,LA	BC	X	
PMVK	P	P		X
PNMAL1	C,P	C,P	X	X
POLE	BC,LA	BC,LA	X	X
POLH	AF,C	AF,C		X
POLR2A	M,D	M,D	X	X
POLR2E	BC,AF,C	BC,AF,C		X
POLR2F	BC,AF	BC,AF	X	X
POLR2L	BC,P,C	N		
POP1	C,P	C,P	X	X
PPCDC	LA	LA		X
PPP1R16A	P,C	P,C	X	X
PPP2R5E	N	N		X
PQBP1	N,C	N,C	X	X
PRC1	LA,C	LA,C		X
PRDM8	P,LA	P,LA	X	X
PRELP	P,LA	P,LA		X
PRKAB1	P,C	P,C		X
PRKAG2	BC	BC		X
PRRX2	BC,P	C	X	
PRSS22	BC,LA	BC,LA		X
PSMA6	C,M	C,M		X
PSMD1	P,C	P,C	X	X
PSMD3	M	M	X	X
PSMD8	M,C	M,C	X	X
PTDSS2	P,AF	BC	X	
PTGES	BC,P,C	BC,P,C	X	X
PTPN13	C,BC,AF	C,BC,AF	X	X
PTPN20B	P	P		X
PTPRE	BC	BC	X	X
PTRH2	C,M,BC	C,M,BC		X
PUM1	AF,BC	AF,BC		X
PVRL3	N,BC	N,BC	X	X
PXMP2	LA	LA		X
PZP	BC,P	BC,P		X
RAB17	BC,LA	BC,LA		X
RAB1B	BC,AF	BC,AF		X
RAB3D	P,M	P,M	X	X
RAD51	P,BC,AF	P,BC,AF	X	X
RAD51C	BC	BC		X
RAN	BC,AF,LA	BC,AF,LA		X
RAP2C	AF,BC	AF,BC	X	X
RAPH1	BC,AF	BC,AF	X	X
RASA1	P	P		X
RBBP9	C,M	C,M	X	X
RBM8A	M,D	M,D	X	X
RBP1	C	C		X
RCN3	C,M	C,M		X
RFWD2	BC	BC		X
RHBG	P	P		X
RHOJ	C,M	N	X	
RIC8B	N,P	N,P	X	X

RND3	P,C	P,C	X	X
RPA1	P,M	P,M	X	X
RPA2	C,P	C,P	X	X
RPA3	M,C	M,C	X	X
RPH3AL	BC,LA	BC,LA	X	X
RPL10L	BC,LA	BC,LA	X	X
RPL14	BC	BC	X	X
RPL18	C,BC	C,BC	X	X
RPL24	BC,C	BC,C	X	X
RPL28	BC,M	BC,M	X	X
RPL30	C,BC,AF	C,BC,AF	X	X
RPL34	BC,C	BC,C	X	X
RPL35	BC,AF	BC,AF	X	X
RPL35A	BC	C	X	
RPL38	C	C	X	X
RPL39L	BC,P	BC,P	X	X
RPL4	BC,C	BC,C	X	X
RPL7A	BC,AF,C	BC,AF,C	X	X
RPL8	C	C	X	X
RPLP0	BC,AF	BC,AF	X	X
RPLP1	C,BC	C,BC	X	X
RPS11	C	C	X	X
RPS13	C,M	C,M	X	X
RPS14	C	C		X
RPS19	C	C	X	X
RPS21	C,BC	C,BC	X	X
RPS24	C	C	X	X
RPS28	C	C	X	X
RPS29	C	C	X	X
RPS3A	C	C	X	X
RPS5	C,BC	C,BC	X	X
RPS9	C,BC	C,BC	X	X
RPSA	C,P	C,P	X	X
RSC1A1	N,BC	N,BC	X	X
RTN1	LA,AF	C	X	
RUNDC2A	BC,LA	BC,LA		X
RUVBL2	P,D	P,D	X	X
SBNO1	P	N	X	
SC65	BC	BC	X	X
SCGB1A1	C,P	C,P	X	X
SEC24D	P,LA	P,LA		X
SEMA6A	LA	LA		X
SERINC1	BC,LA	BC,LA		X
SESN3	P,LA	P,LA	X	X
SETD8	P	P	X	X
SF3A3	C,M	C,M	X	X
SF3B1	P,M,D	P,M,D	X	X
SF3B14	BC,M	BC,M	X	X
SF3B4	M,D	M,D	X	X
SH2B2	P	BC	X	
SHCBP1	N,LA	N,LA	X	X
SHH	AF,C	C	X	
SHROOM2	AF	AF	X	X
SLC25A17	BC	BC		X
SLC26A1	BC,AF	BC,AF	X	X
SLC2A13	BC,AF	BC,AF	X	X
SLC39A1	LA	LA		X
SLC39A2	C,P	C,P	X	X
SLC3A2	P,C	P,C	X	X
SLC45A2	BC,P	BC,P	X	X
SLC46A1	N,C	N,C		X
SLC46A2	BC,AF	BC,AF		X
SLC4A2	LA	LA		X
SLC6A4	N	BC	X	
SLITRK3	P,C	P,C		X
SMARCD1	P,LA	N	X	
SMU1	M,BC	M,BC	X	X
SMUG1	C,AF	BC	X	
SMURF1	BC	BC	X	X
SOCS2	P,C,D	P,C,D		X
SOCS7	C,LA	C,LA	X	X
SOLH	BC,M	BC,M	X	X
SON	M,BC	M,BC	X	X

SPATA20	BC,AF	P	X	
SPATA7	N	N		X
SPIC	P	P	X	X
SPIN2A	BC,AF	BC,AF	X	X
SPP2	P	P	X	X
SPRY2	LA,BC	LA,BC		X
SPSB3	BC,AF	BC,AF		X
SPTA1	P	P	X	X
SSBP3	BC,C	BC,C		X
STAP1	C	C		X
STAR	BC,LA	BC,LA		X
STK39	P,C	N	X	
STRA6	P,C	P,C		X
SUPT6H	P,C	P,C	X	X
SUV39H1	M,AF	M,AF		X
SYT4	P,C	C		
SYTL2	P,C	P,C	X	X
TAGLN	P,C	P,C	X	X
TAS2R49	M,BC	M,BC		X
TBX21	BC,LA	BC,LA		X
TENC1	N	N		X
TESK2	LA	LA		X
THAP3	BC,AF	BC,AF		X
THRA	BC,LA,M	BC,LA,M		X
THSD3	BC,P	BC,P		X
TIMM10	BC,LA	BC,LA		X
TLN1	P,C	P,C	X	X
TMBIM4	P,C,M	P,C,M	X	X
TMEM61	BC,P,AF	BC,P,AF	X	X
TMOD1	C	C	X	X
TMOD2	N	N		X
TMPRSS9	N,BC	N,BC	X	X
TNFRSF1A	AF	AF	X	X
TNPO2	P,M,C	P,M,C	X	X
TP53BP1	P,AF	N	X	
TP53I13	BC,M	BC,M		X
TPCN1	BC,AF	BC,AF		X
TPPP2	C	C		X
TPRG1	C,LA	C,LA		X
TPX2	M,P	M,P	X	X
TRA2A	N	N		X
TRAIP	P,C	P,C	X	X
TRAPPC1	P	P		X
TRAPPC2L	BC,AF	BC,AF		X
TRAT1	LA,C	C		
TRIM17	P,C	P,C	X	X
TRIM32	C	C		X
TRIM9	LA,AF	LA,AF	X	X
TRPM8	BC,AF	BC,AF	X	X
TSPAN9	C	C	X	X
TTC22	LA	LA		X
TUBE1	P	P	X	X
UBB	AF,BC	AF,BC		X
UBC	LA,BC,M	LA,BC,M		X
UBE2D2	C,M	C,M	X	X
UBOX5	BC,AF,C	BC,AF,C	X	X
UGCGL1	N,C,M	N,C,M		X
UNC93A	BC,AF	BC,AF		X
UNG	N	N		X
UPK1A	M,AF	M,AF		X
USO1	BC	BC		X
USP1	C,LA	C,LA	X	X
USP18	BC,P	BC,P	X	X
VARS2	N,C,LA	N,C,LA		X
VAX1	AF,C	AF,C	X	X
VIT	C,LA	C,LA		X
VNN3	C,AF	C,AF		X
WBSCR22	LA,P	LA,P	X	X
WDHD1	LA,P	C	X	
WDR21A	BC,AF,C	BC,AF,C		X
WEE1	M,D	M,D	X	X
WFS1	P,C,M	P,C,M		X
WHSC1L1	M,P,LA	M,P,LA	X	X

WIPI1	BC	BC		X
WISP1	P,C	P,C		X
WRN	C,M	C,M		X
WWP2	P,C,M	C	X	
YARS	BC	C	X	
YIPF4	BC,AF,LA	BC,AF,LA		X
ZBTB48	P	P		X
ZCCHC13	BC,AF	BC,AF		X
ZDHHC19	C,BC	C,BC		X
ZFAND1	C,LA	C,LA		X
ZIM3	N,M	N,M		X
ZNF16	BC	BC		X
ZNF177	BC,AF	BC,AF		X
ZNF212	C	C		X
ZNF225	N	N		X
ZNF234	AF,M	AF,M		X
ZNF331	BC,LA	BC,LA	X	X
ZNF442	C	C		X
ZNF507	BC,P	BC,P		X
ZNF585A	P,C	P,C	X	X
ZNF595	C	C	X	X
ZNRF4	M,P	M,P		X

Table X: Manual annotation of the retest phenotypes using the Qiagen library. HGNC is the target HGNC gene symbol. HeLa and U2OS phenotypes are the manually observed retest phenotypes in HeLa and U2OS cells (respectively), expressed in terms of phenotypic classes, as defined in Table SII. HeLa reproducibility is the reproducibility of the HeLa phenotypes between the primary screen and the retest screen. The X mark indicates that the phenotype is reproducible. Qiagen reproducibility is the reproducibility of the retest phenotypes between the HeLa and the U2OS cells. In total, 280 candidates reproduced their phenotypes between the primary and the retest screens, in both HeLa and U2OS cells.

HGNC	Nb. of siRNAs	Pool phenotype
A1BG	3/4	P, C
ANKRD31	4/4	P, C
ANLN	3/4	BC, P
APOC3	2/4	P
ATM	1/4	P
ATP6V1B1	2/4	BC, P
AURKB	4/4	P, C
BCAR3	1/4	P, C
BLR1	2/4	C, arrest
BMPER	1/4	P, C
BRCA1	0/4	N
C9ORF90	2/4	P
CADM1	2/4	BC, AF
CAPN3	4/4	P
CARD10	3/4	P
CASP1	2/4	P
CD3EAP	3/4	BC, P, AF, M
CGRRF1	0/4	P
CKAP5	4/4	Viability
COL11A1	3/4	P, binuclei
COL6A1	2/4	P
DAOA	1/4	P
DDX4	3/4	P
DONSON	3/4	C, M, P, BC
ERCC1	3/4	C, P
SUSD4	1/4	P, BC
FANCI	3/4	P
CCDC49	2/4	P
GIPR	1/4	P
GPR124	1/4	P
GPR34	1/4	P
GPR34	0/4	P
GPS1	4/4	P
HAAO	1/4	P
IK	4/4	C, arrest
KIF23	3/4	BC, C, P
TUBB	3/4	Viability, arrest
LUC7L2	0/4	P
STK40	4/4	P, C
MIA	2/4	P, C
MRE11A	0/4	BC
MTMR6	2/4	P, C
NARF	3/4	P
NDST3	2/4	P
NTN2L	2/4	P
PBOV1	2/4	P
RAB17	2/4	P
REC8	2/4	P
REEP3	3/4	P
AJAP1	1/4	P
SLC25A37	2/4	P
SLC41A3	3/4	P
SON	3/4	M, BC
SPOCK1	3/4	P
STXBP5L	2/4	P
TEKT3	2/4	C, P
TMEM61	3/4	BC, P, AF
TPM1	2/4	P, C
TRAIP	1/4	P, BC
TRAPPC2L	2/4	P, C
TRAPPC3	4/4	P

Table XI: Manual annotation of deconvoluted Dharmacon siRNA phenotypes. HGNC is the target HGNC gene symbol. Number of siRNAs is the number of individual siRNAs showing the same phenotype as the corresponding Dharmacon siRNA pool (out of the total number of siRNAs in the pool). Pool phenotype is the phenotype observed with corresponding Dharmacon siRNA pool.

HGNC	Source	Pool ID	siRNA ID	Sequence
ABCB10	Dharmacon	M-007300-00	D-007300-01	GAAGAACGGTGTTAGTTAT
			D-007300-02	CGAGAAATATGCCAGCAAA
			D-007300-03	CATCGTCTGTCCACCATTA
			D-007300-04	GCCCAGAGGTGCCCATATT
	Qiagen	29D3	SI00096950	TAGACCCTAAGAAGTAATTAA
			SI00096957	ACCCTGCTTCTGGAACTATTA
			SI00096964	CCCAGTGTGGCTGAGATCCAA
			SI03030062	AACGGTGTTAGTTATTGCCCA
ADAMTS18	Dharmacon	M-005769-01	D-005769-01	ACAAGAACCTGGAGGATTA
			D-005769-03	GCCAGTATCTCAAGAAATT
			D-005769-04	GGGCACAACTTTGGTATGA
			D-005769-05	GGTGTGAGACCAAGTTTAT
	Qiagen	222F2	SI00292103	CAGGTTTAATAAGGACACGAA
			SI00292110	AACCAGCATAAAGCAAATGAA
			SI00292117	CTGGCTTGTCAGGTTTAATAA
			SI00292124	TGGAGGTTACATAAATGTAAA
AGXT2	Dharmacon	M-009818-00	D-009818-01	GGAAAGAAGAGCTAAGTAA
			D-009818-02	GGACCTACATGTTACTAAA
			D-009818-03	GGAAGCAGATACCTGGATT
			D-009818-04	CATAACCACTCCAGAGATT
	Qiagen	2B4	SI00293545	TGGGACCTACATGTTACTAAA
			SI03045931	AGGGCGCACTCAAACAACATA
			SI03050999	ATGGAGTTGTCCAGTACCCAA
			SI03107097	GTGGGACAGGTTGCCAACCAA
ANAPC7	Dharmacon	M-021035-01	D-021035-02	GGAATGCTGTGAGTAAGTA
			D-021035-03	GCTCGCACCTTGTCGCTTA
			D-021035-04	GGAACGCACTGGCTAATCA
			D-021035-05	GCACAGACCCTTACCCTTT
	Qiagen	11E2	SI00114688	ATGGATGTATATGGCTACCTA
			SI00114709	ACCGTTTGTCTTGAAGACCCA
			SI02652895	CCCAAAGGCCAGATTACATTA
			SI02653532	CAGCTTCTATAGCAAACGCTA
ANLN	Dharmacon	M-006838-02	D-006838-01	GGAGATGGATCAAGCATTA
			D-006838-02	GAAATCCGCTTGCCTCTAA
			D-006838-03	GGATAAATCTGGCTAATTG
			D-006838-05	ACGCAACACTTTTGAATTA
	Qiagen	61E4	SI00122703	AAGGTTTCACTGAATGCGAAA
			SI02777859	CACCGTTTCCATCGTCTCGTA
			SI02777866	CTGATGCTTGCTACAAACCTA
			SI03120285	TGGCGATGCCTCTTTGAATAA
APBB1IP	Dharmacon	M-015662-00	D-015662-01	GAATACGGATAGCCAAGTA
			D-015662-02	CAGAAGGAGTCCCAGTATA
			D-015662-03	TTAAGAAGCTCGTCGTCAA
			D-015662-04	ATAAAGCGCCCACTGACTA
	Qiagen	136B2	SI00297871	AAGATTTAAATGAGTCCTTAA
			SI00297878	CAGCATCTCTACAAGCATCAA
			SI00297885	CAGAATATCTGCCCAAATGTA
			SI00297892	CAGCCTCTCTTGGTTATGGAA
ARCN1	Dharmacon	M-013063-00	D-013063-01	AAACAGAGAGTGTAAGATA
			D-013063-02	GATCAGAACCTTCACAGAA
			D-013063-03	GACGGAGGATTACAGAATA
			D-013063-04	TGAAATATCTGAGCACTGT
	Qiagen	90H7	SI00299754	CCCACTTGTGTCAATATTAAA
			SI00299761	AAGGCAAATTCTTTAATCAAA
			SI00299768	CCCATTAATATGGAAAGTGTA
			SI00299824	AAGGCTGAGATGCGTCGTAAA
ARFGEF1	Dharmacon	M-012207-00	D-012207-01	GAACAGGTCTCCAACAATT
			D-012207-02	GATCACAAATGGATGGTTA
			D-012207-03	GAACTACGATCCAAGATTC
			D-012207-04	GAACAGGAACTTGGTATTA
	Qiagen	118G3	SI00300825	CAGGATTTATTTAGAATTGTT
			SI00300832	TCCGGTATTACTGAAATGAAA
			SI00300839	AGGGATAGATTTATTTAATAA
			SI00300853	CAAGATTGTGATGATACTGAA
ASNSD1	Dharmacon	M-020489-00	D-020489-01	CAAGGTCCCTGGTCATTTA
			D-020489-02	GCATTTCAGTCAAGATTTA
			D-020489-03	GCAGTAATATTTCCAATGT
			D-020489-04	GGAGTGAAATCCTATCAGA
	Qiagen	44E9	SI00123872	GCGGGACTAAAGGAACTACAA
			SI03031014	AAGAAGAACTCGAATATGTCA
			SI03099201	CTGGGTCGAATTTCTTCTAGA
			SI03101287	GACAGAGTTATTGGTGATCAT

HGNC	Source	Pool ID	siRNA ID	Sequence
ASPH	Dharmacon	M-004294-00	D-004294-01	GGTTTGATCTTGTTGACTA
			D-004294-02	AAACTAGGAATCTATGATG
			D-004294-03	GAGGAAAGGCGGACTCTCA
			D-004294-04	GCATGGAGGACACAAGAAT
	Qiagen	12F7	SI00062601	CTGTAGAAGATTCACAGGTAA
			SI03023958	TTGCACCATGATACAGATGAT
			SI03111591	TAGGACTTAAAGAGAGATCTA
			SI03113824	TCCAGTGAACCAGTAGTAGAA
ATP7A	Dharmacon	M-019280-00	D-019280-01	GGAGATGGCTCATAAGGTA
			D-019280-02	GATAAACGCTCCCTAAACA
			D-019280-03	GCAAAGGAGTCCATCATAT
			D-019280-04	GGAAAGAATTCATCTAAGT
	Qiagen	31G6	SI00000854	CAGCCAGTTATTCTTCCATTA
			SI00000875	TAGCAGCTTGTAGTATTGAAA
			SI03075730	CCAGTGGCCCATCTTATAATA
			SI03095568	CTGCGTAGCTCCAGAGGTTTA
BCAR3	Dharmacon	M-011469-00	D-011469-01	GGAAGAACCTCGCTCAGCA
			D-011469-02	GGACCCAACTGTGGAATAT
			D-011469-03	GGACATAATTGAAAGACAC
			D-011469-04	GCGAGATGGTGACTTCCTA
	Qiagen	60A10	SI00053095	AAGGTATCAGTTATATGATAT
			SI00053102	GCCCAACGAGTTTGAGTCAAA
			SI03080196	CCGAGCGGCCACTCTGAGTAA
			SI03081603	CCGGAACTCTGGCGTCAACTA
BCL2L1	Dharmacon	M-003458-00	D-003458-01	CAGCTTGGATGGCCACTTA
			D-003458-02	ACAAGGAGATGCAGGTATT
			D-003458-03	CCTACAAGCTTTCCCAGAA
			D-003458-04	GGTAGTGAATGAACTCTTC
	Qiagen	41B10	SI00023191	CTGCTTGGGATAAAGATGCAA
			SI03025141	TTGGCTTTGGATCTTAGAAGA
			SI03068352	CAGCTGCCTCACTTCCTACAA
			SI03112018	TAGGGTGGCCCTTGCAGTTCA
BRD9	Dharmacon	M-014250-00	D-014250-01	CAATGAAGATACAGCTGTT
			D-014250-02	GGCCAGATACCGTGTACTA
			D-014250-03	CACGCAGGCTTTAAGATGA
			D-014250-04	AGTCAGTTACGGAATTTAA
	Qiagen	218F6	SI00313341	CTGGATATTCAATGATAATAA
			SI00313348	TGGATATTCAATGATAATAAA
			SI00313355	CTCCTGGATATTCAATGATAA
			SI00313362	CAAGTCAGTTACGGAATTTAA
C13ORF3	Dharmacon	M-015700-00	D-015700-01	GATCGTACTTCGTTGGTTT
			D-015700-02	AATCCAGGCTCAATGATAA
			D-015700-03	GTACATCGTATCCCAAGTT
			D-015700-04	TACCAAACAATCACTAGTA
	Qiagen	187E11	SI00317933	AAGGATGATGTTAATATTCTT
			SI00317940	CAGCTGGAAAGTATTATCTAA
			SI00317947	AGGGAATATATTCAAAGTGTA
			SI00317954	AAAGACAAACATGAACATTAA
C16ORF68	Dharmacon	M-014309-00	D-014309-01	CAAGGTACATCCCATGATT
			D-014309-02	ACAGAGATGTTCACACAAA
			D-014309-03	CAAGGCAGCCCGCACGATA
			D-014309-04	TGTCAGATGTCCACCTCTA
	Qiagen	152G9	SI00636251	CCGCACGATATCATCAGAATA
			SI00636258	TTAGAGTGTATTTCTAGTAAA
			SI00636265	AAGGTACATCCCATGATTCTA
			SI00636272	CCAGCGAAACATTGCCCTCAA
C1QA	Dharmacon	M-013136-00	D-013136-01	CCATATCGCTGGCCTCTAT
			D-013136-02	GCACTGTACCCGGCTACTA
			D-013136-03	AGGAAGAACCGTACCAGAA
			D-013136-04	CGTGGCATCCCGGGAATTA
	Qiagen	91E5	SI00323729	CCCGGGAATTAAAGGCACCAA
			SI00323736	ACGGTCATCACCAACCAGGAA
			SI00323743	ACAGGCATCCAAGGCCTTAAA
			SI00323750	CCCAGGAAACATCAAGGACCA
C20ORF20	Dharmacon	M-006381-00	D-006381-01	GAAGAACTCCTCAGACTTG
			D-006381-02	GAACTTCGTCCTTCCAGAA
			D-006381-03	GAACCGACACTTCCACATG
			D-006381-04	ACAAAGTCCTGACCGCAAA
	Qiagen	140F4	SI00325325	CTCGGATTAGCAAGCAATAAA
			SI00325332	TCGTGTGACTGCGAACATTAA
			SI00325339	CCCACCCACCTGGGAAACTAA
			SI00325346	CAGAGAATTTGTAGCGGTTAT

