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Supporting document to the Genomic Allergen Rapid Detection Test Method for Skin Sensitisation (GARD™skin), described in Test Guideline 442E

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FOREWORD

This document provides information supporting the Genomic Allergen Rapid Detection (GARD) Test Method for Skin Sensitisation (GARD™skin), included as Annex IV of OECD Test Guideline 442E on *in vitro* skin sensitisation. It includes the origin and biological relevance of the GARDskin Genomic Prediction Signature, as well as a detailed description of the analytical workflow and how the prediction model was defined. It was developed by the developers of the GARD™skin test method. During the development of the test method, the data contained in the present document were treated as Confidential Business Information but are now publicly released. This is in line with the OECD policy for confidential elements in candidate Test Guidelines under development and after adoption [Link].

The Working Party of the National Coordinators of the Test Guidelines Programme approved Annex IV of TG 442E and endorsed the supporting document in its 34th meeting in April 2022, on the basis of a project led by Sweden. This document is published under the responsibility of the Chemicals and Biotechnology Committee.

Supporting document to the Genomic Allergen Rapid Detection Test Method for Skin Sensitisation (GARD™skin)

1. Origin and biological relevance of the GARDskin GPS

1. The genomic biomarkers of the Genomic Allergen Rapid Detection Test Method for Skin Sensitisation (GARD™skin) Genomic Prediction Signature (GPS) were identified by a so-called data-driven approach. Here, *data-driven* is to be interpreted as opposed to the *hypothesis-driven* designs typically utilized in the design of *in vitro* methods. In this context, the biomarker selection and prediction model design were not driven by *a priori* knowledge, e.g. an assumption that expression-levels of certain recognized disease-associated genes or proteins would change following chemical exposure. Rather, genome-wide dataset generated by a reference panel of chemicals, a so-called *discovery dataset,* were interrogated to learn of actual measurable effects, in the context of the specified cellular system (1).

2. For identification of the GPS, a tiered approach for feature selection, combining a filter method and stepwise backward elimination, was applied (1). Following this feature selection strategy, 200 potential predictors were identified. At the stage of NanoString transfer, the signature was reduced to 196 genes, as four probes could not be appropriately designed due to technical constraints (2). The 196 genes, henceforth referred to as the GPS, are listed in Table 1, with target sequences disclosed in Table 2.

3. The biological relevance of the GARDskin GPS in the context of skin sensitization was originally explored together with the original findings of the then proposed biomarkers, in which the product molecules of the GPS transcripts were characterized with regards to the interactome, known functions and canonical pathways (1). It may be noted that a complete understanding of the biological context of all utilized biomarkers is currently not available. This is expected, as data-driven approaches may generate novel hypotheses, as well as confirm existing ones.

4. The dominating functions identified were small molecule biochemistry, cell death, lipid metabolism, hematological system development, cell cycle, molecular transport, cellular growth and proliferation and carbohydrate metabolism. This suggests that the cell line which GARDskin employs has the metabolic capacity required to recognize, process and react to a wide range of xenobiotic biochemistries, and further, that these functions are provoked by xenobiotic stimuli, as evidenced by the findings of these very transcripts following a data-driven analysis of differentially expressed genes in a genome-wide discovery dataset.

5. Similarly, the signaling pathways that were populated by the highest number genes from the GPS were NRF2-mediated oxidative response, xenobiotic metabolism signaling, protein ubiquitination pathway, LPS/IL-1 mediated inhibition of RXR function, aryl hydrocarbon receptor (AHR) signaling, protein kinase A (PKA) signaling and Toll-like receptor (TLR) signaling. These pathways are known to

take part in reactions provoked by foreign substances and largely relate to the generation of so-called danger signals (3), which in turn leads to the induction of pro-inflammatory cytokines and chemokines, as well as co-stimulatory molecules needed for a specific T-cell response upon DC - T-cell interaction.

6. Taken together, the GARDskin GPS monitors mechanistic events associated with Key Event (KE) 3 of the OECD Adverse Outcome pathway (AOP), such as xenobiotic recognition, generation of immunological danger signals, DC maturation and differentiation and regulation of immunological signaling pathways that ultimately contribute to the successful priming of specific T-cells upon exposure to chemical skin sensitizers. Of note, certain mechanistic events associated with the GARDskin GPS may also be associated with other KE:s, albeit monitored in a DC cell line. For additional details, please refer to original work (1).

