

sgRNA-PSM: Predict sgRNAs On-Target Activity Based on Position-Specific Mismatch

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As a key technique for the CRISPR-Cas9 system, identification of single-guide RNAs (sgRNAs) on-target activity is critical for both theoretical research (investigation of RNA functions) and real-world applications (genome editing and synthetic biology). Because of its importance, several computational predictors have been proposed to predict sgRNAs on-target activity. All of these methods have clearly contributed to the developments of this very important field. However, they are suffering from certain limitations. We proposed two new methods called “sgRNA-PSM” and “sgRNA-ExPSM” for sgRNAs on-target activity prediction via capturing the long-range sequence information and evolutionary information using a new way to reduce the dimension of the feature vector to avoid the risk of overfitting. Rigorous leave-one-gene-out cross-validation on a benchmark dataset with 11 human genes and 6 mouse genes, as well as an independent dataset, indicated that the two new methods outperformed other competing methods. To make it easier for users to use the proposed sgRNA-PSM predictor, we have established a corresponding web server, which is available at <http://bliulab.net/sgRNA-PSM/>.

INTRODUCTION

Three main genome editing tools, including zinc-finger nucleases (ZFNs),¹ transcription activator-like effector nucleases (TALENs),² and CRISPR-Cas9 RNA-guided technologies,^{3,4} can be used to recognize and cleave specific DNA sequences.⁵ Compared with ZFNs and TALENs, CRISPR-Cas9 has been widely applied in various cell types and organisms in recent years. In the type II CRISPR-Cas9 system, single-guide RNA (sgRNA) directs Cas9 protein to the target site to cleave the DNA target sequences, and sgRNA should be designed to have around a 20-nt sequence to be complementary to the guide sequence in the DNA target sequences.^{6,7} Rational design of sgRNA is a crucial part for CRISPR-Cas9. Therefore, the prediction of sgRNAs on-target activity is very important for CRISPR-Cas9.

Researchers have proposed several computational methods for sgRNAs on-target activity prediction. Most of them treat the prediction problem of sgRNA as a binary classification task or a regression task, and the computational predictors were constructed based on machine learning algorithms. The differences between these approaches are feature extraction methods and machine learning

techniques, such as gradient boosting regression (GBR),⁸ support vector machines (SVMs),^{9–18} ensemble classifiers^{19–24}, and deep learning,^{25–32} among others. As shown in the aforementioned studies,^{33,34} discriminative features are critical for constructing the computational predictors. Accordingly, some features have been proposed to capture the characteristics of sgRNAs, for example, because the position of a nucleotide in sgRNA will affect its activity, and thus the position-specific (PS)³⁵ feature was proposed to incorporate these sequence patterns, which has been used in ge-CRISPR,³⁶ Azimuth,³⁷ and CRISPRpred.³⁸ Kaur et al.³⁶ proposed an integrated pipeline called ge-CRISPR to predict and analyze the genome editing efficiency of sgRNAs. Azimuth³⁷ employed GBR to train the model, achieving state-of-the-art performance. CRISPRpred³⁸ is another efficient predictor, combining the discriminative features selected by random forest (RF)³⁹ and the SVM regression.

All of the aforementioned predictors have obtained encouraging results and played a role in the development of computational predictors for sgRNAs on-target activity prediction, but they are also suffering from some problems or limitations. Further work is required for the following reasons: (1) these predictors are only able to consider the short-range sequence information of the DNA sequences, otherwise they will cause “high-dimension disaster”;^{40,41} and (2) these predictors failed to incorporate the evolutionary information, ignoring information between non-consecutive nucleotides.

In order to solve these aforementioned problems, we proposed a novel feature, PS mismatch (PSM), sharing the advantages of both PS³⁵ and mismatch features.⁴¹ RNA sequence evolution involves single nucleotides, insertions and deletions of several nucleotides, and other factors. With the long-term accumulation of these changes in evolution, although the similarities between the initial and the final RNA sequences are gradually reduced, these RNA sequences still have many features in common. PSM is such a method for extracting

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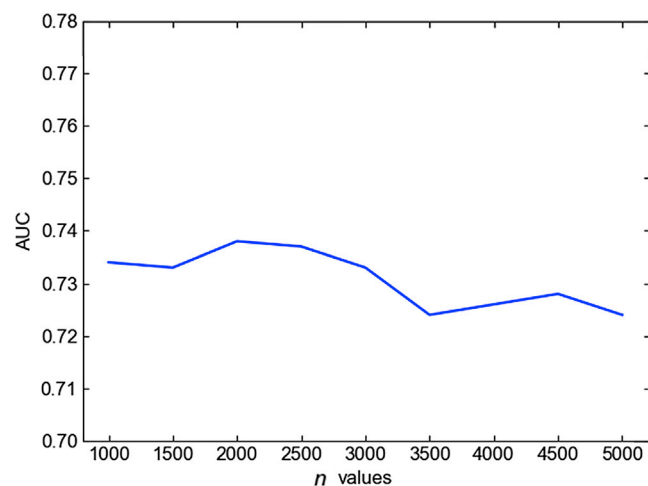


Figure 1. Graph Showing AUC Scores of the sgRNA-PSM Predictors with Different n Values, where n Denotes the Number of Selected Features

the evolutionary information from RNA sequences by allowing mismatches occurring in k -mers from specific positions.⁴¹ PSM has been applied to predict sgRNAs on-target activity, and two predictors were established called “sgRNA-PSM” and “sgRNA-ExPSM” (sgRNA-extended PSM). Finally, a corresponding web server has been constructed (<http://bliulab.net/sgRNA-PSM/>).

RESULTS AND DISCUSSION

Parameter Optimization

According to Equations 9 and 10, there are two parameters in PSM, k and m , and three parameters in the XGBoost algorithm, C , R , and F . These parameters were optimized according to AUC (area under the curve) by using leave-one-gene-out cross-validation on the benchmark dataset S (cf. Equation 3). In this study, these parameters were optimized in the ranges listed in the following:

$$\begin{cases} 1 \leq k \leq 6, & \text{with step } \Delta k = 1 \\ 0 < m \leq k - 1, & \text{with step } \Delta m = 1 \\ 3 \leq c \leq 10, & \text{with step } \Delta c = 1 \\ 0.05 \leq R \leq 0.1, & \text{with step } \Delta R = 0.05 \\ 100 \leq F \leq 1000, & \text{with step } \Delta F = 100 \end{cases} \quad (\text{Equation 1})$$

The final optimal values of the five parameters (cf. Equation 1) were optimized based on the AUC on the benchmark dataset S (cf. Equation 3), as given by

$$\begin{cases} k = 5, m = 2, c = 3, R = 0.1, F = 800 & \text{for sgRNA - PSM} \\ k = 5, m = 2, c = 3, R = 0.1, F = 800 & \text{for sgRNA - ExPSM} \end{cases} \quad (\text{Equation 2})$$

Feature Selection and Analysis

In order to remove the redundant features and reduce the dimension of the resulting feature vectors, here we used SelectKBest in scikit-learn⁴² to select the top number of features with the highest scores

based on the scoring function $f_{\text{regression}}$, which can avoid the over-fitting risk with low computational cost.⁴³ We investigated the influence of the value n (number of selected features) in SelectKBest on the predictive performance of sgRNA-PSM, and the results are shown in Figure 1, from which we can see that the values of n have little impact on the performance, and sgRNA-PSM can achieve the best performance when n is equal to 2,000.

The importance of each feature can be analyzed based on F_{score} . To explore the reason why the proposed sgRNA-PSM predictor works so well, we analyzed the contribution of each feature. Table 1 lists the 10 most important features, from which we can see that (1) the top 9 most important features belong to the features generated in the sequence positions from 23 to 30. In the CRISPR-Cas9 system, the DNA target sequences are composed of two parts:⁴⁴ one is the guide sequence, and the other is the protospacer adjacent motif (PAM). The guide sequence is complementary to around a 20-bp sequence in sgRNA, and PAM is the downstream short sequence of the guide sequence⁶ and is recognized by the Cas9 protein.⁴⁵ In the benchmark dataset S (cf. Equation 3), the guide sequence is in the sequence positions from 5 to 24, and PAM is the short sequence in the sequence positions from 25 to 27.³⁷ Therefore, the top 9 most important features all cover PAM, indicating that the proposed PSM is able to incorporate this important sequence pattern. (2) PAM is composed of any nucleotide in sequence position 25 followed by GG in positions 26 and 27.^{6,37} 7 of the 10 most important features capture this sequence pattern.

Comparison with Other Methods

The results obtained by sgRNA-PSM and sgRNA-ExPSM on the benchmark dataset S are listed in Table 2, from which we can see that the AUC achieved by sgRNA-PSM was 73.8%. The corresponding AUC achieved by sgRNA-ExPSM was even better, which was 74.4%. This is reasonable because the acid cut position and percent peptide features referred to in Equation 11 are complementary with the PSM features in Equation 9. The PSM feature vector reflects long-range sequence information, while the amino acid cut position and percent peptide are guide-positional features corresponding to the start distance of the protein coding region of the gene where the cleavage site of the sgRNA is positioned.³⁷

Then, we made a comparison of the sgRNA-PSM and sgRNA-ExPSM with ge-CRISPR,³⁶ Azimth,³⁷ and CRISPRpred.³⁸ All of these predictors were examined by the leave-one-gene-out cross-validation on the benchmark dataset S (cf. Equation 3). For facilitating comparison, the corresponding results obtained by the ge-CRISPR predictor, the Azimth predictor, and the CRISPRpred predictor are also given in Table 2 and Figure 2. Here, Figure 2 includes the corresponding receiver operating characteristic (ROC) curves showing the performance of the five predictors. A diagonal from the point (0,0) to (1,1) means a random guess. The better performance of the predictor corresponds to a larger AUC.

The following conclusions can be drawn from Table 2 and Figure 2: (1) the AUC score achieved by the proposed sgRNA-PSM predictor is higher than that of ge-CRISPR, and even higher than those of

Table 1. The 10 Most Important Features in the sgRNA-PSM Predictor

No.	PSM Feature ^a	Sequence Position ^b	F_score ^c
1	*G*GG	23–27	185.6
2	G*GG*	24–28	185.6
3	C*G*G	24–28	136.2
4	C**GG	24–28	136.2
5	*C*GG	23–27	129.0
6	C*GG*	24–28	129.0
7	**GGG	24–28	128.0
8	*GGG*	25–29	128.0
9	GGG**	26–30	128.0
10	**TTC	20–24	113.0

^aParameters were $k = 5$, $m = 2$.

^bThe sequence position of mismatches.

^cCalculated by F regression.

Azimuth and CRISPRpred based on the wet experiment features, such as amino acid cut position and percent peptide. Please note that these two features are not sequence-based features, and they are often unavailable. (2) The sgRNA-ExPSM predictor outperforms the sgRNA-PSM predictor by incorporating the amino acid cut position feature and percent peptide feature.

In addition, the sgRNA-PSM predictor was further compared with Azimuth³⁷ and DeepCRISPR (pt+aug CNN)⁴⁶ on the on-target dataset.^{46,47} In order to make a fair comparison, the sgRNA-PSM predictor was trained on the training set of on-target dataset reported in Chuai et al.⁴⁶ and tested on the independent test dataset⁴⁶ for the hct116, hela, and hl60 cell types. The hek293t dataset reported in Doench et al.³⁷ is a subset of our benchmark dataset S (cf. Equation 3). Therefore, our method was not tested on the hek293t dataset again. For sgRNA-PSM, SelectKBest with the scoring function chi2 in scikit-learn was used to select 1,100 dimensions of the PSM features and fed into XGBoost for classification. The predictive results of sgRNA-PSM, DeepCRISPR (pt+aug CNN), and Azimuth are shown in Table 3. As shown in this table, our method outperformed Azimuth and DeepCRISPR (pt+aug CNN) on the hct116 and hela cell types, and it is highly comparable to DeepCRISPR (pt+aug CNN) on the hl60 cell type.

To further explore the reasons why our method cannot perform well on the hl60 cell type, we retrained the sgRNA-PSM classifier with each of the three datasets (hct116, hela, and hl60). For each dataset, 20% of the samples were used as the test dataset, which were stratified by labels following Chuai et al.,⁴⁶ and the remaining 80% of the samples were used as the training dataset. The results are also listed in Table 3, from which we can see that the sgRNA-PSM trained with the hl60 dataset outperformed the corresponding classifier trained with the training data consisting of all four cell types, and it even outperformed Azimuth. The results are not surprising because the four different cell types have different data distributions. Noise informa-

Table 2. List of AUC Scores Obtained by Various Methods via the Leave-One-Gene-Out Cross-Validation on the Same Benchmark Dataset S (cf. Equation 3)

Methods	AUC (%) ^a
Azimuth ^b	71.9
ge-CRISPR ^c	71.7
CRISPRpred ^d	71.6
sgRNA-PSM ^e	73.8
sgRNA-ExPSM ^f	74.4

^aAUC means the area under the ROC curve;^{56,57} the better predictor corresponds to larger AUC values.

^bResults obtained by in-house implementation from Doench et al.³⁷

^cResults obtained by in-house implementation from Kaur et al.³⁶

^dResults obtained by in-house implementation from Rahman and Rahman.³⁸

^eFor the proposed predictor in this article, see Equations 9 and 10 with $k = 5$, $m = 2$, $\zeta = 3$, $R = 0.1$, $F = 800$.

^fFor the proposed predictor in this article, see Equations 10 and 11 with $k = 5$, $m = 2$, $\zeta = 3$, $R = 0.1$, $F = 800$.

tion was introduced when combining all four cell types to train a computational predictor. Therefore, the overall performance of sgRNA-PSM is better than that of all of the other competing methods.

Web Server and User Guide

Providing a user-friendly and freely accessible web server for a new predictor can obviously improve its impact.⁴⁸ To make it easier for users to use the proposed predictor, we established the corresponding sgRNA-PSM web server. Because the sgRNA-ExPSM predictor requires two features obtained from wet experiments, which are often unavailable, its corresponding web server is not able to be constructed. The web server has the following functions: (1) it allows users to input sgRNA sequences in reverse-complementary order, and (2) it allows users to input longer sequences (30–1,000 bp). The web server will detect all of the possible sgRNAs and predict their on-target activities. The steps for using the sgRNA-PSM web server are as follows:

Step 1. Click on the website address <http://bliulab.net/sgRNA-PSM/> to open the sgRNA-PSM web server, at which point the homepage of the website will appear as shown in Figure 3. The detailed introduction to the web server can be obtained by clicking on the “Read Me” button.

Step 2. Click on the “Browse” button to upload the input file or type your query DNA sequences in FASTA format.

Step 3. Click on the “Submit” button to get the final predictive results. When inputting the four DNA sequences in the “Example” window, you will see that the first and second are predicted as high on-target activity sgRNAs, while the third is the sequence in reverse-complementary order, which is predicted as low on-target activity sgRNA, and the fourth has four low on-target activity sgRNAs and one high on-target activity sgRNA. These results are consistent with the experimental results. In order to help the users to solve the problems when using the web server, the

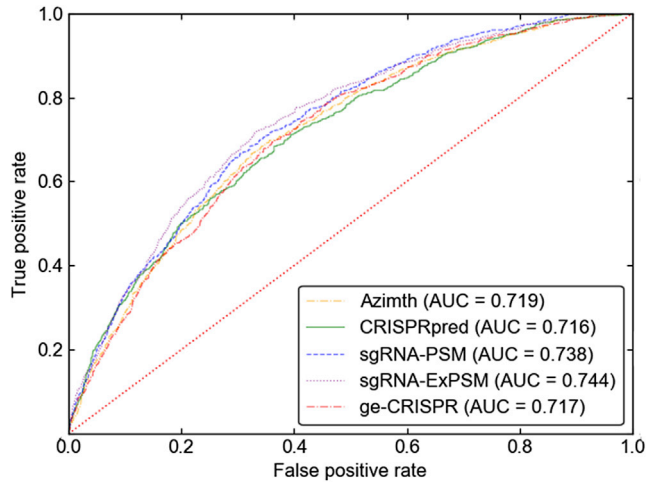


Figure 2. Graph Showing the Predictive Quality of the Aforementioned Predictors via the ROC Curves

The corresponding AUC scores are 0.717, 0.716, 0.719, 0.738, and 0.744 for ge-CRISPR, CRISPRpred, Azimuth, sgRNA-PSM, and sgRNA-ExPSM predictors via the leave-one-gene-out cross-validation on the same benchmark dataset S , respectively.

Frequently Questioned Answers (FQA) are provided by clicking on the FQA button.

MATERIALS AND METHODS

Benchmark Datasets

In this study, a widely used benchmark dataset³⁷ constructed by the FC dataset³⁵ and the RES dataset³⁷ was employed to evaluate the performance of different methods. The benchmark dataset consists of 5,310 sequences from 11 human genes (CD33, MED12, NF2, CD13, TADA2B, CUL3, TADA1, HPRT, NF1, CD15, CCDC101) and 6 mouse genes (Cd45, Cd43, Cd28, H2-K, Cd5, Thy1). There are 1,059 high on-target activity sgRNAs and 4,251 low on-target activity sgRNAs. The benchmark dataset S is as follows:

$$S = S_1 \cup S_2 \cup S_3 \cup \dots \cup S_{16} \cup S_{17} = \bigcup_{i=1}^{17} S_i, \quad (\text{Equation 3})$$

where

$$S_i = S_i^+ \cup S_i^- (i = 1, 2, \dots, 17) \quad (\text{Equation 4})$$

with

$$\frac{|S_1^+|}{|S_1^-|} \approx \frac{|S_2^+|}{|S_2^-|} \approx \frac{|S_3^+|}{|S_3^-|} \approx \dots \approx \frac{|S_{16}^+|}{|S_{16}^-|} \approx \frac{|S_{17}^+|}{|S_{17}^-|} \approx \frac{1}{4}, \quad (\text{Equation 5})$$

where \cup represents the union symbol between two sets, S_i denotes the subset whose sgRNAs are from the i th targeting gene, the positive subset S_i^+ contains high on-target activity sgRNAs, the negative subset S_i^- contains the low on-target activity sgRNAs, $|S_i^+|$ represents the number of sgRNAs in S_i^+ , $|S_i^-|$ represents the number of

Table 3. List of the AUC Scores Obtained by Various Methods on the On-Target Dataset Reported in Chuai et al.⁴⁶

Cell Type ^a	Methods	AUC (%)
<i>hct116</i>	Azimuth ^b	74.1
	DeepCRISPR (pt+aug CNN) ^c	87.4
	sgRNA-PSM ^d	91.7
	Retrained sgRNA-PSM ^e	74.0
<i>Hela</i>	Azimuth ^b	67.5
	DeepCRISPR (pt+aug CNN) ^c	78.2
	sgRNA-PSM ^d	82.8
<i>hl60</i>	Retrained sgRNA-PSM ^e	72.1
	Azimuth ^b	79.2
	DeepCRISPR (pt+aug CNN) ^c	73.9
	sgRNA-PSM ^d	77.6
	Retrained sgRNA-PSM ^e	83.7

^aThe cell type of the independent test dataset.

^bResults reported in Chuai et al.⁴⁶

^cResults reported in Chuai et al.⁴⁶

^dThe sgRNA-PSM predictor trained with the dataset reported in Chuai et al.;⁴⁶ see Equations 9 and 10 with $k = 4$, $m = 2$, $\zeta = 9$, $R = 0.05$, $F = 2,300$.

^eThe sgRNA-PSM predictor trained with each of the three datasets (*hct116*, *hela*, and *hl60*).

sgRNAs in S_i^- , and $|S_i^+|/|S_i^-|$ denotes the number of sgRNAs in $|S_i^+|$ and $|S_i^-|$ in a ratio of about 1:4. The corresponding detailed sequences can be found in [Data S1](#).

The most updated on-target dataset established in Chuai et al.⁴⁶ was employed to further evaluate the performance of the proposed method. This on-target dataset was constructed based on *hct116*,⁴⁹ *hek293t*,³⁷ *hela*,⁴⁹ and *hl60*.⁵⁰ Those datasets were also employed by Haeussler et al.⁴⁷

PSM

Feature extraction is very important for constructing a computational predictor.⁵¹ Inspired by the PS³⁵ and mismatch features,⁴¹ here a novel feature extraction method, PSM, was proposed to capture the long-range sequence information and evolutionary information. Furthermore, PSM is able to efficiently reduce the dimension of the feature vectors. The detailed procedures of generating PSM are described as follows.

A DNA sample D can be represented as follows:

$$D = R_1 R_2 R_3 \dots R_i \dots R_L \quad (i = 1, 2, 3, \dots, L), \quad (\text{Equation 6})$$

where

$$R_i \in \{A(\text{adenine}), C(\text{cytosine}), G(\text{guanine}), T(\text{thymine})\}, \quad (i = 1, 2, 3, \dots, L) \quad (\text{Equation 7})$$

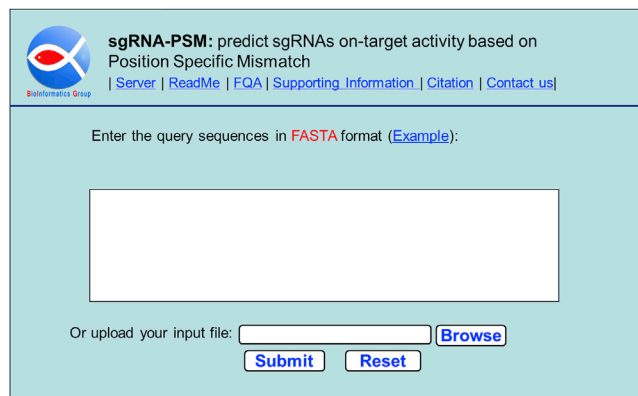


Figure 3. Graphic of the Homepage of the Web Server <http://bliulab.net/sgRNA-PSM/>

represents the i th nucleobase in the sequence, the symbol \in denotes “member of” in the set, and L represents the length of \mathbf{D} .

The PS feature is an important and useful feature extraction method widely used in previous studies.^{35–38} Because the position of nucleotide in a sgRNA affects its activity, the PS feature incorporates the local sequence position information by representing the k -mers^{41,52} along a DNA sample \mathbf{D} (cf. Equation 6) by “one-hot” encoding.⁵³ By using the PS feature, \mathbf{D} can be represented as follows:^{35–38}

$$\mathbf{D} = \left[f_1^{\text{PS}} \cdots f_{4^k}^{\text{PS}} f_{4^k+1}^{\text{PS}} \cdots f_{2 \times 4^k}^{\text{PS}} f_{2 \times 4^k+1}^{\text{PS}} \cdots f_{(L-k) \times 4^k}^{\text{PS}} f_{(L-k) \times 4^k+1}^{\text{PS}} \cdots f_{(L-k+1) \times 4^k}^{\text{PS}} \right]^{\text{T}}, \quad (\text{Equation 8})$$

where T represents the transpose symbol, $f_{(i-1) \times 4^k + j}^{\text{PS}}$ denotes the j th feature in the one-hot encoding at the i th position in \mathbf{D} , whose value is 0 or 1, and k is the number of adjacent nucleotides in a k -mer.

From Equation 8, we can see that the dimension of the PS vector will increase rapidly with the incensement of k values. For example, when k is equal to 6, the dimension of the PS feature vector will be $4^6 \times (30 - 6 + 1) = 1.024 \times 10^5$, which will cause high-dimension disaster.^{40,41,54} Therefore, Equation 8 is useful only when k is small, and it ignores the information of non-consecutive nucleotides. As a result, it can only incorporate the short-range and consecutive nucleotide information without considering the long-range and non-consecutive nucleotide information.

The mismatch feature considers the evolutionary process and allows mismatches occurring in k -mers. Therefore, the dimension of the corresponding feature vectors can be obviously decreased compared with those of k -mers. In this study, we combined the mismatch with the PS feature and proposed a novel feature, i.e., PSM, which is defined as follows:

$$\mathbf{D} = \left[f_1^{\text{PSM}} \cdots f_{\alpha}^{\text{PSM}} f_{\alpha+1}^{\text{PSM}} \cdots f_{2 \times \alpha}^{\text{PSM}} f_{2 \times \alpha+1}^{\text{PSM}} \cdots f_{(L-k) \times \alpha}^{\text{PSM}} f_{(L-k) \times \alpha+1}^{\text{PSM}} \cdots f_{(L-k+1) \times \alpha}^{\text{PSM}} \right]^{\text{T}}, \quad (\text{Equation 9})$$

where $f_{(i-1) \times \alpha + j}^{\text{PSM}}$ represents the j th feature in one-hot encoding at the i th position in \mathbf{D} , whose value is 0 or 1, and α denotes the number of mismatch features considering the one-hot encoding, which can be defined as follows:

$$\alpha = 4^{k-m} \times C_k^{k-m} = 4^{k-m} \times \frac{k!}{(k-m)!m!}, \quad (\text{Equation 10})$$

where m is the number of mismatches in k -mers.

As shown in Equations 9 and 10, the first $4^{k-m} \times C_k^{k-m}$ components reflect the one-hot-encoded feature vector corresponding to the first sequence position, whereas the components from $4^{k-m} \times C_k^{k-m} + 1$ to $2 \times 4^{k-m} \times C_k^{k-m}$ reflect the one-hot-encoded feature vector corresponding to the second sequence position, and so forth. A feature vector formed with $(L - k + 1) \times 4^{k-m} \times [k! / (k - m)!m!]$ components is called the PSM vector for \mathbf{D} as defined in Equation 9. A schematic diagram illustrating how to generate the PSM vector for \mathbf{D} is shown in Figure 4. Compared to the PS vector defined in Equation 8, the dimension of the PSM vector will be significantly reduced. For example, when $k = 6$, the PS feature vector’s dimension (cf. Equation 8) is 1.024×10^5 , while the PSM feature vector’s dimension is $(L - k + 1) \times 4^{k-m} \times [k! / (k - m)!m!]$ as defined in Equations 9 and 10. Now, when we assume $m = 5$, the dimension will be $(30 - 6 + 1) \times 4^{6-5} \times [6! / (6 - 5)!5!] = 600$. The size of the latter is around 1/170th that of the former. Namely, PSM can obviously reduce the dimension of the feature vector compared with PS. It is especially true for larger k values (see Table 4).

Therefore, the PSM vector (cf. Equation 9) should be used to represent the DNA samples, because PSM can overcome the aforementioned limitations for large values of k , while avoiding the high-dimension disaster problem.

Finally, we can augment the PSM vector (cf. Equation 9) to

$$\tilde{\mathbf{D}} = \left[f_1^{\text{PSM}} \cdots f_{\alpha}^{\text{PSM}} f_{\alpha+1}^{\text{PSM}} \cdots f_{2 \times \alpha}^{\text{PSM}} f_{2 \times \alpha+1}^{\text{PSM}} \cdots f_{(L-k) \times \alpha}^{\text{PSM}} f_{(L-k) \times \alpha+1}^{\text{PSM}} \cdots f_{(L-k+1) \times \alpha}^{\text{PSM}} a b \right]^{\text{T}}, \quad (\text{Equation 11})$$

where $\tilde{\mathbf{D}}$ is the augmented PSM, a is the amino acid cut position, and b is the percent peptide given in Doench et al.³⁷ Both of these two features were obtained by wet experiments, which are often unavailable. The feature vector formed with $(L - k + 1) \times 4^{k-m} \times [k! / (k - m)!m!] + 2$ components is the ExPSM vector for \mathbf{D} .