HGNC	Source	Pool ID	siRNA ID	Sequence
C2ORF60	Dharmacon	M-016468-00	D-016468-01	GGTGATGTATTATTCATTC
			D-016468-02	GGACTTCTATGCACGACGA
			D-016468-03	CGAGATGCCCAGTATTTAT
			D-016468-04	CCGAGTTACCAGAGGAATA
	Qiagen	174D10	SI00411572	CAGATTGTTATAATTAAAGAA
			SI00411579	ATGCCCAGTATTTATATTTAA
			SI00411586	CAGCAAGAGAATTGATACAAA
			SI00411593	ATGGATAATTTGTTAATACAA
C6ORF182	Dharmacon	M-018100-00	D-018100-01	GAACATCAGCGTAAGCTAT
			D-018100-02	CTAAAGCACTCCAAGGAAA
			D-018100-03	GAACAACTTCCTGGTGTAA
			D-018100-04	GCACCAAGAACTACTGAAA
	Qiagen	193E7	SI00331233	CTGGTGGGTTCCAAATAATAA
			SI00331240	TCACTTGGATATAATAATATA
			SI00331247	ATGCTTTATAATAAATTTACA
			SI00331254	TACTAGATTGACAATATTCAA
CADM1	Dharmacon	M-016565-00	D-016565-01	GAAGTCAACTGCACTGCTA
			D-016565-02	GGAAAGCTCACTCGGATTA
			D-016565-03	GTACATACTTCACTCATGA
			D-016565-04	GAGAGTCGATGATGAAATG
	Qiagen	212E11	SI00446740	CAGAATTTAGTGTATCCATAA
			SI00446747	CTGGCCCTATTTAGATGATAA
			SI00446754	TCCGACCATAGTATAATCATA
			SI00446761	TTGGGTGAACAAACAATGAAA
CAPRIN1	Dharmacon	M-016057-00	D-016057-01	AGGGTAAGCTTGATGATTA
			D-016057-02	GCACGTCGGGAGCAGCTTA
			D-016057-03	GGAAATTGTTGAGCGTGTT
			D-016057-04	TAGTCAGCCTCACCAAGTA
	Qiagen	205D7	SI00626003	CGGGATTACTCTGGCTATCAA
			SI00626010	TTGGATGAATTCTATAAGCTA
			SI00626017	CAGCCTATGAATCCAACACAA
			SI00626024	TAGCAGTGGAATCAATGTAAA
CARS	Dharmacon	M-010335-00	D-010335-01	GAAGAGTGTTGAAGGATTA
			D-010335-02	GGACAACGGTTACGGCTAT
			D-010335-03	GAAGACAGCAATTCACAAA
			D-010335-04	CGACAAATACTCCAAGTTT
	Qiagen	7H8	SI00338513	AAGGAAGTGTTCATACCTCAA
			SI00338520	CACCCTTGGGTCCTAAATTAA
			SI00338527	CTGGTAGACAGAAACACCTTA
			SI03072384	CAGGTGTTATCAGAATTCCGA
CASP8AP2	Dharmacon	M-012413-00	D-012413-01	GAACAGAGCTCTATGATAC
			D-012413-02	TGGCATAGTTGATCGTTTA
			D-012413-03	GAGAGTAAGTCGTGTCATC
			D-012413-04	GCACATGTTACGAATGATA
	Qiagen	40E9	SI00097272	CAGCTGATGTGCGGAAGTCAA
			SI00097279	AACGAAGTTTCGAGATTCTTA
			SI02638937	CAGTCTGATCTCAATAAGGAA
			SI03056501	CACATACGTAGATCTAACGAA
CD3EAP	Dharmacon	M-020021-00	D-020021-01	GAAAGAAACCTTCGAGCCA
			D-020021-02	GATTAACACTGAGCCTCTA
			D-020021-03	ATACGGAGCTGTGGCTTAT
			D-020021-04	GAAAGAGAGAGGTCACACA
	Qiagen	119D5	SI00305249	CCGGGAAACTGAGGAACTAAA
			SI00305256	AAGGAGCTGTTTCCTGGGTAA
			SI00305263	CAAGGGCAAATTGGCAGGCAA
			SI00305270	CAGATTAACACTGAGCCTCTA
CDC37L1	Dharmacon	M-020779-00	D-020779-01	TAAACTCGGTGGTACATAA
			D-020779-02	GCTTAGCACTGCATAATTC
			D-020779-03	ACATCAAGCTGTTGTAATG
			D-020779-04	TCACAAAGTTTTCAACCTA
	Qiagen	142F2	SI00341005	TTGGTGTTTCATCACATTAAA
			SI00341012	CAGATTATCTTCAGTATTCTA
			SI00341019	CAGGAGCATGCCAAAGCACAA
			SI00341026	ATGGAACAAATAGCACATCAA
CDC42	Dharmacon	M-005057-00	D-005057-01	GGAGAACCATATACTCTTG
			D-005057-02	GATTACGACCGCTGAGTTA
			D-005057-03	GATGACCCCTCTACTATTG
			D-005057-04	CGGAATATGTACCGACTGT
	Qiagen	42C4	SI03028935	AACCTAATTCTTGTAGATGCA
			SI03049914	ATGCATTAGTGTTGAACCAAT
			SI03068261	CAGCTGAAGACCTGTTATGTA
			SI03072118	CAGGTGAGGCTCTCTAGTTTA

HGNC	Source	Pool ID	siRNA ID	Sequence
CDCA5	Dharmacon	M-015256-00	D-015256-01	GAAAGCCCATCGTCTTAAA
			D-015256-02	GGTCCCAGCTGTCCAATCA
			D-015256-03	GATCGTGGCCCATGCTGTA
			D-015256-04	CCTGAAATCTGGCCGAAGA
	Qiagen	39C6	SI00148708	CAGAAAGCCCATCGTCTTAAA
			SI00148715	ACCCGAGAAACAGAAACGTAA
			SI02757965	CTCGGAAAGTTTCCTCGCGTA
			SI02757972	GAGGAACTAAATTTAAGGAAA
CDCA8	Dharmacon	M-021163-00	D-021163-01	GAAGAGAACTCAGTCCATA
			D-021163-02	GGAGAGAGCCTGCGATTAT
			D-021163-03	TGAACTGGCTTGACTACTT
			D-021163-04	GAAAGGTAATACAGGTAGA
	Qiagen	61C4	SI00120582	ACGAAAGGTAATACAGGTAGA
			SI00120589	CTGGTACCTACTTTCAATAAA
			SI03065636	CAGCAGCATACGGACCCACAA
			SI03092740	CTGAAAGACTTCGACCGTGAA
CDKN2A	Dharmacon	M-011007-00	D-011007-01	CCGCATAGATGCCGCGGAA
			D-011007-02	GCGGAAGGTCCCTCAGACA
			D-011007-03	CACCAGAGGCAGTAACCAT
			D-011007-04	CGGAAGGTCCCTCAGACAT
	Qiagen	81E8	SI00001470	CCCGATTGAAAGAACCAGAGA
			SI02659503	CACGCCCTAAGCGCACATTCA
			SI02664396	CAGAACCAAAGCTCAAATAAA
			SI02664403	TACCGTAAATGTCCATTTATA
CENPE	Dharmacon	M-003252-01	D-003252-05	GAAGACAGCTCAAATAATA
			D-003252-06	CAACAAAGCTACTAAATCA
			D-003252-07	GGAAAGAAGTGCTACCATA
			D-003252-08	GGAAAGAAATGACACAGTT
	Qiagen	39B6	SI00028679	AAGATGGTTGGCATAGATAAA
			SI00028693	ACCACCTTAGAGGATATATAA
			SI02653217	CAGGTTAATCCTACCACACAA
			SI02653756	CACGATACTGTTAACATGAAT
CENPI	Dharmacon	M-005268-00	D-005268-01	GGTACAAGGTGAATAATTA
			D-005268-02	GAATAGAAGTGGATCATTT
			D-005268-03	GAAGGTGTGTGACATATAT
			D-005268-04	GGAATTCTCTCTCAGTTAT
	Qiagen	95B5	SI00421876	TCAGAAGAAATTGATATTCTA
			SI00421883	CAAGACTTATCAAGAATTTAA
			SI00421890	TACAAGGTGAATAATTATGAA
			SI00421897	CCAGCTAATGTTCGTCCTCTA
CEP192	Dharmacon	M-032250-00	D-032250-01	GGACTTAAGTGCTACTAGT
			D-032250-02	GAGGTAGGTTGGACATCAA
			D-032250-03	CAGCTATTGTTTATGTTGA
			D-032250-04	GCTCAGCGGTATTTGGGAA
	Qiagen	215H11	SI00343581	AAGGAACATTATCATCTATTA
			SI00343588	CAGAAGTTAGTAGATATGAAA
			SI00343595	ACCCATATTCTAATACCTTAA
			SI00343602	AACAGTGAATGTGCAAGTAAA
CFL1	Dharmacon	M-012707-00	D-012707-01	TGACAGGGATCAAGCATGA
			D-012707-02	GCGGTGCTCTTCTGCCTGA
			D-012707-03	GTCAAGATGCTGCCAGATA
			D-012707-04	GCTATGCCCTCTATGATGC
	Qiagen	41A4	SI00078190	CAGTAAGGGACCTTCGATTAA
			SI02635381	CTGACAGGGATCAAGCATGAA
			SI02635388	CAAGGTGTTCAACGACATGAA
			SI02654134	CAAGCATGAATTGCAAGCAAA
CGRRF1	Dharmacon	M-006933-00	D-006933-01	GAAGATAGCCTCCTTACAT
			D-006933-02	GACCTTAGCTGATGAGGAT
			D-006933-03	TATGAATACTCGCCGCTTT
			D-006933-04	CTACATCGCGGTGGTCTTT
	Qiagen	60H5	SI00089740	CTGATAGGACTTATAAACTAT
			SI03025680	TTGGTTGGGATGTTCCAGTAA
			SI03101658	GACCGGGAAATTTATGATATT
			SI03120019	TGGCATAACCTTGACAACAGA
CHEK1	Dharmacon	M-003255-02	D-003255-06	GCAACAGTATTTCGGTATA
			D-003255-07	GGACTTCTCTCCAGTAAAC
			D-003255-08	AAAGATAGATGGTACAACA
			D-003255-09	CCACATGTCCTGATCATAT
	Qiagen	81A9	SI00287658	AAGAAAGAGATCTGTATCAAT
			SI00605094	CCCGCACAGGTCTTTCCTTAT
			SI02625798	CCACCTCATCATAACAACAAT
			SI02660007	TTGGAATAACTCACAGGGATA

HGNC	Source	Pool ID	siRNA ID	Sequence
CHN1	Dharmacon	M-010251-00	D-010251-01	GAATATAGACCTCCTGTTT
			D-010251-02	TATGAGATCTCCAGAACTA
			D-010251-03	CAATTCCACTCATTACATA
			D-010251-04	GACCTACACTTTGGCTTTA
	Qiagen	92D5	SI00345989	AAGGTTATCCATACCAATAAA
			SI00345996	ACCCTGTTTGATACAGATGAA
			SI00346003	CACGTAGGATACACAACCTTA
			SI00346010	CTGGCTGTTACATTACCATAA
CHST12	Dharmacon	M-008238-00	D-008238-01	GCGCGCACCTGACCTTCAA
			D-008238-02	CTACGAGGCCGACTTTGTT
			D-008238-03	AGAGCGACCTTCCCAGAAA
			D-008238-04	CCAGATCGACTACGACTTC
	Qiagen	141F4	SI00346465	CAGGATTTCTAGGATTTCTAA
			SI00346472	CAGAGGTAAACCGGTCAGTTA
			SI00346479	CAGCGCGCACCTGACCTTCAA
			SI00346486	AAGATTAATATATTTCAGGTA
CHST5	Dharmacon	M-012800-00	D-012800-01	GCGTTGCCCTTCACTAAGA
			D-012800-02	GCCGAAACCTGTCCGCCTT
			D-012800-03	GCAAGCAGGACGTATGCAA
			D-012800-04	GCAAGCCAATCGAGGCCTT
	Qiagen	212E10	SI00346605	AGGGAGTAAGTTACTGCTAAA
			SI00346612	CAGGGAGTAAGTTACTGCTAA
			SI00346619	TTACTGCTAAATTAAATTAAA
			SI00346626	TAGAGTGATTCAACCACCTTA
CKAP5	Dharmacon	M-006847-00	D-006847-01	GGAAATAGCTGTTCACATA
			D-006847-02	GAAGAAACCTCAAGTGGTA
			D-006847-03	GGCCAAAGCTCCAGGATTA
			D-006847-04	CAAGAAACCTGGATGGAAA
	Qiagen	1C7	SI00107961	CAGCTTTAGTTTACTAAACTA
			SI00107975	CACAGTGTCCTCCATAGGTAA
			SI02653588	AAGGGTCGACTCAATGATTCA
			SI02654043	CAGGTATTATTAATGACGCAA
CLDN11	Dharmacon	M-019258-00	D-019258-01	GAAGAGTGCCCACGTATAA
			D-019258-02	GCCCAGGCCTTTGGTGAAA
			D-019258-03	GATGATTGCTGCCTCGGTC
			D-019258-04	AGACCACCATCGTGAGCTT
	Qiagen	101F4	SI00347725	TAGACTTTATGCAATAAATAA
			SI00347732	AACATAAATTGTACTGTTGAA
			SI00347739	AAGTGAAATCTGTGCAATAAA
			SI00347746	CTGCCAGGCTCTAAAGCCAAA
CLN8	Dharmacon	M-013304-00	D-013304-01	GTTCTAACCTACCACATGT
			D-013304-02	GACAGCAACGGGATTCTTT
			D-013304-03	CATATTGGACCCATAAGAA
			D-013304-04	TCAATCCGGTGGACTGGAA
	Qiagen	3A7	SI00123193	TACGCTAATCATTAATCCATA
			SI00123200	ACCAAGGTGTATAGTAACCTA
			SI00123207	CCGGACCGTGTCAAGCATCTA
			SI00123214	CCCGGACAACTTGAATGAAAT
CLSPN	Dharmacon	M-005288-00	D-005288-01	GGAAATACCTGGAGGATGA
			D-005288-02	GGACGTAATTGATGAAGTA
			D-005288-03	GCAGATGGGTTCTTAAATG
			D-005288-04	GAATTTATATGCTGGGAAA
	Qiagen	149E7	SI00348593	CTGCAGTATTTACAACATCAA
			SI00348600	AACAGTGATCACCATAGTAAA
			SI00348607	AAGAGTCATTAGAATCAATAA
			SI00348614	AAGCACATACATGATAAAGAA
CLTC	Dharmacon	M-004001-00	D-004001-01	GAAAGAATCTGTAGAGAAA
			D-004001-02	GCAATGAGCTGTTTGAAGA
			D-004001-03	TGACAAAGGTGGATAAATT
			D-004001-04	GGAAATGGATCTCTTTGAA
	Qiagen	92F6	SI02651733	ACAGTTCTACTTAGAATTCAA
			SI02651740	CCGGAGAGATTTCTTCGTGAA
			SI02651747	ATGGCTGTACGTAATAACTTA
			SI02651754	CACGTGTTATGGAGTATATTA
CLUAP1	Dharmacon	M-014449-00	D-014449-01	CTAAAGACCTGCTCAATAA
			D-014449-02	TGACTTATCTGGAACAACA
			D-014449-03	GAGATGCTCATGCAAGGAA
			D-014449-04	TAACGATGACTCGGACATA
	Qiagen	212G5	SI00348761	CTGGAAATAAACGAGACTGAA
			SI00348768	ACCCTCAGACTTGTAGGTAAA
			SI00348775	TTCCACCTTATTTATCTTCTA
			SI00348782	AACCCTCAGACTTGTAGGTAA

HGNC	Source	Pool ID	siRNA ID	Sequence
CNTFR	Dharmacon	M-007856-00	D-007856-01	GGACAATGAGATTGGGACA
			D-007856-02	GCGGTGACGTGGCGGGTAA
			D-007856-03	CTGCATGGCTCCAAAATTA
			D-007856-04	GGACTGAGGAACCGCGACA
	Qiagen	22A10	SI00153825	ACGCCGGGAAGGAGTACATTA
			SI00153832	AAACGTCACCATTTCATGAAA
			SI00153839	CTGCGGTGACGTGGCGGGTAA
			SI03068338	CAGCTGCCGCTCCAACACTTA
COL9A3	Dharmacon	M-011624-00	D-011624-01	GACCTTCAGTGCCCAAGTA
			D-011624-02	GATGATCAGCGAACAAATT
			D-011624-03	CCAAGGAGCCGTGTTAGGA
			D-011624-04	CGGCATTGACGGAGAAGCT
	Qiagen	92E7	SI00351029	CAGGCTCTCGAAGCTCATAAA
			SI00351036	CAGGGTGACAGAGGAGACAAA
			SI00351043	AAGGTAGGGTGTGTATATATA
			SI00351050	AGCGAACAAATTGCACAGTTA
COPA	Dharmacon	M-011835-00	D-011835-01	ACTCAGATCTGGTGTAATA
			D-011835-02	GCAATATGCTACACTATGT
			D-011835-03	GATCAGACCATCCGAGTGT
			D-011835-04	GAGTTGATCCTCAGCAATT
	Qiagen	92D10	SI00351477	TCCCACTGAGTTCAAATTCAA
			SI00351484	CTGGATTTCAACAGCTCCAAA
			SI00351491	CTGGCGCATGAATGAATCAAA
			SI00351498	AAGCTTAATGACCTCATCCAA
COPB1	Dharmacon	M-017940-00	D-017940-01	CGACACAGCTATGTTAGAA
			D-017940-02	TATAAGGTCTGTCATGCTA
			D-017940-03	CCTCATGACTTCGCAAATA
			D-017940-04	GCTGTTACCGGCCATATAA
	Qiagen	92E10	SI02655702	CAGGATCACACTATCAAGAAA
			SI02655709	CAAGGATTGGTTATAATATAA
			SI02655716	CAGAATTGCTAGAACCTTTAA
			SI02655723	CACCAACATGGTTGATTTAAA
COPB2	Dharmacon	M-019847-01	D-019847-02	GAAGGGAGCATCATTGTTA
			D-019847-03	CAACAGCATTGTAAAGATA
			D-019847-04	GGACACACCCATTATGTTA
			D-019847-05	TATGGGCAGTTGTGAAATA
	Qiagen	36H10	SI00068096	CAGTACGTATTTGGCATTCAA
			SI02664809	ACGATTCTTCAGAGTATGCAA
			SI02664816	CAGGTTTCAAGGGTAGTGAAA
			SI03095792	CTGCTAGATCTGATCGAGTTA
COPG	Dharmacon	M-019138-00	D-019138-01	GAGGGTGGCTTTGAGTATA
			D-019138-02	GCAAACACGCCGTCCTTAT
			D-019138-03	GAAGAGGCTGTGGGTAATA
			D-019138-04	GGAGGCCCGTGTATTTAAT
	Qiagen	37G2	SI00113666	CCGAGCCACCTTCTACCTAAA
			SI02641905	CACCGACTCCACTATGTTGAA
			SI02641912	AGGCCCGTGTATTTAATGAAA
			SI03115546	TCCGTCGGATGTGCTACTTGA
COPZ1	Dharmacon	M-020293-00	D-020293-01	CCAAAGAACAGATCAAGTG
			D-020293-02	GGCTGTGGATGAAATTGTA
			D-020293-03	GAACCTTCCCTGTATACTG
			D-020293-04	CAACAAGACCCATCGGACT
	Qiagen	121G8	SI00351729	AGCGATTTAAATTGTATTGAA
			SI00351736	TTGGCTGTGGATGAAATTGTA
			SI00351743	TTGGGAATAGTTCATAGGGAA
			SI00351750	TCCCAGCATATTTAGATAATA
COX6A2	Dharmacon	M-012021-00	D-012021-01	CGAGTTCCGTCCCTACCAA
			D-012021-02	CAACTCCTATCTCCACTCG
			D-012021-03	GGACGGCAACCACACTCTG
			D-012021-04	CCACAATAGCCACGTGAAC
	Qiagen	92B11	SI00352317	CCCGAGTTCCGTCCCTACCAA
			SI00352324	CACCTTCAACTCCTATCTCCA
			SI00352331	CAATAAAGGTGTGAAGCTTAA
			SI00352338	CAACCACACTCTGTTCCACAA
CR2	Dharmacon	M-007861-00	D-007861-01	GAAATGAAGTCTCTTATGA
			D-007861-02	GCAAATGGATACAAGATAT
			D-007861-03	GGATAAACCTGCTCCTAAA
			D-007861-04	TAACGACACTGTGATATTT
	Qiagen	19F3	SI00029428	CACGCAATTATTATACAGATA
			SI00029435	GCCGGATTAGTTATTATTCTA
			SI00029442	TACCTTATACGTGATATCAAA
			SI03057502	CACCATCCGTTGTACAAGCAA