7. Following the proposal of utilizing the individual predictors of the GPS as variable inputs in a prediction algorithm (4), a *training dataset* was created. To this end, samples of the discovery dataset were reproduced in independent cellular experiments, and targeted gene expression analysis was performed using the NanoString nCounter system, considering only the now *a priori* defined biomarkers (2). Using this training dataset, a prediction algorithm was trained and frozen. Once finalized, the prediction algorithm may be utilized to evaluate so-called *test datasets*, i.e., datasets continuously being generated as a direct consequence of the procedure described in the main body of this TG.

8. The construction of a prediction algorithm from a training dataset, as well as its utilization for classification of samples in a test dataset, is described in sections below.

2. GARD Data Processing

9. The entire GARD analytical workflow subsequent to the generation of raw data files, including data preprocessing, normalization, analysis and application of prediction models for test chemical classification, is automated in the GARD Data Analysis Application (GDAA), a cloud-based software specifically designed by the method developers in order to facilitate streamlined GARD data analysis.

10. On a step by step basis, the GDAA performs the following procedures: Data is quality controlled, by evaluating a set of quality metrics, according to NanoString standards. Raw data is normalized using a single-sample normalization algorithm based on gene specific counts per total counts (CPTC) algorithm (2). Following this, batch variations between the training data set originally used to fit the prediction algorithm and the test data set are eliminated using an algorithm for Batch Adjustment by Reference Alignment (BARA) (5). Lastly, normalized data are analysed by a Support Vector Machine (SVM) (6) prediction algorithm, which in turn feeds the GARDskin prediction model. For a schematic overview of the GDAA and the stepwise processes performed, see Figure 1.

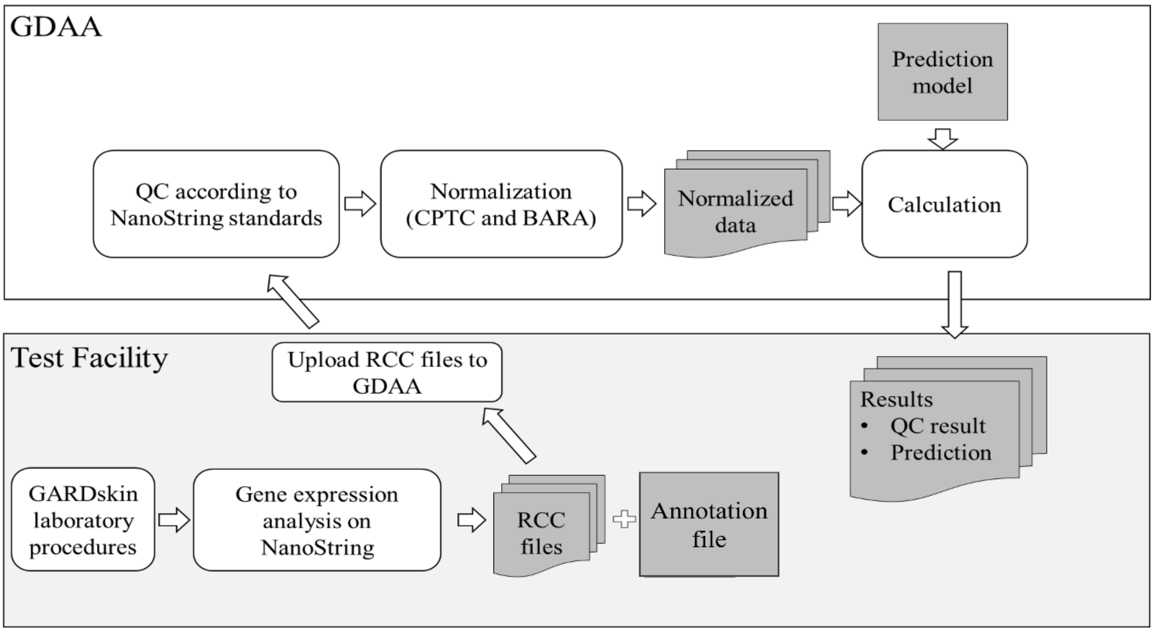

Figure 1. A schematic of the GDAA workflow, including input and output files. RCC; Reporter Code Count (raw gene expression data), CPTC; Counts-per-total-counts (RNA content normalization), BARA; Batch Adjustment by Reference Alignment (batch adjustment normalization)

11. In the following sections, each of these steps of the analytical workflow is described in detail.

2.1. Nanostring Quality Control Parameters

12. The GDAA automatically checks the quality of all generated gene expression data of uploaded RCC files, by evaluating a set of quality metrics. The quality metrics are imaging quality, linearity of the spike-in RNA control probes, limit of detection (LOD), and binding density, as listed in Table 5 of the main body of this Test Guideline.