XGBoost Algorithm

The XGBoost algorithm⁵⁵ is a technique for classification and regression tasks, which is based on tree boosting.⁸ The most important advantage

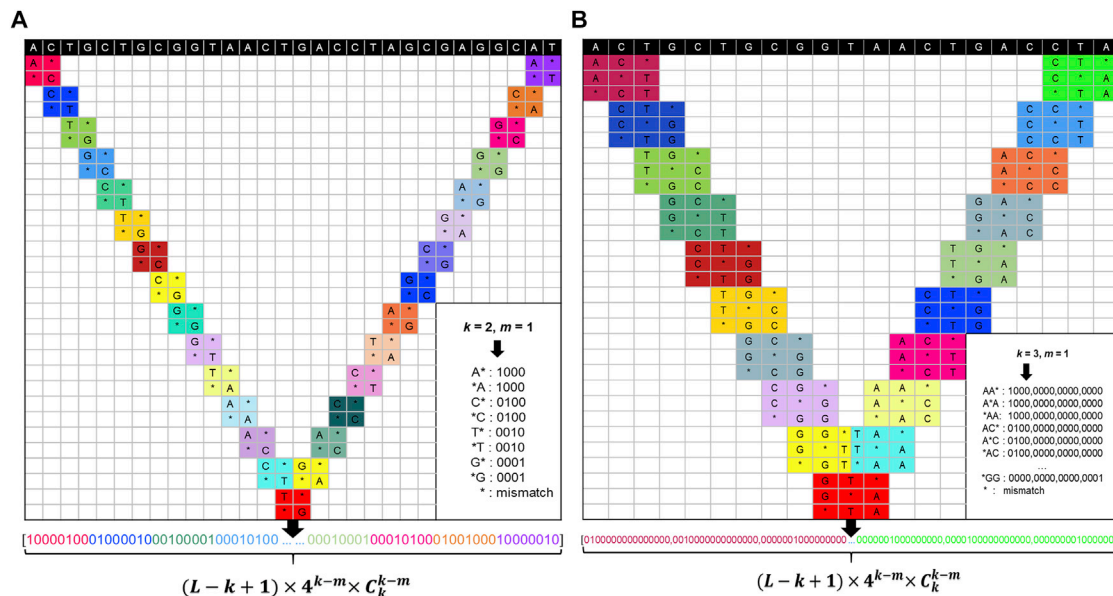


Figure 4. Schematic Diagram Illustrating How to Generate the PSM Vector for a DNA Sequence

(A) Example of PSM with parameters of $k = 2, m = 1$. (B) Example of PSM with parameters of $k = 3, m = 1$.

of XGBoost is its scalability in all scenarios. For more detailed information on XGBoost, please refer to Chen and Guestrin.⁵⁵

In this study, the regression model of the XGBoost algorithm was employed. We used the scikit-learn package⁴² to implement the XGBoost algorithm. The values of its three main parameters (maximum depth of a tree C , boosting learning rate R , and number of boosted trees F)

are given in the following sections, and all the other parameters were set as default values.

Finally, according to Equations 9 and 11, two predictors have been proposed as follows:

$$\begin{cases} sgRNA - PSM, & \text{if use } D \text{ of Eq.7 to denote DNA samples} \\ sgRNA - ExPSM, & \text{if use } \tilde{D} \text{ of Eq.9 to denote DNA samples} \end{cases} \quad \text{(Equation 12)}$$

Table 4. Comparison between the PS Feature Vector's dimension (cf. Equation 8) and the PSM Feature Vector's Dimension (cf. Equation 9)

k	Dimension of PS Vector ^a	m	Dimension of PSM Vector ^b	Ratio γ^c
2	464	1	232	~ 2
3	1,792	1	1,344	~ 1.3
		2	336	~ 5.3
4	6,912	1	6,912	1
		2	2,592	~ 2.7
		3	432	~ 16
5	26,624	2	16,640	~ 1.6
		3	4,160	~ 6.4
6	102,400	4	520	~ 51.2
		4	6,000	~ 17.07
		5	600	~ 170.67
⋮	⋮	⋮	⋮	⋮
⋮	⋮	⋮	⋮	⋮

^aCalculated by Equation 8.

^bCalculated by Equation 9.

^cRatio of the number of column 2 and the number of column 4; it is the same with $\gamma = 4^m \times [(k - m)! / k!]$, where m is given in column 3.

Evaluation Method of Performance

The AUC, as it pertains to the ROC curve,^{56–58} is a widely used measure for evaluating the performance of the predictors. The better predictor corresponds to larger AUC values.

Cross-Validation

The cross-validation method is an important step for evaluating the performance of a predictor.⁵⁹ In this study, in order to ensure that a predictor can be generalized across genes, the leave-one-gene-out cross-validation^{35,37} was used, where each of the 17 subsets of S_i (cf. Equation 3) was selected one by one as the test set, while the other 16 subsets were used to construct the training set to train the predictor. This process was repeated for 17 times, and each subset was selected as the test set once.

Implementation of the Competing Methods

In this study, we compared the proposed methods with three state-of-the-art methods, including ge-CRISPR,³⁶ Azimuth,³⁷ and CRISPRpred.³⁸ The detailed processes of these three approaches were introduced as follows: for ge-CRISPR, the 464 dinucleotide (1-

degree) binary features were finally fed into SVM regressor with a radial basis function (RBF) kernel with a c value of 2^5 for regression. For Azimuth, seven features were used to represent the samples, including position-independent, position-specific, GC count, NGGN, thermodynamic features, amino acid cut position, and percent peptide. These features were combined with GBR with the parameters `learning_rate = 0.1`, `max_depth = 3`, and `n_estimators = 100` to construct the predictor. For CRISPRpred, five different feature extraction methods were employed, including position-independent, position-specific, thermodynamic features, amino acid cut position, and percent peptide. Please note that ViennaRNA package version 2.0⁶⁰ was used to generate thermodynamic features. RF³⁹ was then performed on these features to select 2,899 relevant features according to the importance scores (Mean Decrease Gini) with the maximum number of trees of 500. These features were finally fed into the SVM regressor with linear kernel function with a c value of 2^{-2} for regression.

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.omtn.2020.01.029>.

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OMTN, Volume 20

Supplemental Information

sgRNA-PSM: Predict sgRNAs On-Target Activity Based on Position-Specific Mismatch

Bin Liu, Zihua Luo, and Juan He

Online Supporting Information S1. This benchmark dataset \mathcal{S} consists of 5310 guide sequences targeting 11 human genes (CD13, CD15, CD33, CCDC101, MED12, TADA2B, TADA1, HPRT, CUL3, NF1, NF2) and 6 mouse genes (Cd45, Cd28, Cd43, Cd5, H2-K, Thy1). There are 1059 high on-target activity sgRNAs, and 4251 low on-target activity sgRNAs. See the text of the paper for further explanation.