HGNC	Source	Pool ID	siRNA ID	Sequence
CRNKL1	Dharmacon	M-019013-00	D-019013-01	GATCAAGTATGCCCGCTTT
			D-019013-02	GAAAGGGTACGAGTGATTT
			D-019013-03	CAATTATGATGCATGGTTT
			D-019013-04	CGAGCGTGCTTTAGATGTA
	Qiagen	133E9	SI00354193	TGCGAGTGGATTAATAATTTA
			SI00354200	TCCAAAGAACAAATTATTTAA
			SI00354207	TAGGACTGTTGTTGAGATAAA
			SI00354214	CACAGATGAAGAAGAATTAAA
CXXC4	Dharmacon	M-008812-00	D-008812-01	CACCAGATCTGCAAATTTA
			D-008812-02	GCAAGAGGCTCATCAACTG
			D-008812-03	AGACAGTGCGTTTCAAATT
			D-008812-04	GAACACTGCAGACCTTTGG
	Qiagen	25G2	SI00138495	CAGCAGTTGCAGGAACCGCAA
			SI00138502	TTCAAGGCATTTGGAAATGAA
			SI00138509	CCAGATCTGCAAATTTAGAAA
			SI00138516	TTGGAAATGAAGGGCAAACTA
CYBRD1	Dharmacon	M-017132-00	D-017132-01	GCAGAGATCTACCATGTAA
			D-017132-02	GAACCACAATGTTAACAAT
			D-017132-03	GGAGCGCACTAGAGTTTAA
			D-017132-04	GTTAAACAATGAAGTAGCA
	Qiagen	155B11	SI00358365	AACCACAATGTTAACAATATA
			SI00358372	AAGGATGTGATTAATATAAAT
			SI00358379	AAGGGATTAGATAGCGACTAA
			SI00358386	TAGTATCAATATTTACTTTAA
DNAJB9	Dharmacon	M-012815-00	D-012815-01	GGAGGTGGATTATTTGATG
			D-012815-02	GGACAAAGAGGTAGTGGAA
			D-012815-03	GAGGAAATATGGTTACTAC
			D-012815-04	GAAGCAAAATTCAGAGAGA
	Qiagen	8E4	SI00099442	CAGAGTGTACATGAAACTGTA
			SI02663045	TCGGATAGACTTATTTCTTTA
			SI02663052	CAAGTGCATGATTTCACTTTA
			SI03049067	ATGAAGTACCACCCTGACAAA
DONSON	Dharmacon	M-017453-00	D-017453-01	CCTGTGGACTGGAGTATTA
			D-017453-02	CAGCAGAGCCTTATCTATT
			D-017453-03	GGTCTTGTCCAGCATTGTA
			D-017453-04	CTACCACTGTTCCCTCGTA
	Qiagen	214D5	SI00372841	CTGGAGCAACTTAGTCAAATA
			SI00372848	TAGCAGGTTCTTGTTTCATAA
			SI00372855	AAGGAATATACTGAAATGTTT
			SI00372862	TTCAAGATTCTTGAAGTTGAA
DUX1	Dharmacon	M-019955-00	D-019955-01	GCAAGCATCCGGTGCAATG
			D-019955-02	GAATGATACTCCTTTCGAC
			D-019955-03	TCAAAGTGATGCCCTGCGA
			D-019955-04	AGACGAAAGCGGACTGCCA
	Qiagen	128D5	SI00375025	CCGGTGTGGCGTGGAACCTCA
			SI00375032	CCGGAAGGACTGGGACGCGCA
			SI00375039	TGGCAGCACCTGCGCAGTGAA
			SI00375046	AGGGTGCTCGTCTGCACTCCA
DYNC1I2	Dharmacon	M-012574-00	D-012574-01	GTAAAGCTTTGGACAACTA
			D-012574-02	GATGTTATGTGGTCACCTA
			D-012574-03	GCATTTCTGTGGAGGGTAA
			D-012574-04	GGGATAACCGTAGCAATAA
	Qiagen	93D11	SI00371665	CAGGTGCTAAACTGTCATTAA
			SI00371672	TGGGATAACCGTAGCAATAAA
			SI00371679	CTCGATCGTGTCAGTTTGTAA
			SI00371686	TTCTGTCTAAATGATAATTAA
EIF3C	Dharmacon	M-009036-00	D-009036-01	TCAATGAGCTGATGGATAT
			D-009036-02	GGACACAGGTTCCACATCT
			D-009036-03	GAAGATACCAAGAGAGTTG
			D-009036-04	ACGAATGGATGAAGAATTT
	Qiagen	7G11	SI00055454	GGGCGTCATTGTCAAGATCAA
			SI00055468	ACCGTGATTTCGAGTCCCATA
			SI02781261	CCGCCGACGCATGATCAGCAA
			SI02781289	AACGAATGGATGAAGAATTTA
EIF3I	Dharmacon	M-019531-00	D-019531-01	GTGGAGAGCTCAACCAGTA
			D-019531-02	GAAAGCAGCTGGCCCTTCT
			D-019531-03	GAAGATCCCTTGCAATGAC
			D-019531-04	CCACAGTACTTTGAATTTG
	Qiagen	110B7	SI00377713	CAGATTAAGTATAACCGCGAA
			SI00377720	AAGAAATAAATTGGTTTGGTA
			SI00377727	CCCACAGTACTTTGAATTTGA
			SI00377734	AAGGACCCTATCGTCAATGTA

HGNC	Source	Pool ID	siRNA ID	Sequence
EIF4A3	Dharmacon	M-020762-00	D-020762-01	GAAAGCGGCTGCTCAAAGA
			D-020762-02	GAACGTTGCTGATCTTATC
			D-020762-03	GGTGAAACGTGATGAATTG
			D-020762-04	ACTATGATCTCCCTAATAA
	Qiagen	55F8	SI00107828	AAAGAGCAGATTTACGATGTA
			SI00107835	CCGGAAGGGTGTGGCCATTAA
			SI02663794	CCGCATCTTGGTGAAACGTGA
			SI03049676	ATGATTCGTCGCAGAAGCCTA
ELAC2	Dharmacon	M-015640-00	D-015640-01	GAGCACAAGTTAAAGGTTG
			D-015640-02	GGTAGAATGTCCAGATGAA
			D-015640-03	GTGGAAAGATTGATCAGTT
			D-015640-04	GAGAAGGCGTTCAGAGACT
	Qiagen	56C2	SI00120708	GTGGTAGAATGTCCAGATGAA
			SI03087798	CTACGTCTTCTCCGAGTTCAA
			SI03089163	CTCATGCAGGAGCACAAGTTA
			SI03109526	TACGAGGATGAAACCATGACA
ELL3	Dharmacon	M-014601-00	D-014601-01	GGAAGCAGTACCCAAGTTA
			D-014601-02	GGACATGGACCCCAGATTA
			D-014601-03	GGGAGCGCCTCATTATTTG
			D-014601-04	GGACACAACCTGACTGAAG
	Qiagen	157C7	SI00378609	AAGGAACAAAGCAGCTATAAA
			SI00378616	CAGAAATTGTCCCACATTAAA
			SI00378623	CAAGATAATCCAGGAATATAA
			SI00378630	CCCGTGCTGCTTGCACTCGAA
ELMO2	Dharmacon	M-019222-00	D-019222-01	ACAAGGAGGTGTTGGAATT
			D-019222-02	GCTATGACTTTGTCTATCA
			D-019222-03	TTAAGCAGATTGCAGGGTA
			D-019222-04	CAAATTGCGTAGCCTGAGT
	Qiagen	218E2	SI00378693	CCGGTTGGCACTGAACCACAA
			SI00378700	ACGCAAAGCCATGTACACAAA
			SI00378707	CCGGTCTATAATCCTGAATCA
			SI00378714	CTGAGTTACTCTGAGATTCTA
EPSTI1	Dharmacon	M-015094-00	D-015094-01	GAACAGAGCTAAACCGGTT
			D-015094-02	GAAGAGAAGCATTTAGAGA
			D-015094-03	GATGAAGGATGAACAACAT
			D-015094-04	GGTGGAAGCCAGTCAGAAA
	Qiagen	220G6	SI00380765	ACCGGAGAAATGAGATACAAA
			SI00380772	TTACACAAATTTATAAATAAA
			SI00380779	CACAAATTTATAAATAAATTT
			SI00380786	TAGGTGGAAGCCAGTCAGAAA
ERAF	Dharmacon	M-020729-00	D-020729-01	CAGCAGGTCTTCAATGATC
			D-020729-02	AAGAAGACATGGTGACTGT
			D-020729-03	CTCATGAGCTCCCGAGTCA
			D-020729-04	CCGCAGGATTGAAGGAGTT
	Qiagen	133F8	SI00380793	CTGGATGAACTTCTACATCAA
			SI00380800	AAGGCAGATGGCTCTTCTTAA
			SI00380807	CAGGGACTTCCTGAAGTCTCA
			SI00380814	CCGCAGGATTGAAGGAGTTCA
ESF1	Dharmacon	M-015235-00	D-015235-01	GGAGAGAATTAGATAAAGA
			D-015235-02	TCAAACGACTGAAGTACTA
			D-015235-03	TGAGATTACACGTCGATTA
			D-015235-04	CCAAAGGAGGTGTAATATT
	Qiagen	134B7	SI00326109	CTGGGATAGATTAAAGGCAAA
			SI00326116	TTGGTCGAGATTAAGAATTAA
			SI00326123	TCCATAAATAATTGTACTTAA
			SI00326130	CTGCATTATAGGGTTTATAAA
FAM12B	Dharmacon	M-013033-00	D-013033-01	GCACACTGCTTGTACAGAG
			D-013033-02	GGTCCAGAATCCTCTCAAA
			D-013033-03	ATGGATCGCTTCCGAAATG
			D-013033-04	GGTAGAACCTATCGGCAAC
	Qiagen	150A2	SI00382921	GACGGGTATGTTGATAGCATA
			SI00382928	ATGGCATCTGTTCTTGATTAA
			SI00382935	CTGCTTGTACAGAGCAAAGAA
			SI00382942	CACATGTTTATCTATATCTCA
FAM195B	Dharmacon	M-031000-00	D-031000-01	GCACAGAGTTCCAGGGCTG
			D-031000-02	TTTGAGGGCTGGACCATTG
			D-031000-03	CAGTCTACCTGTTACCTGA
			D-031000-04	GCCCTTGAGCCGTGGGATT
	Qiagen	196B3	SI00506436	CAGAAAGGAAATCAAGGCTCA
			SI00506443	AACGTCCGCTTCATTTACGAA
			SI00506450	CAGCTCTTTGGGCCTAGGATA
			SI00506457	CAGGTGCATGCTGCCACACCA

HGNC	Source	Pool ID	siRNA ID	Sequence
FAM69B	Dharmacon	M-016278-00	D-016278-01	GGAAGAAGATCTCCAACAC
			D-016278-02	TTACGGGACTTTCTACATG
			D-016278-03	GGCGGGAGCTGGTACTGTT
			D-016278-04	GGGACAAGGATGTAACCAT
	Qiagen	176A10	SI00634823	CAGGCTCATGAGGCAGTGCAA
			SI00634830	GAAGAACGTAATGTCAATAAA
			SI00634837	CACAGCCACCTACGACTTCAA
			SI00634844	CTGGCTGGTGTACGTGCACTA
FBXL6	Dharmacon	M-012425-00	D-012425-01	GAGCTCAACCTGCAACTTT
			D-012425-02	GCACCGGCATCAACCGTAA
			D-012425-03	TGTCGAGGCTCTGCAGAAA
			D-012425-04	GCTTATGCCCAATCGGTTT
	Qiagen	213H6	SI00385413	CCCGGGCCTGCTCTACCTCAA
			SI00385420	CCGGCTGACTCTAGCCAAGGA
			SI00385427	CAGGCCCTGGCTGCCTTCTTA
			SI00385434	CTGGGCCTGTATGGCACGTCA
FGF22	Dharmacon	M-013171-00	D-013171-01	GAAGAGAACGGCCACAACA
			D-013171-02	GATCCGCTCTGTACACGTG
			D-013171-03	GCTTCTACGTGGCCATGAA
			D-013171-04	GGTCGCGACTCTACACCGT
	Qiagen	128D8	SI00386981	CCGGGAGCGCATCGAAGAGAA
			SI00386988	AGGCTTCTACGTGGCCATGAA
			SI00386995	GTGGGCGTCGTGGTCATCAAA
			SI00387002	ATCCTGGAGATCCGCTCTGTA
FGFRL1	Dharmacon	M-013064-00	D-013064-01	GGACACTGAGCCTGAAGAA
			D-013064-02	GAACACGACGGTGGACTTC
			D-013064-03	GGCTGAAGCGCGTGGAGTA
			D-013064-04	ACTCACACGTGGAGGGCAA
	Qiagen	22A8	SI02661988	CACCGTGCTGCCAGACCCAAA
			SI02662527	CTTGGTATTTATATTTAAGAA
			SI03061653	CACGTGGATGAAGGACGACCA
			SI03086216	CGGCCGGAGGACAGCGGCAAA
FIBIN	Dharmacon	M-031927-00	D-031927-01	GAAGAGAGCTATGGCAAGT
			D-031927-02	TGTCAAGGCTACTTCGATG
			D-031927-03	GCAAAAGCATCTCCTACGA
			D-031927-04	ACGAGGACTTTCTGGGAAT
	Qiagen	197B10	SI00508396	CAGGTCTACATTATTTAATTA
			SI00508403	AAGAAGATTAATGATCACTTA
			SI00508410	CCTGGTCTTCTTAAATTTAAA
			SI00508417	CAGTGCTATAGTAAATTACAA
FOSL1	Dharmacon	M-004341-00	D-004341-01	GGAGGAAGGAACTGACCGA
			D-004341-02	AGAGGAGCGCCGCCGAGTA
			D-004341-03	AGTGGATGGTACAGCCTCA
			D-004341-04	GAGGAGCGCCGCCGAGTAA
	Qiagen	53E7	SI00420420	CCCACCTAGAACACTAACTCA
			SI00420427	CCGAGTAAGGCGCGAGCGGAA
			SI00420434	CACAATTTGCACTAAATCAGA
			SI00420441	CTGGACAGTATCCCACATCCA
FOSL2	Dharmacon	M-004110-00	D-004110-01	GGCCCAGTGTGCAAGATTA
			D-004110-02	GAAATTCCGGGTAGATATG
			D-004110-03	GCTCACCGCAGAAGCAGTA
			D-004110-04	GCAGCTGTCTCCTGAAGAG
	Qiagen	52F11	SI02780379	GCGGATCATGTACCAGGATTA
			SI02780421	TTGGGTTTGCCAAACGCCTAA
			SI03041584	ACGGCCCAGTGTGCAAGATTA
			SI03090913	CTCGAACCTCGTCTTCACCTA
FZD2	Dharmacon	M-005501-01	D-005501-02	CGGTCTACATGATCAAATA
			D-005501-03	CATCCTATCTCAGCTACAA
			D-005501-04	CCACGTACTTGGTAGACAT
			D-005501-05	TCAAATACCTCATGACGCT
	Qiagen	71H11	SI00422975	CACGTACTTGGTAGACATGCA
			SI00422982	CACCATGGTGTCGGTGGCCTA
			SI00422989	CACGGTGAGACCACCGTGTGA
			SI02757433	CACGGTCTACATGATCAAATA
GABRA3	Dharmacon	M-006164-00	D-006164-01	GAGATAATCCGGTCTAGTA
			D-006164-02	CCAACAAGCTGCTCAGATT
			D-006164-03	GATGAAAGACTGAAATTTG
			D-006164-04	GAACAAATCCGTGGAAGTG
	Qiagen	34G7	SI00016065	TACAATGAGGTTAACAATTCA
			SI00016079	CCCGACTGAGACCAAGACCTA
			SI00016086	CAGAGATAATCCGGTCTAGTA
			SI03052959	CAACCGGGAGTCAGCTATCAA

HGNC	Source	Pool ID	siRNA ID	Sequence
GCNT1	Dharmacon	M-011284-00	D-011284-01	GGACACCTGACGACTATAT
			D-011284-02	GAAGCGGTATGAGGTCGTT
			D-011284-03	GAATCCTAGTAGTGATATT
			D-011284-04	CTATAGTGGTTCATCACAA
	Qiagen	95H8	SI00426132	CTGCATCTGATTTATATTTAA
			SI00426139	CACCTGTATATTCATTTGAAA
			SI00426146	TAGAAAGGTGATAGCATTAAA
			SI00426153	TGGGCTTGATTTAACATTGAA
GDF3	Dharmacon	M-004852-00	D-004852-01	GAATATGTCTTTCTCCAAT
			D-004852-02	GCTTTCAGCTTCCTGTTAA
			D-004852-03	GCTAAGGATTGGAATGACA
			D-004852-04	TGGCACAAGTGGATCATTG
	Qiagen	61A5	SI00127057	CCGAGACTTATGCTACGTAAA
			SI00127064	AAGGAGTGTTCTTAGGGTAAA
			SI03073952	CATGCTCTACCAGGACAATAA
			SI03099012	CTGGGCGTCCGCGGGAATGTA
GFM1	Dharmacon	M-013685-00	D-013685-01	GAGTATGGCTGTCCTTGTA
			D-013685-02	GGAATTAACCGACGCCATG
			D-013685-03	GTCCAGAACTATGCTATTC
			D-013685-04	GTAGGTCGATTTGGACAAT
	Qiagen	165H7	SI00426804	CGGGTTGTTTATCATATAATA
			SI00426811	TAGGTCGATTTGGACAATTAA
			SI00426818	CCCGTTTGACTTTACACATAA
			SI00426825	CACATGGTTGATTCTAATGAA
GIMAP5	Dharmacon	M-013342-00	D-013342-01	GGAAAGTCCTGGTGGTTGA
			D-013342-02	CCCAAGAGCTGTACAAGAA
			D-013342-03	GGGCAAATATGGAACTATG
			D-013342-04	CCACCGGCATTGAGGATTA
	Qiagen	140E11	SI00427364	CAGGTGGAGAAGCACAAGCAA
			SI00427371	CAGAAGATAACTTGTCTGCAA
			SI00427378	CAGCACATGGCTCCTCCTTAA
			SI00427385	ATAGATTTCCTACTTATTTAA
GNA12	Dharmacon	M-008435-00	D-008435-01	GAGCATGACTTCGTTATTA
			D-008435-02	GGATCGGCCAGCTGAATTA
			D-008435-03	GGGAGTCGGTGAAGTACTT
			D-008435-04	AGAAGGCGCTGCTGGAGTT
	Qiagen	61F9	SI00096558	CCGGATCGGCCAGCTGAATTA
			SI00096565	GAGGTAGTTGTGCCTCAATTA
			SI00096572	GTCCGTTTAACTCGATAGAAA
			SI03086195	CGGCCGCGAGTTCGACCAGAA
GNAI1	Dharmacon	M-010404-01	D-010404-03	CCACAGATACTAAGAATGT
			D-010404-04	GCAGTGGTCTACAGTAACA
			D-010404-05	CAAATTACATCCCGACTCA
			D-010404-06	GTGGAAAGATAGTGGTGTA
	Qiagen	23C11	SI00032256	ATGGACGATTACACTTAGAAA
			SI00032270	CTGCATAAGTGTAAATATGCA
			SI03087140	CGGGCGGATGATGCACGCCAA
			SI03109414	TACGACCTGGTTCTAGCTGAA
GOLPH3L	Dharmacon	M-006413-00	D-006413-01	GCAAAGAACCTAGTAGAGA
			D-006413-02	GCACTGAAATAAGCAAGAA
			D-006413-03	GAATCGAGCCAAGGACTTA
			D-006413-04	GTACTAGAGCGGTGGGTAA
	Qiagen	139D10	SI00429436	AAGGGCTAATTTGGTATTGAA
			SI00429443	TCAGCATTTATTATACTTTAA
			SI00429450	TAGGGCAAATGTCTAAATGAA
			SI00429457	CAGCCTTCAATAAATCTTAAA
GPR89A	Dharmacon	M-005725-00	D-005725-01	GGAGATCCCTTTCCCATTC
			D-005725-02	CATAATCACTGAAGTCCTT
			D-005725-03	CCAATTTGATGTGAAGTTT
			D-005725-04	CCAAGGAGAGAATAGAATA
	Qiagen	75B4	SI00115409	ACGGAGAACAATGTTCCAGAA
			SI03065895	CAGCATCATGATTACCTCCCA
			SI03084354	CGCCATGAGTTTCCTGATCGA
			SI03105235	GCGCCAATTGTTTAAAGACTA
GTF3A	Dharmacon	M-012635-00	D-012635-01	GAAACAAGGGCAAGGCTTA
			D-012635-02	CCATAAAGAGGAAATACTA
			D-012635-03	GCAATGAAACAAAGTCTCA
			D-012635-04	GACCATTTGTTTGTGACTA
	Qiagen	96A4	SI00432208	AAGGCTTATCTTTGTGTCAAA
			SI00432215	CACGAGGGCTATGTATGTCAA
			SI00432222	ACCCATAAAGAGGAAATACTA
			SI00432229	AAGGCTGTGGAAGAACCTATA