13. The imaging quality is calculated as the ratio between the number Fields of View (FOV) and the number of successfully counted FOVs. A ratio above 0.75 (>0.75) is required for a sample to pass the imaging quality control.

14. In addition to the custom probes targeting the different transcripts of the GPS, the reagents of each nCounter® XT CodeSet includes a set of five positive and eight negative control probes, termed POS_A-POS_E and NEG_A-NEG_H, respectively. The positive control probes are a set of probes with corresponding target transcripts readily spiked-in into the nCounter® XT CodeSet reagents. The five target transcripts are spiked in a range of concentrations across five orders of magnitude, with POS_A having the highest concentration and POS_E the lowest concentration. The negative control probes consist of so-called scrambled oligos, with no expected target in the assayed sample RNA.

15. The linearity of the positive spike-in controls is calculated using the positive control probes (POS_A-E) and their known RNA concentrations, as specified by the nCounter® XT CodeSet gene expression assay. The acquired counts for the positive control probes and their respective concentrations should be logarithmized (log2) before calculating the R^2 value of a linear fit to the data points. An R^2 value above 0.95 ($R^2 > 0.95$) is required for a sample to pass the linearity quality control.

16. The limit of detection (LOD) quality control uses all the negative controls (NEG_A-H) and the positive control with the lowest concentration (POS_E). The LOD is defined as the mean counts of the negative control probes plus 2 standard deviations of the counts, see Equation 18.

$$LOD = \mu + 2 * \sigma \tag{18}$$

where μ and σ are the mean value and the standard deviation of the negative control probes' counts, respectively. For a sample to pass the LOD quality control, the positive control probe POS_E must be above the estimated LOD (POS_E > LOD).

17. The binding density is a measure of the number of probes observed per cartridge surface area during the gene expression acquisition. For a sample to pass the binding density quality control, the binding density must be above 0.05 and below 2.25 (0.05< binding density <2.25).

18. All acceptance criteria thresholds are based on default values provided by the instrument's manufacturer.

2.2. Counts-per-total-counts (CPTC)

19. The aim of the CPTC-normalization is to scale the observed gene expression levels for a given sample by a value estimated to reflect the amount of RNA that was loaded during the NanoString acquisition analysis, thereby reducing technical variance between samples. This normalization is performed by scaling each gene's count by the sum of counts for that specific sample. The normalization algorithm for a sample is described in equation 1.

$$x_i = \frac{c_i}{\sum_{j=1}^{n} c_j}, i = 1, 2, \ldots, n \tag{1}$$

20. Where x_i represents the normalized expression value for gene *i*, c_i and c_j the counts for gene *i* and gene *j*, respectively, and *n* the number of genes in the prediction signature.

2.3. Batch Adjustment by Reference Alignment (BARA)

21. The aim of the BARA algorithm is to reduce the systematic differences that are frequently observed between datasets acquired at different time points. These systematic differences are referred to as batch effects. BARA is used in the GARD data processing pipelines to remove batch effects between the training set, which was used to define the prediction model (2), and the test dataset under evaluation.

22. BARA performs batch correction by identifying adjustment values based on the values of reference samples, that are present in both the training set and the test sets and are expected to render identical results given the absence of batch effects, in a latent data space. In the GARD assays, these reference samples are comprised of unstimulated controls, i.e. samples acquired from cellular exposure experiments but where no xenobiotic agent was added to the cell medium.