(1) \mathcal{S}_1^+ : 78 high on-target activity sgRNAs targeting CD13

```

>CD13_HsgRNA1
ATTGAAGAGAGACAGTACATGCCCTGGGAG
>CD13_HsgRNA2
TGACAATGAAGGCCAGCAAGTACGTGGACA
>CD13_HsgRNA3
GTGGAATGACCTGTGGCTGAACGAGGGCTT
>CD13_HsgRNA4
CAGCACCCAGGTACTCCACGTAGGAGGCGA
>CD13_HsgRNA5
GGGAACCTGGTGACCATAGAGTGGTGGAAAT
>CD13_HsgRNA6
GTGAACTACGACGAAGAGAAGTGGAGGAAG
>CD13_HsgRNA7
TGGAACTCAGTGACATTCCAGTTGGGGTCT
>CD13_HsgRNA8
TCGCACTGTCAGTGGTGTACTCCCAGGAGA
>CD13_HsgRNA9
TTGAAGAGAGACAGTACATGCCCTGGGAGG
>CD13_HsgRNA10
AGTCAGCACCCAGGTACTCCACGTAGGAGG
>CD13_HsgRNA11
GGGAAGCCCATCTGCAGGGTCCAGCGGTTC
>CD13_HsgRNA12
TCTCATACTGGCTGTCCTTACCAGGGAGC
>CD13_HsgRNA13
GGTCATCACGGTGGATAACCAGCACGGGGAC
>CD13_HsgRNA14
TCTTCAGCACATCAGGCAATGAGTGGGTCC
>CD13_HsgRNA15
TCAACATCACGCTTATCCACCCCAAGGACC
>CD13_HsgRNA16
CGGTCATCACGGTGGATAACCAGCACGGGGA
>CD13_HsgRNA17
CCATCCAACCTCCCACCACCGTGCGGGACA
>CD13_HsgRNA18
CACACCAGGATCCACCCCAACCTGCGGTCC

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>CD13_HsgRNA19
TGTGCCCATCACATCCATCAGAGATGGCAG
>CD13_HsgRNA20
TGCACCTCAAGGGCTCCCTGGTGAAGGACA
>CD13_HsgRNA21
ACCACCTTGGACCAAAGTAAAGCGTGAAT
>CD13_HsgRNA22
TGAACGAGGGCTTCGCCTCCTACGTGGAGT
>CD13_HsgRNA23
GGGCCGGCGTGTGATCTCCGAGGCGGGTG
>CD13_HsgRNA24
TGGCCGGCTCATCGAAGCATGGGAAGGACT
>CD13_HsgRNA25
AGGACGTATTC AAGCAGGGCCTGGCGGTGA
>CD13_HsgRNA26
GCACCGTCCGTTTCACCTGCAAGGAGGCCA
>CD13_HsgRNA27
ACCGCGTGATGGCAGTGGATGCACTGGCCT
>CD13_HsgRNA28
CCGTCTACTGCAACGCTATCGCCCAGGGCG
>CD13_HsgRNA29
TCTCCTCACACTCTGGA ACTCCGTTGGAGC
>CD13_HsgRNA30
TGGTGAAGGACAGCCAGTATGAGATGGACA
>CD13_HsgRNA31
TGATGACCGGAAGCCCATCTGCAGGGTCC
>CD13_HsgRNA32
AAGAGAGACAGTACATGCCCTGGGAGGCCG
>CD13_HsgRNA33
ATGAGATGGACAGCGAGTTCGAGGGGGAGT
>CD13_HsgRNA34
TACTGCAACGCTATCGCCCAGGGCGGGGAG
>CD13_HsgRNA35
CAACGCCGGCGCCATGGAGAACTGGGGACT
>CD13_HsgRNA36
TCCAGCGTTTCATGATGTCCCGCACGGTGG
>CD13_HsgRNA37
TCAAGCTCATGTTTGACCGCTCCGAGGTCT
>CD13_HsgRNA38
GTGGGCTCCGCATAGTCAGCACCCAGGTAC
>CD13_HsgRNA39
GGATGCTCTCCAGCTTCTGTCCGAGGACG
>CD13_HsgRNA40
CCCTGCTTGAATACGTCCTCGGACAGGAAG

>CD13_HsgRNA41
TGGTGGAGCCCACCGAGTACCTGGTGGTGC
>CD13_HsgRNA42
TCTGGGCCGGCGTGTGATCTCCGAGGCGG
>CD13_HsgRNA43
GATTGGCCTGCCAGACTTCAACGCCGGCGC
>CD13_HsgRNA44
CCGAGGCCGGTGTGGACAGCGGGTGGGAGG
>CD13_HsgRNA45
AGATGGGCTTCCCGGTCATCACGGTGGATA
>CD13_HsgRNA46
ACCCGGTAATAGCCCGTCACATTGAGGTTC
>CD13_HsgRNA47
GTGAGGTACGGTCTCAGCGTCACCCGGTAG
>CD13_HsgRNA48
GAGGGGTGGCAGACACTCACCGAGTGGTCT
>CD13_HsgRNA49
GCAAGTACGTGGACATCTTGGGCGTGGTGT
>CD13_HsgRNA50
TGCAGTAGACGGTGGACCGCAGGTTGGGGT
>CD13_HsgRNA51
TGAAGTAGCTCAGGCTGCTCAGGGCGGCCT
>CD13_HsgRNA52
CGTAGTCGAACTCACTGACAATGAAGCCA
>CD13_HsgRNA53
GCCAGTGCATCCACTGCCATCACGCGGTAC
>CD13_HsgRNA54
CTACGTGGAGAAGCAGGCATCCAATGGTGT
>CD13_HsgRNA55
AGCGGTTCATGATGTCCCGCACGGTGGTGG
>CD13_HsgRNA56
CTCCGTTGGAGCAGGCGGTGCTGATGGCAT
>CD13_HsgRNA57
ACCATAGAGTGGTGAATGACCTGTGGCTG
>CD13_HsgRNA58
AAGCTCAACTACACCCTCAGCCAGGGGCAC
>CD13_HsgRNA59
GTCATCACGGTGGATACCAGCACGGGGACC
>CD13_HsgRNA60
CTCTTCAGCACATCAGGCAATGAGTGGGTC
>CD13_HsgRNA61
AGACTCAGCTGCAGAGAGACCACTCGGTGA
>CD13_HsgRNA62
CAGCTCAGTCTTGTCAATGTCGGGGGGCTG

>CD13_HsgRNA63
 TCCATCCAAC TCCCCACCACCGTGCGGGAC
 >CD13_HsgRNA64
 GATCTCCGAGGCGGGTGTGGACAGCGGGTG
 >CD13_HsgRNA65
 AGCATCCTGAGGACTGAGGCGCCCTGGGGT
 >CD13_HsgRNA66
 ACTGTCTCTCTTCAATCAGGAAGAGGGTGT
 >CD13_HsgRNA67
 CAGTTCTCTTCGTCGTAGTTCACCCGGTAA
 >CD13_HsgRNA68
 ATGATCTGTGCCCGATTGATGACAGGGATG
 >CD13_HsgRNA69
 GTGATGACCGGAAGCCCATCTGCAGGGTC
 >CD13_HsgRNA70
 GAGGTGCACCACCAGGTACTCGGTGGGCTC
 >CD13_HsgRNA71
 ACCATGCACCTCCGTACCTTCATGGGGCCA
 >CD13_HsgRNA72
 ACTCTGGAAC TCCGTTGGAGCAGGCGGTGC
 >CD13_HsgRNA73
 TTCATGGCCGGCTCATCGAAGCATGGGAAG
 >CD13_HsgRNA74
 CAGCTGGCTTACCAAGTTCAGGTGGGCTC
 >CD13_HsgRNA75
 TTCATGGGGCCATAGACCTCGGAGCGGTCA
 >CD13_HsgRNA76
 GTGCTGGTATCCACCGTGATGACCGGGAAG
 >CD13_HsgRNA77
 ATGATGTGTACCGCGTGATGGCAGTGGATG
 >CD13_HsgRNA78
 GTGTTGTTTCAGCGCCAGAGTGACAGGGACC

(2) S_2^+ : 55 high on-target activity sgRNAs targeting CD15

>CD15_HsgRNA1
 TGTGACCGTGGACGTGTTCCGGCCGGGGCGG
 >CD15_HsgRNA2
 TAGGACGCGCGGTTCGGTGAGCAGGCGGCAG
 >CD15_HsgRNA3
 GTCCACGTGGATGAAGGCGCCGCGGGGCAC
 >CD15_HsgRNA4
 ACCAACTGAGCCAACATGTGACCGTGGACG
 >CD15_HsgRNA5
 CGCCACTGTCCAGGAAACAGGGGCTGGTGG

>CD15_HsgRNA6
CACCAGCCCCTGTTTCCTGGACAGTGGCGG
>CD15_HsgRNA7
CGGTAGGAGAGCGTCCAGTTGAAGAGGTTA
>CD15_HsgRNA8
TTCGAGTCGCCCTCGCACTCCCCGGGGCTG
>CD15_HsgRNA9
CATCCAAACCCAGCGCTGGCCCCGGGGGCCT
>CD15_HsgRNA10
GGCACAAAGACGTCCGAGTCCGCCCGGTAG
>CD15_HsgRNA11
TCTTCAACTGGACGCTCTCTACCGGGCGG
>CD15_HsgRNA12
CTCCCACCACAGCAGCACGCCACCGGTCCG
>CD15_HsgRNA13
AAAGCACGGCCTGAGCCTCTCCGTAGGACG
>CD15_HsgRNA14
GAGGCACTTGGGAAGTCGTCCACGTGGATG
>CD15_HsgRNA15
GTCCGAACCCCGTCGCGACCGGTGGGCGT
>CD15_HsgRNA16
GGCACCAAGGCTCGTCCCAGAAGGAGGTGA
>CD15_HsgRNA17
TTTTCCACCACCGCGACCTCGTGAAGGGGC
>CD15_HsgRNA18
TCGTCCACGTGGATGAAGGCGCCGCGGGGC
>CD15_HsgRNA19
AGGCCCCCGGGCCAGCGCTGGGTTTGGATG
>CD15_HsgRNA20
CAGCCCCTGTTTCCTGGACAGTGGCGGGGC
>CD15_HsgRNA21
GGCCCCGCCACTGTCCAGGAAACAGGGGCT
>CD15_HsgRNA22
GGGGCCTGGGGCTGGAGGTGCCAGGGCTT
>CD15_HsgRNA23
TCACCGACCGCGCTCCTACGGAGAGGCTC
>CD15_HsgRNA24
GCCCCGAGGCCGCCCTGACTGCCGGCTG
>CD15_HsgRNA25
GCTTCGCAGCCCCGGGGAGTGCGAGGGCGA
>CD15_HsgRNA26
GCCCCGCCACTGTCCAGGAAACAGGGGCTG
>CD15_HsgRNA27
ACCGCGCTCCTACGGAGAGGCTCAGGCCG

>CD15_HsgRNA28
GAGCCTCTCCGTAGGACGCGCGGTTCGGTGA
>CD15_HsgRNA29
GCCACTGGGACGAGCGCCAGGCCCGGGTCC
>CD15_HsgRNA30
GCCCTGTTTCCTGGACAGTGGCGGGGCCA
>CD15_HsgRNA31
ACGACTTCCCAAGTGCCTCCTCCCTGGCCT
>CD15_HsgRNA32
GCCTGAGCCTCTCCGTAGGACGCGCGGTTCG
>CD15_HsgRNA33
CGTCGCCAACCCCGTCGCGACCGGTGGGCG
>CD15_HsgRNA34
GCCCGCCCCGGCCGAACACGTCCACGGTCA
>CD15_HsgRNA35
GGGGGCCCTTCACGAGGTTCGCGGTGGTGG
>CD15_HsgRNA36
TATCGCCGCTACTTCCACTGGCGCCGGAGC
>CD15_HsgRNA37
AGTGGCGGGCCAGGCCTGAGGGCGGGTTCG
>CD15_HsgRNA38
TGCTGCTGTGGTGGGAGCCCTTCGGGGGGC
>CD15_HsgRNA39
TGGTGGCATGGGTGGTGGAGCCACTGGGACG
>CD15_HsgRNA40
ACCCGGGCTGGCGCTCGTCCCAGTGGCTC
>CD15_HsgRNA41
TCGGGGGGCCCTTCACGAGGTTCGCGGTGG
>CD15_HsgRNA42
GACCGGTGGGCGTGCTGCTGTGGTGGGAGC
>CD15_HsgRNA43
GCGGGTTGCGGTTCGAGGAAAAGCAGGTAC
>CD15_HsgRNA44
TGCGGTTCGAGGAAAAGCAGGTACGAGGCCA
>CD15_HsgRNA45
CGAGGTTCGCGGTGGTGGAAAAGCACGGCCT
>CD15_HsgRNA46
GGCAGTGTGCGCCTGGATGCCCCAGGGCGG
>CD15_HsgRNA47
CTCAGTTGGTGGTAGTAGCGGACCCGGGCC
>CD15_HsgRNA48
CAACTACGAGCGCTTTGTGCCCCGCGGCGC
>CD15_HsgRNA49
CTCTTCAACTGGACGCTCCTACCGGGCG

>CD15_HsgRNA50
 ACGGTCACATGTTGGCTCAGTTGGTGGTAG
 >CD15_HsgRNA51
 TAGCTCCGGCGCCAGTGGAAAGTAGCGGCGA
 >CD15_HsgRNA52
 GGCTTCGCAGCCCCGGGAGTGCGAGGGCG
 >CD15_HsgRNA53
 GAGGTGATGTGGACAGCGTAGCTCCGGGCGC
 >CD15_HsgRNA54
 TACTTGCCAGGCTTCGCAGCCCCGGGAGT
 >CD15_HsgRNA55
 AACTTGTAGCGGGCCACTGTGTGCAGGAGC

(3) S_3^+ : 28 high on-target activity sgRNAs targeting CD33

>CD33_HsgRNA1
 CCTCATCCCTGGCACTCTAGAACCCGGCCA
 >CD33_HsgRNA2
 GGGTATGGGATGGAAGAAAGTGCAGGGCAC
 >CD33_HsgRNA3
 ACAGCCACTCACCTGCCACAGCAGGGGCA
 >CD33_HsgRNA4
 TCCTCCTGGCGTCTACGATGCTCAGGGAGC
 >CD33_HsgRNA5
 TCCTCGGTGCTCATAATCACCCACGGCCC
 >CD33_HsgRNA6
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 GCAGGAGTCAGTGACGGTACAGGAGGGTTT
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 GGCTGCAAGTGCAGGAGTCAGTGACGGTAC
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 AAGTGCAGGAGTCAGTGACGGTACAGGAGG
 >CD33_HsgRNA11
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 TGGTGCCGTGGTCCCTGGGGCCGTGGGGTGA
 >CD33_HsgRNA13
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>CD33_HsgRNA16
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 >CD33_HsgRNA19
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 >CD33_HsgRNA24
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 >CD33_HsgRNA25
 CACCTGTCACATGCACAGAGAGCTGGGGAG
 >CD33_HsgRNA26
 TTCTTGTTCGTAGTAGGGTATGGGATGGAAG
 >CD33_HsgRNA27
 TGTTTGTGGCCACTGGAGAGTCCCTGGATA
 >CD33_HsgRNA28
 CAGTTGTTCCCTACTGGGATCCCCAAGGAGG

(4) S_4^+ : 30 high on-target activity sgRNAs targeting CCDC101

>CCDC101_HsgRNA1
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 >CCDC101_HsgRNA2
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 >CCDC101_HsgRNA3
 ACTCAGCCTCTGCATCGGCCTTGGCGGTTG
 >CCDC101_HsgRNA4
 AAACAGGACCGAGTAGTCATCCTGGGGCTG
 >CCDC101_HsgRNA5
 CTGGAGGCTGCTTTACCCGCTGTGGGGGCG
 >CCDC101_HsgRNA6
 ATCAAGTCTCTGTTGGAAGAGAGGCGGATT
 >CCDC101_HsgRNA7
 TGGCATGGCTGTAAGTACCACCTCGGCCA
 >CCDC101_HsgRNA8
 CCCTCAGCATCCTTCGAAAGCTCTGGACA

>CCDC101_HsgRNA9
CAAACAGGACCGAGTAGTCATCCTGGGGCT
>CCDC101_HsgRNA10
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>CCDC101_HsgRNA11
GGGTCATGGCCGACTGCTGCAGCAGGGTCA
>CCDC101_HsgRNA12
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>CCDC101_HsgRNA13
GTCACCAGGCTTCCCGATCCACAGGGGCAG
>CCDC101_HsgRNA14
CACCCCGGAAGACCATGCGCAGAGGGGTGC
>CCDC101_HsgRNA15
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>CCDC101_HsgRNA16
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>CCDC101_HsgRNA17
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>CCDC101_HsgRNA18
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>CCDC101_HsgRNA19
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>CCDC101_HsgRNA20
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>CCDC101_HsgRNA22
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>CCDC101_HsgRNA25
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>CCDC101_HsgRNA26
TCCATCAGCTGATCAAACAAACCCAGGTAA
>CCDC101_HsgRNA27
CGTCTCCGGGTTGGCCTTCCACTGGGGCAG
>CCDC101_HsgRNA28
TATCTCTGAGCCACATTGAGGGGAGGGGAA
>CCDC101_HsgRNA29
CAGGTCTGGCCACGTAGTCTCCTGAGGCAG
>CCDC101_HsgRNA30
GCGATCTTGTCCAGAGCTTTCCGAAGGATG

(5) S_5^+ : 370 high on-target activity sgRNAs targeting MED12

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>MED12_HsgRNA2
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>MED12_HsgRNA3
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>MED12_HsgRNA4
CGATAAATGCCAGGAAGCTACTGCAGGTAT
>MED12_HsgRNA5
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>MED12_HsgRNA6
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>MED12_HsgRNA7
GAGGAACAGAAGAAGCTTCCAGAGGAGGAGG
>MED12_HsgRNA8
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>MED12_HsgRNA9
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>MED12_HsgRNA10
AAGGAAGACTGGCGCATGGTCCACTGGTCC
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>MED12_HsgRNA264
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>MED12_HsgRNA267
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>MED12_HsgRNA268
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>MED12_HsgRNA269
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>MED12_HsgRNA274
CCCCGTCCAACCTGCCCATGCCAGAGGGTA
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CCCCGTCCAACCTGCCCATGCCAGAGGGTA
>MED12_HsgRNA276
TCTGGTCCTGGTTGAGGATGAGGCAGGCAT
>MED12_HsgRNA277
TGTAGTGAACAGGACTCTGAGCCAGGGGCC
>MED12_HsgRNA278
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>MED12_HsgRNA279
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>MED12_HsgRNA283
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TGAGGTGGGCAGTTTAGCAATGAGGGGGGC
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>MED12_HsgRNA286
CTCCGTGTACAGAAGTAGGCAAGCCGGCGG
>MED12_HsgRNA287
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GCCTGTGTATCCAGAACTGCAGGAGGACA
>MED12_HsgRNA289
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TGCGGTGTCTTGAAAAGGTGAAGGAGGATG
>MED12_HsgRNA291
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>MED12_HsgRNA292
ATTTGTTCTTTAAATGGCTACAGGAGGTGT
>MED12_HsgRNA293
ACTTGTGTGGCCCTGGCAGGTGGGGGGCA
>MED12_HsgRNA294
TTGCTAAACTGCCACCTCAGTCCAGGGAC
>MED12_HsgRNA295
TTGCTAAACTGCCACCTCAGTCCAGGGAC
>MED12_HsgRNA296
CCTTTAACACATGTCCCTGGACTGAGGTGG
>MED12_HsgRNA297
CCTTTAACACATGTCCCTGGACTGAGGTGG
>MED12_HsgRNA298
AGTTTAAGCAATTCATCCTCTCCAGGGCGG
>MED12_HsgRNA299
AGTTTAAGCAATTCATCCTCTCCAGGGCGG
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CGTGTACAGAAGTAGGCAAGCCGGCGGGAC
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AGGATACAGCTGAGGCCAAAAACCAGGGGC
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>MED12_HsgRNA304
CTACTAGCCTGTGCCTGTGCATCGTGGCTG
>MED12_HsgRNA305
GTGGTAGGGGTCCGTACTCAGCATGGGAGC
>MED12_HsgRNA306
GTGGTAGGGGTCCGTACTCAGCATGGGAGC
>MED12_HsgRNA307
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>MED12_HsgRNA308
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GTGCTATGGTGGTAGCCAAGCTCCTGGAGA
>MED12_HsgRNA311
GTGCTATGGTGGTAGCCAAGCTCCTGGAGA
>MED12_HsgRNA312
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>MED12_HsgRNA313
TAGTTCACCAGCATTAAAGGAGTGAAGGGAT
>MED12_HsgRNA314
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>MED12_HsgRNA315
CAAGTCACTGAGTGCAGAATGGCTAGGAGT
>MED12_HsgRNA316
AGAATCAGAAGCCGCAGATGAGAAGGGTTC
>MED12_HsgRNA317
AGAATCAGAAGCCGCAGATGAGAAGGGTTC
>MED12_HsgRNA318
GCTGTCAGCTGCAAGCGTTCTGGTCGGCAT
>MED12_HsgRNA319
GCTGTCAGCTGCAAGCGTTCTGGTCGGCAT
>MED12_HsgRNA320
TGGGTCATCGGCAGGATCATCAAAGGGAGA
>MED12_HsgRNA321
GGGCTCCAAAGGCAAGGTCCCCTCGGGAGA
>MED12_HsgRNA322
GGGCTCCAAAGGCAAGGTCCCCTCGGGAGA
>MED12_HsgRNA323
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TGCTCCAGAACCGCATCGTGGATGGAGC
>MED12_HsgRNA327
GCCTTCCCCAGACAAGCCTACAGTAGGAAT
>MED12_HsgRNA328
ACCCTCTGGCATGGGCAGGTTGGACGGGGC
>MED12_HsgRNA329
ACCCTCTGGCATGGGCAGGTTGGACGGGGC

>MED12_HsgRNA330
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>MED12_HsgRNA331
TTGTTCTGTCATCTTGCAGCGTTGTGGAGA
>MED12_HsgRNA332
TCCTTCTTACTGAAAATGGGGACCTGGATG
>MED12_HsgRNA333
GTCTTGAAAAGGTGAAGGAGGATGCGGCAG
>MED12_HsgRNA334
GTCTTGAAAAGGTGAAGGAGGATGCGGCAG
>MED12_HsgRNA335
GTAGTGAACAGGACTCTGAGCCAGGGGCC
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GTAGTGAACAGGACTCTGAGCCAGGGGCC
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GGATTGAGCTGCGGTGTCTTGAAAAGGTGA
>MED12_HsgRNA338
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>MED12_HsgRNA339
AGGCTGAGCTGCTTCTCAAATCCTCGGATC
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TGGCTGCCTCCCAGAACCGCATCGTGGATG
>MED12_HsgRNA341
TGGCTGCCTCCCAGAACCGCATCGTGGATG
>MED12_HsgRNA342
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>MED12_HsgRNA343
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>MED12_HsgRNA344
CTGATGCTGAGTGAATATTCCATGAGGTCC
>MED12_HsgRNA345
AAGGTGCTGGGAATAGTACCTGGGGGATG
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AAGGTGCTGGGAATAGTACCTGGGGGATG
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CCATTGGACGGGTACTTCATACTTTGGAAG
>MED12_HsgRNA348
CCTCTGGCATGGGCAGGTTGGACGGGGCAA
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CCTCTGGCATGGGCAGGTTGGACGGGGCAA
>MED12_HsgRNA350
TTTTTGGCCTCAGCTGTATCCTACAGGTAG
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>MED12_HsgRNA352
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 >MED12_HsgRNA353
 AAAATGGGAGCACTGGGAGCAGAAAGGGAG
 >MED12_HsgRNA354
 GTTCTGGTCGGCATCGTGCTATGGTGGTAG
 >MED12_HsgRNA355
 GTTCTGGTCGGCATCGTGCTATGGTGGTAG
 >MED12_HsgRNA356
 TGCCTGTGCATCGTGGCTGTCCGCGGCAC
 >MED12_HsgRNA357
 TGCCTGTGCATCGTGGCTGTCCGCGGCAC
 >MED12_HsgRNA358
 CCCTTTAGCAGAGTCAGGGCATGTTGGGAC
 >MED12_HsgRNA359
 CACATTATGACCAACACCAGGTCACGGCTC
 >MED12_HsgRNA360
 CACATTATGACCAACACCAGGTCACGGCTC
 >MED12_HsgRNA361
 ACCTTTCACATTATGACCAACACCAGGTCA
 >MED12_HsgRNA362
 ACCTTTCACATTATGACCAACACCAGGTCA
 >MED12_HsgRNA363
 AGCGTTCTGGTCGGCATCGTGCTATGGTGG
 >MED12_HsgRNA364
 AGCGTTCTGGTCGGCATCGTGCTATGGTGG
 >MED12_HsgRNA365
 ATACTTGCACCTCATCTCCCGAGGGGACC
 >MED12_HsgRNA366
 ATACTTGCACCTCATCTCCCGAGGGGACC
 >MED12_HsgRNA367
 CCCTTTGTAACCGAATCTTTGGATTGGGAC
 >MED12_HsgRNA368
 CCCTTTGTAACCGAATCTTTGGATTGGGAC
 >MED12_HsgRNA369
 ACTTTTGTTGCCATCCTCATCGCTCGGCAG
 >MED12_HsgRNA370
 ACTTTTGTTGCCATCCTCATCGCTCGGCAG

(6) S_6^+ : 38 high on-target activity sgRNAs targeting TADA2B

>TADA2B_HsgRNA1
 CGTGACAGACCACACCTGTCCCAGCGGAGG
 >TADA2B_HsgRNA2
 CATTACGTGAGCATGTACATCCACGGGAAC

>TADA2B_HsgRNA3
CTGGAGATCCAGCCGCTTTCTGTGAGGAAA
>TADA2B_HsgRNA4
GCTCAGCCACAGAGATGTCCAGCGGGGGCA
>TADA2B_HsgRNA5
CGGAAGCTGAAAGAGAGACAGCGGCGGAAG
>TADA2B_HsgRNA6
GGGGAGTCCGGGAAGCACCAACGTGGGCAG
>TADA2B_HsgRNA7
TAATAGTCTTCACAGTCACGTAGCGGGCTG
>TADA2B_HsgRNA8
TGCTCAGCCACAGAGATGTCCAGCGGGGGC
>TADA2B_HsgRNA9
CTTGCATGACATGAACTGGTACAGCGGCCT
>TADA2B_HsgRNA10
CGGGCCAAGATCCGAGAAGTGCAGCGGTAC
>TADA2B_HsgRNA11
CGCGCCCACGTGGACATGTACGTGCGGAAG
>TADA2B_HsgRNA12
GCTTCCGCACGTACATGTCCACGTGGGCGC
>TADA2B_HsgRNA13
AGTACTGCGTGTACTGCCTGGCCGAGGTGA
>TADA2B_HsgRNA14
GCTGCTGGACGCCATCGAGCAGTTCGGCTT
>TADA2B_HsgRNA15
GGCGCTTCACGCTCTGGGGGCCCGAGGCCG
>TADA2B_HsgRNA16
AGCGGAAGCGCAGCGGGCTCACCTCGGCCA
>TADA2B_HsgRNA17
CTGGGACAGGTGTGGTCTGTACGCGGTTG
>TADA2B_HsgRNA18
CAGAGAGCCCGCTGATGAGCGTCTCGGCAT
>TADA2B_HsgRNA19
AAGCGCAGCGGGCTCACCTCGGCCAGGCAG
>TADA2B_HsgRNA20
TCGAGCAGTTCGGCTTCGGAAACTGGGTGA
>TADA2B_HsgRNA21
CGCTGCAGTTCTCGGATCTTGGCCCGGAGC
>TADA2B_HsgRNA22
CTCAGCCACAGAGATGTCCAGCGGGGGCAG
>TADA2B_HsgRNA23
GGTAGCGGCGGTGGTGGCCGATCTCGGCGC
>TADA2B_HsgRNA24
CACGGCTACCAGCTGGTGGACGGCGGGCGC

>TADA2B_HsgRNA25
 GTGCGGAAGCTGAAAGAGAGACAGCGGCGG
 >TADA2B_HsgRNA26
 CGGGGCAGCGGGGTGGTGTAGGCTGGGTGA
 >TADA2B_HsgRNA27
 CTCTGTGGCTGAGCAGCAGCAGCTGGGCTA
 >TADA2B_HsgRNA28
 CACGTAATGCTCCATCACCTCTTGGGGAGT
 >TADA2B_HsgRNA29
 GCATTACGTGAGCATGTACATCCACGGGAA
 >TADA2B_HsgRNA30
 AGTTTCCGAAGCCGAAGTCTCGATGGCGT
 >TADA2B_HsgRNA31
 AGCTTCCGCACGTACATGTCCACGTGGGCG
 >TADA2B_HsgRNA32
 GCACTCGGTGCAGCGGAAGCGCAGCGGGCT
 >TADA2B_HsgRNA33
 TTGGTGCTTCCCGACTCCCCAAGAGGTGA
 >TADA2B_HsgRNA34
 AGGCTGGCACCAGATTGTAGTCACGGGCGA
 >TADA2B_HsgRNA35
 AGCATGTACATCCACGGGAACCTGGGGAAG
 >TADA2B_HsgRNA36
 TCGATGTCCTGGCACTCGGTGCAGCGGAAG
 >TADA2B_HsgRNA37
 AGTCTTACAGTCACGTAGCGGGCTGGACT
 >TADA2B_HsgRNA38
 GCCCTTTGTCATCGTAGGAAGATATGGCTG

(7) S_7^+ : 22 high on-target activity sgRNAs targeting TADA1

>TADA1_HsgRNA1
 AGACAACAGCTGAAACAGCCTCCTCGGTGA
 >TADA1_HsgRNA2
 TGACAACGCGTGAGAATGGCCAGGAGGAAA
 >TADA1_HsgRNA3
 CAAGAAGAACTTAAGCGAGGCCCTGGGGGA
 >TADA1_HsgRNA4
 CCAAAAATCTGACAACGCGTGAGAATGGCCA
 >TADA1_HsgRNA5