HGNC	Source	Pool ID	siRNA ID	Sequence
GUCA2A	Dharmacon	M-021488-00	D-021488-01	GGGCACATGTGAAATCTGT
			D-021488-02	GAAGAACTCAAGCCTCTCT
			D-021488-03	GCCCAATGCCCAGGAGATA
			D-021488-04	TCACCGTGCAGGATGGAAA
	Qiagen	96D4	SI00432600	CAGGGTTGGGAAACTCAGGAA
			SI00432607	AACCCGAACTTTCCAGAAGAA
			SI00432614	CAGCTAATAAACCAGATTCCA
			SI00432621	ACCCATGATACTCCACTCCCA
GZMM	Dharmacon	M-005892-00	D-005892-01	GGTCTGCACTGACATCTTC
			D-005892-02	GGTCTCACCTTCCACATCA
			D-005892-03	GCCCGTACATGGCCTCACT
			D-005892-04	CGCCTTACGTGTCCTGGAT
	Qiagen	13G4	SI00075726	CAGGGAGGGACCAATAAATCA
			SI00075733	CCAATAAATCATAATGAAGAA
			SI03087427	CGGTCTCACCTTCCACATCAA
			SI03095477	CTGCGGGAGCTGGACCTCCAA
HDAC1	Dharmacon	M-003493-02	D-003493-01	CTAATGAGCTTCCATACAA
			D-003493-02	GAAAGTCTGTTACTACTAC
			D-003493-04	GGACATCGCTGTGAATTGG
			D-003493-09	CCGGTCATGTCCAAAGTAA
	Qiagen	12E5	SI00070609	CACAGCGATGACTACATTAAA
			SI00070630	CGGGATTGATGACGAGTCCTA
			SI02634149	CCCGTTCTTAACTTTGAACCA
			SI02663472	CACCCGGAGGAAAGTCTGTTA
HEBP1	Dharmacon	M-013115-00	D-013115-01	GAAGTTGCCTATGAAGAAA
			D-013115-02	GGATGAGGCTCTACGGGAA
			D-013115-03	AATGAGATCTGGCTGTTGA
			D-013115-04	ACAAAAGCGTTAAGATTGA
	Qiagen	131A9	SI00435260	CCAGCTGCAAGTCCAACTTAA
			SI00435267	CAACATGTTGGGCATGATCAA
			SI00435274	AAGAAGTTGCCTATGAAGAAA
			SI00435281	TCCAGGCATCTGGGTCACTAA
HIPK2	Dharmacon	M-003266-03	D-003266-06	GAGAATCACTCCAATCGAA
			D-003266-07	AGACAGGGATTAAGTCAAA
			D-003266-08	GGACAAAGACAACTAGGTT
			D-003266-09	GCACACACGTCAAATCATG
	Qiagen	87H6	SI00134330	CCGAGTCAGTATCCAGCCCAA
			SI00134337	ACGGGTCGGGACACCAGTGAA
			SI02659811	AACCAGTACCCTTACATATAA
			SI02659818	TCCCGAAGTCTCCATACTAAA
HIST1H2AE	Dharmacon	M-013146-00	D-013146-01	TAAATAAGCTTCTAGGTCG
			D-013146-02	TGGAATATCTGACGGCCGA
			D-013146-03	CGGCAAAGCTCGGGCAAAA
			D-013146-04	TCTTAGAGCTAGCTGGCAA
	Qiagen	96G5	SI00436940	GAGGAGCTAAATAAGCTTCTA
			SI00436947	CAAGGGCAAGTGAAATGATTA
			SI00436954	ACGGCCGAGATCTTAGAGCTA
			SI00436961	TCCCGAGTCCCAGAAACCAAA
HIST1H2BO	Dharmacon	M-011447-00	D-011447-01	CAAAGGCCGTCACCAAGTA
			D-011447-02	GTTACTCTATCTACGTGTA
			D-011447-03	CGAAGGCCATGGGCATCAT
			D-011447-04	CGTAACCAAGGCCCAGAAA
	Qiagen	6B7	SI03084361	CGCCATGCCCGACCCGGCTAA
			SI03091298	CTCGCAGCTGCCAGCAATCCA
			SI03104402	GAGTTACTCTATCTACGTGTA
			SI03104871	GCCGCAAAGAGAGTTACTCTA
HLA-DQB2	Dharmacon	M-018944-00	D-018944-01	GGAGACAGCCGGTGTTGTG
			D-018944-02	TCTATAACCGCGAGGAGTA
			D-018944-03	CAACTACGAGGCGGAGCTA
			D-018944-04	TGGAACAACTATAAGGACT
	Qiagen	96E9	SI00438956	CAAGAGAAGCATGACAAACAA
			SI00438963	AAGGATTTCTTGGTCCAGTTT
			SI00438970	CGAGGACTGGAACAACTATAA
			SI00438977	TAAACCTGATTCTGAGTTAAA
HN1	Dharmacon	M-021065-00	D-021065-01	GAACAACCTGTGAGGAAGA
			D-021065-02	CAAAATGGCCTCTAATATC
			D-021065-03	GAATAGCTCCCGAGTTTTG
			D-021065-04	GCAGGTGCCAAGTCTAGTG
	Qiagen	214H7	SI00439712	AAGGGAGGCAATCACACTGAA
			SI00439719	AAGGCTTGGATGTACAATGAA
			SI00439726	CGGAGACTTCTTAGATCTGAA
			SI00439733	CTGGACTGTTGCTTCAAGTAA

HGNC	Source	Pool ID	siRNA ID	Sequence
HTRA2	Dharmacon	M-006014-02	D-006014-03	GCGCAGAGTCCGTGTGAGA
			D-006014-04	TCGCAGATGTGGTGGAGAA
			D-006014-05	GCTAAGCGGCGACACGTAT
			D-006014-06	GAGAGTTTCTGCATCGTGG
	Qiagen	14B8	SI00100877	AACGCTGAGGATTCAGACTAA
			SI00100891	CCGCGAGGTCCCTATCTCGAA
			SI03042389	AGAGTCCGTGTGAGACTGCTA
			SI03065496	CAGCACCTGCCGTGGTCTATA
INF2	Dharmacon	M-014097-00	D-014097-01	GCGATGTCCTAACCACTGA
			D-014097-02	AAACAAAGAAACTGTGTGT
			D-014097-03	GGAAGAAGCGTCCCTCCAG
			D-014097-04	AGCCGGAAGTTCAAGGCAA
	Qiagen	66C3	SI00133959	CAGCGATGTCCTAACCACTGA
			SI00133973	CAAGATCAGCACATTGCTGAA
			SI02778615	CCCGGCCTTGATGCTACAACA
			SI02778622	CCTGATTCTGATGATAATAAA
JMJD6	Dharmacon	M-010363-01	D-010363-01	GAACTGGGATTCACATCGA
			D-010363-02	GGATAACGATGGCTACTCA
			D-010363-04	GACCAAAGTTATCAAGGAA
			D-010363-05	GGACCCGGCACAACTACTA
	Qiagen	27F5	SI00109851	AAGGAAATATCGGAACCAGAA
			SI00109858	CTGCTTCCTAAGGATAGATTA
			SI03068037	CAGCTATGGTGAACACCCTAA
			SI03078593	CCCGGCGGCCGTGGCGGATAA
KCNIP1	Dharmacon	M-013559-00	D-013559-01	GAAGACACATTCAAGCAGA
			D-013559-02	GGACGGATACATAAACAAA
			D-013559-03	AGGCGACCCTCGAAAGATA
			D-013559-04	TAACCGCTCTGTCGATTTT
	Qiagen	32B8	SI00107100	CTGGTAGTACAAGTCCTTTAA
			SI00107107	TGGGATAGGACTGAATTATTA
			SI00107121	TCCAGAAACGAGGACCAATAA
			SI03054359	CAAGGACGGATACATAAACAA
KCNK16	Dharmacon	M-006259-00	D-006259-01	CAGCAAGCATTATATCTCA
			D-006259-02	GGTCTTCTGTGTCTTCTAT
			D-006259-03	TGGCAGCAGTTTCTTCTTT
			D-006259-04	GCACAGTTGTCACTACCAT
	Qiagen	32H9	SI00142079	AAGGCTCCTCTTACCTCCCAA
			SI03076640	CCCAGCAAGCATTATATCTCA
			SI03100881	CTTGAGATTGACAGACAGCAA
			SI03106775	GTGGACAAGCCTCTTGGTTAA
KCNN3	Dharmacon	M-006270-01	D-006270-01	GGACGTAACTAGTAACTTT
			D-006270-03	GGAAACATGGTTAATCTAT
			D-006270-04	GAAGATTGACCATGCCAAA
			D-006270-05	GTACACAAGTTCAAGCAGT
	Qiagen	32C4	SI00035126	CAGGACGTAACTAGTAACTTT
			SI00035133	CCCATAGGTCTTAAGATGCAA
			SI00035140	AAGAGAGACCGAGCTAATTAA
			SI00035147	CCGAGCTAATTAACTAACTCA
KCNT2	Dharmacon	M-027333-00	D-027333-01	GAATAGAGCTGAATGATGT
			D-027333-02	GGTCCTCGATACATTATGA
			D-027333-03	CGAGTTATCTACCTTCAAG
			D-027333-04	CGACATAGAGCTCAAACTG
	Qiagen	32A11	SI00726075	CACATAGAGATTAACCAACAA
			SI00726082	CAGGGTACAAGTTGAATTCTA
			SI03034934	AAGGATACGCCTGTTCAATTT
			SI03071957	CAGGTCCTCGATACATTATGA
KEAP1	Dharmacon	M-012453-00	D-012453-01	GGACAAACCGCCTTAATTC
			D-012453-02	CAGCAGAACTGTACCTGTT
			D-012453-03	GGGCGTGGCTGTCCTCAAT
			D-012453-04	CGAATGATCACAGCAATGA
	Qiagen	210F3	SI00451668	GCGAATGATCACAGCAATGAA
			SI00451675	CCGGGAGTACATCTACATGCA
			SI00451689	CTGCATCAACTGGGTCAAGTA
			SI03246439	CCAGGATGCCTCAGTGTTAAA
KERA	Dharmacon	M-012764-00	D-012764-01	GAGAATGCCACCCAGCTAA
			D-012764-02	CCAAGAAGTTTAGAACAAT
			D-012764-03	AAGAATGCCCTGAGGAATA
			D-012764-04	CATCAATTCTAGATCTTCA
	Qiagen	120A8	SI00451752	CAGTATAAATGTAATAATCAA
			SI00451759	ATGGATAAATCTAAACAAGAA
			SI00451766	AACAATTACATTCTTATACAA
			SI00451773	AAGATAGTTTATCAACTCAAA

HGNC	Source	Pool ID	siRNA ID	Sequence
KIAA1026	Dharmacon	M-022166-00	D-022166-01	GAGCGAGGATGCGGTCAAA
			D-022166-02	GCCAAACAGTCCTTAGCTA
			D-022166-03	GCGAGACGGTGCTCAATGG
			D-022166-04	GCTGATCGGAAGCGCTTAA
	Qiagen	199D11	SI00416052	CAGGGACATCGTGAGGATTAA
			SI00416059	CACAGAAATGATATAGAGCTA
			SI00416066	CCCGATTTCCATGATGACTAT
			SI00416073	CTGGAGGTCACCAACGTGTAA
KIAA1407	Dharmacon	M-014068-00	D-014068-01	GAAGGTACCACGAGCTATA
			D-014068-02	GGAAACGGTTCACAAGGAA
			D-014068-03	GATGAGACATAAGCAGGTA
			D-014068-04	GAGTATAACCGGAAACAAG
	Qiagen	147D3	SI00458500	CTGGTTAGACACCAAACTTAA
			SI00458507	ATGAATTGTGTTAGAGAATTA
			SI00458514	CACATTTATTATATAACAAAT
			SI00458521	CTGGAGTACCAGAGAATAGAA
KIAA1529	Dharmacon	M-026179-00	D-026179-01	GAAGGAAGCTGCCCGGATA
			D-026179-02	GAAATGGAGTCCTTCATAA
			D-026179-03	TGAAAGAACTCAACTCCTA
			D-026179-04	ACAATTCCATCGAGACTAA
	Qiagen	147A7	SI00459172	CAGCATGATTAGGATGAACAA
			SI00459179	CAGGTGGGAAAGGAAATGGAA
			SI00459186	CAGGATACCCATGATGAAGAA
			SI00459193	CAGGAAGAGCAAGAGAGTTTA
KIAA1604	Dharmacon	M-023101-00	D-023101-01	GGAATGTGGCCTCAAATTA
			D-023101-02	AAATTAACCTGGTCTCATT
			D-023101-03	CTTATTAGCTGGGCGATTT
			D-023101-04	GAAACAAACAAGTTGCGAA
	Qiagen	147D9	SI00459704	CAGGAACAGATTACAGATAAA
			SI00459711	CAGCAAACAAATGATAGGAAA
			SI00459718	CAGAAGTAAAGAGGTAGATAA
			SI00459725	ATGGAGTTTCCTGAAAGCCAA
KIAA1622	Dharmacon	M-013007-00	D-013007-01	GAACAAGTGTGATTGCAAA
			D-013007-02	TGAAAGGGCTGTTTATCTG
			D-013007-03	GATTGACAGTCGATGAAGA
			D-013007-04	GCGATGGATTTCAGTCAGA
	Qiagen	217B10	SI00459872	AAGGAACAAGTGTGATTGCAA
			SI00459879	ACCGGAAGAAATAGAAAGATT
			SI00459886	CGCGATGGATTTCAGTCAGAA
			SI00459893	CTGGTCAAGATGTCCAAGGAA
KIF11	Dharmacon	M-003317-01	D-003317-05	GCAGAAATCTAAGGATATA
			D-003317-06	CAACAAGGATGAAGTCTAT
			D-003317-07	CAGCAGAAATCTAAGGATA
			D-003317-08	CTAGATGGCTTTCTCAGTA
	Qiagen	42F7	SI00064855	CTAGATGGCTTTCTCAGTATA
			SI02653693	ACGGAGGAGATAGAACGTTTA
			SI02653770	GCCGATAAGATAGAAGATCAA
			SI03104038	GAGGGCGTACAAGAACATCTA
KIF12	Dharmacon	M-008252-01	D-008252-01	ACAGCAAGCTCACCAAGTT
			D-008252-03	GATCTACAATGAGCAGGTT
			D-008252-05	TGGCAGAGATGTTGACGGA
			D-008252-06	GGTCTCAGCCGTCGAAGGA
	Qiagen	43E2	SI00150794	ACCCTTTACATCAGCCGTCAA
			SI00150801	CGCCTCTTATCTGGAGATCTA
			SI00150808	ACAGGAGTTCATGCTAGAGAA
			SI00150815	AAGAGAGGCATCAGCTCCAAA
KIF13A	Dharmacon	M-008257-01	D-008257-02	GTGATGATATGGATAGTTA
			D-008257-04	GAACCATGCTGTTGTGAAT
			D-008257-05	AGACGTACATTGAGAAGTA
			D-008257-06	GCAAATTTGTGCCTTATCG
	Qiagen	42E11	SI00462322	AACCTATGAAATAGTATCCAA
			SI00462329	CCGGCAGGCCGTCACAGTCAA
			SI03031133	AAGAAGTGTCCCGTAGCCCTA
			SI03071530	CAGGGTCATTCCCGTAGAGTA
KIF15	Dharmacon	M-004960-00	D-004960-01	GAAGAGAGCTTGCTTGCTA
			D-004960-02	GGACATAAATTGCAAATAC
			D-004960-03	GGGAAGACATTTACTATGA
			D-004960-04	AATCAGAGCTTCAGTCTTT
	Qiagen	21C11	SI00125615	CAGGATTCCTATGACAACTTA
			SI02643914	TTGAGATTGACCAACTTTCAA
			SI03029390	AACGAGCAGATATATGATCTA
			SI03102386	GACGTGTGGCATCAACATCAA

HGNC	Source	Pool ID	siRNA ID	Sequence
KIF20A	Dharmacon	M-004957-01	D-004957-01	GCAAGAACCTGCTATCAGA
			D-004957-02	GAAGAGGGCCAGAAGAATA
			D-004957-03	GCAATGAGATGGTAGAACA
			D-004957-05	CTGAAGAGTTGCATAAGTA
	Qiagen	42C9	SI02654064	AACGAACTGCTTTATGACCTA
			SI03019828	ACCACTTGTGATGACATCTTA
			SI03060015	CACGATTCAAGGTACCATCAA
			SI03118976	TGCGGCTATGCGAGGATCAAA
KIF23	Dharmacon	M-004956-01	D-004956-01	CGACATAACTTACGACAAA
			D-004956-02	GACATGATCTTTAACAGTA
			D-004956-04	GAACAAATCACTATAAGTC
			D-004956-05	GCATAGAAGTGATCAATAA
	Qiagen	42A9	SI02653483	AAGGCTGAAGATTATGAAGAA
			SI02653910	CAGAAGTTGAAGTGAAATCTA
			SI03026121	AAACGACATAACTTACGACAA
			SI03060050	CACGCACAACCCAAGCGCAAA
KLK1	Dharmacon	M-005906-00	D-005906-01	TCAGAGTGCTGTCTTATGT
			D-005906-02	CAACTTGTTTGACGACGAA
			D-005906-03	AGGCGGCTCTGTACCATTT
			D-005906-04	TGACAGAGCCTGCTGATAC
	Qiagen	13F5	SI00035329	CGCCGTCAGAGTGCTGTCTTA
			SI03055360	CACAACTTGTTTGACGACGAA
			SI03089583	CTCCAGTGTGTGGACCTCAAA
			SI03097003	CTGGAGAACCACACCCGCCAA
LEPROT	Dharmacon	M-032248-00	D-032248-01	GTCGGGAACTGGCATATTT
			D-032248-02	CCAAAAGAGTCACCTATGA
			D-032248-03	CTACTGGAATTGTTGTTTC
			D-032248-04	CCTTATATTTGGAAGAGGA
	Qiagen	1G11	SI00118608	CTGGCCCTTATTCGTCCTGAT
			SI00118615	ATGGCGTTTACTGGCCCTTAT
			SI00118622	AAGCATCATCATAGAGAAGTA
			SI03113831	TCCAGTGGCTAAACCACTTAA
LILRB1	Dharmacon	M-017168-00	D-017168-01	TCACAGAGCTCCAAACCCT
			D-017168-02	CGGTATCGCTGTTACTATG
			D-017168-03	GATCAACGTACCAATCTCA
			D-017168-04	GCACACACAGCCTGAGGAT
	Qiagen	119G5	SI00090937	CAGAAAGTGCATTAAACTGAA
			SI00090951	ACCCATGGCGTCTAAGATCAA
			SI02657200	ATGAATGAATTAGGAAAGAAA
			SI02657207	CACAATGTAAATATTACACAT
MAGED1	Dharmacon	M-006682-00	D-006682-01	GAAGACAGCGCCTTGCTTA
			D-006682-02	GGAAAGAGCAAATAAGTTG
			D-006682-03	TAAGGAAACTTCTCACCTA
			D-006682-04	GGGATGACATTGAGTTTGA
	Qiagen	22F4	SI00020384	TAGGCCTAAGTCAGCCTTTAA
			SI00020391	CTCCTTGGAGATCTAAGGAAA
			SI00020405	CTGAGAGATATCATCCGTGAA
			SI03048857	ATCTGGAGTCCCGGACAATAA
MAGEE1	Dharmacon	M-014189-00	D-014189-01	GGACAGAACTAGTGGTACT
			D-014189-02	GATCAGAGCAAGTACCCTA
			D-014189-03	GCACATTGTTTAGCTCTAG
			D-014189-04	TATAGACAGTTTACGGGTT
	Qiagen	147E8	SI00626955	CGGGAATATATTGTTAAAGAA
			SI00626962	CAGCGCTATATAGACAGTTTA
			SI00626969	TAGCATATAGCTATAGATATA
			SI00626976	TAGCTTAAAGTGATAAACTAA
MAGEE2	Dharmacon	M-015813-00	D-015813-01	GAGACCCACTCAAGAATAT
			D-015813-02	CCAGATCACCGATAGGATA
			D-015813-03	CGATTGCTTTGGTGAATTT
			D-015813-04	AGAACTGGCCAGAACAATA
	Qiagen	177A3	SI00626983	TAGGTTAATGACCAATATTTA
			SI00626990	CAGGCTGACACCTACAATTTA
			SI00626997	CCGGTCTTGTTTCAGCATAAA
			SI00627004	CAGCTGAGTGGCATAAGTTAA
MAGEH1	Dharmacon	M-009135-00	D-009135-01	GAGGGTACCTGATTTATAA
			D-009135-02	CGAAGAAGATCGTCACAGA
			D-009135-03	GCAGTCCGGTGGAGTATGA
			D-009135-04	GGACGATGATGCAGAGGTT
	Qiagen	129G10	SI00627039	CAGAGGGTACCTGATTTATAA
			SI00627046	CAGCAGCTTCTTACGGTATAA
			SI00627053	CGGCTTGTTTATTGCTACAAA
			SI00627060	CCGAAGAAGATCGTCACAGAA