23. For the GARDskin assay, equations 2-8 have already been calculated during assay development, using the indicated training data set (2). Therefore, results obtained in equations 2, 4, and 6, comprise fixed parameters that are employed during the normalization. These parameters are readily hosted in the GDAA, thus, only the steps described by equations 9-15 are executed in response to a novel test dataset in the GDAA. Fixed parameters derived from equations 2, 4 and 16 are listed in Table 3. Fixed parameters derived from equation 6 are listed in Table 4.

24. *The initial steps of the algorithm require a training dataset, here denoted A. The (j, i) element of the matrix is referred to as* a_{ji}*. The training dataset is a matrix with m samples in rows and n variables in columns. Here, the input values of variables i correspond to the gene expression levels of the GPS, as quantified by NanoString nCounter system. The training dataset contains reference samples in rows* $r \subseteq \{1, \ldots, m\}$*.*

25. *Each variable in the training set is first centered to form the matrix X.*

$$\bar{a}_i = \frac{1}{m} * \sum_{j=1}^{m} a_{ji}\,;\ i = 1, \ldots, n \qquad 2$$

$$x_{ji} = a_{ji} - \bar{a}_i;\ j = 1, \ldots, m; i = 1, \ldots, n \qquad 3$$

26. *The centered training dataset is then factorized using singular value decomposition (SVD).*

$$USV^T = SVD(X) \qquad 4$$

27. *The first k principal components are calculated for the dataset, where k is an adjustable hyperparameter of the algorithm. For GARDskin, k is a constant set to 4.*

$$C = XV_{ji};\ j = 1, \ldots, n; i = 1, \ldots, k \qquad 5$$

28. *For each component, a mean value is calculated using only the reference samples. For GARDskin, the value of* $|r|$ *is 3.*

$$\bar{c}_i = \frac{1}{|r|} * \sum_{j \in r} c_{ji}\,;\ i = 1, \ldots, k \qquad 6$$

29. *The training set can then be reconstructed, and the previously estimated mean values can be added, rendering the matrix* A^k *which can be used for construction of a predictive model.*

$$X^k = CV_{ji}^T; j = 1, \ldots, n; i = 1, \ldots, k \qquad 7$$

$$a_{ji}^k = x_{ji}^k + \bar{a}_i; j = 1, \ldots, m; i = 1, \ldots, n \qquad 8$$

30. The test dataset is represented by a matrix B with p samples in rows and n variables (same variables as for the training set) in columns. The rows at indices $r_b \subseteq \{1, \ldots, p\}$ represent the reference

samples in the test set. The variables in matrix B is adjusted by subtracting the column-wise mean values of the training matrix A, forming matrix Z.

$$z_{ij} = b_{ji} - \bar{a}_i; j = 1, \dots, p; i = 1, \dots, n \qquad 9$$

31. The matrix Z is then projected onto the k first singular vectors that were calculated from the training set, generating a new matrix D, describing the location of the test set in the data space spanned by A.

$$D = ZV_{ji};\ j = 1, \dots, n; i = 1, \dots, k \qquad 10$$

32. Using the mean values of the reference samples in the test set, adjustment factors are calculated in each of the k directions by estimating the differences to the mean values in the training set's reference samples.

$$\bar{d}_i = \frac{1}{|r_b|} * \sum_{j \in r_b} c_{ji}\,; i = 1, \dots, k \qquad 11$$

$$g_i = \bar{c}_i - \bar{d}_i; i = 1, \dots, k \qquad 12$$

33. The location of the test samples in the training set's data space is then adjusted by the estimated correction factors, generating the adjusted matrix D*.

$$d^*_{ji} = d_{ji} + g_i; j = 1, \dots, p; i = 1, \dots, k \qquad 13$$

34. Finally, the adjusted test set can be reconstructed to the original data space.

$$Z^k = D^* V^T_{ji}; j = 1, \dots, n; i = 1, \dots, k \qquad 14$$

$$b^k_{ji} = z^k_{ji} + \bar{a}_i; j = 1, \dots, p; i = 1, \dots, n \qquad 15$$

35. Now, predictions can be obtained on the matrix B^k.

2.4. Support Vector Machine (SVM) classifications

36. The classification algorithm employed by the GARDskin assay is an SVM. Prior to classifying a sample in the SVM, variables of preprocessed samples (CPTC- and BARA normalized) are standardized using mean values and standard deviations estimated from the training set, equation 16, where b_i represents the preprocessed value of variable i, μ_i the mean value of the training set of variable i, σ_i the standard deviation of the training set of variable i, and n the number of variables. Here, the input values of variables i correspond to the gene expression levels of the GPS, as quantified by NanoString nCounter system.