 AGATACTGGGCTAACCTAAAGCTGTGGTTC
 >TADA1_HsgRNA6
 TCTTACTGTTTCACGTTGTCCCCAGGGCC
 >TADA1_HsgRNA7
 AAGAAGAACTTAAGCGAGGCCCTGGGGGAC

>TADA1_HsgRNA8
 GTTAAGAGCATAGACAGTATGTGTAGGGAT
 >TADA1_HsgRNA9
 TTTTCAGCTGTTGTCTATGCTGTGGAGGTTG
 >TADA1_HsgRNA10
 AATGATAGTACTGCTTATGAGCATGGGCT
 >TADA1_HsgRNA11
 GGTTC AAGCAGAAGATCAGCAAAGAGGAGT
 >TADA1_HsgRNA12
 CTTACTGTTTCACGTTGTCCCCAGGGCCT
 >TADA1_HsgRNA13
 AGAAGA ACTTAAGCGAGGCCCTGGGGGACA
 >TADA1_HsgRNA14
 CCAAGAAGAACTTAAGCGAGGCCCTGGGGG
 >TADA1_HsgRNA15
 CCTCGAGTGGGAAGCATCATTGTGTGGGAA
 >TADA1_HsgRNA16
 TAGGGATGACTTCCCTGTGCACCTGGGATT
 >TADA1_HsgRNA17
 AGGCGCCAAGAAGAACTTAAGCGAGGCC
 >TADA1_HsgRNA18
 CAATGGCGACCTTTGTGAGCGAGCTGGAGG
 >TADA1_HsgRNA19
 ATGATAGTACTGCTTATGAGCATGGGCTG
 >TADA1_HsgRNA20
 AGCATGGGCTGGACAATGTCACCGAGGAGG
 >TADA1_HsgRNA21
 CTGTTTCAGCTGTTGTCTATGCTGTGGAGG
 >TADA1_HsgRNA22
 TCCATTCTCACAATGATTTCCCTCCTGGCCA

(8) S_g^+ : 13 high on-target activity sgRNAs targeting HPRT1

>HPRT1_HsgRNA1
 TTATAGCCCCCTTGAGCACACAGAGGGCT
 >HPRT1_HsgRNA2
 TTGTAGCCCTCTGTGTGCTCAAGGGGGGCT
 >HPRT1_HsgRNA3
 GCCGAGCTGCTCACCACGACGCCAGGGCTG
 >HPRT1_HsgRNA4
 AATCATTATGCTGAGGATTTGGAAAGGGTG
 >HPRT1_HsgRNA5
 TGGTCAGGCAGTATAATCCAAAGATGGTCA
 >HPRT1_HsgRNA6
 TTAAGTAGAATGACCAGTCAACAGGGGACA

>HPRT1_HsgRNA7
 TTTGGAAAGGGTGTATTATTCTCATGGACT
 >HPRT1_HsgRNA8
 TGGCGACCCGCAGCCCTGGCGTCGTGGTGA
 >HPRT1_HsgRNA9
 TATAGCCCCCTTGAGCACACAGAGGGCTA
 >HPRT1_HsgRNA10
 TGTAGCCCTCTGTGTGCTCAAGGGGGGCTA
 >HPRT1_HsgRNA11
 GGCAGTATAATCCAAAGATGGTCAAGGTCG
 >HPRT1_HsgRNA12
 CTCCGTTATGGCGACCCGCAGCCCTGGCGT
 >HPRT1_HsgRNA13
 TTGCTCGAGATGTGATGAAGGAGATGGGAG

(9) S_9^+ : 31 high on-target activity sgRNAs targeting CUL3

>CUL3_HsgRNA1
 TCAAAAAGCATGTCTTGGTGCTGGTGGGATG
 >CUL3_HsgRNA2
 AAACAAGGTGAATCCGACCCAGAGAGGAAA
 >CUL3_HsgRNA3
 GCACAAGTAACTGGCTCTAATACACGGAAG
 >CUL3_HsgRNA4
 GGCCAATATCCTGTCTGTGAGCACCCGGACT
 >CUL3_HsgRNA5
 TCAAACACAACGATGGATGAATTCAGGCAA
 >CUL3_HsgRNA6
 TCTTACAGTCCGGGTGCTCACGACAGGATA
 >CUL3_HsgRNA7
 GTTTACCACAGGCGAGGGACTGTAGGGCTC
 >CUL3_HsgRNA8
 GATAAGCTGAAAAAGGGAGTCAAAGGGGTA
 >CUL3_HsgRNA9
 CTAAATAACTTGTACATGCAACCAAGGTCT
 >CUL3_HsgRNA10
 GAACCAATTGTAAAGGTGGTTGAAAGGGAA
 >CUL3_HsgRNA11
 GAAACAGGAAGATGGATCTGAAGTTGGTGT
 >CUL3_HsgRNA12
 ACGCCGAGGAGAGACTCACCCGAAAGGCC
 >CUL3_HsgRNA13
 AGGGCTCTAACAAGCTCTCTTTCAGGGATA
 >CUL3_HsgRNA14
 TTTACTTACCTGGATATAGTCAACAGGATT

>CUL3_HsgRNA15
 TGCAC TTTGGTGTGGCTGACTGAGTGGGCC
 >CUL3_HsgRNA16
 ATATGAGCATCTCAAACACAACGATGGATG
 >CUL3_HsgRNA17
 TGATGCACTGCCTTGACAAATCAACGGAAG
 >CUL3_HsgRNA18
 TAGAGCCCTACAGTCCCTCGCCTGTGGTAA
 >CUL3_HsgRNA19
 GTCCGGGTGCTCACGACAGGATATTGGCCC
 >CUL3_HsgRNA20
 TATGGGTGTATTAGGGATCATCTACGGCAA
 >CUL3_HsgRNA21
 TGATTAGAGACATACTAATGTACATGGTAA
 >CUL3_HsgRNA22
 AGCTTATCATCAATAAATAATGAGAGGTAT
 >CUL3_HsgRNA23
 ATAATGAGAGGTATTCAGGAGACCTGGAGT
 >CUL3_HsgRNA24
 GCTGTGTTGGTTTACCACAGGCGAGGGACT
 >CUL3_HsgRNA25
 TTTTTTAGGTA ACTCAGCAGTTGAAGGCGC
 >CUL3_HsgRNA26
 AAGGTTCTACTTAGCCAAACACAGTGGTCG
 >CUL3_HsgRNA27
 TCTCTTGGATATTACAGATGACCATGGATG
 >CUL3_HsgRNA28
 CCTTTTTAACTGGTCCATAAAAATGTGGCAT
 >CUL3_HsgRNA29
 CTGTTTTACATAGGTATCTTTAGGTGGTGT
 >CUL3_HsgRNA30
 TGTTTTTCCTCCACAGACTGAATGTGGATG
 >CUL3_HsgRNA31
 GCACTTTGGTGTGGCTGACTGAGTGGGCCA

(10) S_{10}^+ : 148 high on-target activity sgRNAs targeting NF1

>NF1_HsgRNA1
 TTTTAAAAAACCTACCGTAAACTCGGGTCA
 >NF1_HsgRNA2
 TTTAAAACAGACTTTCTCTCTAAGTGGTTT
 >NF1_HsgRNA3
 ATGCAAAGCCATATGAAATTGTAGTGGACC
 >NF1_HsgRNA4
 TGCAAAATTAAAACGACTCCTGAAGGGTAA

>NF1_HsgRNA5
CACAAACCTGTGGCAGATACACACTGGTCC
>NF1_HsgRNA6
CTTCAAGCCCCTTTCGATTCTAGGTGGTGG
>NF1_HsgRNA7
TTCGAAGTTGAGGGGGGAATTCTGAGGAGG
>NF1_HsgRNA8
GTTAAATAGCATTGGATACAGAGCAGGACT
>NF1_HsgRNA9
GCTCAATATCGCATTACTTAATTTAGGCAG
>NF1_HsgRNA10
AGTAAATCCACTTACCTATAGGAAGGGTCA
>NF1_HsgRNA11
TGGCACACACTTCGAAGTTGAGGGGGGAAT
>NF1_HsgRNA12
AGTCACACATGCCAGAGATTGCTCAGGAAG
>NF1_HsgRNA13
AGTTACAGTTATAGATATAGACTGCGGAGA
>NF1_HsgRNA14
AGGTACATGAAAAAGAAGAATTC AAGGCTT
>NF1_HsgRNA15
ACGGACCAATGTTAAGGATCTGGTGGTCT
>NF1_HsgRNA16
TCCTACTGCACCGATGCTGTTCTGAGGGAA
>NF1_HsgRNA17
ATACACTGGAAAAATGTCTTGCTGGGGTAA
>NF1_HsgRNA18
AGATACTTATAGCTTCTTGCTCTCCAGGTCT
>NF1_HsgRNA19
CTGAACTTCGGAATTCTGCCTCTGGGGTTT
>NF1_HsgRNA20
ACTAAGAAAGTAACAACGTGGAAGAGGTAG
>NF1_HsgRNA21
GGTTAGAACCATCAGAGAGCCTTGAGGAAA
>NF1_HsgRNA22
TGCCAGAGATTGCTCAGGAAGCAATGGAGG
>NF1_HsgRNA23
TCAGAGAGCCTTGAGGAAAACCAGCGGAAC
>NF1_HsgRNA24
TACCAGCACATAGTGAAATGTAGAAGGTGA
>NF1_HsgRNA25
GAGCAGCACTTCAGAAAAGAGTGATGGCAC
>NF1_HsgRNA26
CAAAAGCCAAAATGGAAGATGGCCAGGTAA

>NF1_HsgRNA27
AAAAAGCCACCACCTAGAATCGAAAGGGGC
>NF1_HsgRNA28
TCTGAGGAGGAACTGATGATGGCATGGAAG
>NF1_HsgRNA29
AGAAAAGTAACAACGTGGAAGAGGTAGGGAA
>NF1_HsgRNA30
CCAAAAGTCAGTACTGAGCACAAACAAGGAAT
>NF1_HsgRNA31
GGACAGTCTACGAAAAGCTCTTGCTGGCCA
>NF1_HsgRNA32
TTGCAGTGCCACTCCAGAGGATTCGGATT
>NF1_HsgRNA33
GACCAGTGGACAGAAGCTAGCTCAAAGGTAT
>NF1_HsgRNA34
TCAAAGTTTGAGGAATTTATGACTAGGTAA
>NF1_HsgRNA35
CAAGATAAGGAGAATGATTTGTAGTGGCCA
>NF1_HsgRNA36
CCAGATCCCACAGACTGATATGGCTGGTAA
>NF1_HsgRNA37
AGCAATCTCTGGCATGTGTGACTGAGGGAC
>NF1_HsgRNA38
GGATATGAATGATAGACTGGACAATGGCTT
>NF1_HsgRNA39
ACCAATGCTCTCACCTTAAAGTGTGGTTG
>NF1_HsgRNA40
TGATATTAATGACCAGTCCATGTGTGGAAG
>NF1_HsgRNA41
CCACATTAGGCTTAGGTTACCACAAGGATC
>NF1_HsgRNA42
CAAGATTCGGCCAAAAGATGTCCCTGGGAC
>NF1_HsgRNA43
CAGGATTGATAAATCTGAGGAACATGGCAC
>NF1_HsgRNA44
CTCCATTGCTTCCTGAGCAATCTCTGGCAT
>NF1_HsgRNA45
TAGAATTGTTACAGTATATCAATGTGGATT
>NF1_HsgRNA46
CTACCAAGCTGGGACTTCCAAAAGCTGGGAA
>NF1_HsgRNA47
GTGACAATACACAGCATCAATCTTAGGCCA
>NF1_HsgRNA48
CTGCCACATCAAGGGAATTGTTGAAGGACA

>NF1_HsgRNA49
CCTACAGGAATGGATCAACATGACTGGCTT
>NF1_HsgRNA50
CGCACAGGCCGGTGGAAATGGGTCCAGGCCG
>NF1_HsgRNA51
CAGTCATGTTGATCCATTCTGTAGGGAGT
>NF1_HsgRNA52
ACACCCAAAGACAACAAGAGCTCTTGGTTG
>NF1_HsgRNA53
AAAGCCACCACCTAGAATCGAAAGGGGCTT
>NF1_HsgRNA54
TCAACCACCATGGACTGAACAAGTAGGAAA
>NF1_HsgRNA55
TCAACCACGTCTTTGGATATATCTTGGATT
>NF1_HsgRNA56
CAATCCATGGAATTGTGCAGAGTGTGGTGT
>NF1_HsgRNA57
TTTTCTACTTGTTCAGTCCATGGTGGTTG
>NF1_HsgRNA58
TGGCCGCGCACAGGCCGGTGGAAATGGGTCC
>NF1_HsgRNA59
TGAGCGCGGTGCCCTGGTTTGCAATGGTTA
>NF1_HsgRNA60
GAGTCGGGCTGTGACAGTTCCCAGCGGGTC
>NF1_HsgRNA61
GTGGCTACTAAGAAAGTAACAACGTGGAAG
>NF1_HsgRNA62
CCTGCTCGTCGAAGCGGCTGACCACGGCCT
>NF1_HsgRNA63
TCGCCTCTGCACAAAGCCCTCTTTTGGGTA
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AGTTCTGACAAAAATCCTTCAACAAGGCAC
>NF1_HsgRNA65
TGGTCTGGCCGACAGTTGGATAGGTGGCTG
>NF1_HsgRNA66
TGTCTGTTTCCGCCACCTCTGTGAGGAAG
>NF1_HsgRNA67
CAATCTTAGGCCACCAATCCAATGCGGACT
>NF1_HsgRNA68
CACTCTTCCAAAAATTCTAACGTGAGGTGT
>NF1_HsgRNA69
ATAGCTTCTTGTCTCCAGGTCTGTAGGTTT
>NF1_HsgRNA70
TTATCTTGTGTCCAGAAATAATCCAGGATA

>NF1_HsgRNA71
AACAGAAACTACCTGCTGCCACCTTGGCTT
>NF1_HsgRNA72
TTCAGAACCTTTGGGAGAGGACCATGGCTG
>NF1_HsgRNA73
TAGGGAAGATGAGCTGCCACATCAAGGGAA
>NF1_HsgRNA74
GTAGGACAATCAGATGCTATATCAAGGAAA
>NF1_HsgRNA75
CAATGAGATTAGATGAAACGATGCTGGTCA
>NF1_HsgRNA76
TTGTGAGCTAGCTTGAGAGCATTGTGGAAT
>NF1_HsgRNA77
CACAGAGGTGGCGGAAACAGGACATGGCAA
>NF1_HsgRNA78
CATGGAGTCATGTATTCCAAACAAAGGTGT
>NF1_HsgRNA79
CAGAGATTGCTCAGGAAGCAATGGAGGTAA
>NF1_HsgRNA80
CCTTGCAGCCACCTATCCAACCTGTCGGCCA
>NF1_HsgRNA81
TTAGGCAGTTCTGACCCGAGTTTACGGTAG
>NF1_HsgRNA82
GCGTGCCTGGTTTGCAATGGTTAAGGTGA
>NF1_HsgRNA83
TTTGGCCGAATCTTGGTGTGTTGGGGGATA
>NF1_HsgRNA84
TATGGCTTTAAAGTCAGTAAGACATGGTAT
>NF1_HsgRNA85
GTGAGGAAGCAGATATCCGGTGTGGGGTGG
>NF1_HsgRNA86
GACTGGACAATGGCTTCACACTCCTGGTGC
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CATGGGACATTCGCCTCTTAACAATGGTCT
>NF1_HsgRNA88
TACAGGGCCACTTCTAGTTTGGTCTGGGCT
>NF1_HsgRNA89
AGTCGGGCTGTGACAGTTCCCAGCGGGTCC
>NF1_HsgRNA90
AAAGGGGCTTGAAGTTAATGTCAAAGGTGA
>NF1_HsgRNA91
AGATGGTAGAATACCTGACAGACTGGGTTA
>NF1_HsgRNA92
GATTGGTGGAACTGGTCACAATGATGGGTG

>NF1_HsgRNA93
TCAGGGTTCCACAGAAACATGTACAGGGCC
>NF1_HsgRNA94
GAAAGTAACAACGTGGAAGAGGTAGGGAAG
>NF1_HsgRNA95
GGCAGTACAGCAGAATTAATTACAGGGCTC
>NF1_HsgRNA96
GGCTGTGACAGTCCCAGCGGGTCCGGATA
>NF1_HsgRNA97
ATTGGTGGAAGTGGTCACAATGATGGGTGA
>NF1_HsgRNA98
AATGGTGTGTAACCATGAGAAAGTGGGACT
>NF1_HsgRNA99
CTTGGTGTGTTGGGGGATAGAGTCGGGCTG
>NF1_HsgRNA100
CAGGGTTCCACAGAAACATGTACAGGGCCA
>NF1_HsgRNA101
CCTTGTGTGCTCAGTACTGACTTTGGTAT
>NF1_HsgRNA102
CTTTGTTTGAATACATGACTCCATGGCTG
>NF1_HsgRNA103
AATTTAAAGAAAAACCTACAGACCTGGAGA
>NF1_HsgRNA104
TCTATAACTGTAACCTCCTGGGTCAGGGAGT
>NF1_HsgRNA105
GTGCTACCTATCTACAAAAACTCCTGGATC
>NF1_HsgRNA106
ATGTTACCTTAAGATCAACCACCATGGACT
>NF1_HsgRNA107
GTCTTACTAATAGAGACAATAAAGAGGGTG
>NF1_HsgRNA108
CCCTTAGAGCTTCCACACATGGACTGGTCA
>NF1_HsgRNA109
TACGTAGTAATTCTTCATGATCCATGGACA
>NF1_HsgRNA110
ATTGTAGTGGACCTTACCCATACCGGGCCT
>NF1_HsgRNA111
TCTATATCTATAACTGTAACCTCCTGGGTCA
>NF1_HsgRNA112
TGTGTCAATTAGTTGAAGTAATGATGGCAA
>NF1_HsgRNA113
TGCTTCATACGGTGAGACAATGGCAGGATT
>NF1_HsgRNA114
TCTATCATTCATATCCGGACCCGCTGGGAA

>NF1_HsgRNA115
AGACTCCATGCAGACTCTCTTCCGAGGCAA
>NF1_HsgRNA116
GAATTCCGAAGTTCAGCTGCATGCTGGTTT
>NF1_HsgRNA117
CGGGTCCGGATATGAATGATAGACTGGACA
>NF1_HsgRNA118
GAATTCGTTGATCAAACATCATCTGTGGTAT
>NF1_HsgRNA119
CTCTTCTAAAGCCAAGGTGGCAGCAGGTAG
>NF1_HsgRNA120
CCCATCTATTCAAGCAAAAATATGGGGAAG
>NF1_HsgRNA121
AAGGTGAACTGGTTCTCATCTACTAGGCAG
>NF1_HsgRNA122
TGCATGAAGGTGAGCGGCGTGCCCTGGTTT
>NF1_HsgRNA123
CTGTTGACATCATATTGCTGACAGAGGCAA
>NF1_HsgRNA124
TGGCTGATCGGTTTGAGAGATTGGTGAAC
>NF1_HsgRNA125
AATGTGCAGAAAAGCTATTTGACTTGGTGG
>NF1_HsgRNA126
TTTTTGCATCTTGGCAGGCTACACTGGTAA
>NF1_HsgRNA127
CGATTGCTAGGCCCGGTATGGGTAAGTCC
>NF1_HsgRNA128
ACAATGGCAGGATTGATAAATCTGAGGAAC
>NF1_HsgRNA129
GAAGTGGCCCTGTACATGTTTCTGTGGAAC
>NF1_HsgRNA130
AAGATGGTAGAATACCTGACAGACTGGGTT
>NF1_HsgRNA131
CCAATGTGGTTCCTTGTCTCAGTGGGTAA
>NF1_HsgRNA132
GGCATGTGTGACTGAGGGACCAGTTGGACG
>NF1_HsgRNA133
GAAGTGTGTGCCACTGTTTATAACCAGGTAT
>NF1_HsgRNA134
GGACTTACATTGGTGATGATTCGATGGAGT
>NF1_HsgRNA135
ATCCTTACCAGCCATATCAGTCTGTGGGAT
>NF1_HsgRNA136
TCATTTAGAAAGACTGATTGCCCTAGGACT

>NF1_HsgRNA137
 TGTATTAGCAAACGAGTGTCTCATGGGCAG
 >NF1_HsgRNA138
 TGGATTATTTCTGGACACAAGATAAGGAGA
 >NF1_HsgRNA139
 TGGCTTCACACTCCTGGTGCATGAAGGTGA
 >NF1_HsgRNA140
 TTTGTTTCGCTCTGCTGAAGTTACTTGGACA
 >NF1_HsgRNA141
 CACCTTCTACATTTCACTATGTGCTGGTAA
 >NF1_HsgRNA142
 GCAGTTCTGACCCGAGTTTACGGTAGGTTT
 >NF1_HsgRNA143
 GAAGTTGAGGGGGGAATTCTGAGGAGGAAC
 >NF1_HsgRNA144
 TGGTTTGCAATGGTTAAGGTGAACTGGTTC
 >NF1_HsgRNA145
 GTCATTGCCTTCCGTTCCAGTTACCGGGAC
 >NF1_HsgRNA146
 TCTTTTGGCCGAATCTTGGTGTGTTGGGGG
 >NF1_HsgRNA147
 TGGTTTGTCTACAAATTGAGTATTGGTAT
 >NF1_HsgRNA148
 CTGTTTTAAAGCGATTGCTAGGCCCGGTATGGACGTGTTTCGGCCGGGGCGG

(11) S_{11}^+ : 45 high on-target activity sgRNAs targeting NF2

>NF2_HsgRNA1
 ATGAAAAGATCTACTGCCCTCCTGAGGCTT
 >NF2_HsgRNA2
 AAGCAACAATGGCCAACGAAGCACTGGTGA
 >NF2_HsgRNA3
 AAGCAACCCAAGACGTTACCGTGAGGATC
 >NF2_HsgRNA4
 TAAAAAGGGCACAGAGCTGCTGCTTGGAGT
 >NF2_HsgRNA5
 GACTACGACCCCAAGTGTTCACAAGCGGGGA
 >NF2_HsgRNA6
 AGGTACTGGATCATGATGTTTCAAAGGAAG
 >NF2_HsgRNA7
 CCACAGATTCTCCAGCTATGTATCGGGAAC
 >NF2_HsgRNA8
 GTTCAGCAGATGAAAGCCCAGGCCAGGGAG
 >NF2_HsgRNA9
 TTCTAGCCTTCTCCTCCCTGGCCTGGGCTT

>NF2_HsgRNA10
AAAAATCCCCGCTTGTGAACACTGGGGTCG
>NF2_HsgRNA11
GACGATCCTCACGGTGAACGTCTTGGGTTG
>NF2_HsgRNA12
CGAGATGTTTCGGATTTCATTCCACGGGAA
>NF2_HsgRNA13
TTTGATTGGTGTGCCGACTCTGGGGCTC
>NF2_HsgRNA14
AGGCCACAGCGATTTCGCACGGAGGAGGAGA
>NF2_HsgRNA15
GGCTCACCGGTACGTGGGCTTGGTGGCAA
>NF2_HsgRNA16
CGTTCACCGTGAGGATCGTCACCATGGACG
>NF2_HsgRNA17
GAAACATCTCGTACAGTGACAAGGAGGTAG
>NF2_HsgRNA18
CATTCCACGGGAAGGAGATCTTGGGGGTCA
>NF2_HsgRNA19
AGGACCTGCAGGAAGCACGCGAGGCGGAGC
>NF2_HsgRNA20
ACGCCGAGATGGAGTTCAATTGCGAGGTAA
>NF2_HsgRNA21
TGGCCTGGCTCAAAATGGACAAGAAGGTTG
>NF2_HsgRNA22
AGGAGAAGCGCCTGATGGAGCAGAAGGTGC
>NF2_HsgRNA23
TGACGATCCTCACGGTGAACGTCTTGGGTT
>NF2_HsgRNA24
CTTTGATTGGTGTGCCGACTCTGGGGCT
>NF2_HsgRNA25
AGAAGCCAGGAGCACAGAAGCCTCAGGAGG
>NF2_HsgRNA26
ATCGGAACCATGATCTATTTATGAGGAGA
>NF2_HsgRNA27
AAATGGAATATCTGAAGATAGCTCAGGACC
>NF2_HsgRNA28
GCCAGGAGCACAGAAGCCTCAGGAGGGCAG
>NF2_HsgRNA29
TGAGGGAGGAGGCTGAACGCACGAGGGATG
>NF2_HsgRNA30
TCAGGGTCATAAATGTGAAGCCCCAGGGCA
>NF2_HsgRNA31
TGCAGTACACAATCAAGGACACAGTGGCCT

>NF2_HsgRNA32
 CGGCGTCCATGGTGACGATCCTCACGGTGA
 >NF2_HsgRNA33
 TTCTTACGCCGTCCAGGCCAAGGTAGGCTC
 >NF2_HsgRNA34
 GCTGTCACCAATGAGGTTGAAGCTTGGTAT
 >NF2_HsgRNA35
 TGTATCAGATGACTCCGGAAATGTGGGAGG
 >NF2_HsgRNA36
 TCATTCCACGGGAAGGAGATCTTGGGGGTC
 >NF2_HsgRNA37
 AGAGTCCGGCACACCAAATCAAAGAGGTCC
 >NF2_HsgRNA38
 TTCTTCTTTGAGCCTACCTTGGCCTGGACG
 >NF2_HsgRNA39
 TCTTTGAGCCTACCTTGGCCTGGACGGCGT
 >NF2_HsgRNA40
 GTTTTGCCTCCTCCTCGGTGATCTGGGCCT
 >NF2_HsgRNA41
 TCTTTGGACTGCAGTACACAATCAAGGACA
 >NF2_HsgRNA42
 ATCTTGGGGGTCAGTCTGTTCTCAGGGTCA
 >NF2_HsgRNA43
 GAGATGTTTCGGATTTTCATTCCACGGGAAG
 >NF2_HsgRNA44
 AATTTTATCCTGAGAATGCTGAAGAGGAGC
 >NF2_HsgRNA45
 CAGGTTTCTCGGAGCCCCAGAGTCCGGCAC

(12) S_{12}^+ : 48 high on-target activity sgRNAs targeting CD5

>CD5_HsgRNA1
 CTTACACCAGCTTCTTGTAGACCAGAGGACC
 >CD5_HsgRNA2
 CCACACTGCAGAGACTTACAGATGAGGTTC
 >CD5_HsgRNA3
 AGAGACTTACAGATGAGGTTCCCAGGCC
 >CD5_HsgRNA4
 GTGGAGATCCAGATGGAAAACAAGTGGAAA
 >CD5_HsgRNA5
 ATCCAGGCCAAGACCCAAACCCAGCGGGCC
 >CD5_HsgRNA6
 CTGTAGTGAGACACAGCTCCCGTTCGGGGC
 >CD5_HsgRNA7
 TTGGATATAGACCACGGAGATCCTTGGCAG

>CD5_HsgRNA8
ACAGATGAGGTTCCCCAGGCCAGGGGCCT
>CD5_HsgRNA9
GCCAATTCGATGGGAGGCCCGAACGGGAG
>CD5_HsgRNA10
TGTTCAATGAAGGGAAAGGACCAAGGGCCA
>CD5_HsgRNA11
AGGCCACCCCTTCCAGACTGTCCGAGGCAG
>CD5_HsgRNA12
CACACACTGCTGCCCCGACCAGGCGGCTC
>CD5_HsgRNA13
CCAGCAGCACCACCAGGAGTACAAGGGTCA
>CD5_HsgRNA14
CACCCAGCGTCCCAGCAGGTATGTGGCAG
>CD5_HsgRNA15
ATTGCAGCTGGTGCCAGGACACGAAGGCCT
>CD5_HsgRNA16
AAAACAGTGTGCAGTTCCAGTTGGAGGCTG
>CD5_HsgRNA17
CCTTCCGCTGAGCCTGATCTGCCTAGGTGG
>CD5_HsgRNA18
CCCACCTAGGCAGATCAGGCTCAGCGGAAG
>CD5_HsgRNA19
TCATCCTGACCCTTGTACTCCTGGTGGTGC
>CD5_HsgRNA20
GTGGCGACCTCATCTCCTTCCACACGGTGG
>CD5_HsgRNA21
TCCGCTGAGCCTGATCTGCCTAGGTGGGTG
>CD5_HsgRNA22
GCTGCTGGCTGCCACATACCTGCTGGGAAC
>CD5_HsgRNA23
TCTCCTGGGCACAGAGGAACCCGGGGGAGG
>CD5_HsgRNA24
CACGGAGATCCTTGGCAGAAGACCTGGTTC
>CD5_HsgRNA25
CTCAGATATCCAGGTGATGCTAAGTGGCTC
>CD5_HsgRNA26
GTTTGCACACTGCAGAGGCCTGCTGGGCAT
>CD5_HsgRNA27
TACAGCAGTGCTTCCAGAAAACAACGGCCC
>CD5_HsgRNA28
TCCAGCCCAAGGTTTCAGAGCCGCCTGGTTCG
>CD5_HsgRNA29
AACAGCTGAGATGTGGTGACCCCTTGGCCC

>CD5_HsgRNA30
 TGCTGCTGGCTGCCACATACCTGCTGGGAA
 >CD5_HsgRNA31
 GAAGGGAAAGGACCAAGGGCCAAGGGGTCA
 >CD5_HsgRNA32
 TCCTGGCACCAGCTGCAATCTGGGAGGAGC
 >CD5_HsgRNA33
 CCTAGGCAGATCAGGCTCAGCGGAAGGCAC
 >CD5_HsgRNA34
 AAGTGGCTCCAATTCCAAGTGCAGGGTCA
 >CD5_HsgRNA35
 TGAAGGGAAAGGACCAAGGGCCAAGGGGTCA
 >CD5_HsgRNA36
 CAGCGGGCCTGGCCCCAGGCACTGTGGCAA
 >CD5_HsgRNA37
 GTCAGGGTCAAGTGGAGATCCAGATGGAAA
 >CD5_HsgRNA38
 CTGGGGTCTGTTCAATGAAGGGAAAGGACC
 >CD5_HsgRNA39
 CACAGGTGTGGTGAATTCTACAATGGCAG
 >CD5_HsgRNA40
 TCTTGTAGACCAGAGGACCACACATGGCCA
 >CD5_HsgRNA41
 GCCTGTCTTGGCCTTGTAGAGGATGGTGC
 >CD5_HsgRNA42
 TGCAGTGTGCAAACAGCTGAGATGTGGTGA
 >CD5_HsgRNA43
 CAGATCAGGCTCAGCGGAAGGCACTGGTCT
 >CD5_HsgRNA44
 TGGTCTGCGGGTCTGTTCAATGAAGGGAAA
 >CD5_HsgRNA45
 CAGGTCTTCTGCCAAGGATCTCCGTGGTCT
 >CD5_HsgRNA46
 CCGCTGAGCCTGATCTGCCTAGGTGGGTGA
 >CD5_HsgRNA47
 TATGTGGCAGCCAGCAGCACTTCGTGGGAG
 >CD5_HsgRNA48
 GTTGTTCAGTTGGATATAGACCACGGAGA

(13) S_{13}^+ : 15 high on-target activity sgRNAs targeting CD28

>CD28_HsgRNA1
 GACTACATGAACATGACTCCCCGGAGGCCT
 >CD28_HsgRNA2
 CACGACCAGTGCCCAAAACAGCTTAGGAGA

>CD28_HsgRNA3
 CTCTCGTTGTCTAGGTAAGGCGGAGGGTAC
 >CD28_HsgRNA4
 TTACCTAGACAACGAGAGGAGCAATGGAAC
 >CD28_HsgRNA5
 GCTCCTCTCGTTGTCTAGGTAAGGCGGAGG
 >CD28_HsgRNA6
 CAATGACACTCAGGCTGCTGTTCTTGGCTC
 >CD28_HsgRNA7
 CCCTGCTTGTGGTAGATAGCAACGAGGTCA
 >CD28_HsgRNA8
 CCTCGTTGCTATCTACCACAAGCAGGGGCG
 >CD28_HsgRNA9
 GCCCTCATCAGAACAATGACACTCAGGCTG
 >CD28_HsgRNA10
 GAACTCGGCATTCGAGCGAAACTGGGGCTG
 >CD28_HsgRNA11
 TGATTGACGTGCAGATTCCAGAGACGGAAC
 >CD28_HsgRNA12
 AGGTTGTAGGAATACCTGCAGCTGAGGCTG
 >CD28_HsgRNA13
 GGAATTCGGGCATCCCTGTACAAGGGCGT
 >CD28_HsgRNA14
 CAACTTCTTCTCAGTTCAAGTAACAGGTAA
 >CD28_HsgRNA15
 CTCGTTGCTATCTACCACAAGCAGGGGCGA

(14) S_{14}^+ : 34 high on-target activity sgRNAs targeting H2-K

>H2-K_HsgRNA1
 GCGGAGAATCCGAGATATGAGCCGCGGGCG
 >H2-K_HsgRNA2
 AAGCAGAGAGACTCAGGGCCTACCTGGAGG
 >H2-K_HsgRNA3
 CACCAGCCTGCTCCCACTTGTGTTTGGTGA
 >H2-K_HsgRNA4
 TCGTAGGCGTACTGCTGGTACCCGCGGAGG
 >H2-K_HsgRNA5
 CAGGAGGGGCCCCGAGTATTGGGAGCGGGAG
 >H2-K_HsgRNA6
 AGGGCAATGAGCAGAGTTTCCGAGTGGACC
 >H2-K_HsgRNA7
 CCACCACAGATGCCCACTTCTGGAAGGTTC
 >H2-K_HsgRNA8
 TGATCACCAAACACAAGTGGGAGCAGGCTG

>H2-K_HsgRNA9
ACTTCCATGTACCGGGGCTCCCCGAGGCCG
>H2-K_HsgRNA10
GTGACGAAATACCTCAGCGAGTGTGGGCCT
>H2-K_HsgRNA11
TGAACGAAGACCTGAAAACGTGGACGGCGG
>H2-K_HsgRNA12
GCGGCGCTGATCACCAAACACAAGTGGGAG
>H2-K_HsgRNA13
CTCCCGGCCCGTACTCACCCGCGCGGGTC
>H2-K_HsgRNA14
TAGGCGTACTGCTGGTACCCGCGGAGGAGT
>H2-K_HsgRNA15
TCCACGTAGCCGACTTCCATGTACCGGGGC
>H2-K_HsgRNA16
AGACCTGAAGATAAAGTCACCCTGAGGTGC
>H2-K_HsgRNA17
TGCTCTGGTTGTAGTAGCCGAGCAGGGTCC
>H2-K_HsgRNA18
AAATCTTCCACACAGATTCCCCAAAGGCC
>H2-K_HsgRNA19
CTCGGAAACTCTGCTCATTGCCCTTGGCTT
>H2-K_HsgRNA20
CAGAGAGACTCAGGGCCTACCTGGAGGGCA
>H2-K_HsgRNA21
CCGAGATATGAGCCGCGGGCGGGTGGATG
>H2-K_HsgRNA22
CCGAGCAGGGTCCTCAGGTCCACTCGGAAA
>H2-K_HsgRNA23
GCGGGCGCGGTGGATGGAGCAGGAGGGGCC
>H2-K_HsgRNA24
CGGCGCTGATCACCAAACACAAGTGGGAGC
>H2-K_HsgRNA25
TCTGGCTGTGAAGTGGGGTCCGACGGGCGA
>H2-K_HsgRNA26
CCCTGGCTCCGACTCAGACCCGCGGGGTG
>H2-K_HsgRNA27
CGCGGGTCTGAGTCGGAGCCAGGGCGGCCG
>H2-K_HsgRNA28
CCCCGTACATGGAAGTCGGCTACGTGGACG
>H2-K_HsgRNA29
CCACGTAGCCGACTTCCATGTACCGGGGCT
>H2-K_HsgRNA30
CGGGTACCAGCAGTACGCCTACGACGGCTG

>H2-K_HsgRNA31
CACGTAGCCGACTTCCATGTACCGGGGCTC
>H2-K_HsgRNA32
CAGGTCTGCTGTGATGGGTCACATGGGCCT
>H2-K_HsgRNA33
AGGCTGGTGAAGCAGAGAGACTCAGGGCCT
>H2-K_HsgRNA34
TCTGTGTCTCCCGCTCCCAATACTCGGGCC

(15) S_{15}^+ : 56 high on-target activity sgRNAs targeting CD45

>CD45_HsgRNA1
TGACAAAGACTTCTGTGTCCAGAAGGGCAA
>CD45_HsgRNA2
CCAGAAATGATGATTGCTGCTCAGGGGCCA
>CD45_HsgRNA3
CAGAAACGCCTAAGCCTAGTTGTGGGGATC
>CD45_HsgRNA4
AGCTAAGGCGACAGAGGTGTCTGATGGTGC
>CD45_HsgRNA5
CCAGAAGTTTGAGCCACAAACCCATGGTCA
>CD45_HsgRNA6
AGACAATAGTATAAATGTTACATGTGGTCC
>CD45_HsgRNA7
CATTAATGCATCCTTTGTGATGGTAGGTAC
>CD45_HsgRNA8
CATCAATGTAGCTGGCATTATGTAGGTGG
>CD45_HsgRNA9
TTGGAATGTCTCAGCTCAAAAGTTCGGAGA