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MAGI1	Dharmacon	M-011922-00	D-011922-01	GGACGTGGCTTCAAATAGT
			D-011922-02	GGAAAGTGATCACGACGGA
			D-011922-03	GAAAGAAGGGGATCTCATA
			D-011922-04	GGGATAACCTTTACCGCCA
	Qiagen	112A5	SI00310149	AAGGAATACCACCAAACCAAA
			SI00310156	CAAATGGGTTATAATATGTTA
			SI00310163	TCGCTTGTTCTGAAATCTCTA
			SI00310170	GAGGATAATTTAGGTCCTCTA
MAST1	Dharmacon	M-004672-01	D-004672-01	CGACAGGAGTCACCTTTGA
			D-004672-03	GACACTAGCTACTTTGACA
			D-004672-04	GAGCCTCACCACCAACTTA
			D-004672-05	ACATCAAGCTCACAGATTT
	Qiagen	89G8	SI00628173	CCCGAGGTCATCCTGCGTCAA
			SI03058251	CACCGAGAGCATCACAGACGA
			SI03061233	CACGGTCTACTTCTATGAATT
			SI03115161	TCCGCGCTTCAGCAAGGTGTA
MAX	Dharmacon	M-010092-02	D-010092-04	CGAGGTGGAGAGCGACGAA
			D-010092-05	GACAAACGGGCTCATCATA
			D-010092-06	GTAGGGACCACATCAAAGA
			D-010092-07	TTTCACAGTTTGCGGGACT
	Qiagen	49B4	SI03026177	AAACGTAGGGACCACATCAAA
			SI03093027	CTGACAAACGGGCTCATCATA
			SI03111451	TAGGAAATGAGCGATAACGAT
			SI03116995	TCGGCTTGTTGTTGTCGGTGA
MC1R	Dharmacon	M-005657-01	D-005657-01	CAAAGAGGATGGACTAAAT
			D-005657-02	GATATTGTGTGGTCTGGTT
			D-005657-03	GGGAAGCTCCGGACTCCTA
			D-005657-05	TGGCTATGCTGGTGCTCAT
	Qiagen	72F11	SI00036946	CCAGGAAAGTCTGGTAATAAA
			SI00036953	CACCAGGGCTTTGGCCTTAAA
			SI00036960	CACGCTCTTCATCGCCTACTA
			SI03050684	ATGGACTAAATGATCTCTGAA
MFAP1	Dharmacon	M-020071-00	D-020071-01	GGAGAAAGCAGAAATTGAA
			D-020071-02	GCTCAGGTCGCACCAAATA
			D-020071-03	AAGTGAAGGTAAAGCGTTA
			D-020071-04	TATGAGGCATGGAAAGTTC
	Qiagen	99A6	SI00630651	TAGCATGATACTGGAAATAAA
			SI00630658	CTGGAGGATCATTTCAATAAA
			SI00630665	AAGGAGAAAGCAGAAATTGAA
			SI00630672	AAGGTGAGATTTCAATGGAAA
MGAT5	Dharmacon	M-011334-00	D-011334-01	GTACTGAACCCGAATTTAA
			D-011334-02	CAAATTATGCCCAATCGAA
			D-011334-03	CCGAGTCCTTGATTCATTT
			D-011334-04	AACCCTTGCTGTGTTATTA
	Qiagen	99F6	SI00631099	TACAATAATTATACATAATAA
			SI00631106	CTCATTTACATTGATATTGTA
			SI00631113	CTGGAAGAATAAGAAGATCTA
			SI00631120	TAGCTAGAATTTATAATTTAT
MGC29891	Dharmacon	M-016074-00	D-016074-01	GAAGAGAAGTTGCCACTAA
			D-016074-02	AGAATCAGGTGAATGTTAA
			D-016074-03	GGCCAGCCATTTATTGTAA
			D-016074-04	GTTAACCTCGCAAGCCTTA
	Qiagen	173C10	SI00637483	AAGGAAATATACAGAAGACAA
			SI00637490	CACCAATATATATGCCTTTAA
			SI00637497	CTGGGTAATATCCAAACTTCA
			SI00637504	AAGACTGTATCTCAAAGGAAA
MID1IP1	Dharmacon	M-015884-00	D-015884-01	CAGAAGCACTCGCTCTTTA
			D-015884-02	GAGATCGGCTTCGGCAATT
			D-015884-03	GCAAATCTGCGACACCTAC
			D-015884-04	TCTCGAAACTCACGCGCAA
	Qiagen	148D6	SI00645659	CCAGATGTAGACTATATTCTA
			SI00645666	TCGGTAATCGGTACTACTTTA
			SI00645673	CAGCCACTACGTGCTTCTCAA
			SI00645680	CTCGCTCTTTAACGCCATGAA
MLN	Dharmacon	M-012641-00	D-012641-01	AGAAATCCCTGAGTGTATG
			D-012641-02	GGAACGGAATAAAGGGCAA
			D-012641-03	GGAATGAGGATGAACTCCA
			D-012641-04	GACTGCTCCTCTGGAAATT
	Qiagen	24A2	SI00037422	CTCCAAGATGGTATCCCGTAA
			SI00037429	CAGCCGGACACCAGAAGACAA
			SI02628521	AAGGAACGGAATAAAGGGCAA
			SI03036922	AAGTGAGGCCCTGGGAATTTA

HGNC	Source	Pool ID	siRNA ID	Sequence
MSL3L1	Dharmacon	M-012319-00	D-012319-01	GCGCAAAGCTGAGCCAGAA
			D-012319-02	CAGCGTAAATTGGCAAGAA
			D-012319-03	GGTGTGGACTCTGTCTTAA
			D-012319-04	AAAGGTGACTTCGTCTAAA
	Qiagen	211E8	SI00650307	CAGGAGGAAACGGTTAGTGAA
			SI00650314	ACAGCGTAAATTGGCAAGAAA
			SI00650321	CTGGTGTGGACTCTGTCTTAA
			SI00650328	CAGAAGCATTGCAGTCTCTGA
MSTN	Dharmacon	M-012039-00	D-012039-01	ACAAAGATGTCTCCAATTA
			D-012039-02	GGAAACAGCTCCTAACATC
			D-012039-03	CAACTTAGGCATTGAAATA
			D-012039-04	GCATGTACTTGGAGACAAA
	Qiagen	23A10	SI00074627	CTGATGCTATCTCAACAATAA
			SI00074634	ACGGTACAAGGTATACTGGAA
			SI00074641	AGGAGTATGCTTTAAAGTCTA
			SI00074648	CTCAGTAAACTTCGTCTGGAA
MT3	Dharmacon	M-012728-00	D-012728-01	CAAGTGCGAGGGATGCAAA
			D-012728-02	GAAGTGTGCCAAGGACTGT
			D-012728-03	GTGCAAAGGCGGAGAGGCA
			D-012728-04	AGGCAGAAGCAGAGAAGTG
	Qiagen	99B9	SI00650727	ACCTTGGAGGAATGACAATAA
			SI00650734	CAGGTGGCTCAGTGCCACCTA
			SI00650741	CGCGTCCAGTTGCTTGGAGAA
			SI00650748	CTGCAAGTGCGAGGGATGCAA
MYH9	Dharmacon	M-007668-00	D-007668-01	GAAGTCAGCTCCCTAAAGA
			D-007668-02	GCACAGAGCTGGCCGACAA
			D-007668-03	GGCCAAACCTGCCGAATAA
			D-007668-04	GAACATGGCCCTCAAGAAG
	Qiagen	42F3	SI00038346	TCGGAGCACAAGCGCAAGAAA
			SI00038353	CACGGAGATGGAGGACCTTAT
			SI00038360	AACCGGGACGAAGCCATCAAA
			SI02654911	CAGGAGCAGCTCCAGGCAGAA
NANS	Dharmacon	M-013399-00	D-013399-01	TGAAACAGGCATAGCGATA
			D-013399-02	GGTAGATAATCATGGCAAA
			D-013399-03	GGTGTTGGAACGTCACATA
			D-013399-04	CCGGAAGGCACCATTCTAA
	Qiagen	135A7	SI00654843	TAGGGTATTCTGGGCATGAAA
			SI00654850	TTGGTAGATAATCATGGCAAA
			SI00654857	ATGGATGAGATGGCAGTTGAA
			SI00654864	TGAGCTAGAATTCAAGTTTAA
NCR1	Dharmacon	M-020866-00	D-020866-01	GGAGAAGGCTGAACACACA
			D-020866-02	AGACGGGACTCCAGAAAGA
			D-020866-03	GGTGGTAACAGAAATGTAT
			D-020866-04	GTACAGCGCGGATACGGGA
	Qiagen	40G11	SI00068908	TCGGTTCATCCTGGACCCGAA
			SI00068915	AAGCATGTTCTTACTGCTCAA
			SI00068929	CTGGATCTGGTGGTAACAGAA
			SI03093475	CTGAGCGGATTAACAAAGTCA
NDC80	Dharmacon	M-004106-00	D-004106-01	GAAGAAAGCTACTCTAATT
			D-004106-02	GCGAATAAATCATGAAAGA
			D-004106-03	GAAGATGGAATTATGCATA
			D-004106-04	GAGTAGAACTAGAATGTGA
	Qiagen	39F5	SI00084539	CACAATTAGCAGAGTATCACA
			SI02653224	CCGAGACCACTTAATGACAAA
			SI02653567	TCCCTGGGTCGTGTCAGGAAA
			SI03067442	CAGCGGGAATACCAACTAGTT
NDUFA7	Dharmacon	M-012693-00	D-012693-01	GGACCAGCCTTACCTGTGA
			D-012693-02	GGTCCTAGCCACAAGCTCT
			D-012693-03	CCATAAAGAGGTGGGAGCT
			D-012693-04	TCATCATGTCGTCGCAGAA
	Qiagen	100F4	SI00656495	CAGGGAGAATGTGACCTAATT
			SI00656502	TAGCCACAAGCTCTCCAACAA
			SI00656509	ACCAGGAGATCTCCAAGCGAA
			SI00656516	CATCATCATGTCGTCGCAGAA
NEDD4	Dharmacon	M-007178-01	D-007178-02	GGAGAGACCATATACATTT
			D-007178-03	GGGATTCTTTGAACTAATA
			D-007178-04	GGAGGGAACATACAAAGTA
			D-007178-05	TAGCTGGAATGGCAGTTTA
	Qiagen	10C6	SI03051419	ATGGCGATTTGTAAACCGAAT
			SI03062843	CAGAACGACTACTTGGACAAA
			SI03648925	ATGGAGTTGATTAGATTACAA
			SI03649072	CCGGAGAATTATGGGTGTCAA

HGNC	Source	Pool ID	siRNA ID	Sequence
NEDD8	Dharmacon	M-020081-00	D-020081-01	GAAAGGAGATTGAGATTGA
			D-020081-02	AGATTGAGATTGACATTGA
			D-020081-03	CAGACAAGGTGGAGCGAAT
			D-020081-04	GGAGATTGAGATTGACATT
	Qiagen	15H9	SI00657335	CTGGAAAGAAGATGCTAATTA
			SI00657349	CTCATAATGAGGCATCATATA
			SI00657356	AGCGGTAGGAGCAGCAATTTA
			SI03102827	GAGATTGACATTGAACCTACA
NFIA	Dharmacon	M-008661-00	D-008661-01	GAAAGAATTTGTCCAACTT
			D-008661-02	GGAAAGTTCTTCATACTAC
			D-008661-03	CAAGTGACGCTGACATTAA
			D-008661-04	GGCAAGATGCGAAGAATTG
	Qiagen	100A8	SI00657979	AAGGATGAATTGCTAAGTGAA
			SI00657986	CAGATTCAAGTCAATCTGAAA
			SI00657993	ACCGATTCAAATCAACTTGTA
			SI00658000	CAGCAGTTAAGTATATAACAT
NGFR	Dharmacon	M-009340-01	D-009340-03	CTACCAGCCCGAGCACATA
			D-009340-04	TCCAGAACAAGACCTCATA
			D-009340-05	GCGAGGACACCGAGCGCCA
			D-009340-06	CGTATTCCGACGAGGCCAA
	Qiagen	39A7	SI00038703	ATGGCAATTCTTTGACCTCAA
			SI02628731	AACGTTAAGTGATGAACATTA
			SI03056151	CACAGCGGTGAGTGCTGCAAA
			SI03080119	CCGAGCACATAGACTCCTTTA
NHP2L1	Dharmacon	M-019900-00	D-019900-01	GAATGTGCCCTACGTGTTT
			D-019900-02	TTGAAAGGCTCTTAGTCTA
			D-019900-03	GACTGAGGCTGATGTGAAT
			D-019900-04	CAGCAGATCCAATCCATTC
	Qiagen	206D3	SI00658539	CAGCTACTCTCTATTGTTATA
			SI00658546	CAGGGTGGTGGCACCGTTGAA
			SI00658553	CTGAGGTTGTGTATCATATTA
			SI00658560	AACAGAGATGGTGGAGTCCAA
NINJ2	Dharmacon	M-020844-00	D-020844-01	CAACGCAGCCACCATCTTG
			D-020844-02	GAAAAGCAGTGGCGACTCA
			D-020844-03	GAGAAAACATCGACCTTCA
			D-020844-04	GACCATCCTCTCACTACTA
	Qiagen	100A10	SI00658882	ACGCAGGTACTGCCAGCCATA
			SI00658889	CTGAACCTGAATGAGGTAGAA
			SI00658896	TACCCACAGCACCTGAGTTAA
			SI03246460	AATGGAATCTATATCTATAAA
NKD2	Dharmacon	M-018641-00	D-018641-01	GAACTACACGTCCAGATTC
			D-018641-02	GGGCAGCGCCTCAACATTG
			D-018641-03	GCAAGACCCTCCGTGTGAA
			D-018641-04	GGACGTTCACGCTCTATGA
	Qiagen	22C4	SI00145453	CAGCCTCATGCACACCATCTA
			SI00145460	CACGGAGCGCAGAAACCACTA
			SI00145467	CACGCTCTATGACTTTGACAA
			SI03062122	CACTATGTTTCCTGGCTCTAA
NOS3	Dharmacon	M-006490-00	D-006490-01	TGAAGCACCTGGAGAATGA
			D-006490-02	CGGAACAGCACAAGAGTTA
			D-006490-03	CGAGGAGACTTCCGAATCT
			D-006490-04	AGGAGATGGTCAACTATTT
	Qiagen	44D7	SI00012677	TCAGGAGTATCTTACCTGTAA
			SI03061674	CACGTGGCTAAGCCAGCTCAA
			SI03082464	CCGGGACTTCATCAACCAGTA
			SI03114748	TCCCTGGTATTTCCACGGAAA
NOX4	Dharmacon	M-010194-00	D-010194-01	GAATTACAGTGAAGACTTT
			D-010194-02	CAGGAGGGCTGCTGAAGTA
			D-010194-03	GGGCTAGGATTGTGTCTAA
			D-010194-04	GATCACAGCCTCTACATAT
	Qiagen	30F3	SI00117642	TCCATTTGCATCAATACTCAA
			SI00117649	CAAGATGACCGTCACATTACA
			SI02642500	AACCAGGAGATTGTTGGATAA
			SI02642507	CAGCATCTGTTCTTAACCTCA
NR2F6	Dharmacon	M-003423-00	D-003423-01	CGACGCCTGTGGCCTCTCA
			D-003423-02	CAGCCGGTGTCCGAACTGA
			D-003423-03	CAACCGTGACTGCCAGATC
			D-003423-04	GTACTGCCGTCTCAAGAAG
	Qiagen	48B7	SI00074172	AAGGCCAATAATAAAGACATT
			SI00074179	ATGACTCAAGGCCAATAATAA
			SI00074186	CAGACACTACATGATGACTCA
			SI03085320	CGCGGTGCTGGGCATCGACAA

HGNC	Source	Pool ID	siRNA ID	Sequence
NSUN4	Dharmacon	M-027291-00	D-027291-01	ACACTAGCGTTGCTTCAGA
			D-027291-02	CCGCGGAGACATCGATATA
			D-027291-03	GACCGCCACTCCCTTCATG
			D-027291-04	ATGGTGCACTGGTCAATAA
	Qiagen	70D4	SI00661892	CTGGAATATTCACATAATAGA
			SI02779588	TACGTATGTCTGGCTTGATTA
			SI03083486	CCTGGGTGTCATGGAGTACTA
			SI03114377	TCCCGCGGAGACATCGATATA
NUCB1	Dharmacon	M-015822-00	D-015822-01	CGAGCAGGATCCCAATGTA
			D-015822-02	GGTCATCGATGTACTGGAG
			D-015822-03	CGACGCAGCCCATCATGAA
			D-015822-04	GAACCAGCATACATTCGAG
	Qiagen	101G2	SI00662403	CTGCATGATATCAACAGTGAT
			SI00662410	CTCAGTGATCGGCTTAACTTA
			SI00662417	CCGCGAGCACCCTAAAGTCAA
			SI00662424	CTGGATGAAGTGGCACAGTCA
NUF2	Dharmacon	M-005289-01	D-005289-02	GAACGAGTAACCACAATTA
			D-005289-03	GGACTCCTATGCTAAGATA
			D-005289-04	GAATTCGACTGGAACATTT
			D-005289-05	TAGCTGAGATTGTGATTCA
	Qiagen	61D4	SI00140630	CAGGAGCTACAACAATCACTA
			SI00140637	CACAGTAATTGAGGATTGCAA
			SI00140644	AAGCATGCCGTGAAACGTATA
			SI03032141	AAGATACGGTCCAGAAGCTTA
NUMBL	Dharmacon	M-012682-00	D-012682-01	CAGAAGAACTCGCCTTTCA
			D-012682-02	GCACTGACTTCCAGGTGAA
			D-012682-03	GCAAAGCCACTGTAGAGAA
			D-012682-04	CCAAGGATCTTCTGGTCGA
	Qiagen	112F5	SI00662879	CCGCACTGACTTCCAGGTGAA
			SI00662886	AACTTGAAGATTTGTATTATA
			SI00662893	GCCAATAAAGGAAGAATATAA
			SI00662900	CCAGAAGAACTCGCCTTTCAA
NXF1	Dharmacon	M-013680-00	D-013680-01	CGAGATCGCATTCATGTTA
			D-013680-02	GCACACGCGTCTCAACGTT
			D-013680-03	GGCTATGTATTGTAAATGA
			D-013680-04	GCGAACGATTTCCCAAGTT
	Qiagen	117C9	SI00663495	CAGAACAAGTAGAACAGCTAA
			SI00663502	AACGCGTTAATTTCCCTCAAA
			SI00663509	CCGAAGGATATCTATCATCAT
			SI00663516	CGCGAACGATTTCCCAAGTTA
ORC4L	Dharmacon	M-003286-02	D-003286-06	GAAAGCACATTCCGTTTAT
			D-003286-07	TGAAAGAACTCATGGAAAT
			D-003286-08	GCTGAGAAGTGGAATGAAA
			D-003286-09	CCAGTGATCTTCATATTAG
	Qiagen	206G4	SI00675031	CAGAAGTTTGTTCAAAGGAAA
			SI00675038	AAGCATTTCAATATCAGCAAA
			SI00675045	CCGGCAGATACACTTAATGAA
			SI00675052	AAGGGTGGTCTCATAAGATTA
PAX2	Dharmacon	M-003921-01	D-003921-01	GAAGTCAAGTCGAGTCTAT
			D-003921-03	GGACAAGATTGCTGAATAC
			D-003921-04	CATCAGAGCACATCAAATC
			D-003921-05	CGACAGAACCCGACTATGT
	Qiagen	57E9	SI00006083	CACAGCTACACGCCCATTAAA
			SI00006090	CCCGTAGTTGCTCTTTCGGTA
			SI00006104	CAGGAACTGAACAGAACCACA
			SI03077508	CCCGACTATGTTCGCCTGGGA
PCDHB10	Dharmacon	M-013278-00	D-013278-01	CGAACAACCTTTCAAATCA
			D-013278-02	CCGATGATAACAAACAATA
			D-013278-03	GGGACAGCATTTAGACTAG
			D-013278-04	TAACATTAGTGGCGGTGAT
	Qiagen	143D11	SI00679315	AAGGAATTAATTACTATTATA
			SI00679322	ATGCCTTATAATTGAAATAAA
			SI00679329	TTGGATTTAATATTCAGTAAA
			SI00679336	CAAATTTAAGTTATTATGCAA
PCDHB7	Dharmacon	M-013526-00	D-013526-01	GAACTAGAATTGTTTCAGA
			D-013526-02	GAACCAACAGCCTGAGTAA
			D-013526-03	TTAAAGCGCAATTGGACTA
			D-013526-04	CATTAACTATTCAGGCCAA
	Qiagen	143G11	SI00679595	CTGAGTAGGAATATTACATAA
			SI00679602	TTGGACTATGAGGCAATTCAA
			SI00679609	CCCGAATTGGTGCTGAATCAA
			SI00679616	TAGAATTGTTTCAGACCAGAA

HGNC	Source	Pool ID	siRNA ID	Sequence
PCDHB9	Dharmacon	M-013279-00	D-013279-01	GAAACCGTCTGTTGACAAT
			D-013279-02	GGAAAGACAATTTGCTATG
			D-013279-03	AAACTCTCCTGGGATAGTA
			D-013279-04	GACCTCCACTATACGCATT
	Qiagen	143E11	SI00679651	AAGGATCAATCTCTTATTTAA
			SI00679658	CCCACTTAATAAAGACATTTA
			SI00679665	ATGCTTAACTTCACAAGTTAA
			SI00679672	ATCCTGCTAAATTTCAATTAA
PDE4DIP	Dharmacon	M-021870-00	D-021870-01	CTAACGAGCTGGAGAAATA
			D-021870-02	GAAGGGAATAGTAAACTTA
			D-021870-03	AGAGCGAGATCATGACTTA
			D-021870-04	GCAAGAAAATGGTCCCTTA
	Qiagen	210F2	SI00681338	CTGGTTGATCCTGAAGACATA
			SI00681345	CAAGCGGAACATTGAGCTGAA
			SI03171301	CAGCCTCAAGCTGCGCATCTA
			SI03224522	TACCAGGTAATTGAAGGTCAA
PEG3	Dharmacon	M-006544-00	D-006544-01	GGAGAGACCTTCAATAAGA
			D-006544-02	GCGAAGACCTCAACACAAA
			D-006544-03	GAAAGAGGCGCTATCATTT
			D-006544-04	GGTAAGTCCTTTATTCATA
	Qiagen	101A8	SI00682115	AAGGATGACCCTGATGACAAA
			SI00682122	CCGGATGTCATCATAGGAGAA
			SI00682129	GAGGCTTTAGGTTTAATTCAA
			SI00682136	CAGCGAAGACCTCAACACAAA
PEX11A	Dharmacon	M-012622-00	D-012622-01	GTACCTCGCTTATGCTTAA
			D-012622-02	GGTCTTGTGTCCTCTATAG
			D-012622-03	GCTCACCACTACTACTATT
			D-012622-04	CGTAAATGGTTCAGACTAG
	Qiagen	110A11	SI00682395	TAGATATTTGTTAGAGCCCAA
			SI00682402	CAAAGAGAAGGTGGTAATGAA
			SI00682409	TTGGAACTAGTACCTACTTTA
			SI00682416	CTTGTTCATGTGAGCATTTAA
PEX13	Dharmacon	M-012591-00	D-012591-01	CAGCGGATGTTAGGTTTAA
			D-012591-02	GATGATCTTCCACCCAGTA
			D-012591-03	TTTCAGGGCTGTATTGGAT
			D-012591-04	AAACGGTGGAATCAAGTAA
	Qiagen	35E10	SI00040558	CTGGCTAGCCTTGATGGCCAA
			SI00040565	TTGACTTGGAATCCTTAGTAA
			SI00040572	TACCAACCCAACACTAACTAA
			SI00040579	TACAGCGGATGTTAGGTTTAA
PEX26	Dharmacon	M-019128-00	D-019128-01	CCTGGGTCCTTCAGTATTA
			D-019128-02	GAGGTGAAGTGCTCCCTGT
			D-019128-03	GATGTTGGTTCGCCAGCTT
			D-019128-04	GCTCCAAGACCCAGCCAAT
	Qiagen	142B3	SI00682563	CAGGATGTTAATGGAGCTGGA
			SI00682570	TAAATTCTTCATGGAATTGAA
			SI00682577	AACATAGAACAGATACCTTTA
			SI00682584	ACAAATGATAGTAGTCACATA
PGLYRP2	Dharmacon	M-008638-00	D-008638-01	GGAGATACCTTTCCAGATG
			D-008638-02	CCTCGGACCTTTACGCTTT
			D-008638-03	GCACGTCTATTCAGGAAAC
			D-008638-04	GGCGCAGGGTCATAAATTT
	Qiagen	57G5	SI00147056	CACGTCTATTCAGGAAACCTA
			SI00147063	CACCTGGACAATCTCGTGCTA
			SI00147070	GCCCTTGATCGCCATCACTAA
			SI00147077	CTGGACTTTGACAGTGGTCAA
PHCA	Dharmacon	M-009430-00	D-009430-01	GATTATACCTCCAATGTTC
			D-009430-02	CCACATGACTCTGAAATAT
			D-009430-03	AACGGTACATTGCTTCTTA
			D-009430-04	GGACTGGGTTATACATCAT
	Qiagen	140G10	SI00683711	AAGGAAATCCTTAAAGATCTA
			SI00683718	ATGGATGGTTCTCAAAGGTAA
			SI00683725	TCAGATTTGATTAATATTGTA
			SI00683732	ACGCTCCAGTTTATAAAGAAA
PIK3R4	Dharmacon	M-005025-01	D-005025-01	GAGGAGAACTTGCTATATT
			D-005025-03	GCACAGAATTGTCTACCTT
			D-005025-04	GTAAGTCGTTCTATATTTG
			D-005025-05	CAGCTGATGTCTACTGTAA
	Qiagen	87B8	SI00107184	TAGAGGCAGAAGATTACTTAA
			SI02224537	AAGCAGAATTCTAGATCAGAA
			SI02660392	AAGATGTACTTGACTAGTTTA
			SI02660399	CAAGCAATGCGTGGACTTTAA