$$x_i = \frac{b_i - \mu_i}{\sigma_i}; i = 1, \dots, n \qquad 16$$

37. The SVM was defined using linear kernels, meaning that feature-specific coefficients can be extracted for the respective model. Therefore, classification of a single sample with either prediction model comprises the calculation of a decision value according to the linear equation described below. A binary classification is then obtained by evaluating the sign of the decision value (DV).

$$DV = b + \sum_{i=1}^{n} w_i x_i \qquad 17$$

where n is the number of variables (196 for GARDskin), b is the SVM's intercept, w_i the weight for variable i, and x_i the normalized gene expression value for variable i.

38. The identities and variable weights utilized by equation 17 for each gene of the GARDskin GPS's are listed in Table 1.

Table 1. The GARDskin GPS, including weights used for predictive modeling.

Parameter	Gene Symbol	Accession	SVM Value[1]
SVM Intercept	NA	NA	0.528954482
8133549	NA	GPS_8133549b.1	0.056599609
8140170	NA	GPS_8140170.1	1.91E-05
8145244	NA	GPS_8145244b.1	-0.01117444
AAMDC	AAMDC	NM_024684.2	0.033898422
ABAT	ABAT	NM_020686.5	0.006863548
ABHD5	ABHD5	NM_016006.4	0.041541088
ACER2	ACER2	NM_001010887.2	0.007719248
ACLY	ACLY	NM_001096.2	-0.017245566
ACTR10	ACTR10	NM_018477.2	0.020013467
ADAM20	ADAM20	NM_003814.4	-0.023978172
ALDH18A1	ALDH18A1	NM_001017423.1	-0.020013964
ALDH1B1	ALDH1B1	NM_000692.3	-0.019072892
ALKBH6	ALKBH6	NM_032878.3	0.004020885
ANAPC1	ANAPC1	NM_022662.3	-0.012602236
ANAPC5	ANAPC5	NM_016237.4	-0.016164334
ANKRA2	ANKRA2	NM_023039.4	0.013175619
ARFGAP3	ARFGAP3	NM_001142293.1	0.03897404
ARHGAP9	ARHGAP9	BC006107.1	0.002467956
ASB7	ASB7	NM_024708.3	0.00648298
ATP6V0D1	ATP6V0D1	NM_004691.4	0.007358478
ATP6V0E1	ATP6V0E1	NM_003945.3	0.018124205
ATP6V1H	ATP6V1H	NM_213620.2	0.037470329
BCL7A	BCL7A	NM_001024808.1	-0.021273517
BIN2	BIN2	NM_016293.2	0.040497079
BLMH	BLMH	NM_000386.3	-0.007151042
C12orf57	C12orf57	NM_138425.2	0.08230072
C19orf54	C19orf54	NM_198476.3	-0.009594629
C1orf174	C1orf174	NM_207356.2	-0.021818173
C20orf24	C20orf24	NR_026562.1	0.068356418
C3orf62	C3orf62	ENST00000343010.1	-0.022648434
C9orf89	C9orf89	NM_032310.3	0.004228944
CARM1	CARM1	NM_199141.1	-0.017612592
CD33	CD33	NM_001082618.1	-0.001644182
CD86	CD86	NM_175862.4	-0.005984092
CD93	CD93	NM_012072.3	-0.024492284