>CD45_HsgRNA10
ACTTACATAGCTGCACACCACCCAGGCCG
>CD45_HsgRNA11
TGTAACATTTATACTATTGTCTGTCGGCCG
>CD45_HsgRNA12
TCACACGATGTGAAGAAGGAAACAGGGTAA
>CD45_HsgRNA13
CTGCACTTTCCAAGAGATTGAACAAGGCAC
>CD45_HsgRNA14
GCGCAGAATACTGGCCAAGCATGGAGGAAG
>CD45_HsgRNA15
GATGAGACAGTTGATGACTTCTGGAGGATG
>CD45_HsgRNA16
CCTTAGTGCTGGTGTGGGCGTACAGGTAC
>CD45_HsgRNA17
AACTATAGATTTATATGTACCACCAGGTGA

>CD45_HsgRNA18
TCTTATAGCATAAAAACATATCCATGGGGTT
>CD45_HsgRNA19
TTTGATAGGTCCGGACAAGGTCAATGGAAT
>CD45_HsgRNA20
TTTAATCAGATGATTATAACCGTGTGGAAC
>CD45_HsgRNA21
TTTGATCAGGGCTTCAAGGAACCCAGGAAA
>CD45_HsgRNA22
CAGGCAGCTCTTCCCCTTTCCATGTGGTAC
>CD45_HsgRNA23
CCAGCATGGCATCAATTCCAATGTAGGTAC
>CD45_HsgRNA24
AATACATTAATGCATCCTTTGTGATGGTAG
>CD45_HsgRNA25
AGTACCAGTGTACCACATGGAAAGGGGAAG
>CD45_HsgRNA26
AAGGCCTGGAAGCAGAGGGCAAAGTGGATG
>CD45_HsgRNA27
GCTACCTGGTATTTCAGCCTCCAGAGGGGAG
>CD45_HsgRNA28
CTCTCTGAAATAAATGGAGATGCAGGGTCC
>CD45_HsgRNA29
GACAGAGATGGATCCCAGCAGACAGGGTTG
>CD45_HsgRNA30
AGGTGAGGGTCTTCAGGAACCCCATGGTCT
>CD45_HsgRNA31
GACAGAGGTGTCTGATGGTGCAAGTGGAGG
>CD45_HsgRNA32
ACCTGAGTCTGCATCTAAACCCCATGGATA
>CD45_HsgRNA33
TCTTGCAGCTGGATCCCCACAACCTAGGCTT
>CD45_HsgRNA34
CCCAGCATCGTACCTGGCTCACAGTGGAGT
>CD45_HsgRNA35
GATGGGAAACTTGCTGAATACCCGTGGAAT
>CD45_HsgRNA36
AGCTGGATCCCCACAACCTAGGCTTAGGCGT
>CD45_HsgRNA37
TCAGGGGCCACTAAAAGAAACGATCGGTGA
>CD45_HsgRNA38
TTTAGGGCCATTAGTTTCATAAGGAGGACC
>CD45_HsgRNA39
ACTTGTACTTAACTCCTAGGGCCCCGGGAT

>CD45_HsgRNA40
 ATGTGTAGCAGAAATCTTATATCGCGGTGT
 >CD45_HsgRNA41
 ATTTGTATCTTTCAGAGCATTCCACGGGTA
 >CD45_HsgRNA42
 AGAGGTGTCTGATGGTGCAAGTGGAGGTAC
 >CD45_HsgRNA43
 GTTATAAATGTGCAGACAGATTTGGGGAGT
 >CD45_HsgRNA44
 TTCCTAACCTGCAGTGGACGAGGATGGATG
 >CD45_HsgRNA45
 CTTGTACTTAACTCCTAGGGCCCCGGGATG
 >CD45_HsgRNA46
 CTTATAGCATAAAAACATATCCATGGGGTTT
 >CD45_HsgRNA47
 TTCTTATAGCATAAAAACATATCCATGGGGT
 >CD45_HsgRNA48
 TTTGTATCTTTCAGAGCATTCCACGGGTAT
 >CD45_HsgRNA49
 GAAGTCATCAACTGTCTCATCCCGGGGCC
 >CD45_HsgRNA50
 CCTTTCCATGTGGTACACTGGTACTGGTAC
 >CD45_HsgRNA51
 GCTTTGCGTAGAGACTTTACCACTTGAAAA
 >CD45_HsgRNA52
 ATCGTGTGACCATGACAATAACTGTGGCCT
 >CD45_HsgRNA53
 GTCTTTACCTGCAGTGCACCACAATGGGAC
 >CD45_HsgRNA54
 CCATTTATTTTCAGAGAGTTCCACACGGTTA
 >CD45_HsgRNA55
 CCAATTCACCAGCTGGCCAGACCATGGGGT
 >CD45_HsgRNA56
 TATGTTGTCAAGCTAAGGCGACAGAGGTGT

(16) S_{16}^+ : 13 high on-target activity sgRNAs targeting THY1

>THY1_HsgRNA1
 AGCCAACCTCACCACCAAGGATGAGGGCGA
 >THY1_HsgRNA2
 GTGCCAGTCTTGCAGGTGTCCCGAGGGCAG
 >THY1_HsgRNA3
 TTCTCATGGCGGCAGTCCAGGCGAAGGTTT
 >THY1_HsgRNA4
 TGTGCCAGTCTTGCAGGTGTCCCGAGGGCA

>THY1_HsgRNA5
 TTACCCTAGCCAACTTCACCACCAAGGATG
 >THY1_HsgRNA6
 TTATCCTTGGTGTATTCTCATGGCGGCAG
 >THY1_HsgRNA7
 GGTACGTGTGCTCGGGTATCCCAAGGGTGC
 >THY1_HsgRNA8
 AGGGCTGGTTGGAGAGGGTGACGCGGGAGC
 >THY1_HsgRNA9
 CATCCTTGGTGGTGAAGTTGGCTAGGGTAA
 >THY1_HsgRNA10
 CACAGACAAGCTGGTCAAGTGTGGCGGCAT
 >THY1_HsgRNA11
 CCTTGATATAGGGCTGGTTGGAGAGGGTGA
 >THY1_HsgRNA12
 TCTCGGGTCAGGCTGAACTCATGCTGGATG
 >THY1_HsgRNA13
 TTGGTGGTGAAGTTGGCTAGGGTAAGGACC

(17) S_{17}^+ : 35 high on-target activity sgRNAs targeting CD43

>CD43_HsgRNA1
 ACAGAACTGGTTGCTGTGGTAGCAGGGAGT
 >CD43_HsgRNA2
 CGCCACAACAGCAGTAGCGCCACGAGGGCC
 >CD43_HsgRNA3
 GAAGACAATTCAGTAGTTTCCAAGGGGGTTC
 >CD43_HsgRNA4
 AAGAAGACAATTCAGTAGTTTCCAAGGGGG
 >CD43_HsgRNA5
 CTGCAGTTCCGTCTGTCCACAGGATTGGCTG
 >CD43_HsgRNA6
 AAGACAATTCAGTAGTTTCCAAGGGGGTCA
 >CD43_HsgRNA7
 GTCACCACAGCTACTGGGTCTCTGGGGCCC
 >CD43_HsgRNA8
 AATGCCAGCCCATCAGTTTCTGTGGGGTCA
 >CD43_HsgRNA9
 TCTACCCAAGATCCCATAACCACCAGGTCA
 >CD43_HsgRNA10
 TGGACCCAGCATGCCCAAAGAGGAGGAGA
 >CD43_HsgRNA11
 GTCCCTGACCCACAGAACTGATGGGCTG
 >CD43_HsgRNA12
 GGAGCTTACTGTTGTAGCCACAGAGGGTCC

>CD43_HsgRNA13
ATGTCTTGCTGGAAACTTCCTGAGAGGCAG
>CD43_HsgRNA14
GCTGGAAACTTCCTGAGAGGCAGTAGGCTC
>CD43_HsgRNA15
AGAAGACAATTCAGTAGTTTCCAAGGGGGT
>CD43_HsgRNA16
ACAGGATTGGCTGCAGTGACAGGAGGGTCA
>CD43_HsgRNA17
CCTTGCACCTTCTCCTCCTCTTTGGGGCAT
>CD43_HsgRNA18
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA19
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA20
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA21
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA22
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA23
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA24
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA25
CACTGCAGCCAATCCTGTGACAGACGGACC
>CD43_HsgRNA26
ATTGGCTGCAGGTCCGTCTGTCACAGGATT
>CD43_HsgRNA27
AGATGCTGCAGTTCCGTCTGTCACAGGATT
>CD43_HsgRNA28
ATGGGCTGGCATTCTGGGCTTCAGAGGTAC
>CD43_HsgRNA29
TGGAGCTGTGATATGTGGGGTAGATGGTAG
>CD43_HsgRNA30
ACCTGGACCCAGCATGCCCCAAAGAGGAGG
>CD43_HsgRNA31
TCTGGGGCCCTCGAGTGAGATGCATGGACT
>CD43_HsgRNA32
TTGTGGTCTGCCCCAGGGGCTGATGGTCT
>CD43_HsgRNA33
AGAGGTACTTGGAGCTGTGATATGTGGGGT
>CD43_HsgRNA34
TCTTTGGGGCATGCTGGGTCCAGGTGGCGA

>CD43_HsgRNA35
TTGATTCTTGGCTTGGTGACCTGGTGGTTA

(18) S_1 : 377 low on-target activity sgRNAs targeting CD13

>CD13_LsgRNA1
TCAGAAATAATACCAACAACCTGGAGGGAGA

>CD13_LsgRNA2
GTCAAACAGCTCACTGATCTGGGCCGGCGT

>CD13_LsgRNA3
CATGAACCGCTGGACCCTGCAGATGGGCTT

>CD13_LsgRNA4
CCAGAACGATCTCTTCAGCACATCAGGCAA

>CD13_LsgRNA5
CGGTAACGATTCCACGCTTTACTTTGGTCC

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>CD13_LsgRNA348
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>CD13_LsgRNA349
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>CD13_LsgRNA368
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>CD13_LsgRNA370
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>CD13_LsgRNA371
TACTTTGGTCCAAGGTGGTGGCCGAGGCGG
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GGGGTGGTGGTGGCTGAGGCGGACGGGGT

>CD13_LsgRNA373
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 >CD13_LsgRNA374
 ACGCTTTACTTTGGTCCAAGGTGGTGGCCG
 >CD13_LsgRNA375
 ATTATTTCTGAAGTGAATGAAGAGGGGTGT
 >CD13_LsgRNA376
 CATGTTTGACCGCTCCGAGGTCTATGGCCC
 >CD13_LsgRNA377
 CACCTTTGGGAAGCATGTTGGACAGGGCTG

(19) S_2^- : 218 low on-target activity sgRNAs targeting CD15

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 >CD15_LsgRNA2
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 >CD15_LsgRNA3
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 >CD15_LsgRNA4
 GTGGAAGTAGCGGCGATAGACCGCGGGGT
 >CD15_LsgRNA5
 CCGAAATTGGGCTCCTGCACACAGTGGCCC
 >CD15_LsgRNA6
 CCGAACACGTCCACGGTCACATGTTGGCTC
 >CD15_LsgRNA7
 GGAAACAGGGGCTGGTGGCATGGGTGGTGA
 >CD15_LsgRNA8
 TTCCACCACCGCGACCTCGTGAAGGGGCC
 >CD15_LsgRNA9
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 >CD15_LsgRNA10
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 >CD15_LsgRNA11
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 >CD15_LsgRNA12
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>CD15_LsgRNA17
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>CD15_LsgRNA37
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>CD15_LsgRNA38
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>CD15_LsgRNA39
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>CD15_LsgRNA145
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>CD15_LsgRNA169
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>CD15_LsgRNA170
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>CD15_LsgRNA171
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>CD15_LsgRNA215
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>CD15_LsgRNA216
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>CD15_LsgRNA217
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>CD15_LsgRNA218
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(20) S_3^- : 126 low on-target activity sgRNAs targeting CD33

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>CD33_LsgRNA6
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>CD33_LsgRNA37
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>CD33_LsgRNA38
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>CD33_LsgRNA40
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 >CD33_LsgRNA124
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 >CD33_LsgRNA125
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 GGAGTTCTTGTCTAGTAGGGTATGGGATG

(21) S_4 : 119 low on-target activity sgRNAs targeting CCDC101

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>CCDC101_LsgRNA2
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>CCDC101_LsgRNA3
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>CCDC101_LsgRNA4
ACTCACAGGCCCCACCCCTCTGTGGGGCC
>CCDC101_LsgRNA5
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>CCDC101_LsgRNA7
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>CCDC101_LsgRNA8
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>CCDC101_LsgRNA9
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>CCDC101_LsgRNA10
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>CCDC101_LsgRNA11
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>CCDC101_LsgRNA12
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>CCDC101_LsgRNA15
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>CCDC101_LsgRNA16
GAGACAAGGTGGCTGCCCGGGTGAAGGCCG
>CCDC101_LsgRNA17
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>CCDC101_LsgRNA18
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>CCDC101_LsgRNA19
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>CCDC101_LsgRNA20
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>CCDC101_LsgRNA28
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>CCDC101_LsgRNA29
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>CCDC101_LsgRNA31
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>CCDC101_LsgRNA67
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>CCDC101_LsgRNA113
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>CCDC101_LsgRNA116
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>CCDC101_LsgRNA117
CCTCTGTGGGGCCATCCCTGCCTCAGGAGA
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(22) S_5^- : 1478 low on-target activity sgRNAs targeting MED12

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>MED12_LsgRNA4
TGAGAAACATAAGGAGTATAGCCCTGGAGG
>MED12_LsgRNA5
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>MED12_LsgRNA6
CCAAAAACCAGGGGCCGGTGCTGAGGGCAC
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CCGCAAAGGGACAGCAGAACTGGTGGGTT
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>MED12_LsgRNA12
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>MED12_LsgRNA13
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 >MED12_LsgRNA1476
 AGGGTTTGGGTGGTGCAGGAGGTCCGGAGG
 >MED12_LsgRNA1477
 CAAATTTGTTCTTTAAATGGCTACAGGAGG
 >MED12_LsgRNA1478
 CAAATTTGTTCTTTAAATGGCTACAGGAGG

(23) S_6^- : 152 low on-target activity sgRNAs targeting TADA2B

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 >TADA2B_LsgRNA3
 CAAAAACCTAGCCGGCTCCAAACGGGGAAA
 >TADA2B_LsgRNA4
 CCAAAAAGCCGCCTTCCTAGCTACCTGGACA
 >TADA2B_LsgRNA5
 GAGGAAGGAGAACAAAAACCTAGCCGGCTC
 >TADA2B_LsgRNA6
 CTACAATCTGGTGCCAGCCTTCCTGGGGAA
 >TADA2B_LsgRNA7
 TCTGACAGGAGCTCGAAGCCTGGAAGGTTTC

>TADA2B_LsgRNA8
GAGTACGAGGCAGCGCGGCATAAACGGGAG
>TADA2B_LsgRNA9
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>TADA2B_LsgRNA10
GTGGACGGCGGGCGCTTACGCTCTGGGGG
>TADA2B_LsgRNA11
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>TADA2B_LsgRNA12
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>TADA2B_LsgRNA13
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>TADA2B_LsgRNA14
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>TADA2B_LsgRNA15
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>TADA2B_LsgRNA16
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>TADA2B_LsgRNA17
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>TADA2B_LsgRNA18
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>TADA2B_LsgRNA19
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>TADA2B_LsgRNA20
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>TADA2B_LsgRNA21
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>TADA2B_LsgRNA22
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>TADA2B_LsgRNA23
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>TADA2B_LsgRNA24
TACAATCTGGTGCCAGCCTTCTGGGGAAG
>TADA2B_LsgRNA25
GAGCATGTACATCCACGGGAACCTGGGGAA
>TADA2B_LsgRNA26
TTGAATTTCTCACAGAAAGCGGCTGGATC
>TADA2B_LsgRNA27
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>TADA2B_LsgRNA28
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>TADA2B_LsgRNA29
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>TADA2B_LsgRNA30
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>TADA2B_LsgRNA31
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>TADA2B_LsgRNA32
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>TADA2B_LsgRNA33
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>TADA2B_LsgRNA34
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>TADA2B_LsgRNA35
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>TADA2B_LsgRNA36
GCTCCATCACCTCTTGGGGAGTCCGGGAAG
>TADA2B_LsgRNA37
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>TADA2B_LsgRNA38
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>TADA2B_LsgRNA39
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>TADA2B_LsgRNA40
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>TADA2B_LsgRNA41
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>TADA2B_LsgRNA42
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>TADA2B_LsgRNA43
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>TADA2B_LsgRNA44
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>TADA2B_LsgRNA46
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>TADA2B_LsgRNA47
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>TADA2B_LsgRNA48
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>TADA2B_LsgRNA62
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>TADA2B_LsgRNA63
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>TADA2B_LsgRNA65
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>TADA2B_LsgRNA66
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>TADA2B_LsgRNA67
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>TADA2B_LsgRNA69
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>TADA2B_LsgRNA70
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>TADA2B_LsgRNA72
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>TADA2B_LsgRNA74
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>TADA2B_LsgRNA76
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>TADA2B_LsgRNA77
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>TADA2B_LsgRNA84
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>TADA2B_LsgRNA92
GACGGCGGGCGCTTCACGCTCTGGGGGCC
>TADA2B_LsgRNA93
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>TADA2B_LsgRNA94
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>TADA2B_LsgRNA103
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>TADA2B_LsgRNA104
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>TADA2B_LsgRNA105
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>TADA2B_LsgRNA106
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>TADA2B_LsgRNA107
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>TADA2B_LsgRNA109
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>TADA2B_LsgRNA110
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>TADA2B_LsgRNA111
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>TADA2B_LsgRNA112
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>TADA2B_LsgRNA113
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>TADA2B_LsgRNA114
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>TADA2B_LsgRNA115
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>TADA2B_LsgRNA116
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>TADA2B_LsgRNA117
AGCTGGTAGCCGTGGTAGCGGCGGTGGTGG

>TADA2B_LsgRNA118
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>TADA2B_LsgRNA119
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>TADA2B_LsgRNA120
ATCTGGTGCCAGCCTTCCTGGGGAAGGACA
>TADA2B_LsgRNA121
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>TADA2B_LsgRNA122
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>TADA2B_LsgRNA123
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>TADA2B_LsgRNA124
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>TADA2B_LsgRNA125
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>TADA2B_LsgRNA126
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>TADA2B_LsgRNA128
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>TADA2B_LsgRNA129
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>TADA2B_LsgRNA130
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>TADA2B_LsgRNA131
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>TADA2B_LsgRNA132
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>TADA2B_LsgRNA133
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>TADA2B_LsgRNA134
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>TADA2B_LsgRNA137
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>TADA2B_LsgRNA138
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>TADA2B_LsgRNA139
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>TADA2B_LsgRNA140
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 >TADA2B_LsgRNA141
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 >TADA2B_LsgRNA142
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 >TADA2B_LsgRNA143
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 >TADA2B_LsgRNA144
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 >TADA2B_LsgRNA145
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 >TADA2B_LsgRNA146
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 >TADA2B_LsgRNA147
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 >TADA2B_LsgRNA148
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 >TADA2B_LsgRNA149