HGNC	Source	Pool ID	siRNA ID	Sequence
PKIB	Dharmacon	M-008224-01	D-008224-02	GAGGACAGATTCATCAAAA
			D-008224-04	AAACAACACAAGACCAATT
			D-008224-05	AGACGGAACCTCAGATTTG
			D-008224-06	AGTCTGGGGTCGCCAATTT
	Qiagen	84A3	SI00162218	AAGGCTCATAATCTATCAAGA
			SI00288575	CAGCATGTGTATATTAGATAA
			SI00288582	CCGGAATGCCTTACCAGACAT
			SI03052336	ATGTCTGTATACAGTAACCAA
PLK1	Dharmacon	M-003290-01	D-003290-05	CAACCAAAGTCGAATATGA
			D-003290-06	CAAGAAGAATGAATACAGT
			D-003290-07	GAAGATGTCCATGGAAATA
			D-003290-08	CAACACGCCTCATCCTCTA
	Qiagen	83H11	SI00071624	CAACGGCAGCGTGCAGATCAA
			SI00071631	CACCATATGAATTGTACAGAA
			SI02223837	CCGGATCAAGAAGAATGAATA
			SI02223844	CGCGGGCAAGATTGTGCCTAA
PNMAL1	Dharmacon	M-021021-00	D-021021-01	AGAAAGCCCTGTGTGAATA
			D-021021-02	TGTTAAAGCTGCCCTCATT
			D-021021-03	CGATGAACCTTCTGGAGGA
			D-021021-04	GAGCAGTGGTGCAGATCAT
	Qiagen	140D2	SI00389837	CAGGTGTATGGTAGTAAGTAA
			SI00389844	CACCATGACTAGTAAATGTAA
			SI00389851	AAGGAAGAAGTACCAAGTCAA
			SI00389858	CTCGTGATGATTCATTTCAAA
POLE	Dharmacon	M-020132-00	D-020132-01	AGAGAAGGCTGGCGGATTA
			D-020132-02	GGAAACCTCTAAGAAGATA
			D-020132-03	TGAAGGAGATCACCCAGTA
			D-020132-04	GAAGAGGTATGCTGTGTTC
	Qiagen	46C7	SI00086023	CCGCATCATCCTCTGTACAAA
			SI00086030	CTGGATGGATCCATCTAACTA
			SI03028872	AACCGTATTTCTACATTGCGA
			SI03037755	ACAGATCGGAATATTCCGGAA
POLR2A	Dharmacon	M-011186-01	D-011186-02	CAACATCTCCTACTTATTC
			D-011186-03	TAATAGAGGTCATCGAGAA
			D-011186-04	GAAGGTGACTGCCAACACA
			D-011186-05	GGGATGAGATGAACTTGCA
	Qiagen	102B3	SI00688975	CTCGGGAAGAACAAAGCTAAA
			SI00688982	CACCACAGTCTCCAACCTATA
			SI00688989	CCGACTTAAGGAGCTCATCAA
			SI00688996	CAGGACATTCAGAACACTATT
POLR2F	Dharmacon	M-004723-00	D-004723-01	CAGACAACGAGGACAATTT
			D-004723-02	GGAGAATGCCGAAGAGGAA
			D-004723-03	GATGGGAGCTATGAAGACT
			D-004723-04	CATCATCATTCGCCGTTAC
	Qiagen	102F3	SI00689087	TCACTTTATATGTGTAAATAA
			SI00689094	CACACCATACATGACCAAGTA
			SI00689101	TTGGAGAATGCCGAAGAGGAA
			SI00689108	CTGCCAGATGGGAGCTATGAA
POP1	Dharmacon	M-014148-00	D-014148-01	GAACCGGACGCTAGAATTT
			D-014148-02	CGATGGAGATGAACAGATT
			D-014148-03	GCAGTGCATTCTCAGTATA
			D-014148-04	GCCAAGCGGTTTCATATGG
	Qiagen	119E9	SI00689759	CAGGGCATAGATAATACGTTA
			SI00689766	TCCCTTAAATGTCAAATGCAA
			SI00689773	CTCCCTGGAAACAAGAATAAA
			SI00689780	CTGGTGGATAGAAACCTGTAA
PPP1R16A	Dharmacon	M-018795-00	D-018795-01	GGGCCGACCTGAACGCAAA
			D-018795-02	CCTATGACCTGTGTGATGA
			D-018795-03	CACCAGTGCTGCATTGATG
			D-018795-04	GAGCCAGCCTGAGCGCTAA
	Qiagen	164F11	SI00144921	CCCGAGCAGCCCTGTGGGCAA
			SI02658187	CCGAGCCAGCCTGAGCGCTAA
			SI02658194	CCGGAAGCTGGAACCTTGTTA
			SI02658201	CAGCCCTGACTTGGCCAACGA
PQBP1	Dharmacon	M-012716-00	D-012716-01	TCAAACATCTGGAGCCTGA
			D-012716-02	GATCATTGCCGAGGACTAT
			D-012716-03	CCATGGACCCTAGCTCATA
			D-012716-04	ACGATGATCCTGTGGACTA
	Qiagen	210A7	SI00691691	AGCCGAAAGGATGAAGAGTTA
			SI00691698	CCGAAAGGATGAAGAGTTAGA
			SI00691705	CTCAAACATCTGGAGCCTGAA
			SI00691712	CCCAACTCCGTGGTTACCAAA

HGNC	Source	Pool ID	siRNA ID	Sequence
PRDM8	Dharmacon	M-020669-00	D-020669-01	GACGAGGAGTTACTAGTTT
			D-020669-02	GCAATGAGTCCTTCAGGGA
			D-020669-03	CATATGAGGTCGCACCACA
			D-020669-04	CCGTATATCTTTCGGGTAG
	Qiagen	52D3	SI00125468	CTCGCATAATTGACTCGGAAA
			SI00125475	CCGCTGGAAAGCGGTCATAAA
			SI00125482	TCCAACAATGTCTGACAGATA
			SI00125489	CGCGCGCGCAAGCACAGTTAA
PSMD1	Dharmacon	M-011363-00	D-011363-01	GCAATGATATCGTTAGACA
			D-011363-02	GAGATAATTTGGAATGGTT
			D-011363-03	GTGCCTGGATCCACTAATA
			D-011363-04	CGAATGATGTCCCAGGAAT
	Qiagen	102F9	SI00694750	TTGGAAGGCATCGTAAATAAA
			SI00694757	CTGCATGTCTTTAATGCAGAA
			SI03246649	AAGCAGTGCATTTGTAGGAAA
			SI03246985	CAGGCTGTGAGTGATATCTTA
PSMD3	Dharmacon	M-011364-00	D-011364-01	CCGCAAAGTGTTACTATTA
			D-011364-02	GGACCTACACCCTAATTAT
			D-011364-03	CAGCTACGCTTCGGCATGA
			D-011364-04	ACCACTATGTTCTGTATAA
	Qiagen	102G9	SI00694883	CAAGGAGATGATTGACATCTA
			SI00694890	CACGTGAAACAGCTAGAGAAA
			SI00694897	CAGATGGGACCTACACCCTAA
			SI00694904	CACGAGAAGGGCTATGTCCAA
PSMD8	Dharmacon	M-017583-00	D-017583-01	CCACAGAACTGGCCAAACA
			D-017583-02	GCTACTACTTTGATTACAA
			D-017583-03	CAGTGTCCCTGGAGCAATA
			D-017583-04	GAGGGCAGCTACAACAAAG
	Qiagen	102A10	SI00694967	TCCAACTGACATGTTCATTAA
			SI00694974	AAGGGCGAGTGGAACCGTAAA
			SI00694981	CTGCAGGGTTTCGCCCAATAA
			SI00694988	ATGCTACTACTTTGATTACAA
PTGES	Dharmacon	M-008462-01	D-008462-01	GCACGCTGCTGGTCATCAA
			D-008462-03	GGGCTTCGTCTACTCCTTT
			D-008462-04	GGATGCACTTCCTGGTCTT
			D-008462-05	TGGCACACACCGTGGCCTA
	Qiagen	45G7	SI00069573	TTGGGTGACCAGCCACTCAAA
			SI00069587	CGGGCTAAGAATGCAGACTTT
			SI00069594	CAGCACGCTGCTGGTCATCAA
			SI03035816	AAGGGAGACTCTATTTAAGAT
PTPN13	Dharmacon	M-008065-00	D-008065-01	GAACAAACCATGAAGATTC
			D-008065-02	GAAGAAATATGGGCTGTAT
			D-008065-03	GGAAAGAAGAGTTCGTTTA
			D-008065-04	CAGATCAGCTTTCCTGTAA
	Qiagen	78G11	SI00086660	AACCTTTGGATCAGTGTCTAA
			SI02637047	TCCAGGTACATTAAAGATGAA
			SI02659342	CGGTCTATTCTTACTAAGAAA
			SI02659349	TCGATGGATAAGTATCATATA
PTPRE	Dharmacon	M-008068-02	D-008068-02	GCGAACAGGTACATTCATA
			D-008068-03	GAATGGAAATCCCACACTA
			D-008068-04	CGATTGAGATAAAGAATGA
			D-008068-06	AAACGGATATGCAGTACAC
	Qiagen	79E2	SI00089068	ACCACGGGCAATTAAACTTTA
			SI00089075	GACCATCGTCATGTTAACAAA
			SI00089082	CAGTGAATTCACAACCCTGAA
			SI02665635	CCGAGTGATCCTTTCCATGAA
PVRL3	Dharmacon	M-013952-01	D-013952-02	GGAATATTCTGCTATAGGA
			D-013952-03	GCGAATTACTTGTGTTGTA
			D-013952-04	ACAATGGCCTGATGGTTTA
			D-013952-05	CCGATACTCTTTCATATTA
	Qiagen	26A11	SI00696262	CACATGTAGATGGTTCCGTAA
			SI00696269	ATCGAGGATCTAGCAACAGAA
			SI03024343	TTGCTAGAGGAAGGCGAATTA
			SI03029565	AACGATTATCAGCCAGTACAA
RAB3D	Dharmacon	M-010822-01	D-010822-02	TGACATCGCCAATCAGGAA
			D-010822-03	GTTCAAACTGCTACTGATA
			D-010822-04	GTACTGTGGGCATCGATTT
			D-010822-05	GGACGAACGTGTTGTGCCT
	Qiagen	36C4	SI00062181	CAGGCCCTGTTTAGCTGTTTA
			SI00062195	CTGGAACTATGGACCACATTA
			SI00062202	AAGCAAGTTCTTGCCCAATCA
			SI03052595	CAAACTGCTACTGATAGGCAA

HGNC	Source	Pool ID	siRNA ID	Sequence
RAD51	Dharmacon	M-003530-03	D-003530-02	GAAGCTATGTTCGCCATTA
			D-003530-05	GCAGTGATGTCCTGGATAA
			D-003530-07	CCAACGATGTGAAGAAATT
			D-003530-08	AAGCTATGTTCGCCATTAA
	Qiagen	56G2	SI00045010	CAGGATAAAGCTTCCGGGAAA
			SI02663682	AAGGGAATTAGTGAAGCCAAA
			SI03061338	CACGGTTAGAGCAGTGTGGCA
			SI03072272	CAGGTGGTAGCTCAAGTGGAT
RAP2C	Dharmacon	M-010057-00	D-010057-01	CAACTTGTGTCGTCCAGTA
			D-010057-02	GAAGATTTCTACCGCAAAG
			D-010057-03	GCAAATCTGCCCTTACTGT
			D-010057-04	GAGATCAAATTGTCAGAGT
	Qiagen	26H3	SI00130039	ATGGCTAATATACAAGGGTTA
			SI03069794	CAGGATATCAAGCCAATGAGA
			SI03076458	CCCACTAATCCTAGTAGGAAA
			SI03117611	TGAGATCGTCAGGCAAATGAA
RAPH1	Dharmacon	M-031919-00	D-031919-01	GGAAGCAGCTCTATATGAA
			D-031919-02	CGACATACATTGAAACATG
			D-031919-03	GCGAGCATCTGGTATCTAC
			D-031919-04	GCATGGACTCTTTGGATAT
	Qiagen	218H5	SI00698635	AAGGATTATCTTCTTCATCTA
			SI00698642	CTGGATCATGTCAACGTTTAT
			SI00698649	CAGCTCTATATGAACTACCAA
			SI00698656	ATGGCTGATCTTTGCTCTATA
RBBP9	Dharmacon	M-017623-00	D-017623-01	TCGAGTATATGCTATTGTA
			D-017623-02	AAACATGCCCGACCCAATT
			D-017623-03	AGAAGTGGCCGATAGGTTG
			D-017623-04	GGCCATGAGGTATGCAGAA
	Qiagen	211H5	SI00699307	CTGAATGGAAATCAACTGTAA
			SI00699314	TTGAATAATAATGTTGTTAAA
			SI00699321	AACAATGTATTTGACTACTAA
			SI00699328	TAGGATAAATGATCCATTTAA
RBM8A	Dharmacon	M-003531-00	D-003531-01	GGTATACTCTAGTTGAATA
			D-003531-02	GTTGAAGGCTGGATTCTCT
			D-003531-03	GGACGAGAGCATTCACAAA
			D-003531-04	TGAGGAAGCCACCGAAGAA
	Qiagen	38A6	SI00699951	ACACGACAAATTCGCAGAATA
			SI03046533	ATACTCTAGTTGAATATGAAA
			SI03070004	CAGGATGGCGATGAACCCGGA
			SI03070536	CAGGCGAACAGGATATCTGAA
RIC8B	Dharmacon	M-021081-00	D-021081-01	CAACATGCTTGATAAACTT
			D-021081-02	GCAAGGACCGGAAATTTAT
			D-021081-03	GGTCACAATTGCGCTATGA
			D-021081-04	AATCGGCCATAGACCATAA
	Qiagen	139H8	SI00444248	CAGAAAGAGCTGGTAAATAAA
			SI00444255	CTCCCTATAAAGAGTTATAAA
			SI00444262	CAGCACCCATTTGTACATATA
			SI00444269	TAGGGCTACTTTCAAATTTGA
RND3	Dharmacon	M-007794-01	D-007794-02	GAACGTGAAATGCAAGATA
			D-007794-03	GAAATTATCCAGCAAATCT
			D-007794-04	TAGTAGAGCTCTCCAATCA
			D-007794-05	AGAATTACACGGCCAGTTT
	Qiagen	90H8	SI00301371	CAGCCAGAAATTATCCAGCAA
			SI00301392	CGGACAGATGTTAGTACATTA
			SI00301399	TTCATTGTGATTGTCATTAAA
			SI00301406	CACCTTGGCATGTGTAAATAA
RPA1	Dharmacon	M-015749-00	D-015749-01	GAAGTCAGCTGAAGCAGTT
			D-015749-02	GGAATGGGTTCTACTGTTT
			D-015749-03	GCAATCCAGTGCCCTATAA
			D-015749-04	GAAGTGCGACACCGAATTT
	Qiagen	46B8	SI00046025	GAGGTGCTACATAGTTGGTAA
			SI00046032	ACCGCATGATCCTGTCAGTAA
			SI02663696	CAGGAATTATGTCGTAAGTCA
			SI02663703	CCGTGTGACGATCCCATGTTA
RPA2	Dharmacon	M-017058-00	D-017058-01	GATCAATGCACACATGGTA
			D-017058-02	CAAAATAGATGACATGACA
			D-017058-03	GAGTGAAGCAGGGAACTTT
			D-017058-04	GTGGAACAGTGGATTCGAA
	Qiagen	46H3	SI00046046	TACCAGGAGAGTACTTACATA
			SI00046060	CCAGGTGTTGAATTTGATTAA
			SI00046067	AAGGCTTGTCCAAGACCTGAA
			SI02664956	AACAGTGGATTCGAAAGCTAT

HGNC	Source	Pool ID	siRNA ID	Sequence
RPA3	Dharmacon	M-003322-01	D-003322-05	GGAAGTGGTTGGAAGAGTA
			D-003322-06	GAAGATAGCCATCCTTTTG
			D-003322-07	CATGCTAGCTCAATTCATC
			D-003322-08	GATCTTGGACTTTACAATG
	Qiagen	46C8	SI00046074	AAGGGAGTAAATCGACCCTCA
			SI00046081	TCGCTGATTGGTGCCGAGAAA
			SI00046088	TCCGCGCATTTAATTGGCGAA
			SI03057180	CACCACGTATCATTCCGCAAA
RPH3AL	Dharmacon	M-017670-00	D-017670-01	GAAAGTCTGCACCAAATGT
			D-017670-02	GACAAACCCTGGAAGGAGT
			D-017670-03	TGTGTAAGATCTGCAGTGA
			D-017670-04	GGGAATGATCAGTGGGTTT
	Qiagen	113B3	SI00705411	CACGTTATGCTTCAGAATTAA
			SI00705418	CAGGAAGAAAGTCTGCACCAA
			SI00705425	CTGCCTTATTGAAACCATCTA
			SI00705432	GAGGTTTGGCTTGGCATGAAA
RPL10L	Dharmacon	M-013264-00	D-013264-01	GAAGTTTAATGCTGACGAA
			D-013264-02	GAGTGCGGCTCCATCCCTT
			D-013264-03	GGTGAAAAGTTGTGGCAGA
			D-013264-04	GTTGTGGAGTCAAGTACGT
	Qiagen	177F7	SI00705551	CTGACTTATGCTTACTAATAA
			SI00705558	ACGAAGTTTAATGCTGACGAA
			SI00705565	CCGTATTTGTGCCAACAAATA
			SI00705572	CCAGAAGATTCATATCTCCAA
RPL14	Dharmacon	M-012948-00	D-012948-01	GCATGCAGCTCACTGATTT
			D-012948-02	AAGCCAAGATGACAGATTT
			D-012948-03	GAAAATTGGTCGCGATTGT
			D-012948-04	CGATGGACCTTGCACTCAA
	Qiagen	111D8	SI00705663	CAGATTGATAGTAGGATTATA
			SI00705670	CACCAGAAGTATGTCCGACAA
			SI00705677	CCTGTTGACAAATGTATTTAA
			SI00705684	AATAAACATTAAATAATCAAA
RPL18	Dharmacon	M-011142-00	D-011142-01	GAAGAACCAACTCCACATT
			D-011142-02	GCAAGGAGCCCAAGAGCCA
			D-011142-03	GAGTGGACATCCGCCATAA
			D-011142-04	GGCTGTTGGTCAAGTTATA
	Qiagen	103A7	SI00705775	GAGGCTGTTGGTCAAGTTATA
			SI00705782	CCGCCATAACAAGGACCGAAA
			SI00705789	ACCCTGGATCCTACTCTCTTA
			SI00705796	CGCCATCATGGGAGTGGACAT
RPL24	Dharmacon	M-011144-00	D-011144-01	TAGAAAGGCTCAACGAGAA
			D-011144-02	TATCAGGGCTGCTAAGGAA
			D-011144-03	GTGCATCTCTTGCTGATAT
			D-011144-04	CGAAATGCGAGTCGGCTTT
	Qiagen	103D7	SI00705971	AAGAGGAATCAGAAACCTGAA
			SI00705978	AAGGCTAAGCAAGCATCTAAA
			SI00705985	CAGGGCTGCTAAGGAAGCAAA
			SI00705992	TAAATAAAGATTGGATTATAA
RPL28	Dharmacon	M-011145-00	D-011145-01	GGAATAAGCAGACCTACAG
			D-011145-02	CGGCAAAGGTGTCGTGGTG
			D-011145-03	CGCAATTCCTTCCGCTACA
			D-011145-04	AATGGATGGTCGTGCGGAA
	Qiagen	103F7	SI00706083	CAGGGTTGATGAGAAGATTAA
			SI00706090	ATGGTGCATATTGAATGTATA
			SI00706097	TAGGAATAAATTAATGACTTT
			SI00706104	CTGCTTGACTGTGCCCACAAA
RPL30	Dharmacon	M-013604-00	D-013604-01	GCACACTGGCTATCATTGA
			D-013604-02	GATCAACTCTAGGCTCCAA
			D-013604-03	GGAAGTACGTCCTGGGGTA
			D-013604-04	AGAGTACTATGCTATGTTG
	Qiagen	103E7	SI00706167	CAGGAAGATGGTGGCCGCAAA
			SI00706174	CTGAAATAGAGTACTATGCTA
			SI00706181	AGGCTCCAACTCGTTATGAAA
			SI00706188	CAGGTGACTCTGACATCATTA
RPL34	Dharmacon	M-013545-00	D-013545-01	GCACAGAGTCAGAAAGCTA
			D-013545-02	AAACTAGGCTGTCCCGAAC
			D-013545-03	CGTTTGACATACCGACGTA
			D-013545-04	TACAATACAGCCTCTAACA
	Qiagen	207G2	SI00706279	CAGTATATGATCACTAATATA
			SI00706286	AAGCACAGAGTCAGAAAGCTA
			SI00706293	TACCAGGAGCTCTGATATATA
			SI00706300	AATGACTTGATTGTTATTATA