COX20	COX20	NM_198076.4	-0.019115552
COX7A2L	COX7A2L	NM_004718.2	0.021765308
CRHBP	CRHBP	NM_001882.3	-0.024430886
CSGALNACT2	CSGALNACT2	NM_018590.4	0.02060306
CYP51A1	CYP51A1	NM_000786.3	-0.017722631
DDRGK1	DDRGK1	NM_023935.1	0.040070336
DDX19A	DDX19A	NM_018332.3	-0.021410478
DDX21	DDX21	NM_004728.3	-0.02812977
DHCR24	DHCR24	NM_014762.3	-0.010878943
DHCR7	DHCR7	NM_001360.2	-0.014314584
DHX33	DHX33	NM_001199699.1	-0.029218496
DNAJB4	DNAJB4	NM_007034.3	0.030279911
DNAJB9	DNAJB9	NM_012328.2	0.032654112
DNAJC5	DNAJC5	NM_025219.2	0.016946662
DNAJC9	DNAJC9	NM_015190.3	-0.024124926
DRAM2	DRAM2	NM_178454.4	0.002699961
DTD1	DTD1	NM_080820.4	-0.024028686
EDEM2	EDEM2	NM_018217.2	0.012247701
EEF2KMT	EEF2KMT	NM_201400.3	-0.019241415
EMC7	EMC7	NM_020154.2	-0.02039051
EVI2B	EVI2B	NM_006495.3	0.029115559
FAM212B	FAM212B	NM_019099.4	0.012209461
FAS	FAS	NM_000043.4	0.029588049
FASN	FASN	NM_004104.4	-0.019929301
FBXO10	FBXO10	NM_012166.2	-0.021511448
FDPSP2	FDPSP2	NR_003262.1	-0.021529896
FDXR	FDXR	NM_004110.4	0.011791525
FOXO4	FOXO4	NM_005938.3	0.032239872
FTH1P2	FTH1P2	ENST00000466086.1	0.075205345
FTH1P5	FTH1P5	J04755.1	-0.017438431
FUCA2	FUCA2	NM_032020.4	0.042008024
GAS2L3	GAS2L3	NM_174942.1	-0.05309023
GDAP2	GDAP2	NM_001135589.2	0.013919689
GDF11	GDF11	NM_005811.3	-0.031418399
GLRX	GLRX	NM_002064.2	0.089675787
GNL3L	GNL3L	NM_001184819.1	-0.006194377
GNPNAT1	GNPNAT1	NM_198066.3	0.002077791
GSR	GSR	NM_000637.3	0.047540691
GTF3C2	GTF3C2	NM_001521.2	-0.003581487
HBP1	HBP1	NM_012257.3	-0.005067692
HIST1H1C	HIST1H1C	NM_005319.3	-0.025973884
HIST1H1E	HIST1H1E	NM_005321.2	-0.034592403
HIST1H2AE	HIST1H2AE	NM_021052.2	-0.072195756
HIST1H2BE	HIST1H2BE	NM_003523.2	-0.022904139
HIST1H3G	HIST1H3G	NM_003534.2	-0.02082623

HIST1H3J	HIST1H3J	NM_003535.2	-0.034477188
HIST1H4A	HIST1H4A	NM_003538.3	-0.025940051
HIST2H2AA3	HIST2H2AA3	BC001629.1	-0.032288343
HIST2H2AA3	HIST2H2AA3	BC001629.1	-0.02960366
HIST2H2BF	HIST2H2BF	NM_001024599.2	-0.070611108
HMGB3	HMGB3	NM_005342.3	-0.016980573
HMGCR	HMGCR	NM_000859.2	-0.018414824
HMGCS1	HMGCS1	NM_002130.7	-0.027092735
HMOX1	HMOX1	NM_002133.2	0.085734124
HNRNPL	HNRNPL	NM_001533.2	-0.01679857
IRS2	IRS2	NM_003749.2	-0.003037465
ISCU	ISCU	NM_014301.3	-0.00553174
ISG20L2	ISG20L2	NM_030980.1	-0.015930029
KCNE3	KCNE3	NM_005472.4	0.089689874
KGFLP1	KGFLP1	NR_003674.2	-0.009080626
KIAA0226L	KIAA0226L	NM_025113.3	0.041543212
LINC00987	LINC00987	NR_036466.1	0.019943767
LPAR1	LPAR1	NM_001401.3	0.034752789
LRPPRC	LRPPRC	NM_133259.3	-0.02054276
LY96	LY96	NM_015364.2	0.006619376
MAP2K1	MAP2K1	NM_002755.3	-0.002786052
MAPK13	MAPK13	NM_002754.4	0.073173694
METTL2A	METTL2A	NM_181725.3	-0.017771146
MGST3	MGST3	NM_004528.2	0.013437201
MRPL30	MRPL30	NM_145212.3	-0.015684134
MRPL4	MRPL4	NM_015956.2	-0.02308159
MRPS17	MRPS17	NM_015969.2	-0.031310556
MSANTD2	MSANTD2	NM_024631.2	0.029145624
MTR	MTR	NM_000254.2	-0.013748335
MYBBP1A	MYBBP1A	NM_014520.3	-0.033943468
NBR1	NBR1	NM_031858.2	0.054638995
NIP7	NIP7	NM_016101.4	-0.017241817
NLRP12	NLRP12	NM_033297.2	0.061787451
NOL6	NOL6	NM_022917.4	-0.019145848
NQO1	NQO1	NM_000903.2	0.061651838
NRBP1	NRBP1	NM_013392.2	0.012364255
NUBPL	NUBPL	NM_025152.2	-0.018151568
NUDT14	NUDT14	NM_177533.4	0.016930578
NUFIP1	NUFIP1	NM_012345.2	-0.009158645
NUP153	NUP153	NM_001278209.1	0.010731489
OR5B21	OR5B21	NM_001005218.1	-0.010121462
OSER1	OSER1	NM_016470.7	0.051759335
OTTHUMT00000400136	OTTHUMT00000400136	OTTHUMT00000400136.1	-0.025893552
PASK	PASK	NM_015148.3	-0.009866345
PAWR	PAWR	NM_002583.2	-0.007707116