 GGGATTCCTTGCCGCTTCTGGAGGTGGTCT
 >TADA2B_LsgRNA150
 GTGCTTCTCGGCCGGCGCCGAGATCGGCCA
 >TADA2B_LsgRNA151
 GATTTTGAATTTCTCACAGAAAGCGGCTG
 >TADA2B_LsgRNA152
 CTTCTTGTCTTCCCCAGGAAGGCTGGCAC

(24) S₇: 87 low on-target activity sgRNAs targeting TADA1

>TADA1_LsgRNA1
 TTCAAAAAGATCGTACATGTTACCCGGAGG
 >TADA1_LsgRNA2
 AAGGAAAGCTTATCGGTTACGAGATGGTCA
 >TADA1_LsgRNA3
 ATTGAAAGGATCATCACGAAACTCTGGCAT
 >TADA1_LsgRNA4
 TTGTAAGCTACTACACTATTCTTCAGGTAT
 >TADA1_LsgRNA5
 CACAAATTGCTGGGCTCCTGAGAGAGGATT
 >TADA1_LsgRNA6
 CCACACAATGATGCTTCCCCTCGAGGCCA
 >TADA1_LsgRNA7
 AGCTACTACACTATTCTTCAGGTATGGCTG
 >TADA1_LsgRNA8
 TCATAGACTTCTCACACAGGATAATGGTAA

>TADA1_LsgRNA9
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>TADA1_LsgRNA10
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>TADA1_LsgRNA11
CCGCAGCAAAACCTGGAAAACCCAAGGGAA
>TADA1_LsgRNA12
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>TADA1_LsgRNA13
CGCCAGCGCTTGGCAGCCAAGGAGGGGCTT
>TADA1_LsgRNA14
TTGAAGCTCATAGACTTCTCACACAGGATA
>TADA1_LsgRNA15
GAGAAGCTGGATTCTGACCAGCACAGGGAG
>TADA1_LsgRNA16
GCACAGGGAGCAGTAAAAGCTGGAGGGCTG
>TADA1_LsgRNA17
CTCGAGTGGGAAGCATCATTGTGTGGGAAC
>TADA1_LsgRNA18
GGGGATCCTTTGCCACAAATTGCTGGGCTC
>TADA1_LsgRNA19
CTAGATGGTGCTGGATCTTTGCCTTGGCCA
>TADA1_LsgRNA20
CACTATTCTTCAGGTATGGCTGCGGGGTCA
>TADA1_LsgRNA21
AAGACAAAGTTCACCGCCAGCGCTTGGCAG
>TADA1_LsgRNA22
ATTCCAGCCTCAAATCCTCTCTCAGGAGC
>TADA1_LsgRNA23
CCGCCAGCGCTTGGCAGCCAAGGAGGGGCT
>TADA1_LsgRNA24
AGCACAGGGAGCAGTAAAAGCTGGAGGGCT
>TADA1_LsgRNA25
CTTCCCACTCGAGGCCAGCTTGAAGGGAGA
>TADA1_LsgRNA26
ACCGCCAGCGCTTGGCAGCCAAGGAGGGGC
>TADA1_LsgRNA27
GCTTCCCACTCGAGGCCAGCTTGAAGGGAG
>TADA1_LsgRNA28
CACCCCCTGATGATGCTGAGCAGCAGGCTG
>TADA1_LsgRNA29
TTCTCCCTTCAAGCTGGCCTCGAGTGGGAA
>TADA1_LsgRNA30
TTCACCGCCAGCGCTTGGCAGCCAAGGAGG

>TADA1_LsgRNA31
AGCCCCCTCCTTGGCTGCCAAGCGCTGGCGG
>TADA1_LsgRNA32
GCAGCCTGCTGCTCAGCATCATCAGGGGGT
>TADA1_LsgRNA33
TCTCCCTTCAAGCTGGCCTCGAGTGGGAAG
>TADA1_LsgRNA34
CCCTCCTTGGCTGCCAAGCGCTGGCGGTGA
>TADA1_LsgRNA35
TGGCCGCTCCAGCTCGCTCACAAAGGTCG
>TADA1_LsgRNA36
GCTGCGGGGTCACGTTACTGCCAAAGGCAT
>TADA1_LsgRNA37
GTCACTATCATTTCTCCCTTCAAGCTGGCCT
>TADA1_LsgRNA38
TACACTATTCTTCAGGTATGGCTGCGGGGT
>TADA1_LsgRNA39
CTCTCTCAGGAGCCAGCAATTTGTGGCAA
>TADA1_LsgRNA40
ACAACCTGACGTCAGTATATCTTTAAGGTGA
>TADA1_LsgRNA41
CAGCCTGCTGCTCAGCATCATCAGGGGGTG
>TADA1_LsgRNA42
GGTGCTGGATCTTTGCCTTGGCCAGGGGGT
>TADA1_LsgRNA43
GTAGCTTACAACAACCTTAATAGAAAGGTAA
>TADA1_LsgRNA44
CGACCTTTGTGAGCGAGCTGGAGGCGGCCA
>TADA1_LsgRNA45
ATCTGACAACGCGTGAGAATGGCCAGGAGG
>TADA1_LsgRNA46
TGGCGACCTTTGTGAGCGAGCTGGAGGCGG
>TADA1_LsgRNA47
TAGTGACTGCTTATGAGCATGGGCTGGACA
>TADA1_LsgRNA48
TTAAGAGCATAGACAGTATGTGTAGGGATG
>TADA1_LsgRNA49
TGGGGATCCTTTGCCACAAATTGCTGGGCT
>TADA1_LsgRNA50
CGCAGCAAACCTTGAAAACCCAAGGGAAA
>TADA1_LsgRNA51
CAAGGCAAAGATCCAGCACCATCTAGGAGA
>TADA1_LsgRNA52
TTTAGCACAGCAAAGCCCTCCTTGGCTG

>TADA1_LsgRNA53
ACCAGCACAGGGAGCAGTAAAAGCTGGAGG
>TADA1_LsgRNA54
GGCTGCACTCCTGCTGGCATGCTCCGGAGA
>TADA1_LsgRNA55
CTGAGCAGCAGGCTGCACTCCTGCTGGCAT
>TADA1_LsgRNA56
TGCAGCCTGCTGCTCAGCATCATCAGGGGG
>TADA1_LsgRNA57
TGCTGCTCAGCATCATCAGGGGGTGGGTGA
>TADA1_LsgRNA58
TTTTGCTGCGGAACCCCTGGCCAAGGCAA
>TADA1_LsgRNA59
ATGGGCTGGACAATGTCACCGAGGAGGCTG
>TADA1_LsgRNA60
TGGTGCTGGATCTTTGCCTTGCCAGGGGG
>TADA1_LsgRNA61
AGAAGCTGGATTCTGACCAGCACAGGGAGC
>TADA1_LsgRNA62
GCCAGGAGGAAATCATTGTGAGAATGGACT
>TADA1_LsgRNA63
TGCTGGATCTTTGCCTTGCCAGGGGGTTC
>TADA1_LsgRNA64
GTAGGGATGACTTCCCTGTGCACCTGGGAT
>TADA1_LsgRNA65
CCAGGGCCTCGCTTAAGTTCTTCTTGCCG
>TADA1_LsgRNA66
GCCAGGGGGTTCCGCAGCAAAAACCTGGAAA
>TADA1_LsgRNA67
TTCTGTTCGTCAGAAATTTGATGTAGGTTG
>TADA1_LsgRNA68
AGCTGTTGTCTATGCTGTGGAGGTTGGTTT
>TADA1_LsgRNA69
CAAAGTTTCAAGTCGTCATCATCTTGGGGA
>TADA1_LsgRNA70
TATTGTTTCTGCCTCTGCAGATACTGGGCT
>TADA1_LsgRNA71
ACACTATTCTTCAGGTATGGCTGCGGGGTC
>TADA1_LsgRNA72
ACACTCTACCTGCATCTTTGCCTCCGGTGA
>TADA1_LsgRNA73
ACTGTCTATGCTCTTAACATTGAAAGGATC
>TADA1_LsgRNA74
ATCTTCTGCTTGAACCACAGCTTTAGGTTA

>TADA1_LsgRNA75
 ATACTGACGTCAGTTGTGTCAAGAAGGAAA
 >TADA1_LsgRNA76
 TGTGTGAGAAGTCTATGAGCTTCAAGGTCA
 >TADA1_LsgRNA77
 CTGCTGCTCAGCATCATCAGGGGGTGGGTG
 >TADA1_LsgRNA78
 GTCTTGCTGCAGCTCTTCATGATTTGGATG
 >TADA1_LsgRNA79
 AGCCTGCTGCTCAGCATCATCAGGGGGTGG
 >TADA1_LsgRNA80
 GTGCTGGATCTTTGCCTTGGCCAGGGGGTT
 >TADA1_LsgRNA81
 GTTGTGTCAAGAAGGAAAGCTTATCGGTTA
 >TADA1_LsgRNA82
 AGAGTGTCTCCGGAGCATGCCAGCAGGAGT
 >TADA1_LsgRNA83
 AAGTTTCAAGTCGTCATCATCTTGGGGATC
 >TADA1_LsgRNA84
 CATGTTACCCGGAGGCAAAGATGCAGGTAG
 >TADA1_LsgRNA85
 ATATTTCTGTCTCCTAGATGGTGCTGGATC
 >TADA1_LsgRNA86
 AAAGTTTCAAGTCGTCATCATCTTGGGGAT
 >TADA1_LsgRNA87
 ATTGTTTCTGCCTCTGCAGATACTGGGCTA

(25) S_8^- : 51 low on-target activity sgRNAs targeting HPRT1

>HPRT1_LsgRNA1
 GGTGAAAAGGACCCACGAAGTGTGGATA
 >HPRT1_LsgRNA2
 TGATAAAATCTACAGTCATAGGAATGGATC
 >HPRT1_LsgRNA3
 AAAAAAGTAATTCACTTACAGTCTGGCTT
 >HPRT1_LsgRNA4
 TTCCAAATCCTCAGCATAATGATTAGGTAT
 >HPRT1_LsgRNA5
 TTTTAACTAGAATGACCAGTCAACAGGGGA
 >HPRT1_LsgRNA6
 GCAAAAATAAATCAAGGTCATAACCTGGTTC
 >HPRT1_LsgRNA7
 AAACAATGCAGACTTTGCTTTCCTTGGTCA
 >HPRT1_LsgRNA8
 GTCAACAGGGGACATAAAAAGTAATTGGTGG

>HPRT1_LsgRNA9
TTTAACTAGAATGACCAGTCAACAGGGGAC
>HPRT1_LsgRNA10
ATGCAGACTTTGCTTTCCTTGGTCAGGCAG
>HPRT1_LsgRNA11
CGCCAGGGCTGCGGGTCGCCATAACGGAGC
>HPRT1_LsgRNA12
TGAAATTCCAGACAAGTTTGTGTAGGATA
>HPRT1_LsgRNA13
AATCCAAAGATGGTCAAGGTCGCAAGGTAT
>HPRT1_LsgRNA14
AGCACACAGAGGGCTACAATGTGATGGCCT
>HPRT1_LsgRNA15
TGCTCACCACGACGCCAGGGCTGCGGGTCG
>HPRT1_LsgRNA16
TTTTTCAGATTAGTGATGATGAACCAGGTTA
>HPRT1_LsgRNA17
TTTGCATACCTAATCATTATGCTGAGGATT
>HPRT1_LsgRNA18
TGCTCGAGATGTGATGAAGGAGATGGGAGG
>HPRT1_LsgRNA19
ATTCCTCATGGACTAATTATGGACAGGTAA
>HPRT1_LsgRNA20
CAGTCTGATAAAATCTACAGTCATAGGAAT
>HPRT1_LsgRNA21
TTACCTGTCCATAATTAGTCCATGAGGAAT
>HPRT1_LsgRNA22
CTGGCTTATATCCAACACTTCGTGGGGTCC
>HPRT1_LsgRNA23
TTTTCTTCTAGAATGTCTTGATTGTGGAAG
>HPRT1_LsgRNA24
ATACCTTGCGACCTTGACCATCTTTGGATT
>HPRT1_LsgRNA25
CCCTGAAGTATTCATTATAGTCAAGGGCAT
>HPRT1_LsgRNA26
GGCCGAGCTGCTCACCACGACGCCAGGGCT
>HPRT1_LsgRNA27
TGGAGATGATCTCTCAACTTTAACTGGAAA
>HPRT1_LsgRNA28
TCGAGATGTGATGAAGGAGATGGGAGGCCA
>HPRT1_LsgRNA29
TCTGGCTTATATCCAACACTTCGTGGGGTC
>HPRT1_LsgRNA30
GTCTGGCTTATATCCAACACTTCGTGGGGT

>HPRT1_LsgRNA31
 AACAGGGGACATAAAAAGTAATTGGTGGAGA
 >HPRT1_LsgRNA32
 CATTGTAGCCCTCTGTGTGCTCAAGGGGGG
 >HPRT1_LsgRNA33
 TTCAGTGCTTTGATGTAATCCAGCAGGTCA
 >HPRT1_LsgRNA34
 GCATGTTTGTGTCATTAGTGAAACTGGAAA
 >HPRT1_LsgRNA35
 GCTATAAATTCTTTGCTGACCTGCTGGATT
 >HPRT1_LsgRNA36
 TACCTAATCATTATGCTGAGGATTTGGAAA
 >HPRT1_LsgRNA37
 ATTGTAGCCCTCTGTGTGCTCAAGGGGGG
 >HPRT1_LsgRNA38
 TGATTAGGTATGCAAAATAAATCAAGGTCA
 >HPRT1_LsgRNA39
 GGCATATCCTACAACAAACTTGTCTGGAAT
 >HPRT1_LsgRNA40
 TGTTTATTCTCATGGACTAATTATGGACA
 >HPRT1_LsgRNA41
 CTGCTCACCACGACGCCAGGGCTGCGGGTC
 >HPRT1_LsgRNA42
 ATGATCTCTCAACTTTAACTGGAAAGGTAT
 >HPRT1_LsgRNA43
 AACGTCTTGCTCGAGATGTGATGAAGGAGA
 >HPRT1_LsgRNA44
 TTTTTGAAAGGATATAATTGACACTGGCAA
 >HPRT1_LsgRNA45
 TCCCTGAAGTATTCATTATAGTCAAGGGCA
 >HPRT1_LsgRNA46
 CCCTTGACTATAATGAATACTTCAGGGATT
 >HPRT1_LsgRNA47
 TCTTTGGATTATACTGCCTGACCAAGGAAA
 >HPRT1_LsgRNA48
 ACATTGTAGCCCTCTGTGTGCTCAAGGGGG
 >HPRT1_LsgRNA49
 GTAATTAACAGCTTGCTGGTGAAAAGGACC
 >HPRT1_LsgRNA50
 ATCATTATGCTGAGGATTTGGAAAAGGTGT
 >HPRT1_LsgRNA51
 GCCCTTGACTATAATGAATACTTCAGGGAT

(26) S₉: 123 low on-target activity sgRNAs targeting CUL3

>CUL3_LsgRNA1
GATGAAAAATATGTAAACAGCATTGGGAC
>CUL3_LsgRNA2
CGTCAAAACTGGAAGGAATGTTTAGGGATA
>CUL3_LsgRNA3
ATGAAAAATATGTAAACAGCATTGGGACC
>CUL3_LsgRNA4
AAAAAACATGATATCTAAGTTAAAGGTAA
>CUL3_LsgRNA5
CTCAAAAGCATGTCTTGGTGCTGGTGGGAT
>CUL3_LsgRNA6
AGGTAAAGCTCTTGTCTTCTGAAGAAGGAGA
>CUL3_LsgRNA7
CCGGAAAGGCCCGGATCCGCATCTTGGTGT
>CUL3_LsgRNA8
ACCCAAATCAAAGGAAATAGAAAATGGTCA
>CUL3_LsgRNA9
TAGAAACAATATTGGATAAAGCAATGGTCC
>CUL3_LsgRNA10
AATCAACGGAAGAACCAATTGTAAAGGTGG
>CUL3_LsgRNA11
TGATAAGCTGAAAAGGGAGTCAAAGGGGT
>CUL3_LsgRNA12
TCTGAATATCTCAAAGCATGTCTTGGTGC
>CUL3_LsgRNA13
TTTGAATCTTGACTCTGTGTAGTTGGATG
>CUL3_LsgRNA14
AACCAATTGTAAAGGTGGTTGAAAGGGAAC
>CUL3_LsgRNA15
CAGAACAAGAAGTAGAAACAATATTGGATA
>CUL3_LsgRNA16
GAGCACCATGTCTGAATCTGAGCAAAGGCAC
>CUL3_LsgRNA17
TCCGACCCAGAGAGGAAAGAAACAAGGCAG
>CUL3_LsgRNA18
TTGAACGTTATTATAAACAACACTTGGCAA
>CUL3_LsgRNA19
AAGGACTTATTGAGAGAGAATATTTGGCAC
>CUL3_LsgRNA20
GAGGAGAGACTCACCGAAAGGCCCGGATC
>CUL3_LsgRNA21
TTAAAGAGCATTAATATGGTCATCTGGAAA
>CUL3_LsgRNA22
CATGAGATAGAAGCTGCTATAGTGCGGATA

>CUL3_LsgRNA23
CGGAAGGACACCAAGATGCGGATCCGGGCC
>CUL3_LsgRNA24
ATTCAGGCAACATCTACAGGCAACTGGTGT
>CUL3_LsgRNA25
TGTGAGTGTATGAGTTCCTATTTGAGGGAG
>CUL3_LsgRNA26
TATGAGTTCCTATTTGAGGGAGCAAGGTAA
>CUL3_LsgRNA27
ATCAATAAATAATGAGAGGTATTCAGGAGA
>CUL3_LsgRNA28
TTCAATACGTTTCTTAATAACAACCTGGACT
>CUL3_LsgRNA29
GACTATAGTAGAAATGGAGAATTCTGGGCT
>CUL3_LsgRNA30
GAGAATATTTGGCACGAACACCTGAGGATC
>CUL3_LsgRNA31
AGAAAATCCAGCGTAAGAATAACAGTGGTCT
>CUL3_LsgRNA32
GGATATGATTGCAAGAGAGCGGAAAGGAGA
>CUL3_LsgRNA33
GTGGATGTCAGTTCACGTCAAACTGGAAG
>CUL3_LsgRNA34
CGTTATTATAAACAACACTTGGCAAGGAGA
>CUL3_LsgRNA35
CTCTATTATTAAGAGCATTAAATATGGTCA
>CUL3_LsgRNA36
AGGTATTCAGGAGACCTGGAGTTGAGGTTG
>CUL3_LsgRNA37
ATTTATTGATGATAAGCTGAAAAAGGGAGT
>CUL3_LsgRNA38
ACGTCAAACTGGAAGGAATGTTTAGGGAT
>CUL3_LsgRNA39
TGAGCAAAGGCACGGGCAGCCGGAAGGACA
>CUL3_LsgRNA40
CCCGCAATAGTTTGTAAAGAGACGGTCA
>CUL3_LsgRNA41
ACTACACAGAGTCAAGATTCAAACAGGTAT
>CUL3_LsgRNA42
ATGTCAGTTCACGTCAAACTGGAAGGAAT
>CUL3_LsgRNA43
AGCACATGAAGACTATAGTAGAAATGGAGA
>CUL3_LsgRNA44
TAAACATGGAGAAAAGCTCTACACTGGACT

>CUL3_LsgRNA45
CGGTCATTGTTGAATGATTCCAGGAGGAAG
>CUL3_LsgRNA46
GAACCCGCTGTGTTGGTTTACCACAGGCGA
>CUL3_LsgRNA47
CTCGCCTGTGGTAAACCAACACAGCGGGTT
>CUL3_LsgRNA48
TTTTTCGAGATCAAGTTGTACGTTATGGGTG
>CUL3_LsgRNA49
TGGGCTAGTACATATGTTGAAAAATGGAAA
>CUL3_LsgRNA50
AGCTCTATAGAAATGCATATACAATGGTTT
>CUL3_LsgRNA51
ACAGCTCACACTCCAGCATCATATGGGTTC
>CUL3_LsgRNA52
CCGTCTCTTTAAACAAACTATTGCGGGTGA
>CUL3_LsgRNA53
AGATCTGCAGAACCCATATGATGCTGGAGT
>CUL3_LsgRNA54
TCGCCTGTGGTAAACCAACACAGCGGGTTC
>CUL3_LsgRNA55
AGCTCTTGT'TTCTGAAGAAGGAGAAGGAAA
>CUL3_LsgRNA56
TTCCCTTTCAACCACCTTTACAATTGGTTC
>CUL3_LsgRNA57
GAAAGAATCCTGTTGACTATATCCAGGTAA
>CUL3_LsgRNA58
CTTGGAATGATCATCAAACAGCTATGGTGA
>CUL3_LsgRNA59
CTAAGACCACTGTTATTCTTACGCTGGATT
>CUL3_LsgRNA60
TCGAGACCTAAAATCATTAAACATCTGGCAA
>CUL3_LsgRNA61
TTTTCGAGATCAAGTTGTACGTTATGGGTGT
>CUL3_LsgRNA62
GTGTGAGCTGTCGACCACTGTGTTTGGCTA
>CUL3_LsgRNA63
CCAAGATGCGGATCCGGGCCTTTCCGGTGA
>CUL3_LsgRNA64
GGAAGATGGATCTGAAGTTGGTGTGGAGG
>CUL3_LsgRNA65
TGCAGCACAATGTTCTAGTAGCGGAGGTGA
>CUL3_LsgRNA66
AGATGCAGCACAATGTTCTAGTAGCGGAGG

>CUL3_LsgRNA67
GGCAGCCGGAAGGACACCAAGATGCGGATC
>CUL3_LsgRNA68
TTCTGCCTTGTTTCTTTCTCTCTGGGTCG
>CUL3_LsgRNA69
CCGTGCCTTTGCTCAGATTGACATGGTGC
>CUL3_LsgRNA70
GACAGCTCACACTCCAGCATCATATGGGTT
>CUL3_LsgRNA71
TAGGGCTCTAACAAGCTCTCTTTCAGGGAT
>CUL3_LsgRNA72
ATAAGCTGAAAAAGGGAGTCAAAGGGGTAA
>CUL3_LsgRNA73
TGGTGCTGGTGGGATGTTGCACTTTGGTGT
>CUL3_LsgRNA74
AAGGGCTTATTGGATCTGAAGAGTAGGTTC
>CUL3_LsgRNA75
GAGCGGAAAGGAGAAGTCGTAGACAGGTAA
>CUL3_LsgRNA76
CAACGGAAGAACCAATTGTAAAGGTGGTTG
>CUL3_LsgRNA77
GGAAGGACACCAAGATGCGGATCCGGGCCT
>CUL3_LsgRNA78
AGATGGATCTGAAGTTGGTGTGGAGGTGC
>CUL3_LsgRNA79
AGACGGTCATTGTTGAATGATTCCAGGAGG
>CUL3_LsgRNA80
GTGTGTATGTACAACAAAATAATGTGGAGA
>CUL3_LsgRNA81
CCATGTTCGAATCTGAGCAAAGGCACGGGCA
>CUL3_LsgRNA82
TAATGTGGAGAACGTCTACAATTTGGGATT
>CUL3_LsgRNA83
TTAGGTGGTGTGATCTTACAGTCCGGGTG
>CUL3_LsgRNA84
ATATGTGTATACTTTGCGATCCTCAGGTGT
>CUL3_LsgRNA85
GTGAGTGTATGAGTTCCTATTTGAGGGAGC
>CUL3_LsgRNA86
CGCTGTGTTGGTTTACCACAGGCGAGGGAC
>CUL3_LsgRNA87
AGTTGTTATTAAGAAACGTATTGAAGGACT
>CUL3_LsgRNA88
ATTGGTCTTCCGTTGATTTGTCAAGGCAG

>CUL3_LsgRNA89
TGGTGTGGAGGTGCACAAGTAACTGGCTC
>CUL3_LsgRNA90
GCATTAATATGGTCATCTGGAAAGTGGAAA
>CUL3_LsgRNA91
TTCTTACAAAAGAACCCAAATCAAAGGAAA
>CUL3_LsgRNA92
GGTTTACCACAGGCGAGGGACTGTAGGGCT
>CUL3_LsgRNA93
TTGTTACCGAACATCTCATAAATAAGGTAT
>CUL3_LsgRNA94
TTGATACCTTATTTATGAGATGTTTCGGTAA
>CUL3_LsgRNA95
TTTCTACTATAGTCTTCATGTGCTTGGAAA
>CUL3_LsgRNA96
ATAATAGAGAAAAATACACATTTGAGGTAT
>CUL3_LsgRNA97
AGAGTAGGTTTCGATCGCTTCCTCCTGGAAT
>CUL3_LsgRNA98
ACTATAGTAGAAATGGAGAATTCTGGGCTA
>CUL3_LsgRNA99
TATTTATTGATGATAAGCTGAAAAAGGGAG
>CUL3_LsgRNA100
TATCTCAAAGCATGTCTTGGTGCTGGTGG
>CUL3_LsgRNA101
GGGATCATCTACGGCAAACCTCTATTGGATA
>CUL3_LsgRNA102
CGGATCCGCATCTTGGTGTCTTCCGGCTG
>CUL3_LsgRNA103
CATGTCGAATCTGAGCAAAGGCACGGGCAG
>CUL3_LsgRNA104
AAATTCTGCAGACATTTCCAAAAAAGGAGC
>CUL3_LsgRNA105
TGGATGAATTCAGGCAACATCTACAGGCAA
>CUL3_LsgRNA106
AATCTGAGCAAAGGCACGGGCAGCCGGAAG
>CUL3_LsgRNA107
TTTCTGCCTTGTTTCTTTCTCTCTGGGTC
>CUL3_LsgRNA108
CTATTGGATATGATTGCAAGAGAGCGGAAA
>CUL3_LsgRNA109
CTGGTGGGATGTTGCACTTTGGTGTGGCTG
>CUL3_LsgRNA110
TCTCTGGGTCGGATTACCTTGTTTGGCAG

>CUL3_LsgRNA111
 TAGGTGGTGTGATCTTACAGTCCGGGTGC
 >CUL3_LsgRNA112
 AAGTTGTACGTTATGGGTGTATTAGGGATC
 >CUL3_LsgRNA113
 ATAATGTGGAGAACGTCTACAATTTGGGAT
 >CUL3_LsgRNA114
 GCCTTGTTCCTTCTCTCTGGGTCCGGATT
 >CUL3_LsgRNA115
 TTTTTTAAAAATGAAACAGGAAGATGGATC
 >CUL3_LsgRNA116
 CAAGTTATTTAGTCGTGTGCCAAATGGTTT
 >CUL3_LsgRNA117
 TTTCTTCAAACGCTAAATCAAGCTTGAAT
 >CUL3_LsgRNA118
 ACGTTTCTTAATAACAACCTGGACTTGGTAA
 >CUL3_LsgRNA119
 TATGTTGAAAAATGGAAAGACAGAAGGTAA
 >CUL3_LsgRNA120
 CAAGTTGTACGTTATGGGTGTATTAGGGAT
 >CUL3_LsgRNA121
 GAGCTTTACCTTGCTCCCTCAAATAGGAAC
 >CUL3_LsgRNA122
 TCTTTTCTTGCATAAACCTAAAAAGGACC
 >CUL3_LsgRNA123
 TTCTTTTGTAAGAACCCGCTGTGTTGGTTT

(27) S_{10}^- : 588 low on-target activity sgRNAs targeting NF1

>NF1_LsgRNA1
 AATAAAAAATAGGATTCCCAGCTTTGGAAG
 >NF1_LsgRNA2
 TTCCAAAAATCTAACGTGAGGTGTGGCTC
 >NF1_LsgRNA3
 TTAGAAAACATGTTCCAGAGCAGTTGGTAG
 >NF1_LsgRNA4
 TCCTAAAAGGCAAGAAATGGAATCAGGGAT
 >NF1_LsgRNA5
 GTGCAAAATTAACGACTCCTGAAGGGTA
 >NF1_LsgRNA6
 AAGAAAACAGGGGCCGAAACCCAAGGCAG
 >NF1_LsgRNA7
 CAGAAAAGAGTGATGGCACTGCTGAGGCGC
 >NF1_LsgRNA8
 ACGAAAAGCTCTTGCTGGCCATGGAGGAAG

>NF1_LsgRNA9
ATCAAAAAGGAGATACTTACACAACAGGAAA
>NF1_LsgRNA10
CCTAAAAGGCAAGAAATGGAATCAGGGATC
>NF1_LsgRNA11
GATGAAAAGTGCGCAAACAGGTGGCAGGAAA
>NF1_LsgRNA12
GTGGAAAATACCAGTCAAATGTCCATGGATC
>NF1_LsgRNA13
GAGTAAATCCACTTACCTATAGGAAGGGTC
>NF1_LsgRNA14
CAGGAAATCCATGAGCCTGGACATGGGGCA
>NF1_LsgRNA15
TTCTAAATGACATTTATTATGCTTCGGAAA
>NF1_LsgRNA16
TCATAAATTCCTCAAACCTTGAAGTGGTAA
>NF1_LsgRNA17
AGACAACAAGAGCTCTTGGTTGCAGGGATG
>NF1_LsgRNA18
TGGAAACAGTCACAGAAGCTTTGTTGGAGA
>NF1_LsgRNA19
CTGTAACAGTGGACGAACTCGCCACGGATC
>NF1_LsgRNA20
TTATAACCAAAGAAAACCTTGTATTTGGAAA
>NF1_LsgRNA21
TCAAAAACCAGTGCAACAGGTGGCTTGGGAT
>NF1_LsgRNA22
CATAAACCTGATGTCTCTAGTAACTGGCCC
>NF1_LsgRNA23
GCTGAACTTCGGAATTCTGCCTCTGGGGTT
>NF1_LsgRNA24
CTCTAACTTTAACTTTGCATTGGTTGGACA
>NF1_LsgRNA25
AGGGAAGATGAGCTGCCACATCAAGGGAAT
>NF1_LsgRNA26
AGGTAAGATGTTTGGTATTGTGGTGGGGAT
>NF1_LsgRNA27
TGTAAGCAAGTACTTACATCAATTGGGAA
>NF1_LsgRNA28
AGAAAAGCTATTTGACTTGGTGGATGGTTT
>NF1_LsgRNA29
TACCAAGCTGGGACTTCCAAAGCTGGGAAT
>NF1_LsgRNA30
GGGTAAGGAGATGTGGGAGTCAGGAGGGAT

>NF1_LsgRNA31
ACTGAAGGCAGCTCTGAACATCTAGGGCAA
>NF1_LsgRNA32
CTGCAAGGTATCCTTCAGAACCTTTGGGAG
>NF1_LsgRNA33
GTAAAATAATGACATTCTGTTTCAAGGTTT
>NF1_LsgRNA34
CAAAAATATGGGGAAGCCTTGGGCAGGTAT
>NF1_LsgRNA35
AGGAAATCCATGAGCCTGGACATGGGGCAA
>NF1_LsgRNA36
TTTTAATGGCTTGTGGCGGTTTGCAGGACC
>NF1_LsgRNA37
CCAAAATGTTTCTACAGGAGCATCAGGATT
>NF1_LsgRNA38
AATTAATTACAGGGCTCGTCCAACCTGGTCC
>NF1_LsgRNA39
TTTGAATTCTGTAGAAGTTATTTCTGGACA
>NF1_LsgRNA40
TCCAAATTTGTTAAATCCAATCCATGGAAT
>NF1_LsgRNA41
CTTAACAATAAGCTCAGCATAAGTCTGGAAT
>NF1_LsgRNA42
TCTGACACAGACTCCCTACAGGAATGGATC
>NF1_LsgRNA43
AGGCACACTCCCCAAGGGCACAAAGGAAG
>NF1_LsgRNA44
GGATACACTGGAAAATGTCTTGCTGGGGT
>NF1_LsgRNA45
TGAAACACTTCATAAAGCAGTGCAAGGTTG
>NF1_LsgRNA46
ACTGACACTTCATCCACCCACACCGGATA
>NF1_LsgRNA47
AAGTACAGAAGAAGCTGACCATAGAGGAGT
>NF1_LsgRNA48
ACTAACCAAGCAACTTCTTAGTGTTGGCCT
>NF1_LsgRNA49
CCCTACCACTGGCCACTGTAACAGTGGACG
>NF1_LsgRNA50
GGCAACCAGAACAGCTTCAGTGTGAGGGTT
>NF1_LsgRNA51
GGAAACCAGCATGCAGCTGAACTTCGGAAT
>NF1_LsgRNA52
CAAAACCAGTGCAACAGGTGGCTTGGGATC

>NF1_LsgRNA53
CTCCACCATTCTATAGGAATAAGATGGTAG
>NF1_LsgRNA54
CTAGACCCACCAGATCCTTAACATTGGTCC
>NF1_LsgRNA55
TCTTACCGGTGCCATTTCGTATTGCTGGGTG
>NF1_LsgRNA56
GCATACCTCAGTGTTCCTGCAGTGGGATG
>NF1_LsgRNA57
AATGACCTGTCCCGGTAACCTGGAACGGAAG
>NF1_LsgRNA58
GTTACCTTAACCATTGCAAACCAGGGCAC
>NF1_LsgRNA59
TTGTACCTTTAATTTAAAAATCGAGGGCCA
>NF1_LsgRNA60
AAATACGGACCAATGTTAAGGATCTGGTGG
>NF1_LsgRNA61
GACCACGGCCTGGACCCATTCCACCGGCCT
>NF1_LsgRNA62
GGAAACGTGGCATGTCTCGGAGGCTGGCAT
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(28) S_{11}^- : 178 low on-target activity sgRNAs targeting NF2

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CCAGGCTCACCGGTACGTGGGCTTGGTGG
>NF2_LsgRNA110
TCCTGCTCAGCCTCTGCGCCTTCTGGGCC
>NF2_LsgRNA111
GATAGCTCAGGACCTGGAGATGTACGGTGT
>NF2_LsgRNA112
TAGAGCTCTTCAAAGAAGGCCACTCGGGAC
>NF2_LsgRNA113
AGCTGCTGCTTGGAGTGGATGCCCTGGGGC
>NF2_LsgRNA114
AGGTGCTGGCACTGAAGATGGCTGAGGAGT
>NF2_LsgRNA115
TACTGCTTGGTACGCAGAGCACCGAGGCCG
>NF2_LsgRNA116
ACATGGAAAAGAGCAAGCATCTGCAGGAGC
>NF2_LsgRNA117
TGCGGGAAGCGATGGCCCCGGCCATGGCGC
>NF2_LsgRNA118
AGCAGGACCTGCAGGAAGCACGCGAGGCGG
>NF2_LsgRNA119
CCAGGGAGGAGAAGGCTAGAAAGCAGGTGA
>NF2_LsgRNA120
GCACGGAGGAGGAGAAGCGCCTGATGGAGC
>NF2_LsgRNA121
GTCAGGAGGCAACGGTGCTGGAATTGGGTT
>NF2_LsgRNA122
AGGAGGCAAACTTCTGGCCCAGAAGGCCG
>NF2_LsgRNA123
TCAAGGCCACAGCGATTTCGCACGGAGGAGG

>NF2_LsgRNA124
AAAAGGCCAGATCACCGAGGAGGAGGCAA
>NF2_LsgRNA125
AATGGCCTCACCTGGCTCGGCCTCGGTGC
>NF2_LsgRNA126
TCGAGGCCTTGAAACTGAAAGAGAGGGAGA
>NF2_LsgRNA127
ATGTGGGAGGAGAGAATTACTGCTTGGTAC
>NF2_LsgRNA128
ATGAGGGAGGAGGCTGAACGCACGAGGGAT
>NF2_LsgRNA129
AGAAGGTGCTGGAAGCCGAGGTGCTGGCAC
>NF2_LsgRNA130
CAACGGTGCTGGAATTGGGTTTCATGGGCTG
>NF2_LsgRNA131
TTGTGTACTGCAGTCCAAAGAACCAGGTTT
>NF2_LsgRNA132
CAGGGTCATAAATGTGAAGCCCCAGGGCAT
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TGCAGTCCAAAGAACCAGGTTTCTCGGAGC
>NF2_LsgRNA134
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>NF2_LsgRNA135
ATTGGTTTGTATTGCAGATGAAGTGAAA
>NF2_LsgRNA136
TTTCTAGCCTTCTCCTCCCTGGCCTGGGCT
>NF2_LsgRNA137
TCAGTATCTTTGAAGTCGAAAGACAGGCTG
>NF2_LsgRNA138
TTGTTATTGCAGATGAAGTGAAAGGGAAG
>NF2_LsgRNA139
GACTTCAAAGATACTGACATGAAGCGGCTT
>NF2_LsgRNA140
CAGATCAGCTGAAGCAGGACCTGCAGGAAG
>NF2_LsgRNA141
TCCCTCATCTGCTTCTCTCGAGCGAGGCGC