HGNC	Source	Pool ID	siRNA ID	Sequence
RPL35	Dharmacon	M-012371-00	D-012371-01	GGAAATCCATTGCCCGTGT
			D-012371-02	CCTAAGAAGACACGTGCCA
			D-012371-03	GCGCGTCGCCAAAGTGACA
			D-012371-04	GGAAGTACGCGGTCAAGGC
	Qiagen	6A11	SI02663871	CCGTGTTCTCACAGTTATTAA
			SI02663878	TGCAGCAATGGCCAAGATCAA
			SI03032260	AAGATCCGAGTCGTCCGGAAA
			SI03056186	CACAGCTGGCTGAGACTGCAA
RPL38	Dharmacon	M-011133-00	D-011133-01	AGGACAACGTGAAGTTTAA
			D-011133-02	GCTCACAGCCCGACGAAAG
			D-011133-03	GATGCCAAATCTGTCAAGA
			D-011133-04	GATGCAGCAGATACCTTTA
	Qiagen	6C10	SI02624762	CACCCTGGTCATCACTGACAA
			SI02624769	CAGTGAAGGAACTGAAATGAA
			SI03042067	ACTGATTGGAACTGTATTATA
			SI03078845	CCCGGTTTGGCAGTGAAGGAA
RPL39L	Dharmacon	M-012971-00	D-012971-01	TAGGGTGGATTCAGTAATA
			D-012971-02	TGTATGCTCTGTGCTAGTA
			D-012971-03	CAAGTTCACGATCATCTTA
			D-012971-04	CAGATGAAACCTGGTAGTA
	Qiagen	170H10	SI00706531	CAGATGAAACCTGGTAGTAAA
			SI00706538	CAGATCGAGATTTGCGTCCTA
			SI00706545	TCGGAGTCTCAGAGACACCAA
			SI00706552	TTGCCTCTTTGGAGTAGGAAA
RPL4	Dharmacon	M-008956-00	D-008956-01	GCAGAGTCCTAAAGAAGAA
			D-008956-02	AGATAAAGTTGAAGGCTAC
			D-008956-03	CTACTACAGAGGAGAAGAA
			D-008956-04	TGTTGAAGCTAAACCCATA
	Qiagen	6E9	SI00019446	CAGGCAGTGAGAAACATGAAA
			SI00019453	AAAGCCTGGAATGATATCAAA
			SI03066294	CAGCCCTATGCTGTCAGTGAA
			SI03102512	GAGAAGAAGCCTGCTGCATAA
RPL7A	Dharmacon	M-011134-00	D-011134-01	GGTGAACTCGGAAGACAAA
			D-011134-02	CCATCGAGCTGGTTGTCTT
			D-011134-03	CTAAGTCTGTGGCTCGTAT
			D-011134-04	GGACGTCCCAACGAAGAGA
	Qiagen	6F9	SI00706699	CAGGTGAACTCGGAAGACAAA
			SI03077949	CCCGCCGCCCAAGATGCCGAA
			SI03087595	CTAAACTGGGTTAAATGTACA
			SI03114230	TCCCATCGAGCTGGTTGTCTT
RPL8	Dharmacon	M-013721-00	D-013721-01	GGGCGTACCACAAATATAA
			D-013721-02	GAACTGCTGGCCACGAGTA
			D-013721-03	CGGGATCCGTATCGGTTTA
			D-013721-04	CAAGAAGACCCGTGTGAAG
	Qiagen	207E2	SI00706755	CCGGGCGTACCACAAATATAA
			SI00706762	CTCAATAAAGTTTGTGTTTAT
			SI00706769	AAAGTTTGTGTTTATGCCAAA
			SI00706776	TCCGGGATCCGTATCGGTTTA
RPLP0	Dharmacon	M-010864-00	D-010864-01	GATCAAGACTGGAGACAAA
			D-010864-02	GGACGAGGATATGGGATTT
			D-010864-03	GAGAAACTGCTGCCTCATA
			D-010864-04	GATTTGGTCTCTTTGACTA
	Qiagen	207H2	SI02650473	TCCGCGGTTTCTGATTGGCTA
			SI02650487	ACGGGCGATGGCGCAGCCAAT
			SI02660798	CTACTTTGTTCGCATTATAAA
			SI02660805	TTGGCTACTTTGTTCGCATTA
RPLP1	Dharmacon	M-011135-00	D-011135-01	CATTAAAGCAGCCGGTGTA
			D-011135-02	GCACGACGATGAGGTGACA
			D-011135-03	TGGCCTGGCTTGTTTGCAA
			D-011135-04	AAGAAGAATCCGAGGAGTC
	Qiagen	207A3	SI00706818	CTGCATCTACTCGGCCCTCAT
			SI00706825	AAAGTGGAAGCAAAGAAAGAA
			SI00706832	TCGGTCCTTCCGAGGAAGCTA
			SI04799970	AAGAAAGTGGAAGCAAAGAAA
RPS11	Dharmacon	M-013569-00	D-013569-01	GAACATGTCTGTACACCTG
			D-013569-02	GAGACTATCTGCACTACAT
			D-013569-03	GATCCTCTCTGGCGTGGTG
			D-013569-04	CCAGATCGGTGACATCGTC
	Qiagen	103C9	SI00707147	CCCTGCGTAATCGATAAGGAA
			SI00707154	CGGGAAGATGGCGGACATTCA
			SI00707161	TGGCGTGGTGACCAAGATGAA
			SI00707168	CCACAATGAAATAAAGTTATT

HGNC	Source	Pool ID	siRNA ID	Sequence
RPS13	Dharmacon	M-011150-00	D-011150-01	GGATAAGGATGCTAAATTC
			D-011150-02	CTAAGGGACTTGCTCCTGA
			D-011150-03	CCAGTCGGCTTTACCCTAT
			D-011150-04	CCGTTTGGCTCGATATTAT
	Qiagen	103D9	SI00707203	ACCGTTTGGCTCGATATTATA
			SI00707210	CTGAAGATCTCTACCATTTAA
			SI00707217	TCGCATAAATTTGTCTGTGTA
			SI00707224	CAGAAAGGATAAGGATGCTAA
RPS19	Dharmacon	M-003771-00	D-003771-01	CCAGCAGGAGTTCGTCAGA
			D-003771-02	CCGTCAAGCTGGCCAAGCA
			D-003771-03	CCTACGATGAGAACTGGTT
			D-003771-04	GCCGAGGCTCCAAGAGTGT
	Qiagen	6E10	SI03077522	CCCGACTTGTGCGCCCGGGAA
			SI03092460	CTCTCTATCCTCTCTCTATTA
			SI03109078	TACCGTCAAGCTGGCCAAGCA
			SI03113649	TCCAGCCACGAACGACGCAAA
RPS21	Dharmacon	M-011153-00	D-011153-01	TCGTAGGATGGGTGAGTCA
			D-011153-02	CAGGTTTAATGGCCAGTTT
			D-011153-03	CCATTCTCCGATTGGCCAA
			D-011153-04	GCATCGTCTCAAAGAACTT
	Qiagen	103F9	SI00707483	TGGAATATTTGTCATAAATAA
			SI00707490	CGGCGAGTTCGTGGACCTGTA
			SI00707497	CAAGGTCACAGGCAGGTTTAA
			SI00707504	GCGGAAATGCTCCGCTAGCAA
RPS24	Dharmacon	M-011155-00	D-011155-01	GAACGACACCGTAACTATC
			D-011155-02	AGACATGGCCTGTATGAGA
			D-011155-03	CAACGAAAGGAACGCAAGA
			D-011155-04	GTACAAGACCACACCGGAT
	Qiagen	207D3	SI00707539	CAAGAACATTAATAAACTAAA
			SI00707546	CGCAAGAACATTAATAAACTA
			SI00707553	CACTAGAAAGTTCATGACCAA
			SI00707560	AAGATAGATCGCCATCATGAA
RPS28	Dharmacon	M-013679-00	D-013679-01	GACACGAGCCGATCCATCA
			D-013679-02	GCAGGTGCGCGTGGAATTC
			D-013679-03	GCGACGTGCTCACCCTTTT
			D-013679-04	GGACCGGTTCTCAGGGACA
	Qiagen	103H9	SI00707714	CTGAGATGCTCCTTTAAATAA
			SI00707721	GCCGATGGGAATGGTCTGTCA
			SI00707728	CCCGGAGGTTGCGCTGAGCTT
			SI03145072	AGCGTTTGTGTTTCAAGTTAA
RPS29	Dharmacon	M-011157-00	D-011157-01	GGTCTGATCCGGAAATATG
			D-011157-02	GGTTCTCGCTCTTGTCGTG
			D-011157-03	CAATATGTGCCGCCAGTGT
			D-011157-04	ACGCGAAGGATATCGGTTT
	Qiagen	103A10	SI00707735	ATGATAATTCTTTGTATATAA
			SI00707749	GAAGGATATCGGTTTCATTAA
			SI02786350	CCGCCAGTGTTTCCGTCAGTA
			SI04861990	CCGGCACGGTCTGATCCGGAA
RPS3A	Dharmacon	M-013603-00	D-013603-01	CATGATGTCTTCGTTAGAA
			D-013603-02	GGTCGTGTGTTTGAAGTGA
			D-013603-03	TGAACGAGCTGATGGATAT
			D-013603-04	GAACAAGCGCCTTACGAAA
	Qiagen	207B3	SI00707819	CACCTGCTATGTTCAATATAA
			SI00707826	CCGGAAGAAGATGATGGAAAT
			SI00707833	TTGAAAGAAGTGGTCAATAAA
			SI00707840	AAAGATTGGTATGATGTGAAA
RPS5	Dharmacon	M-010498-01	D-010498-02	ACATTTCCCTGCAGGATTA
			D-010498-03	CCGCCAAACGCTTCCGCAA
			D-010498-04	GCACCGATGATGTGCAGAT
			D-010498-05	GAACTCCTATGCCATTAAG
	Qiagen	103A9	SI00707959	CACCGATGATGTGCAGATCAA
			SI00707966	CTCGAACTCCTATGCCATTAA
			SI00707973	CCTGGTGAACGCCATCATCAA
			SI00707980	CCGGGAGGACTCCACACGCAT
RPS9	Dharmacon	M-011131-00	D-011131-01	GAACATCCCGTCCTTCATT
			D-011131-02	GCGGAGACCCTTCGAGAAA
			D-011131-03	GAAGCTGATCGGCGAGTAT
			D-011131-04	GGCAAGATGAAGCTGGATT
	Qiagen	103B9	SI00708071	ACGGCGTCTGTTCGAAGGCAA
			SI00708078	CCCGCGGAGACCCTTCGAGAA
			SI00708085	AAACAGGATCAGCGCTTTAAA
			SI00708092	CCCGGGCCGCGTGAAGAGGAA

HGNC	Source	Pool ID	siRNA ID	Sequence
RPSA	Dharmacon	M-013303-00	D-013303-01	GGTCATGCCTGATCTGTAC
			D-013303-02	GCACCAATCTTGACTTCCA
			D-013303-03	GCGCATGCGTGGCACCATT
			D-013303-04	CAACAAGGGAGCTCACTCA
	Qiagen	7B11	SI00467964	TCGACATGAGTTGTACTTCTA
			SI00467971	TACCTGGGATTGCATATCAAA
			SI00467978	TTGCATATCAAAGCATAATAA
			SI03045371	AGGCTCTTAAGCAGCATGGAA
RSC1A1	Dharmacon	M-008895-00	D-008895-01	GAAAGAACTTCATGAACTT
			D-008895-02	GCTCAACAGTCCCTAGTTA
			D-008895-03	GAACATTGGTGCATTGGAT
			D-008895-04	GCAACAGAATCAACACAAA
	Qiagen	60D6	SI00089173	AAGAACCGTTCTGTCACTGTA
			SI00089180	CTCAATCAGACTTCTGAGCAA
			SI00089194	TAGGGAATCCATAAATAAGAA
			SI03027948	AACATCGTAGTTCCTACATGA
RUVBL2	Dharmacon	M-012299-00	D-012299-01	TAACAAGGATTGAGCGAAT
			D-012299-02	CGCAGTACATGAAGGAGTA
			D-012299-03	TCAACGAACTCAAAGGCGA
			D-012299-04	ACGCAAGGGTACAGAAGTG
	Qiagen	119F5	SI00709247	CCGGAGATCCGTGATGTAACA
			SI00709254	CACGCAGTACATGAAGGAGTA
			SI00709261	AACCGTTACAGCCACAACCAA
			SI00709268	CCAGGACGCCTTCCTCTTCAA
SC65	Dharmacon	M-020141-00	D-020141-01	CAGAGTACCTGGCAGTCTT
			D-020141-02	GGACTGTGAGGCCAATTTG
			D-020141-03	CCGCCAAGTATCTCAACTA
			D-020141-04	ACGCGCTGTTCAAGGCTAA
	Qiagen	118G5	SI00711347	CAGCAAGAACTATTTATTAAA
			SI00711354	CCGGGCTGTGAAGCTCTACAA
			SI00711361	CGCCAAGTATCTCAACTACTA
			SI00711368	AATGTTTGTTGTTGAATGAAA
SCGB1A1	Dharmacon	M-016680-00	D-016680-01	GGACACACCCTCCAGTTAT
			D-016680-02	CCAGAGAAAGCATCATTAA
			D-016680-03	GAAACTCGCTGTCACCCTC
			D-016680-04	CAAAGCTCACTGTGTAATT
	Qiagen	2H9	SI00051198	CAGCCTTGCTCTCTTCAATAA
			SI00051205	CTGTGTAATTAGCATTTAGAA
			SI03033002	AAGCATCATTAAGCTCATGGA
			SI03043145	AGCCCAAAGCTCACTGTGTAA
SESN3	Dharmacon	M-018289-00	D-018289-01	GAAAGAAGCCTGAAGGTTT
			D-018289-02	GCGCAGAGCTTTATTTAAC
			D-018289-03	GAAGGAAGTTGTCCAAGCA
			D-018289-04	GAGGATGACATGATTATAA
	Qiagen	178C2	SI00715715	CAGGCTAATATCAGTCAACAA
			SI00715722	AAGCCTGAAGGTTTACATTAA
			SI00715729	CAGGCACTATATTGCAATAAT
			SI00715736	AAGACCTTTCACATAAGATAA
SETD8	Dharmacon	M-031917-00	D-031917-01	ACCCGTGGCTGAAGCATTA
			D-031917-02	GCAACTAGAGAGACAAATC
			D-031917-03	GATTGAAAGTGGGAAGGAA
			D-031917-04	GCACGACATCGACGGCGTA
	Qiagen	43A8	SI02664991	CTGCAGTCTGAAGAAAGGAAA
			SI02664998	AAGAATAGATGAATTGATTGA
			SI03110625	TAGAGGCAGGAAGATGTCCAA
			SI03116484	TCGCCTAGGAAGACTGATCAA
SF3A3	Dharmacon	M-019808-00	D-019808-01	GGAGGGATATGGTCGTTAT
			D-019808-02	GCAAACCTATTCCCTACTG
			D-019808-03	CGTCATGGCTAAAGAGATG
			D-019808-04	TGATAAGGATGGATTACGA
	Qiagen	119H9	SI00715883	AAGGAAGAATGCAGAGTATAA
			SI00715890	CAGAGACTATTCAGTACCAAA
			SI00715897	CAGCGACATCTCACTCATGAA
			SI00715904	CTGGGTTTGGACAGATTGAAA
SF3B1	Dharmacon	M-020061-00	D-020061-01	GGAATTAGATGCTATGTTC
			D-020061-02	GCAAACGAGTCAAACCATA
			D-020061-03	GAACCGCTATTGATTGATG
			D-020061-04	GTAGAATGTTGCAATATTG
	Qiagen	212C9	SI00715911	CAGGTTATTATGACCAGGAAA
			SI00715918	AAGACTCACGAAGATATTGAA
			SI00715925	GTGGCATTGCTTAATGATATA
			SI00715932	ACGATGACTATTCATCATCTA

HGNC	Source	Pool ID	siRNA ID	Sequence
SF3B14	Dharmacon	M-020260-00	D-020260-01	GAACACACCTGAAACTAGA
			D-020260-02	TGAAGTAAATCGGATATTG
			D-020260-03	TAACAGATACCTTGTGGTT
			D-020260-04	GAACAGCTTATGTGGTCTA
	Qiagen	134B9	SI00715939	TCGGATATTGTATATAAGAAA
			SI00715946	AACATTCGACTTCCACCTGAA
			SI00715953	CTGGATGTTGATGTCCTGCAT
			SI00715960	TTGGAATACATTATGTTAATA
SF3B4	Dharmacon	M-017190-00	D-017190-01	GAGAAGTTGCTTTATGATA
			D-017190-02	GAACAAAGCATCAGCTCAC
			D-017190-03	TGATCAAACTCTATGGGAA
			D-017190-04	TAACCGTCCTATCACCGTA
	Qiagen	116H9	SI00716023	CTGGATGAGAAGGTTAGTGAA
			SI00716030	CACAGGCAACTCCAAAGGTTA
			SI00716037	CACCGTATCTTATGCCTTCAA
			SI00716044	CATGAACATGATCAAACTCTA
SHCBP1	Dharmacon	M-016781-00	D-016781-01	GATTGTAGCTACCGTGATA
			D-016781-02	CGATTAAGATTGCATTATG
			D-016781-03	GGAGATGTTTGTTGGGATT
			D-016781-04	TATAAATGCCTGCTTCGAA
	Qiagen	155G3	SI00717843	CTGGGTGTTCTTGTTATCATA
			SI00717850	AAGCAGTTTGTCAAATTGTAA
			SI00717857	TTGCATAATACTTGTCTTAAA
			SI00717864	CAAGATATCCATGGTGAATAA
SHROOM2	Dharmacon	M-011577-00	D-011577-01	GAGAATGCCCTCAATAATT
			D-011577-02	GGATGAGGATTCAACCAGA
			D-011577-03	GGACAAGACTCGTGGCCAG
			D-011577-04	GGTATGTTCCCGATAAGAA
	Qiagen	63D4	SI00299124	TTCACTCATTCTCAGATTAAA
			SI00299180	ATCCTGCTTGACTGTAACAAA
			SI00299201	CACCTATAAAGACCACCTGAA
			SI03101588	GACCCTGAAGCTGGTCGTCAA
SLC26A1	Dharmacon	M-007488-00	D-007488-01	CCACGGAGCTGCTGGTCAT
			D-007488-02	GGGAGTACCTGGCAGGCGA
			D-007488-03	GGGACACGGCTGAGGAGGA
			D-007488-04	TGGCCAAGAGCCTGGTGAA
	Qiagen	211C7	SI00722015	CACGCTGATGACCGGGCTTTA
			SI00722022	CAGCCTCTATACGTCCTTCTT
			SI00722029	CAGCCCATCTACAGCCTCTAT
			SI00722036	AGCCAACAGCAGCACCCTCAA
SLC2A13	Dharmacon	M-007513-00	D-007513-01	GGAAGTAACTATCATCTTT
			D-007513-02	GAACAAATCAACTGTCATT
			D-007513-03	GAAGGGAGATATATTGAAT
			D-007513-04	GGAAATTGAATCACTCTTT
	Qiagen	169B9	SI00722659	GAGGAATATGATAGCATCAAA
			SI00722666	AAGGGAGATATATTGAATATA
			SI00722673	AAGCTTACCTTTGGTAGTTTA
			SI00722680	AAGGGAAATGTCACATATTAT
SLC39A2	Dharmacon	M-007570-00	D-007570-01	GAGCAGGGTTCATGCATAT
			D-007570-02	GCAGTGTTCTCCATACTAT
			D-007570-03	GGTGTTTGGTGTAGGAATG
			D-007570-04	GCTGGTACCTTCCTGTATG
	Qiagen	131C2	SI00724535	CTGGACTAAGACAAAGATATT
			SI00724542	CTCCACAGCCATGGACATTTA
			SI00724549	CAGACTAAATAGCATTCAGTA
			SI00724556	CAGCAAGTGAGAGAAATTCTT
SLC3A2	Dharmacon	M-003542-00	D-003542-01	AGAATGGTCTGGTGAAGAT
			D-003542-02	GAAGAATGGTCTGGTGAAG
			D-003542-03	TCACGGGCCTGTCCAAGGA
			D-003542-04	GAGCATCCGTGTCATTCTG
	Qiagen	207D6	SI02650865	TCGGGACATAGAGAATCTGAA
			SI02650872	CAGCCTGACATGGACCCACTA
			SI02650879	GAGGTGGAGCTGAATGAGTTA
			SI02650893	ATGGAGCTACAGCCTCCTGAA
SLC45A2	Dharmacon	M-013153-00	D-013153-01	GTACGAGTATGGTTCTATC
			D-013153-02	GATAGGTGTCGTTCTCTTT
			D-013153-03	GTGCATCAACTCCGTGTTT
			D-013153-04	GTCTTTACTTCACGGGATA
	Qiagen	45E4	SI00114114	CAGCTTTGATTGCTAACCCAA
			SI00114121	ATGGACGGCCTTCCTGTCCAA
			SI00114128	TCGCAGGGCAATGACATTAAA
			SI03104353	GAGTATGGTTCTATCGAGAAA