>NF2_LsgRNA142
GCCCTCCTGAGGCTTCTGTGCTCCTGGCTT
>NF2_LsgRNA143
TCGCTCGAGAGAAGCAGATGAGGGAGGAGG
>NF2_LsgRNA144
CGCCTCGCTCGAGAGAAGCAGATGAGGGAG
>NF2_LsgRNA145
TGTTTTCGGATTTTCATTCCACGGGAAGGAGA

>NF2_LsgRNA146
CCACTCGGGACTTGGCGCTCTGCAAGGTGA
>NF2_LsgRNA147
CATCTCGTACAGTGACAAGGAGGTAGGACA
>NF2_LsgRNA148
AACTTCTGGCCCAGAAGGCCGAGAGGCTG
>NF2_LsgRNA149
TGGCTGAAAAGGCCAGATCACCGAGGAGG
>NF2_LsgRNA150
AGGCTGAACGCACGAGGGATGAGTTGGAGA
>NF2_LsgRNA151
TCAATGAACTCAAGACAGAAATCGAGGCCT
>NF2_LsgRNA152
ACAATGAATGGGCCTCACCTGGCTCGGCCT
>NF2_LsgRNA153
ATACTGACATGAAGCGGCTTTCCATGGAGA
>NF2_LsgRNA154
ATCCTGAGAATGCTGAAGAGGAGCTGGTTC
>NF2_LsgRNA155
CTCTTGAGAGAGCTGAAGCTCATGCGGGAA
>NF2_LsgRNA156
GGCCTGAGCCCCGCGCCATGGCCGGGGCCA
>NF2_LsgRNA157
CGCATGAGCTTCAGCTCTCTCAAGAGGAAG
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GGTCTGAGGAGACAGCTGACCTGTTGGCTG
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ATTCTGCACAATGAGAACTCCGACAGGGGT
>NF2_LsgRNA161
AGATTGCCACCAAGCCCACGTACCCGGTGA
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CTGCTGCTTGGAGTGGATGCCCTGGGGCTT
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TACGTGGGCTTGGTGGCAATCTCCAGGAGC
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ACACTGGGGTCGTAGTCACCATACTGGAAA

>NF2_LsgRNA168
 TCCTTGTCACGTGACGAGATGTTTCGGATT
 >NF2_LsgRNA169
 ACGGTGTGAACTACTTTGCAATCCGGGTGT
 >NF2_LsgRNA170
 TTTGTTATTGCAGATGAAGTGGAAAGGGAA
 >NF2_LsgRNA171
 TTTCTTCACCCCTCGCAGATGGAGCGGCAG
 >NF2_LsgRNA172
 TTCATTCCACGGGAAGGAGATCTTGGGGGT
 >NF2_LsgRNA173
 TTCCTTCTCCTCATAAATAGATCATGGTTC
 >NF2_LsgRNA174
 TGGCTTCTTACGCCGTCCAGGCCAAGGTAG
 >NF2_LsgRNA175
 GAGGTGAAGCTTGGTATGTCAGGAGGCAA
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 AGTTTTGCCTCCTCCTCGGTGATCTGGGCC
 >NF2_LsgRNA177
 CTTATTGGATCCACAGAATAAAAAGGGCAC
 >NF2_LsgRNA178
 GATCTTGGGGTTCAGTCTGTTCTCAGGGTC

(29) S_{12}^- : 191 low on-target activity sgRNAs targeting CD5

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 >CD5_LsgRNA2
 TCAGAAAAGCAGCGTCAGTGGATTGGCCC
 >CD5_LsgRNA3
 CCAGAAAACAACGGCCAGGAGGGCGGCCA
 >CD5_LsgRNA4
 TGGAAAACAGTGTGCAGTTCCAGTTGGAGG
 >CD5_LsgRNA5
 TGGTAACACTGAGACAGCTTCTCCTGGGCA
 >CD5_LsgRNA6
 CCCAAACCCAGCGGGCCTGGCCCCAGGCAC
 >CD5_LsgRNA7
 AAACAACGGCCCAGGAGGGCGGCCAGGCGC
 >CD5_LsgRNA8
 GGCCAAGGACAGGCCCTGGGCCTGGGGAA
 >CD5_LsgRNA9
 CTACAAGGCCAAGGACAGGCCCTGGGCCT
 >CD5_LsgRNA10
 GCCCAAGGTTTCAGAGCCGCTGGTCGGGGG

>CD5_LsgRNA11
GCTGAAGTGCGCCAGAGATCACAGTGGGAG
>CD5_LsgRNA12
TCACACACACTGCTGCCCCGACCAGGCGG
>CD5_LsgRNA13
GGTAACACTGAGACAGCTTCTCCTGGGCAC
>CD5_LsgRNA14
TGAGACAGCTTCTCCTGGGCACAGAGGAAC
>CD5_LsgRNA15
TGTGACAGTTCTGCAGCCAGGGGCCGGGA
>CD5_LsgRNA16
TGCCACATACCTGCTGGGAACGCTGGGTGA
>CD5_LsgRNA17
CCACACATGGCCAGCAGCACCACCAGGAGT
>CD5_LsgRNA18
ACCCACCACCGTGCCGGAGCCCACAGGTAA
>CD5_LsgRNA19
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>CD5_LsgRNA20
CCCCGACCAGGCGGCTCTGAACCTTGGGCTG
>CD5_LsgRNA21
GAGCACCTCTTACCTGTGGGCTCCGGCAC
>CD5_LsgRNA22
TCTTACCTGTGGGCTCCGGCACGGTGGTGG
>CD5_LsgRNA23
GGGGACGGTGGGAAGAGCTATGTCGGGAGC
>CD5_LsgRNA24
AGAGACTCACCCAGCGTTCCCAGCAGGTAT
>CD5_LsgRNA25
ACTTACTGTTCTGGTTCACTCCTGTGGGGC
>CD5_LsgRNA26
TACAAGAAGCTGGTGAAGAAATGTAGGTAC
>CD5_LsgRNA27
GCCAAGACCCAAACCCAGCGGGCCTGGCCC
>CD5_LsgRNA28
TTACAGATGAGGTTCCCCAGGCCAGGGGC
>CD5_LsgRNA29
CCAGAGCAGATGACGGTGAGCGCTGGCCG
>CD5_LsgRNA30
CTGCAGCCAGGGGCCGGGGACGGTGGGAAG
>CD5_LsgRNA31
CTCCAGCTCCTCCCAGATTGCAGCTGGTGC
>CD5_LsgRNA32
CACCAGCTGCAATCTGGGAGGAGCTGGAGA

>CD5_LsgRNA33
GCCAAGGACAGGCCCTGGGCTGGGGAAC
>CD5_LsgRNA34
ACGAAGGCTGAGGTGCACAGGTGTGGTGG
>CD5_LsgRNA35
ATGAAGGAAAGGACCAAGGGCCAAGGGGT
>CD5_LsgRNA36
CCCAAGGTTTCAGAGCCGCTGGTCGGGGGC
>CD5_LsgRNA37
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>CD5_LsgRNA38
TGACAGTTCTGCAGCCAGGGCCGGGGACG
>CD5_LsgRNA39
CGACATAGCTCTTCCCACCGTCCCCGGCCC
>CD5_LsgRNA40
CATTATCACCCACCTAGGCAGATCAGGCTC
>CD5_LsgRNA41
TCCCATCGAATTGGCAAGGGCTGGGGTCC
>CD5_LsgRNA42
CCTCATCTGTAAGTCTCTGCAGTGTGGCTC
>CD5_LsgRNA43
CAGGATGATGCTTGCCACAGTGCCTGGGGC
>CD5_LsgRNA44
GTGGATGCTGACAAAACCTCCCCGGGTTC
>CD5_LsgRNA45
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>CD5_LsgRNA46
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>CD5_LsgRNA47
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>CD5_LsgRNA56
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>CD5_LsgRNA57
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CGCACAGTTGCTGTGTGGCTTCGATGGAAA
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CTCCCATCGAATTGGCAAGGGCCTGGGGTC
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>CD5_LsgRNA69
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>CD5_LsgRNA70
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>CD5_LsgRNA71
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>CD5_LsgRNA74
TCCTCCCAGATTGCAGCTGGTGCCAGGACA
>CD5_LsgRNA75
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>CD5_LsgRNA77
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>CD5_LsgRNA82
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>CD5_LsgRNA85
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>CD5_LsgRNA86
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>CD5_LsgRNA87
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>CD5_LsgRNA89
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>CD5_LsgRNA90
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GGGCCTGGGGTCCCTCAGCTCTGCAGGAGC
>CD5_LsgRNA94
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>CD5_LsgRNA95
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>CD5_LsgRNA96
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>CD5_LsgRNA97
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>CD5_LsgRNA98
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>CD5_LsgRNA99
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>CD5_LsgRNA100
CATCGAAGCCACACAGCAACTGTGCGGTCC
>CD5_LsgRNA101
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>CD5_LsgRNA112
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>CD5_LsgRNA124
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>CD5_LsgRNA125
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>CD5_LsgRNA126
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>CD5_LsgRNA127
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>CD5_LsgRNA129
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>CD5_LsgRNA131
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GCCTGGGGCCAGGCCCGCTGGGTTTGGGTC
>CD5_LsgRNA133
GGTCGGGGGCAGCAGTGTGTGTGAGGGCAT
>CD5_LsgRNA134
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>CD5_LsgRNA137
GCACGGTGGTGGGTGGGGTGGTTGTGGGTG
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>CD5_LsgRNA139
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>CD5_LsgRNA140
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>CD5_LsgRNA141
AATGGTCCTGGCTCAGCCTCCAACCTGGAAC
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>CD5_LsgRNA146
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>CD5_LsgRNA153
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>CD5_LsgRNA154
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CGTGTCTTGGCACCAGCTGCAATCTGGGAG
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CTTCTCCTGGGCACAGAGGAACCCGGGGGA
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CTTGTGAACTTGTGTTGTTGCAGTTGGATA
>CD5_LsgRNA160
GTAGTGAGACACAGCTCCCGTTCGGGGCCT
>CD5_LsgRNA161
ACGGTGAGCGCCTGGCCGCCCTCCTGGGCC
>CD5_LsgRNA162
AGGATGATGCTTGCCACAGTGCTGGGGCC
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TGTTTGCACACTGCAGAGGCCTGCTGGGCA
>CD5_LsgRNA164
CTGGTGCCAGGACACGAAGGCCTGAGGTGC

>CD5_LsgRNA165
TTTCTGCCTCGGACAGTCTGGAAGGGGTGG
>CD5_LsgRNA166
ACAGTGCCTGGGGCCAGGCCCGCTGGGTTT
>CD5_LsgRNA167
GTGGTGAATTCTACAATGGCAGCTGGGGT
>CD5_LsgRNA168
GAATTGGAGCCACTTAGCATCACCTGGATA
>CD5_LsgRNA169
TCCTTGGCAGAAGACCTGGTTCTGGGGTCT
>CD5_LsgRNA170
TAAGTGGCTCCAATTCCAAGTGCAGGGTC
>CD5_LsgRNA171
CCCCTGGCTGCAGAAGTGCACACAGGGCC
>CD5_LsgRNA172
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>CD5_LsgRNA173
CCCTTGTACTCCTGGTGGTGCTGCTGGCCA
>CD5_LsgRNA174
CTGGTGTCCCTGCTGCCTCTGTCCCGGACA
>CD5_LsgRNA175
CATCTGTCCGGGACAGAGGCAGCAGGGACA
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CCTGTGTGACAGTTCTGCAGCCAGGGGCCG
>CD5_LsgRNA177
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>CD5_LsgRNA184
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CCCGTTCGGGGCCTCCCATCGAATTGGCAA
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>CD5_LsgRNA187
 TCCTTTCTGCAGATTTCCAGCCCAAGGTTC
 >CD5_LsgRNA188
 CTGGTTCTGGGGTCTGTTCAATGAAGGGAA
 >CD5_LsgRNA189
 CCACTTGACCCTGACACTTGGAAATTGGAGC
 >CD5_LsgRNA190
 ATGCTTGCCACAGTGCCTGGGGCCAGGCC
 >CD5_LsgRNA191
 ATCCTTGGCAGAAGACCTGGTTCTGGGGTC

(30) S_{13}^- : 59 low on-target activity sgRNAs targeting CD28

>CD28_LsgRNA1
 AACGAAACAGTGACGTTCCGTCTCTGGAAT
 >CD28_LsgRNA2
 TGGTAAAGCAGTCGCCCCTGCTTGTGGTAG
 >CD28_LsgRNA3
 CTGCAAAGTCTCTGGCAGGGGCGTAGGGCT
 >CD28_LsgRNA4
 CATGAACATGACTCCCCGGAGGCCTGGGCT
 >CD28_LsgRNA5
 TGCAAAGTCTCTGGCAGGGGCGTAGGGCTG
 >CD28_LsgRNA6
 CTCGAATGCCGAGTTCAACTGCGACGGGGA
 >CD28_LsgRNA7
 ATGAACATGACTCCCCGGAGGCCTGGGCTC
 >CD28_LsgRNA8
 TACAACCTTCTCGCAAAGGAATTCCGGGCA
 >CD28_LsgRNA9
 AGCAACGAGGTCAGCCTCAGCTGCAGGTAT
 >CD28_LsgRNA10
 CGGTACGCTGCAAAGTCTCTGGCAGGGGCG
 >CD28_LsgRNA11
 AGTGACTACATGAACATGACTCCCCGGAGG
 >CD28_LsgRNA12
 TTGAACTCGGCATTCGAGCGAAACTGGGGC
 >CD28_LsgRNA13
 GAACAGCGACGTGGAAGTCTGTGTCGGGAA
 >CD28_LsgRNA14
 ACTCAGTCATCTCCTAAGCTGTTTTGGGCA
 >CD28_LsgRNA15
 TGACAGTGGCTCTTTGTGTTATCTGGGTAA
 >CD28_LsgRNA16
 CTGGATAGGGTCCCTGTTCAGGGGCGGTAC

>CD28_LsgRNA17
CGAAATCCCCGTCGCAGTTGAACTCGGCAT
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TCGAATGCCGAGTTCAACTGCGACGGGGAT
>CD28_LsgRNA19
AGGAATTCGGGCATCCCTGTACAAGGGCG
>CD28_LsgRNA20
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>CD28_LsgRNA24
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>CD28_LsgRNA26
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>CD28_LsgRNA28
CTTTCGAGTGAGCCCAGGCCTCCGGGGAGT
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TTCACGCCCTTGTACAGGGATGCCCGGAAT
>CD28_LsgRNA30
CCTCCGCCTTACCTAGACAACGAGAGGAGC
>CD28_LsgRNA31
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>CD28_LsgRNA32
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>CD28_LsgRNA33
ACCTCGTTGCTATCTACCACAAGCAGGGGC
>CD28_LsgRNA34
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>CD28_LsgRNA35
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>CD28_LsgRNA36
TGAACTCGGCATTCGAGCGAAACTGGGGCT
>CD28_LsgRNA37
AAGTCTCTGGCAGGGGCGTAGGGCTGGTAA
>CD28_LsgRNA38
CTTTGCAGCGTACCGCCCCTGACAGGGACC

>CD28_LsgRNA39
 TCTGGCAGGGGCGTAGGGCTGGTAAGGCTT
 >CD28_LsgRNA40
 AACAGCGACGTGGAAGTCTGTGTCGGGAAT
 >CD28_LsgRNA41
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 >CD28_LsgRNA42
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 >CD28_LsgRNA43
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 >CD28_LsgRNA55
 GTCATGTTTATGTAGTCACTTTGAAGGAGT
 >CD28_LsgRNA56
 TTTGTTATGGCTTGCTAGTGACAGTGGCTC
 >CD28_LsgRNA57
 GGTATTCCTACAACCTTCTCGCAAAGGAAT
 >CD28_LsgRNA58
 GGAATTCCTTTGCGAGAAGGTTGTAGGAAT
 >CD28_LsgRNA59
 GGCTTTCGAGTGAGCCCAGGCCTCCGGGGA

(31) S_{14}^- : 135 low on-target activity sgRNAs targeting H2-K

>H2-K_LsgRNA1
CACCAAACACAAGTGGGAGCAGGCTGGTGA
>H2-K_LsgRNA2
CCAGAACAGCAACGGTCGCCATGTTGGAGA
>H2-K_LsgRNA3
CGCCAACAGCAGGAGCAGCGTGCACGGTAC
>H2-K_LsgRNA4
CGGGAACGCGACGCTGCTGCGCACAGGTGC
>H2-K_LsgRNA5
TGAAAACGTGGACGGCGGCGGACATGGCGG
>H2-K_LsgRNA6
GATGAAGATGAGAAGGAGAAACACAGGTAG
>H2-K_LsgRNA7
CTCCAAGGACAACCAGAACAGCAACGGTCG
>H2-K_LsgRNA8
CTGCAATAGTCACTGGAGCTGTGGTGGCTT
>H2-K_LsgRNA9
GGAGACAGTGGATGGAGGAGGCTCTGGGAA
>H2-K_LsgRNA10
TTACACATGCCATGTGTACCATCAGGGGCT
>H2-K_LsgRNA11
CAGGACATGGAGCTTGTGGAGACCAGGCCT
>H2-K_LsgRNA12
CATCACCTGACCTGGCAGTTGAATGGGGA
>H2-K_LsgRNA13
AGTCACCCTGAGGTGCTGGGCCCTGGGCTT
>H2-K_LsgRNA14
AAATACCTCAGCGAGTGTGGGCCTGGGGGC
>H2-K_LsgRNA15
GGTGACGAAATACCTCAGCGAGTGTGGGCC
>H2-K_LsgRNA16
AGCCACTCCACGCACGTGCCCTCCAGGTAG
>H2-K_LsgRNA17
ACGAAGACCTGAAAACGTGGACGGCGGCGG
>H2-K_LsgRNA18
AGAGAGACTCAGGGCCTACCTGGAGGGCAC
>H2-K_LsgRNA19
GAGCAGAGTTTCCGAGTGGACCTGAGGACC
>H2-K_LsgRNA20
ATGGAGCAGGAGGGGCCCGAGTATTGGGAG
>H2-K_LsgRNA21
TAGAAGCCCAGGGCCCAGCACCTCAGGGTG
>H2-K_LsgRNA22
TCGCAGCCGTCGTAGGCGTACTGCTGGTAC

>H2-K_LsgRNA23
TGCCAGGTCAGGGTGATGTCAGCAGGGTAG
>H2-K_LsgRNA24
TTGTAGTAGCCGAGCAGGGTCCTCAGGTCC
>H2-K_LsgRNA25
TGGAAGTCGGCTACGTGGACGACACGGAGT
>H2-K_LsgRNA26
GAAGATAAAGTCACCCTGAGGTGCTGGGCC
>H2-K_LsgRNA27
CTTTATCTTCAGGTCTGCTGTGATGGGTCA
>H2-K_LsgRNA28
TGTGATGGGTCACATGGGCCTTTGGGGAAT
>H2-K_LsgRNA29
CGCCATGTTGGAGACAGTGGATGGAGGAGG
>H2-K_LsgRNA30
AGGTATTTTCGTCACCGCCGTGTCCCGGCC
>H2-K_LsgRNA31
CTCTCACACTATTCAGGTGATCTCTGGCTG
>H2-K_LsgRNA32
ATTACACATGCCATGTGTACCATCAGGGGC
>H2-K_LsgRNA33
AAGTCACCCTGAGGTGCTGGGCCCTGGGCT
>H2-K_LsgRNA34
ACTCCACGCACGTGCCCTCCAGGTAGGCC
>H2-K_LsgRNA35
CGTGCACGCTGCTCCTGCTGTTGGCGGCCG
>H2-K_LsgRNA36
CCCACACTCTCCTTACCCCATCTCAGGGTG
>H2-K_LsgRNA37
CTGCCAGGTCAGGGTGATGTCAGCAGGGTA
>H2-K_LsgRNA38
GCTCCAGTGACTATTGCAGCTCCAAGGACA
>H2-K_LsgRNA39
GAGACAGTGGATGGAGGAGGCTCTGGGAAG
>H2-K_LsgRNA40
ACCCCATCTCAGGGTGAGGGGCTCAGGCAG
>H2-K_LsgRNA41
TGGGCATCTGTGGTGGTGCCTCTTGGGAAG
>H2-K_LsgRNA42
TACACATGCCATGTGTACCATCAGGGGCTG
>H2-K_LsgRNA43
CCAACATGGCGACCGTTGCTGTTCTGGTTG
>H2-K_LsgRNA44
GGCACCACCACAGATGCCCACTTCTGGAAG

>H2-K_LsgRNA45
CCTTCCAGAAGTGGGCATCTGTGGTGGTGC
>H2-K_LsgRNA46
GGAGCCAGGGCGGCCGCAACAGCAGGAGC
>H2-K_LsgRNA47
CCTCCCATTCAACTGCCAGGTCAGGGTGA
>H2-K_LsgRNA48
CCGCCCCAGGCCACACTCGCTGAGGTAT
>H2-K_LsgRNA49
TCCTCCCATTCAACTGCCAGGTCAGGGTG
>H2-K_LsgRNA50
GCTCCCCGAGGCCGGGCCGGGACACGGCGG
>H2-K_LsgRNA51
GGTACCCGCGGAGGAGTCGCCCGTCGGACC
>H2-K_LsgRNA52
ATCACCTGACCTGGCAGTTGAATGGGGAG
>H2-K_LsgRNA53
GGGTCCGACGGGCGACTCCTCCGCGGGTAC
>H2-K_LsgRNA54
ACCGCCGTGTCCCGGCCCGCCCTCGGGGAG
>H2-K_LsgRNA55
CCGGCCTCGGGGAGCCCCGGTACATGGAAG
>H2-K_LsgRNA56
AAGACCTGAAAACGTGGACGGCGGCGACA
>H2-K_LsgRNA57
TCACCCTGACCTGGCAGTTGAATGGGGAGG
>H2-K_LsgRNA58
TGCTCCTGCTGTTGGCGGCCCGCCCTGGCTC
>H2-K_LsgRNA59
CTCTCCTTACCCCATCTCAGGGTGAGGGGC
>H2-K_LsgRNA60
AATCCGAGATATGAGCCGCGGGCGCGGTGG
>H2-K_LsgRNA61
GTCCCGCAGGCTCTCACACTATTCAGGTGA
>H2-K_LsgRNA62
CCACCGCGCCCGCGGCTCATATCTCGGATT
>H2-K_LsgRNA63
CCC CGCGGGTCTGAGTCGGAGCCAGGGCG
>H2-K_LsgRNA64
CGGGCGCGGTGGATGGAGCAGGAGGGGCC
>H2-K_LsgRNA65
TGCTCGGCTACTACAACCAGAGCAAGGGCG
>H2-K_LsgRNA66
GGAGCGGGAGACACAGAAAGCCAAGGGCAA

>H2-K_LsgRNA67
AGTTTCGTGCGCTTCGACAGCGACGCGGAGA
>H2-K_LsgRNA68
CCGCCGTGTCCCGGCCCGCCTCGGGGAGC
>H2-K_LsgRNA69
GGGCTACCTGGAGGGCACGTGCGTGGAGT
>H2-K_LsgRNA70
GCACCTCAGGGTGACTTTATCTTCAGGTCT
>H2-K_LsgRNA71
GTGGCTCCGCAGATACCTGAAGAACGGGAA
>H2-K_LsgRNA72
TCAGCTCCTCCCCATTCAACTGCCAGGTCA
>H2-K_LsgRNA73
CTGCCTGAGCCCCTCACCTGAGATGGGGT
>H2-K_LsgRNA74
CAGGCTGGTGAAGCAGAGAGACTCAGGGCC
>H2-K_LsgRNA75
TCTCCTTACCCCATCTCAGGGTGAGGGGCT
>H2-K_LsgRNA76
GAACCTTCCAGAAGTGGGCATCTGTGGTGG
>H2-K_LsgRNA77
TGTCCCTTGAGCTGCAATAGTCACTGGAGC
>H2-K_LsgRNA78
GGAGCTTGTGGAGACCAGGCCTGCAGGGGA
>H2-K_LsgRNA79
CGGAGAATCCGAGATATGAGCCGCGGGCGC
>H2-K_LsgRNA80
AGTTGAATGGGGAGGAGCTGATCCAGGACA
>H2-K_LsgRNA81
TGTGGAGACCAGGCCTGCAGGGGATGGAAC
>H2-K_LsgRNA82
CGGGGAGCCCCGGTACATGGAAGTCGGCTA
>H2-K_LsgRNA83
GCCTGAGCCCCTCACCTGAGATGGGGTAA
>H2-K_LsgRNA84
AGCTGATCCAGGACATGGAGCTTGTGGAGA
>H2-K_LsgRNA85
CTGTGATGGGTACATGGGCCTTTGGGGAA
>H2-K_LsgRNA86
GGGCGATGTAATCGCAGCCGTCGTAGGCGT
>H2-K_LsgRNA87
TCAGGCAGCCCCTGATGGTACACATGGCAT
>H2-K_LsgRNA88
TGGAGCAGGAGGGGCCCGAGTATTGGGAGC

>H2-K_LsgRNA89
GTGGGCATCTGTGGTGGTGCCCTCTTGGGAA
>H2-K_LsgRNA90
GGTCGCCATGTTGGAGACAGTGGATGGAGG
>H2-K_LsgRNA91
AGAAGCCCAGGGCCCAGCACCTCAGGGTGA
>H2-K_LsgRNA92
CACCGCCGTGTCCCGGCCCGCCTCGGGGA
>H2-K_LsgRNA93
AGCAGCGTCGCGTTCCCGTTCTTCAGGTAT
>H2-K_LsgRNA94
CCTGGCTCCGACTCAGACCCGCGCGGGTGA
>H2-K_LsgRNA95
TCCCGGCCCGGTACTCACCCGCGCGGGTCT
>H2-K_LsgRNA96
GCTCGGCTACTACAACCAGAGCAAGGGCGG
>H2-K_LsgRNA97
CTCTGGCTGTGAAGTGGGGTCCGACGGGCG
>H2-K_LsgRNA98
ACCGGGGCTCCCCGAGGCCGGGCCGGGACA
>H2-K_LsgRNA99
GTGAGGGGCTCAGGCAGCCCCTGATGGTAC
>H2-K_LsgRNA100
CAACGGTCGCCATGTTGGAGACAGTGGATG
>H2-K_LsgRNA101
TTCAGGTGATCTCTGGCTGTGAAGTGGGGT
>H2-K_LsgRNA102
GGAAGGTTCCATCCCCTGCAGGCCTGGTCT
>H2-K_LsgRNA103
CCATGTACCGGGGCTCCCCGAGGCCGGGCC
>H2-K_LsgRNA104
TTTCGTCACCGCCGTGTCCCGGCCCGGCCT
>H2-K_LsgRNA105
TGATGTCAGCAGGGTAGAAGCCCAGGGCCC
>H2-K_LsgRNA106
TCAGGTCTGCTGTGATGGGTCACATGGGCC
>H2-K_LsgRNA107
TCAGGTGATCTCTGGCTGTGAAGTGGGGTC
>H2-K_LsgRNA108
TACCGTGCACGCTGCTCCTGCTGTTGGCGG
>H2-K_LsgRNA109
CCGAGTGGACCTGAGGACCCTGCTCGGCTA
>H2-K_LsgRNA110
AAACGTGGACGGCGGCGGACATGGCGGCGC

>H2-K_LsgRNA111
GACCGTTGCTGTTCTGGTTGTCCTTGGAGC
>H2-K_LsgRNA112
AAGATAAAGTCACCCTGAGGTGCTGGGCCC
>H2-K_LsgRNA113
CATGTACCGGGGCTCCCCGAGGCCGGGCCG
>H2-K_LsgRNA114
GAAATACCTCAGCGAGTGTGGGCCTGGGGG
>H2-K_LsgRNA115
ACTTTATCTTCAGGTCTGCTGTGATGGGTC
>H2-K_LsgRNA116
GTACTCACCCGCGCGGGTCTGAGTCGGAGC
>H2-K_LsgRNA117
CTCCTCCATCCACTGTCTCCAACATGGCGA
>H2-K_LsgRNA118
GCGTTCCCGTTCTTCAGGTATCTGCGGAGC
>H2-K_LsgRNA119
GGGGTCCGACGGGCGACTCCTCCGCGGGTA
>H2-K_LsgRNA120
TGGCTCCGCAGATACCTGAAGAACGGGAAC
>H2-K_LsgRNA121
CTGGTCTCCACAAGCTCCATGTCCTGGATC
>H2-K_LsgRNA122
TTGCTCTGGTTGTAGTAGCCGAGCAGGGTC
>H2-K_LsgRNA123
GCCCTGAACGAAGACCTGAAAACGTGGACG
>H2-K_LsgRNA124
TGCCTGAGCCCCTCACCTGAGATGGGGTA
>H2-K_LsgRNA125
GATATGAGCCGCGGGCGCGGTGGATGGAGC
>H2-K_LsgRNA126
CAGGTGATCTCTGGCTGTGAAGTGGGGTCC
>H2-K_LsgRNA127
GCTGTGATGGGTCACATGGGCCTTTGGGGA
>H2-K_LsgRNA128
GAGCTGCAATAGTCACTGGAGCTGTGGTGG
>H2-K_LsgRNA129
CTCCTGCTCCATCCACCGCGCCCGCGGCTC
>H2-K_LsgRNA130
CTTCTGGAAGGTTCCATCCCCTGCAGGCCT
>H2-K_LsgRNA131
TACCTGGAGGGCACGTGCGTGGAGTGGCTC
>H2-K_LsgRNA132
CATCTGTGGTGGTGCCTCTTGGGAAGGAGC

>H2-K_LsgRNA133
 CTCCTTACCCCATCTCAGGGTGAGGGGCTC
 >H2-K_LsgRNA134
 CATGTTGGAGACAGTGGATGGAGGAGGCTC
 >H2-K_LsgRNA135
 GAGCTTGTGGAGACCAGGCCTGCAGGGGAT

(32) S_{15}^- : 210 low on-target activity sgRNAs targeting CD45

>CD45_LsgRNA1
 ATACAAAAGGAAGATTGCTGATGAGGGCAG
 >CD45_LsgRNA2
 CCAGAAACGCCTAAGCCTAGTTGTGGGGAT
 >CD45_LsgRNA3
 AAGGAAAGCAGACTTATGGAGACATGGAAG
 >CD45_LsgRNA4
 AGCAAAAAGGCCACAGTTATTGTCATGGTCA
 >CD45_LsgRNA5
 TCCAAAATGCTAAGTGTGGAAATGAGGATT
 >CD45_LsgRNA6
 TTCCAACAAAATGTCAGAATGGATTGGCTC
 >CD45_LsgRNA7
 GATGAACAACAGGAACTCGTTGAAAGGGGT
 >CD45_LsgRNA8
 CAGGAACCCCATGGTCTGGCCAGCTGGTGA
 >CD45_LsgRNA9
 CAAGAAGAAAATAAGAAGAAGAACAGGAAT
 >CD45_LsgRNA10
 CTA AAAAGAAACGATCGGTGACTTTTGGCAG
 >CD45_LsgRNA11
 GGCCAAGCATGGAGGAAGGCACTCGGGCTT
 >CD45_LsgRNA12
 TGGAAAGTGCAGAAACAGAAGATGTGGTTG
 >CD45_LsgRNA13
 CCTGAATCATAGACACCAGGTCTTTGGGTT
 >CD45_LsgRNA14
 TGTCAATGGGAAGATTCAAAGAAATGGGAC
 >CD45_LsgRNA15
 ATGAACAACAGGAACTCGTTGAAAGGGGTG
 >CD45_LsgRNA16
 AGGCACAGAACAACCCTGTCTGCTGGGATC
 >CD45_LsgRNA17
 AGGCACAGTATATCCTGATTCATCAGGCTT
 >CD45_LsgRNA18
 AGCTACCACAACGAAGCAAACATGTGGTAA

>CD45_LsgRNA19
ACTTACCACATGTTTGCTTCGTTGTGGTAG
>CD45_LsgRNA20
AGACACCAGGTCTTTGGGTTCTGCAGGCAG
>CD45_LsgRNA21
GTGTACCAGTACCAGTGTACCACATGGAAA
>CD45_LsgRNA22
CAGTACCAGTGTACCACATGGAAAAGGGGAA
>CD45_LsgRNA23
ATCCACCCAGTGACCCCTCCCCTCTGGAGG
>CD45_LsgRNA24
CCTCACCTGCTCCTCAAACCTTCGACGGAGA
>CD45_LsgRNA25
TGCTACCTGGTATTTCAGCCTCCAGAGGGGA
>CD45_LsgRNA26
CTCTACGCAAAGCACGGCCTGGGGTGGTGT
>CD45_LsgRNA27
TTATACTATTGTCTGTGCGCCGGGAGGTTT
>CD45_LsgRNA28
GCAGACTGTTCTGGCTGAATTCAGGTAT
>CD45_LsgRNA29
AACCAGAAATGATGATTGCTGCTCAGGGGC
>CD45_LsgRNA30
AGAGAGAAATTGACATTCACCTGGTGGTAC
>CD45_LsgRNA31
CTGTAGAACAAGTGCGCAGAATACTGGCCA
>CD45_LsgRNA32
CCAAAAGACCTGGTGTCTATGATTCAGGACC
>CD45_LsgRNA33
TGACAGAGATGGATCCCAGCAGACAGGGTT
>CD45_LsgRNA34
TCATAGAGGAACCTGGTATTGCTCCTGGTGA
>CD45_LsgRNA35
CTCCAGAGGGGAGGGGTCACTGGGTGGATC
>CD45_LsgRNA36
TGACAGAGTTAGTGAATGGAGACCAGGTTT
>CD45_LsgRNA37
TTACAGATGATGAAAAGCAGCTGATGGATG
>CD45_LsgRNA38
G TTCAGCTTCTGAATGATGTAATCAGGACA
>CD45_LsgRNA39
ACCCAGGAAATACATTGCTGCACAAGGTAA
>CD45_LsgRNA40
ATCTAGGAAGTCTGTGCTCAGTACTGGGGC

>CD45_LsgRNA41
TTTGAGGAGCAGGTGAGGGTCTTCAGGAAC
>CD45_LsgRNA42
TCACAGGGAAGAATGTCAACATAACGGTTT
>CD45_LsgRNA43
CAGAAATCATCAACTGTCTCATCCCGGGGC
>CD45_LsgRNA44
TAAAAGTCTGATTACTAGATTCATAGGTGT
>CD45_LsgRNA45
ACAGAGTGCCACTTAAGCATGAACTGGAGA
>CD45_LsgRNA46
CAAAAGTTCGGAGAGTGTAGGCTGAGGCTC
>CD45_LsgRNA47
CAGGAGTTGGAGGACACAGCACATTGGAAA
>CD45_LsgRNA48
TGTTATAAATGTGCAGACAGATTTGGGGAG
>CD45_LsgRNA49
GCTAATACTTCAATTTGTTTGGAGTGGAAA
>CD45_LsgRNA50
CCCCATCAGCTTCCTAACCTGCAGTGGACG
>CD45_LsgRNA51
CTGAATCATAGACACCAGGTCTTTGGGTTC
>CD45_LsgRNA52
CTTCATCCCTTCTGGGGAAGCCTTGGGAAG
>CD45_LsgRNA53
GCTCATCTCCAGTTCATGCTTAAGTGGCAC
>CD45_LsgRNA54
TATGATCTGCGCAAGAAAAGATCCAGGTAA
>CD45_LsgRNA55
GTTGATGACTTCTGGAGGATGATCTGGGAG
>CD45_LsgRNA56
CGGGATGAGACAGTTGATGACTTCTGGAGG
>CD45_LsgRNA57
GTCAATGGGAAGATTCAAAGAAATGGGACT
>CD45_LsgRNA58
TGTCATGGTCACACGATGTGAAGAAGGAAA
>CD45_LsgRNA59
GTCTATGGTTATGTTGTCAAGCTAAGGCGA
>CD45_LsgRNA60
AGTAATGTTCCCAAACATGGCAGCTGGAAA
>CD45_LsgRNA61
TGTGATGTTGACAGAGTTAGTGAATGGAGA
>CD45_LsgRNA62
ATACATTACTTACATCAATGTAGCTGGCAT

>CD45_LsgRNA63
TGGTATTCAGCCTCCAGAGGGGAGGGGTCA
>CD45_LsgRNA64
TTTTATTCTGATTGTGGGGCTTTCGGGCAT
>CD45_LsgRNA65
CATACAAAAGGAAGATTGCTGATGAGGGCA
>CD45_LsgRNA66
GTGACAAAGACTTCTGTGTCCAGAAGGGCA
>CD45_LsgRNA67
TGAACAACAGGAACTCGTTGAAAGGGGTGA
>CD45_LsgRNA68
CCCACAAC TAGGCTTAGGCGTTTCTGGAAC
>CD45_LsgRNA69
GCTGCAAGAAAAACGTTAGTCTCTTGGCCT
>CD45_LsgRNA70
TGGCCAAGCATGGAGGAAGGCACTCGGGCT
>CD45_LsgRNA71
GTTTCAAGCTTTCACCTCAAACTGGTCA
>CD45_LsgRNA72
AAGGCACAGAACAACCCTGTCTGCTGGGAT
>CD45_LsgRNA73
AATTCACAGTAATGTTCCCAAACATGGCAG
>CD45_LsgRNA74
AATTCACCAGCTGGCCAGACCATGGGGTTC
>CD45_LsgRNA75
GTCACACGATGTGAAGAAGGAAACAGGGTA
>CD45_LsgRNA76
TCTCCAGATATGACCATGGGTTTGTGGCTC
>CD45_LsgRNA77
TTCACAGCAATTTAGATGAACAACAGGAAC
>CD45_LsgRNA78
CACCCAGTGACCCCTCCCCTCTGGAGGCTG
>CD45_LsgRNA79
CATTCATACCTGAAAGATGTCAGTTGGACA
>CD45_LsgRNA80
CATGCATCCATCCTCGTCCACTGCAGGTTA
>CD45_LsgRNA81
ACTTCATCCCTTCTGGGGAAGCCTTGGGAA
>CD45_LsgRNA82
CCTACATTGGAATTGATGCCATGCTGGAAG
>CD45_LsgRNA83
TCCTCATTTCCACACTTAGCATTTTGGACA
>CD45_LsgRNA84
TATTCCACTAAAGCCTGATGAATCAGGATA

>CD45_LsgRNA85
ACATCCACTTTGCCCTCTGCTTCCAGGCCT
>CD45_LsgRNA86
TCTTCCCATTTGACATAGGCAAGTAGGGACA
>CD45_LsgRNA87
TCTTCCCCTTTCCATGTGGTACACTGGTAC
>CD45_LsgRNA88
GTGTCCCTACTTGCCTATGTCAATGGGAAG
>CD45_LsgRNA89
CCTCCCCTCTGGAGGCTGAATACCAGGTAG
>CD45_LsgRNA90
AGGACCTCAAACAGAAGCTTCCCAAGGCTT
>CD45_LsgRNA91
ATATCCTGATTCATCAGGCTTTAGTGAAT
>CD45_LsgRNA92
GAAGCCTTGGGAAGCTTCTGTTTGAGGTCC
>CD45_LsgRNA93
CCGTGGAAGTTTGAGGAGCAGGTGAGGGTC
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AGCCCGAGTGCCTTCCTCCATGCTTGGCCA
>CD45_LsgRNA95
CTGGCGATGATGTCATAGAGGAAGTGGTAT
>CD45_LsgRNA96
AGTGCGCAGAATACTGGCCAAGCATGGAGG
>CD45_LsgRNA97
TCTGCTACACATGTGTAATTTGTTGGGCA
>CD45_LsgRNA98
TCAGCTCAAAAGTTCGGAGAGTGTAGGCTG
>CD45_LsgRNA99
GTGACTCATATCCAATTCACCAGCTGGCCA
>CD45_LsgRNA100
CAGCCTCCAGAGGGGAGGGGTCACTGGGTG
>CD45_LsgRNA101
AAGTCTCTACGCAAAGCACGGCCTGGGGTG
>CD45_LsgRNA102
GGATCTCTCTTCTTCATGTTGTGTAGGCAT
>CD45_LsgRNA103
CATGCTGGAAGGCCTGGAAGCAGAGGGCAA
>CD45_LsgRNA104
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>CD45_LsgRNA105
CTACCTGGTATTCAGCCTCCAGAGGGGAGG
>CD45_LsgRNA106
TCAACTGTCTCATCCCGGGGCCCTAGGAGT

>CD45_LsgRNA107
TGTTCTGTGCCTTGTTCAATCTCTTGAAA
>CD45_LsgRNA108
TTTTCTTAGAGACTTCCTTCATACAGGAGT
>CD45_LsgRNA109
GAAGCTTCCCAAGGCTTCCCCAGAAGGGAT
>CD45_LsgRNA110
GCAACTTCTTCAGTGGTCCCATTGTGGTGC
>CD45_LsgRNA111
TCCAGAAACGCCTAAGCCTAGTTGTGGGGA
>CD45_LsgRNA112
ACCAGAAATGATGATTGCTGCTCAGGGGCC
>CD45_LsgRNA113
CTAGGAAGTCTGTGCTCAGTACTGGGGCGA
>CD45_LsgRNA114
CGTCGAAGTTTGAGGAGCAGGTGAGGGTCT
>CD45_LsgRNA115
TCTGGACACAGAAGTCTTTGTACAGGTAA
>CD45_LsgRNA116
TAGGGACACTTCATAGTATTTATAAGGTTT
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>CD45_LsgRNA118
TAGAGACTTCCTTCATACAGGAGTTGGAGG
>CD45_LsgRNA119
TTTTGAGCTGAGACATTCCAAGGTAGGTAA
>CD45_LsgRNA120
TCTGGAGGATGATCTGGGAGCAAAAGGCCA
>CD45_LsgRNA121
AGCAGAGGGCAAAGTGGATGTCTATGGTTA
>CD45_LsgRNA122
CAAAGATGTCCAAAATGCTAAGTGTGAAA
>CD45_LsgRNA123
AGATGCAGACTCAGGTTTAGATACAGGCTC
>CD45_LsgRNA124
AGCTGCCTGCAGAACCCAAAGACCTGGTGT
>CD45_LsgRNA125
CCATGCTGGAAGGCCTGGAAGCAGAGGGCA
>CD45_LsgRNA126
TCTAGGAAGTCTGTGCTCAGTACTGGGGCG
>CD45_LsgRNA127
CATTGGAATTGATGCCATGCTGGAAGGCCT
>CD45_LsgRNA128
CAAAGGATGCATTAATGTATTTGCTGGTTT

>CD45_LsgRNA129
TTCTGGCCTTTGGATTTGCCCTTCTGGACA
>CD45_LsgRNA130
CTGGGGCGAAGGAAAGCAGACTTATGGAGA
>CD45_LsgRNA131
AAAAGGCTAATACTTCAATTTGTTTGGAGT
>CD45_LsgRNA132
GTGGGGCTTTCGGGCATCTTTGATGGGAAA
>CD45_LsgRNA133
TGTTGGGCGTACAGGTACCTACATTGGAAT
>CD45_LsgRNA134
TGTGGGGCTTTCGGGCATCTTTGATGGGAA
>CD45_LsgRNA135
CCATGGGTTTGTGGCTCAAACCTTCTGGCCT
>CD45_LsgRNA136
ATGTGGTCCTCCTTATGAAACTAATGGCCC
>CD45_LsgRNA137
TTGAGGTCCTGAATCATAGACACCAGGTCT
>CD45_LsgRNA138
CCATGGTCTGGCCAGCTGGTGAATTGGATA
>CD45_LsgRNA139
CAATGTAGCTGGCATTATGTAGGTGGACC
>CD45_LsgRNA140
CCTGGTATTCAGCCTCCAGAGGGGAGGGGT
>CD45_LsgRNA141
AGAAGTCATCAACTGTCTCATCCCGGGGCC
>CD45_LsgRNA142
CTGTGTCCAGAAGGGCAAATCCAAAGGCCA
>CD45_LsgRNA143
AGTGGTCCCATTTGTGGTGCACCTGCAGGTAA
>CD45_LsgRNA144
CTGTGTCCTCCAACCTCCTGTATGAAGGAAG
>CD45_LsgRNA145
GCTTGTGATACTTCATCCCTTCTGGGGAAG
>CD45_LsgRNA146
CCGTGTGGAACCTCTCTGAAATAAATGGAGA
>CD45_LsgRNA147
GAGTGTGGGTACCTACCATCACAAAGGATG
>CD45_LsgRNA148
GTTTGTTCCTTAGTGCTGGTGTGGGCGT
>CD45_LsgRNA149
ATGCTAAAGCACTGATTATATTCCTGGTGT
>CD45_LsgRNA150
GTGGTAAAGTCTCTACGCAAAGCACGGCCT

>CD45_LsgRNA151
GCATTAACTCTCCGTCTCGAAGTTTGAGGAGC
>CD45_LsgRNA152
CTGCTACACATGTGTAATTTGTTTGGGCAC
>CD45_LsgRNA153
CCAGTACCAGTGTACCACATGGAAAGGGGA
>CD45_LsgRNA154
TCTTTACCTGCAGTGCACCACAATGGGACC
>CD45_LsgRNA155
AGAATACTGGCCAAGCATGGAGGAAGGCAC
>CD45_LsgRNA156
TGAGTAGAAAAAAGAAAAAGCAACTGGAAG
>CD45_LsgRNA157
ATGTTATAAATGTGCAGACAGATTTGGGGA
>CD45_LsgRNA158
CATTTATACTATTGTCTGTCTGGCCGGGAGG
>CD45_LsgRNA159
TTCATATGTACTCCACTGTGAGCCAGGTAC
>CD45_LsgRNA160
CTGGTATTCAGCCTCCAGAGGGGAGGGGTC
>CD45_LsgRNA161
TTTTTATTCTGATTGTGGGGCTTTCGGGCA
>CD45_LsgRNA162
CACCTCAAACTGGTCACATTATTAGGCAA
>CD45_LsgRNA163
AAGGTCAATGGAATGAAAACCTCCCGGCCG
>CD45_LsgRNA164
GATGTCACAATAATCAGAAACACCAGGAAT
>CD45_LsgRNA165
CAATTCACCAGCTGGCCAGACCATGGGGTT
>CD45_LsgRNA166
CACTTCACCTCGGATTGCAGAGGAAGGAGC
>CD45_LsgRNA167
AGACTCAGTTTTAGATACAGGCTCAGGCCA
>CD45_LsgRNA168
AGCCTCCAGAGGGGAGGGGTCACTGGGTGG
>CD45_LsgRNA169
ATCTTCCCATTGACATAGGCAAGTAGGGAC
>CD45_LsgRNA170
AGTGTCCCTACTTGCCTATGTCAATGGGAA
>CD45_LsgRNA171
ACTCTCCGTCTCGAAGTTTGAGGAGCAGGTGA
>CD45_LsgRNA172
AGTCTCTACGCAAAGCACGGCCTGGGGTGG

>CD45_LsgRNA173
AAAGTCTCTACGCAAAGCACGGCCTGGGGT
>CD45_LsgRNA174
ACTCTCTGAAATAAATGGAGATGCAGGGTC
>CD45_LsgRNA175
ATCATCTGAAGACTCATCTGATTCAGGCTC
>CD45_LsgRNA176
CACTTCTGACTACCAAATGTAAAAGGTTT
>CD45_LsgRNA177
AGGGTCTTCAGGAACCCCATGGTCTGGCCA
>CD45_LsgRNA178
ATGATGAAAAGCAGCTGATGGATGTGGAGC
>CD45_LsgRNA179
TACATGACTGCACACCAAAGAAAAGGCTA
>CD45_LsgRNA180
TTGATGACTTCTGGAGGATGATCTGGGAGC
>CD45_LsgRNA181
CCCCTGAGCAGCAATCATCATTTCTGGTTT
>CD45_LsgRNA182
TTGCTGATGAGGGCAGACTGTTCTGGCTG
>CD45_LsgRNA183
GAATTGATGCCATGCTGGAAGGCCTGGAAG
>CD45_LsgRNA184
TAGATGCTGGCGATGATGTCATAGAGGAAC
>CD45_LsgRNA185
CCTCTGCTTCCAGGCCTTCCAGCATGGCAT
>CD45_LsgRNA186
TTTGTGGCTCAAACCTTCTGGCCTTTGGATT
>CD45_LsgRNA187
TCCATGGGGTTTAGATGCAGACTCAGGTTT
>CD45_LsgRNA188
ACACTGGTACTGGTACACAGTTCTGGGCTC
>CD45_LsgRNA189
ATGATGTAATCAGGACATCGTTTGTGGTCA
>CD45_LsgRNA190
CATGTGTAATTTGTTTGGGCACGAAGGTTG
>CD45_LsgRNA191
TGCTTGTGATACTTCATCCCTTCTGGGGAA
>CD45_LsgRNA192
ACCTTGTGCAGCAATGTATTTCTGGGTTC
>CD45_LsgRNA193
AGTCTGTGCTCAGTACTGGGGCGAAGGAAA
>CD45_LsgRNA194
TGTTTGTTCCTTAGTGCTGGTGTGGGCG

>CD45_LsgRNA195
 GGTTTTAGGGCCATTAGTTTCATAAGGAGG
 >CD45_LsgRNA196
 GGCTTTAGTGGGAATACAATCAGTTTGGAGA
 >CD45_LsgRNA197
 ACATTTATACTATTGTCTGTCTGGCCGGGAG
 >CD45_LsgRNA198
 TGTTTTATGCTATAAGAACAATTCAGGTAA
 >CD45_LsgRNA199
 ACTATTCAACTGACTATGAGTTTCTGGTAA
 >CD45_LsgRNA200
 GGTTTTCATTCATTGACCTTGTCCGGACC
 >CD45_LsgRNA201
 AAGCTTCCAAGGCTTCCCCAGAAGGGATG
 >CD45_LsgRNA202
 CAGCTTCCTAACCTGCAGTGGACGAGGATG
 >CD45_LsgRNA203
 AGACTTCCTTCATACAGGAGTTGGAGGACA
 >CD45_LsgRNA204
 TTCTTTGAATCTTCCCATTGACATAGGCAA
 >CD45_LsgRNA205
 AAGGTTGTCCAAGTACATCTTTCAGGTAT
 >CD45_LsgRNA206
 ATGCTTGTGATACTTCATCCCTTCTGGGGA
 >CD45_LsgRNA207
 TACCTTGTGCAGCAATGTATTTCTGGGTT
 >CD45_LsgRNA208
 AGATTTTATACAAAACAACAAGCAAGGCTA
 >CD45_LsgRNA209
 CTCTTTTCACAATGGAGTGTACGAGGGAGA
 >CD45_LsgRNA210
 TATGTTTCCAACAAAATGTCAGAATGGATT

(33) S_{16}^- : 49 low on-target activity sgRNAs targeting THY1

>THY1_LsgRNA1
 CAATAAAAGTATCAGTGTGTATAGAGGTGA
 >THY1_LsgRNA2
 CACAAAAGTAGTCGCCCTCATCCTTGGTGG
 >THY1_LsgRNA3
 AGAGAAGAGGAAGCACGTGCTCTCAGGCAC
 >THY1_LsgRNA4
 ATCCACAGACAAGCTGGTCAAGTGTGGCGG
 >THY1_LsgRNA5
 AAGCACGTGCTCTCAGGCACCCCTTGGGATA

>THY1_LsgRNA6
CGGTACGTGTGCTCGGGTATCCCAAGGGTG
>THY1_LsgRNA7
CATCAGCGTCGCTCTCCTGCTCTCAGGTAC
>THY1_LsgRNA8
GAGCAGGAGAGCGACGCTGATGGCTGGGTT
>THY1_LsgRNA9
ATCCAGGATGTGTTCTGAACCAGCAGGCTT
>THY1_LsgRNA10
GGCTAGGGTAAGGACCTTGATATAGGGCTG
>THY1_LsgRNA11
ACTCATGCTGGATGGAGTTATCCTTGGTGT
>THY1_LsgRNA12
TAGCCAACTTCACCACCAAGGATGAGGGCG
>THY1_LsgRNA13
GGTTCACCAGGCAGGCTGTCAGGCTGGTCA
>THY1_LsgRNA14
GAAGCACGTGCTCTCAGGCACCCTTGGGAT
>THY1_LsgRNA15
AGAGCACGTGCTTCCTCTTCTCTCGGGTCA
>THY1_LsgRNA16
AAGGCACTGCTGTGCCAGTCTTGCAGGTGT
>THY1_LsgRNA17
GGGTCAGGCTGAACTCATGCTGGATGGAGT
>THY1_LsgRNA18
ACTGCCGCCATGAGAATAACACCAAGGATA
>THY1_LsgRNA19
CTGCCCTCGGGACACCTGCAAGACTGGCAC
>THY1_LsgRNA20
TCATCCTTGGTGGTGAAGTTGGCTAGGGTA
>THY1_LsgRNA21
GACGCGGGAGCGGTACGTGTGCTCGGGTAT
>THY1_LsgRNA22
CGCCCTCATCCTTGGTGGTGAAGTTGGCTA
>THY1_LsgRNA23
CCCTCTCCAACCAGCCCTATATCAAGGTCC
>THY1_LsgRNA24
GACCCTTGCCCAGTACCTGAGAGCAGGAGA
>THY1_LsgRNA25
AGGTGACCAGCCTGACAGCCTGCCTGGTGA
>THY1_LsgRNA26
TAAGGACCTTGATATAGGGCTGGTTGGAGA
>THY1_LsgRNA27
GAGCGACGCTGATGGCTGGGTTTCATGGTGC

>THY1_LsgRNA28
CTGAGAGCAGGAGAGCGACGCTGATGGCTG
>THY1_LsgRNA29
GAGAGCACGTGCTTCCTCTTCTCTCGGGTC
>THY1_LsgRNA30
TCTTGCAGGTGTCCCGAGGGCAGAAGGTGA
>THY1_LsgRNA31
TGACGCGGGAGCGGTACGTGTGCTCGGGTA
>THY1_LsgRNA32
TCAGGCTGGTCACCTTCTGCCCTCGGGACA
>THY1_LsgRNA33
TAGGGCTGGTTGGAGAGGGTGACGCGGGAG
>THY1_LsgRNA34
ACGTGCTTCCTCTTCTCTCGGGTCAGGCTG
>THY1_LsgRNA35
AGCAGGAGAGCGACGCTGATGGCTGGGTTC
>THY1_LsgRNA36
TGGCGGCAGTCCAGGCGAAGGTTTTGGTTC
>THY1_LsgRNA37
GTCAGGCTGGTCACCTTCTGCCCTCGGGAC
>THY1_LsgRNA38
GCCTGGTGAACCAAACCTTCGCCTGGACT
>THY1_LsgRNA39
TTTTGGTTCACCAGGCAGGCTGTCAGGCTG
>THY1_LsgRNA40
AAAAGTAGTCGCCCTCATCCTTGGTGGTGA
>THY1_LsgRNA41
TCAAGTGTGGCGGCATAAGCCTGCTGGTTC
>THY1_LsgRNA42
AGGGTAAGGACCTTGATATAGGGCTGGTTG
>THY1_LsgRNA43
TGGCTAGGGTAAGGACCTTGATATAGGGCT
>THY1_LsgRNA44
GAGTTATCCTTGGTGTTATTCTCATGGCGG
>THY1_LsgRNA45
GTGTTATTCTCATGGCGGCAGTCCAGGCGA
>THY1_LsgRNA46
GAGTTCAGCCTGACCCGAGAGAAGAGGAAG
>THY1_LsgRNA47
ACCTTGATATAGGGCTGGTTGGAGAGGGTG
>THY1_LsgRNA48
TGGTTGGAGAGGGTGACGCGGGAGCGGTAC
>THY1_LsgRNA49
CCCCTTCTCTATCCACAGACAAGCTGGTCA

(34) S₁₇: 110 low on-target activity sgRNAs targeting CD43

>CD43_LsgRNA1
ACAGAAACTGATGGGCTGGCATTCTGGGCT
>CD43_LsgRNA2
CCCCAAAGAGGAGGAGAAGGTGCAAGGCCA
>CD43_LsgRNA3
TGGAAACTACTGAATTGTCTTCTTTGGAGA
>CD43_LsgRNA4
CAGAAACTGATGGGCTGGCATTCTGGGCTT
>CD43_LsgRNA5
CTGGAAGCAGTGCTGATGTCTTGCTGGAAA
>CD43_LsgRNA6
CTCGAAGGAGACCATCAGCCCCCTGGGGGCA
>CD43_LsgRNA7
GACAACAAGCTCTAACGAGACCAGTGGACC
>CD43_LsgRNA8
TGTCACAGGATTGGCTGCAGTGACAGGAGG
>CD43_LsgRNA9
TACAACAGTAAGCTCCAAGACCAGTGGTCC
>CD43_LsgRNA10
TGTCACCACAGCTACTGGGTCTCTGGGGCC
>CD43_LsgRNA11
AACCACCACCAAGGCAATAAGCATGGGCAC
>CD43_LsgRNA12
AGAGACCCAGTAGCTGTGGTGACAGGGGGA
>CD43_LsgRNA13
CTGTACCTGAGCCTACTGCCTCTCAGGAAG
>CD43_LsgRNA14
GGTGACCTGGTGGTTATGGGATCTTGGGTA
>CD43_LsgRNA15
CCCACTGGAActCTCCACAGAACTGGTTG
>CD43_LsgRNA16
AGGTACTTGGAGCTGTGATATGTGGGGTAG
>CD43_LsgRNA17
GCCAAGAATCAAGTGGCATGTTACTGGTGC
>CD43_LsgRNA18
CGTTAGAGCTTGTGTGCACAGTGGTGGGGG
>CD43_LsgRNA19
CGCCAGAGGCAAAAGCGGAGGACTGGGGCC
>CD43_LsgRNA20
TTAGAGCTTGTGTGCACAGTGGTGGGGGT
>CD43_LsgRNA21
TCGAAGGAGACCATCAGCCCCCTGGGGGCAG

>CD43_LsgRNA22
TGAGAGGCAGTAGGCTCAGGTACAGGGGTG
>CD43_LsgRNA23
GCTCAGGTACAGGGGTGCTCATGCTGGCAC
>CD43_LsgRNA24
CTGCAGGTCCGTCTGTACAGGATTGGCTG
>CD43_LsgRNA25
AGGGAGTCCATGCATCTCACTCGAGGGCCC
>CD43_LsgRNA26
TAACATGCCACTTGATTCTTGGCTTGGTGA
>CD43_LsgRNA27
CAGCATGCCCCAAAGAGGAGGAGAAGGTGC
>CD43_LsgRNA28
GCCACAACAGCAGTAGCGCCACGAGGGCCA
>CD43_LsgRNA29
TTGTCACAGTGGTGGGGGTGCACTGGTTC
>CD43_LsgRNA30
CTGTCACCACAGCTACTGGGTCTCTGGGGC
>CD43_LsgRNA31
AAACCACCACCAAGGCAATAAGCATGGGCA
>CD43_LsgRNA32
GCGCCAGAGGCAAAAGCGGAGGACTGGGGC
>CD43_LsgRNA33
AGCCCATCAGTTTCTGTGGGGTCAGGGACA
>CD43_LsgRNA34
TGCCCATGCTTATTGCCTTGGTGGTGGTTT
>CD43_LsgRNA35
GTTTCCAAGGGGGTCAAAGAAACTGGGATT
>CD43_LsgRNA36
AGACCCAGTAGCTGTGGTGACAGGGGGACC
>CD43_LsgRNA37
CAGCCCATCAGTTTCTGTGGGGTCAGGGAC
>CD43_LsgRNA38
GAGACCCAGTAGCTGTGGTGACAGGGGGAC
>CD43_LsgRNA39
CAATCCCAGTTTCTTTGACCCCTTGAAAA
>CD43_LsgRNA40
CTGACCCACAGAACTGATGGGCTGGCAT
>CD43_LsgRNA41
AGGGCCCCAGAGACCCAGTAGCTGTGGTGA
>CD43_LsgRNA42
TGGTCCCCCTGTCACCACAGCTACTGGGTC
>CD43_LsgRNA43
GGTCCCCCTGTCACCACAGCTACTGGGTCT

>CD43_LsgRNA44
TTCTCCTCCTCTTTGGGGCATGCTGGGTCC

>CD43_LsgRNA45
TGTCCCTGACCCACAGAACTGATGGGCT

>CD43_LsgRNA46
GTGACCTGGTGGTTATGGGATCTTGGGTAG

>CD43_LsgRNA47
GACTCGAAGGAGACCATCAGCCCCCTGGGGG

>CD43_LsgRNA48
CTAACGAGACCAGTGGACCCTCTGTGGCTA

>CD43_LsgRNA49
GTGGCGAGCCCAGACAGTCTGCAGAGGACG

>CD43_LsgRNA50
AACTCTCCACAGAACTGGTTGCTGTGGTAG

>CD43_LsgRNA51
GTCACTGGCTACATTTGATGGTTCTGGAAG

>CD43_LsgRNA52
TTGGCTTGGTGACCTGGTGGTTATGGGATC

>CD43_LsgRNA53
AGAGCTTGTGTGCACAGTGGTGGGGGGTGC

>CD43_LsgRNA54
TCCTCTTTGGGGCATGCTGGGTCCAGGTGG

>CD43_LsgRNA55
CACAGAACTGGTTGCTGTGGTAGCAGGGAG

>CD43_LsgRNA56
ACTCGAAGGAGACCATCAGCCCCCTGGGGGC

>CD43_LsgRNA57
TGGTGACAGGGGGACCACTGGTCTTGGAGC

>CD43_LsgRNA58
CAGAGACCCAGTAGCTGTGGTGACAGGGGG

>CD43_LsgRNA59
TGCAGACTGTCTGGGCTCGCCACCTGGACC

>CD43_LsgRNA60
TGTGGAGAGTTCCAGTGTGGCCCGTGGCAC

>CD43_LsgRNA61
GTTAGAGCTTGTGTGCACAGTGGTGGGGGG

>CD43_LsgRNA62
CTGAGAGGCAGTAGGCTCAGGTACAGGGGT

>CD43_LsgRNA63
CCACGAGGGCCAAAACCACCACCAAGGCAA

>CD43_LsgRNA64
CAGGGAGTCCATGCATCTCACTCGAGGGCC

>CD43_LsgRNA65
TGCAGCATCTACATCTATCTCTAAAGGAAC

>CD43_LsgRNA66
GAATGCCAGCCCATCAGTTTCTGTGGGGTC
>CD43_LsgRNA67
TGGTGCCCATGCTTATTGCCTTGGTGGTGG
>CD43_LsgRNA68
TTCTGCTGGAAACTGAGGTGCCACGGGGCCA
>CD43_LsgRNA69
TGGAGCTTACTGTTGTAGCCACAGAGGGTC
>CD43_LsgRNA70
CTTGGCTTGGTGACCTGGTGGTTATGGGAT
>CD43_LsgRNA71
TAGAGCTTGTTCACAGTGGTGGGGGGTG
>CD43_LsgRNA72
CACAGGATTGGCTGCAGTGACAGGAGGGTC
>CD43_LsgRNA73
ACTGGGATTGTGGTCTGCCCCAGGGGCTG
>CD43_LsgRNA74
GAGAGGCAGTAGGCTCAGGTACAGGGGTGC
>CD43_LsgRNA75
TTGTGGCGCCAGAGGCAAAAGCGGAGGACT
>CD43_LsgRNA76
TTATGGGATCTTGGGTAGACGTCGTGGATG
>CD43_LsgRNA77
AACTGGGATTGTGGTCTGCCCCAGGGGCT
>CD43_LsgRNA78
AGGAGGGTCACTGGCTACATTTGATGGTTC
>CD43_LsgRNA79
AGGGGGTCAAAGAAACTGGGATTGTGGTCT
>CD43_LsgRNA80
TACTGGTGCCCATGCTTATTGCCTTGGTGG
>CD43_LsgRNA81
ACCAGTAACATGCCACTTGATTCTTGGCTT
>CD43_LsgRNA82
TGGGGTCAGGGACAGTGGACTCGAAGGAGA
>CD43_LsgRNA83
CATCGTCGTCCTCTGCAGACTGTCTGGGCT
>CD43_LsgRNA84
TCTCGTTAGAGCTTGTGTGCACAGTGGTGG
>CD43_LsgRNA85
CTGCTACCACAGCAACCAGTTCTGTGGAGA
>CD43_LsgRNA86
GCGCTACTGCTGTTGTGGCGCCAGAGGCAA
>CD43_LsgRNA87
GAGGTACTTGGAGCTGTGATATGTGGGGTA

>CD43_LsgRNA88
TGCTTATTGCCTTGGTGGTGGTTTTGGCCC
>CD43_LsgRNA89
CAGGTCACCAAGCCAAGAATCAAGTGGCAT
>CD43_LsgRNA90
AGTTTCCAAGGGGGTCAAAGAAACTGGGAT
>CD43_LsgRNA91
CTTCTCCTCCTCTTTGGGGCATGCTGGGTC
>CD43_LsgRNA92
AACTTCCTGAGAGGCAGTAGGCTCAGGTAC
>CD43_LsgRNA93
ATCGTCGTCCTCTGCAGACTGTCTGGGCTC
>CD43_LsgRNA94
GCCCTCGTGGCGCTACTGCTGTTGTGGCGC
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TCCGTCTGTCACAGGATTGGCTGCAGGGAC
>CD43_LsgRNA96
ATTGTCTTCTTTGGAGACTTCTGCTGGTGC
>CD43_LsgRNA97
AAACTGAGGTGCCACGGGCCACACTGGAAC
>CD43_LsgRNA98
CACTTGATTCTTTGGCTTGGTGACCTGGTGG
>CD43_LsgRNA99
GCCTTGCACCTTCTCCTCCTCTTTGGGGCA
>CD43_LsgRNA100
TGGCTGCAGTGACAGGAGGGTCACTGGCTA
>CD43_LsgRNA101
AGAATGCCAGCCCATCAGTTTCTGTGGGGT
>CD43_LsgRNA102
TTTCTGCTGGAACTGAGGTGCCACGGGCC
>CD43_LsgRNA103
AAACTGGGATTGTGGTCTGCCCCAGGGGC
>CD43_LsgRNA104
CTGTTGTAGCCACAGAGGGTCCACTGGTCT
>CD43_LsgRNA105
CTGTTGTGGCGCCAGAGGCAAAAGCGGAGG
>CD43_LsgRNA106
TAGCTGTGGTGACAGGGGGACCACTGGTCT
>CD43_LsgRNA107
GGCATTCTGGGCTTCAGAGGTACTTGGAGC
>CD43_LsgRNA108
CCAGTTCTGTGGAGAGTTCCAGTGTGGCCC
>CD43_LsgRNA109
CAGTTTCTGTGGGGTCAGGGACAGTGGACT

>CD43_LsgRNA110
GGCCTTGCACCTTCTCCTCCTCTTTGGGGC