HGNC	Source	Pool ID	siRNA ID	Sequence
SMU1	Dharmacon	M-021129-00	D-021129-01	CAACTGAGCAGGCATATTA
			D-021129-02	GACCATAGATTTGTTTCGA
			D-021129-03	GATAGCAGTCAGATCCTTA
			D-021129-04	GACATTACATTATTAGTGC
	Qiagen	140G2	SI00727559	CAGAATGTTCAAATACCTTTA
			SI00727566	CAGGTTGTTCTGGAATTGATA
			SI00727573	AAGGATGTGATTGGTATTGCA
			SI00727580	CCAGATGGAAGTAGCAAAGAA
SMURF1	Dharmacon	M-007191-00	D-007191-01	GCACTATGATCTATATGTT
			D-007191-02	AAAGAGATCTAGTCCAGAA
			D-007191-03	GGAAGAAGGTTTGGATTAC
			D-007191-04	GGACTGCAGAGGACTGTTA
	Qiagen	16A10	SI00126497	AAGGATAACCTCGATGATGTA
			SI00126511	CAGAGATACGAAAGAGATCTA
			SI03094756	CTGCCCGAAGGCTACGAACAA
			SI03111276	TAGCGTGTGGAACCATAAGAA
SOCS7	Dharmacon	M-027197-00	D-027197-01	GGAGAAGTGTGGTTGGTAT
			D-027197-02	AAACCCAAGTTGACAAGAA
			D-027197-03	TCCGAAAGTTCTACTACTA
			D-027197-04	AAGCGCAGCTCATTTCCAA
	Qiagen	59F2	SI00729218	CCGAAAGTTCTACTACTATGA
			SI03074400	CCACACTAGAATGGAGCACTA
			SI03102687	GAGAGCCATTATGCACTCCAA
			SI03114356	TCCCGATTCAGCAATGTCAAA
SOLH	Dharmacon	M-006037-00	D-006037-01	GATGGAGTACGGCGACTTT
			D-006037-02	CCAAGTGCACGCTCAGAAA
			D-006037-03	GTGAGGGCATGACCTGCTA
			D-006037-04	GGAGACACCGTGCGTTACA
	Qiagen	13D9	SI00079765	CCGGCACAAGCCCGACCTCAA
			SI00079772	ACGGGTGTCCTCGGCCCAGAA
			SI00079779	CTCGTCCACCCTGCAGAACAA
			SI00079786	CAGGCAGGTCCTGGTGATCTT
SON	Dharmacon	M-012983-00	D-012983-01	GCTGAGCGCTCTATGATGT
			D-012983-02	GATACAGAACTACGATATA
			D-012983-03	GGTCTTTCGTGGTCAGTAA
			D-012983-04	CAATGTCAGTGGAGTATCA
	Qiagen	207F8	SI00729239	CAGAATCTTCAATTACGTTAA
			SI00729246	ATGATGTTGATTTATCTTTAA
			SI00729253	CTCAGTTTAGTTAATAAATAT
			SI00729260	AAAGATATTCATCTTGATTTA
SPIC	Dharmacon	M-016274-00	D-016274-01	GATCTTCTATTCACAGTGT
			D-016274-02	GAGCCTGTCTATAATTGGA
			D-016274-03	GTGCTGCGGACTTCTATTT
			D-016274-04	GTATTCAGTGGGTAGATAA
	Qiagen	172D3	SI00731591	TTGGGAAATTCTGCCAATGAA
			SI00731598	ATCAAGAATATCTCAGTTTAA
			SI00731605	CAGAATTGTCAATTTATTAAT
			SI00731612	AACCATCGTCCTCATGTCAAA
SPIN2A	Dharmacon	M-021182-00	D-021182-01	GCAAATACCATAATTGGCA
			D-021182-02	TAGGTAAGCATGTGGAATA
			D-021182-03	GCTCAAGCACCTATCATGA
			D-021182-04	AGGCAGACCTTCATCCCAA
	Qiagen	135F9	SI00731647	CAGGGACTGGTGGCAGCCCAA
			SI00731654	CAAATTTGTGAATACATGAAA
			SI00731661	CACTGTAGTCTTGTGCAGAAA
			SI00731668	TCACTACTAAGAGGAAACTAA
SPP2	Dharmacon	M-019720-00	D-019720-01	GCACAGAGCAAGAATAAAT
			D-019720-02	GAAGATCCCGCTACATGTG
			D-019720-03	CAGAGGGACTACTATGTGT
			D-019720-04	TACGATCCATCCTCCTTAA
	Qiagen	105E5	SI00732235	CCGGCACAGAGCAAGAATAAA
			SI00732242	CTGATCAGTTTCAATCTGTAA
			SI00732249	AACAACTTGGTCATGAATTTA
			SI00732256	CCGGGAGACTACATGCAGGAA
SPTA1	Dharmacon	M-019726-00	D-019726-01	GGACAAAGCTTGGAGACTA
			D-019726-02	GCACCGAAGTTCTGCATAA
			D-019726-03	GCAGAGGGCAAGTCATATA
			D-019726-04	GAACCACGCATTCAAGAGA
	Qiagen	105C6	SI00732655	TTGGAATGTGTTTAAATTTAA
			SI00732662	CAGGCAAATGTGGAAGATAAA
			SI00732669	TCCGATTATAGAATAAAGTAA
			SI00732676	ATGGTATAGTAGATAAATAAA

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SUPT6H	Dharmacon	M-010540-01	D-010540-01	GAACATGACTTCACAGATG
			D-010540-03	CCAGAGACCTTCTACATTG
			D-010540-04	AAAGAAGGCTCAAGACATT
			D-010540-05	CAGCATAGATTTGAAGGGA
	Qiagen	105D9	SI00736575	TAGGAGCATCTTTGAAATGTA
			SI00736582	CAGCACAATTCAGAAGATCAA
			SI00736589	CAGGACAATTTCCCTGAACTA
			SI00736596	TACAATGAGTATGATGAAGAA
SYTL2	Dharmacon	M-013555-00	D-013555-01	GAAACTAGCTCTCCAGTAT
			D-013555-02	GGGAGAAGATGGTAAACTC
			D-013555-03	CATTTAAGCGCAATAGTTT
			D-013555-04	GGGATAACAAACAGAATAA
	Qiagen	215C9	SI00738143	CCGGTGGAATCTGATCTTGAA
			SI00738150	AAGGGATTTAAATATAACAAA
			SI00738157	AAGAAACTATTTACTCTGTAA
			SI00738164	CTGGGATAACAAACAGAATAA
TAGLN	Dharmacon	M-003714-01	D-003714-02	AGAAAGCGCAGGAGCATAA
			D-003714-03	CCAGACTGTTGACCTCTTT
			D-003714-04	CTCGGCAGATCATCAGTTA
			D-003714-05	CCAAAATCGAGAAGAAGTA
	Qiagen	207D11	SI00739151	CAGCTTGGCAGTGACCAAGAA
			SI00739158	CAGACTGTTGACCTCTTTGAA
			SI00739165	CCCAACTGGTTTATGAAGAAA
			SI00739172	TCCCAACTGGTTTATGAAGAA
TLN1	Dharmacon	M-012949-00	D-012949-01	GGAAATAACAGGGACCTTA
			D-012949-02	GAAGAGATAGGTTCCCATA
			D-012949-03	GAAGATGGTTGGCGGCATT
			D-012949-04	GAGATGAGGAGTCTACTAT
	Qiagen	6C8	SI00086961	CAGCTCGAGATGGCAAGCTTA
			SI00086968	CAGGGCAATGAGAATTATGCA
			SI00086975	CCGCATTGGCATCACCAATCA
			SI00086982	TGGGAAAGCTTTGGACTACTA
TMBIM4	Dharmacon	M-020255-00	D-020255-01	CACACTCACTGATGCATAA
			D-020255-02	CCGAATGGCCTTTCTGAGA
			D-020255-03	ACATGAGAGTCCTGCCTTA
			D-020255-04	GAAGAGTACGTATTAGCTG
	Qiagen	134D9	SI00344477	CCGAATGGCCTTTCTGAGAAA
			SI00344484	TTGATTTAGGATCTCAGTTAA
			SI00344491	ACGGTTTCTGGAAGCAGTTAA
			SI00344498	CACACACTCACTGATGCATAA
TMEM61	Dharmacon	M-018940-00	D-018940-01	CCAAGTGGATCGAGGGATG
			D-018940-02	TATGAGAGCATCAGCCTTG
			D-018940-03	GGGACGCTCTGCTTCGCTT
			D-018940-04	CCTCCACCCTCCGCTATTG
	Qiagen	185G8	SI00485324	CAGCAAACGTTCGTTGTTGAA
			SI00485331	CCCAGAATTTAGTGGCTTAAA
			SI00485338	CAGGTCCTGAATCCAGAGACA
			SI00485345	CACTGTGGAGTCCTCAGAGAA
TMOD1	Dharmacon	M-019747-00	D-019747-01	TGATTAAACCCACACAATA
			D-019747-02	GCAAAGGAGTTTAAGGACC
			D-019747-03	GTAGAAGCCCTCCCATACA
			D-019747-04	ACGCAATGATGAACAACAA
	Qiagen	106C7	SI00748223	TTGAATCTGGTTATTATTTAA
			SI00748230	CCGACGAAGAACCAAATTCAA
			SI00748237	CTGGATGAAGATGAAATCCTT
			SI00748244	CAAGGTGTTGAAGACACTGAA
TMPRSS9	Dharmacon	M-019463-00	D-019463-01	ACAAATACATCCAGCCTGT
			D-019463-02	GACGACAGCTGGCCTCACA
			D-019463-03	GGTCACCGTTCCTAAGCTA
			D-019463-04	GAGCTCACAGGGAGACATA
	Qiagen	15A7	SI00163303	CACGCGCATCACCAGGCTAAA
			SI00163310	CCAGGTGGTCCAGATCGTCAA
			SI00163317	CGGGCCAACCTGCCAACTCAA
			SI00163324	ACCGTTCCTAAGCTACAAGAA
TNFRSF1A	Dharmacon	M-005197-00	D-005197-01	CAAAGGAACCTACTTGTAC
			D-005197-02	GAGCTTGAAGGAACTACTA
			D-005197-03	CACAGAGCCTAGACACTGA
			D-005197-04	TCCAAGCTCTACTCCATTG
	Qiagen	54E3	SI00021462	ACCGGCATTATTGGAGTGAAA
			SI00021476	ACGGTGGAAGTCCAAGCTCTA
			SI03044349	AGGAACCTACTTGTACAATGA
			SI03097192	CTGGAGCTGTTGGTGGGAATA

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TNPO2	Dharmacon	M-020491-01	D-020491-01	GGGCAGAGATGCAGCCTTA
			D-020491-03	GCAGTTCTCTGAGCAATTC
			D-020491-04	AAACAGGAGTGTCTCAACA
			D-020491-05	GCGCTGATGGACAATATTG
	Qiagen	131G2	SI02652027	CCCGAGCATCTCTCTCTGTAA
			SI02652034	ATCGTGCAGGATAAACTCAAA
			SI02652041	CAGGAGTGTCTCAACAACATT
			SI02652048	AAAGATCAGTTTCTTGTGAAA
TPX2	Dharmacon	M-010571-00	D-010571-01	TGACAACACTTACTACAAA
			D-010571-02	GGACGAACCGGTAGTGATA
			D-010571-03	AGACAAAGAACGTCAGTTA
			D-010571-04	GAACTTTACATCTGAACTA
	Qiagen	39B5	SI00097195	TAGGCCTGATAGACTGATTAA
			SI02665075	AAGGATGATATTAACCTGTTA
			SI02665082	AAGGCTAATAATGAGATGTAA
			SI03063368	CAGAATTCGAATGCCCACCAA
TRAIP	Dharmacon	M-006924-00	D-006924-01	AGAATGAACTGGACAATGT
			D-006924-02	GTTGGTGCCTTCCCTATTT
			D-006924-03	ACAGAGTGCTGACAAGGAA
			D-006924-04	GACAGTCTACTCTGAATTG
	Qiagen	40G7	SI00082236	CCGGCTCAGGAGCAAGATGAA
			SI00082243	AAGGAAATCATGAGCCTGAAA
			SI02225608	CCGTGATGATATTGATCTCAA
			SI02225615	CGGGACCAGCCTGAGGTGTAA
TRIM17	Dharmacon	M-006981-00	D-006981-01	GCTAAGAGGCTTTCTAGAG
			D-006981-02	GGAAGAACAACGTGAGTGT
			D-006981-03	GGTCCCACCTGCACACCTA
			D-006981-04	GAGCGGAGAGAACGCATTG
	Qiagen	1F10	SI00113302	CCCGGACAGATTGAAGTGCTA
			SI00113309	CAGGGACAACGTGAGCCGGAA
			SI00113316	CACAGTGACCATGTGGGTGAA
			SI00113323	ACGCATTGTGCTGGAGTTTGA
TRIM9	Dharmacon	M-012974-00	D-012974-01	CCACAGGTCTCATGGAGTA
			D-012974-02	GCTTGGAGGTGATTAAGGA
			D-012974-03	CAACGGCGTCCGCGTGTTT
			D-012974-04	AAACAGGAGTCAGCCCGTA
	Qiagen	21H6	SI00147546	CCCAAGAATCGCGTACTGGAA
			SI03067197	CAGCGCTACGTTGTCCTGGAA
			SI03070634	CAGGCGCTGAACGGACTGTCA
			SI03081162	CCGCGTCAACAAGGAGCATGA
TRPM8	Dharmacon	M-006517-00	D-006517-01	GGAATCAGCTAGAGAAGTA
			D-006517-02	CGAATGTTCTCACCTATTA
			D-006517-03	GAAGAAACCTGTCGACAAG
			D-006517-04	GCAATGGTATGGAGAGATT
	Qiagen	31D3	SI00135744	TCGAATGTTCTCACCTATTAA
			SI00135758	CAGAATGTTATCATACTACAT
			SI00135765	CCGGGACGAGATGGACATAGA
			SI03023118	TTCGGTCATCTACGAGCCCTA
TSPAN9	Dharmacon	M-012293-00	D-012293-01	GAGATGCGATGCTGTGGTG
			D-012293-02	TAAGAAGTACGACGCATGA
			D-012293-03	GCAGAGCTGATCTTACTCA
			D-012293-04	AAGAACGCCTGGAACATCA
	Qiagen	119A6	SI00657587	TTCAGAGAGAACAGAATTTAA
			SI00657594	CTGGTTTGACTTGGAACTAGA
			SI00657601	CTGCTAGAAACTGTCAGACAA
			SI00657608	CTGCATATGCGTATTTGCCAA
TUBE1	Dharmacon	M-006844-00	D-006844-01	CGAAACAGCTCATCACTGA
			D-006844-02	GGACTTGGCACATTTCTTT
			D-006844-03	CAAAGAGTCTGGTTACTTC
			D-006844-04	CGAGCAGTCTTGATTGATA
	Qiagen	42D10	SI00114884	CACGAGCAGTCTTGATTGATA
			SI02777558	TAGTGAAATCTTAGTACCTTA
			SI02777565	CAAGATTTGAAGGGTCCCTTA
			SI03060211	CACGCCGCGGTCAACCAGAAA
UBE2D2	Dharmacon	M-010383-01	D-010383-02	TCAGAAGTATGCGATGTAA
			D-010383-03	CTATCAGGGTGGAGTATTT
			D-010383-04	GTCCATCTGTTCTCTGTTG
			D-010383-05	TGAATGATCTGGCACGGGA
	Qiagen	208H3	SI00754383	TAGCTTGAAACTTGTAAACAA
			SI00754390	ATGATTAATCTGTGTAATAAA
			SI00754397	TTGGATAACCTCTACAAATAA
			SI00754404	TTCCAGGAACTTGATTGTTAA

HGNC	Source	Pool ID	siRNA ID	Sequence
UBOX5	Dharmacon	M-006949-00	D-006949-01	GAACGTCACTGGCCTGGAA
			D-006949-02	GACAGTAACTTTGGTGTAA
			D-006949-03	GTACACATCTGCCTCATCT
			D-006949-04	GAGCAGAAGCTGTCACAAA
	Qiagen	11H11	SI00108899	CAGACAGTAACTTTGGTGTAA
			SI00108920	TCCCTACAACTTGGTACTCTA
			SI03067358	CAGCGGCCGGTTGCTAGCCAA
			SI03077361	CCCGAATGTGCCTCCTGCAAA
USP1	Dharmacon	M-006061-01	D-006061-02	GCATAGAGATGGACAGTAT
			D-006061-03	GAAATACACAGCCAAGTAA
			D-006061-05	CATAGTGGCATTACAATTA
			D-006061-06	TAACGACAGCTATGGATTA
	Qiagen	107E3	SI00758107	TTGGGCCATGACCAGATATAA
			SI00758114	CTCGCGCGCACGAATGGTTAA
			SI00758121	TTCAAAGGACGCCACGTTCAA
			SI00758128	CTGGCGCGGGCGGAGGCTAAA
USP18	Dharmacon	M-004236-02	D-004236-03	GGAATTCACAGACGAGAAA
			D-004236-04	GGAAGAAGACAGCAACATG
			D-004236-05	GGGAAGACATCCAGTGTAC
			D-004236-06	CCAGGGAGTTATCAAGCAA
	Qiagen	16D5	SI00118034	TAAGCGCTTCCTGGAAGTGAA
			SI00118041	AAGATGGAGTGCTAATGGAAA
			SI03022915	TTCGCTTTCCATTCAGTGGAA
			SI03097570	CTGGATCTACGGAGTCTTCTA
VAX1	Dharmacon	M-031769-00	D-031769-01	GAAGAAAGAGCCAGCAAAT
			D-031769-02	CGAAGAACGCGCACAAGGA
			D-031769-03	GTTCGGGAAACCAGACAAA
			D-031769-04	ACGATTCAAACGCGGGATA
	Qiagen	120G4	SI00759451	ACCCTTTATAGTTTACAAATA
			SI00759458	TCGGGAAATCTTTACATTTCA
			SI00759465	CACTGCGTAATTCTTAGTTTA
			SI00759472	TCCCATCTGATGAATCAGAAA
WBSCR22	Dharmacon	M-009383-00	D-009383-01	GAAATACGTTCGCAACTCA
			D-009383-02	GAGAGGTTCCCATTAAGGA
			D-009383-03	GCCCTGCCATGCTGGATGA
			D-009383-04	CATTGGAGCTTCTTTATCT
	Qiagen	2A6	SI00118671	CTGAGTGGAAGTTATCTGTCA
			SI02757993	CAGGGAGTCTGTGTTCACCAA
			SI02758000	CCCTAACAGTGCCAAAGCAAA
			SI03088449	CTCACGGATGATTGATATCCA
WEE1	Dharmacon	M-005050-00	D-005050-01	GCAGAACAATTACGAATAG
			D-005050-02	TAGAACATCTCGACTTATT
			D-005050-03	GATCATATGCTTATACAGA
			D-005050-04	AATCGGCTCTGGAGAATTT
	Qiagen	85B5	SI00051758	CAGGGTAGATTACCTCGGATA
			SI02631076	TTGACTAATAATACTGGCTAA
			SI02758791	CAAGACCTGCTAAGAGAATTA
			SI02758798	ACAATTACGAATAGAATTGAA
WHSC1L1	Dharmacon	M-012875-00	D-012875-01	CAAGACAGGCTTATAATTT
			D-012875-02	GAACGTGCTCAGTGGGATA
			D-012875-03	GTCCACTGGTGTTAAGTTT
			D-012875-04	GCTTGAGGTTCATACTAAA
	Qiagen	51H11	SI03040912	ACGACCAAGATCTGTGCTGAA
			SI03047352	ATCCACTGAGGTTGTGCCAAA
			SI03076773	CCCAGCTTGAGGTTCATACTA
			SI03109505	TACGAGAGTATAAAGGTCATA
ZNF331	Dharmacon	M-021386-00	D-021386-01	GTAAATCCCTTGGCCGTAA
			D-021386-02	CGACGTAGCCATAGACTTT
			D-021386-03	GGAGGTATGTCAATCAGAT
			D-021386-04	GGCCTTTACTCGAGTCAAT
	Qiagen	141H3	SI00772443	CACCAGGATGATTAAATTTAA
			SI00772450	CACCAAATGGCCAATAAGTAA
			SI00772457	CTGGAGGACAAGAGGAAGTAA
			SI00772464	CACGGCCATCAGCTTACACAA
ZNF585A	Dharmacon	M-016843-00	D-016843-01	CGACAGAAGTCAGAGTTGA
			D-016843-02	GGCAAAGCGTTCACACAAA
			D-016843-03	GGACCATAATCAACATAGA
			D-016843-04	AGAAATCAGTGTTCAGTGT
	Qiagen	222C3	SI00777147	AAGGATGTAACTTTCATGTAA
			SI00777154	AAGAAAGATCGTATTAAGTTA
			SI00777161	CAGATTAATAACTTATATGAA
			SI00777168	ATCGTATTAAGTTAACGATAA

HGNC	Source	Pool ID	siRNA ID	Sequence
ZNF595	Dharmacon	M-018879-00	D-018879-01	CCACAACACTGAACGAACA
			D-018879-02	CCACATCACTTAGTAAACA
			D-018879-03	TACCAGTGCTTGTCAACTA
			D-018879-04	CCTCAACTCTTATATTACA
	Qiagen	181D5	SI00777371	AAGTATATGAGTATAATTATA
			SI00777378	CACACATTTCTAAGTCATGAA
			SI00777385	CAGTCCAGTTATACACTTTAA
			SI00777392	CAGGCATATGACATGTAATTA

Table XII: siRNA sequences. HGNC is the target HGNC gene name. Source is the siRNA source. Pool ID is the siRNA pool ID. siRNA ID is the single siRNA ID. Sequence is the siRNA sequence.