PDAP1	PDAP1	NM_014891.6	-0.016002905
PDE1B	PDE1B	NM_000924.3	-0.030225058
PFAS	PFAS	NM_012393.2	-0.025867274
PHLDA3	PHLDA3	NM_012396.3	0.014890414
PIK3AP1	PIK3AP1	NM_152309.2	0.027143988
PINK1	PINK1	NM_032409.2	0.052255635
PMM2	PMM2	NM_000303.2	-0.040695293
PNO1	PNO1	NM_020143.2	-0.032498706
POLR2E	POLR2E	NM_002695.3	-0.022990109
POLR3E	POLR3E	NM_018119.3	-0.020891194
PPM1D	PPM1D	NM_003620.3	0.004270021
PREX1	PREX1	NM_020820.3	0.004360807
PSTPIP1	PSTPIP1	NM_003978.3	0.050454056
RAB33B	RAB33B	NM_031296.1	0.00993255
RENBP	RENBP	NM_002910.5	0.024057248
RFC2	RFC2	NM_181471.2	-0.013597855
RNASEH1	RNASEH1	NM_002936.4	-0.002272294
RNF146	RNF146	NM_030963.2	0.019489208
RNF24	RNF24	NM_007219.2	0.066712482
RNF26	RNF26	NM_032015.3	-0.012358389
RPF2P1	RPF2P1	ENST00000424137.1	-0.023568653
RPSA	RPSA	NM_002295.4	-0.005832863
RPUSD2	RPUSD2	NM_152260.2	-0.020245974
RRP12	RRP12	NM_001145114.1	-0.026416351
RXRA	RXRA	NM_002957.5	0.082351026
SCARB2	SCARB2	NM_005506.3	0.011564037
SERBP1	SERBP1	NM_001018068.1	-0.032160449
SFPQ	SFPQ	ENST00000357214.1	-0.021096571
SLC25A32	SLC25A32	NM_030780.4	-0.035624141
SLC35B3	SLC35B3	NM_001142540.1	0.023512203
SLC37A4	SLC37A4	NM_001164277.1	-0.015958306
SLC5A6	SLC5A6	NM_021095.2	-0.020293403
SMPD4	SMPD4	NM_017751.4	-0.011540004
SNHG1	SNHG1	AK095849.1	-0.034339073
SNHG12	SNHG12	NR_024127.1	-0.022531094
SNORA45B	SNORA45B	NR_002977.1	-0.06987957
SNX27	SNX27	NM_030918.5	0.001528995
SPRY2	SPRY2	NM_005842.2	-0.049116104
SQLE	SQLE	NM_003129.3	-0.04104768
SREBF2	SREBF2	NM_004599.3	-0.017971371
SRP72P2	SRP72P2	ENST00000538672.1	-0.002879943
ST3GAL6	ST3GAL6	NM_001271148.1	0.018381256
STK17B	STK17B	NM_004226.3	0.02495814
TAPT1	TAPT1	NM_153365.2	0.015686607
TAS2R5	TAS2R5	NM_018980.2	-0.010771173

TBCEL	TBCEL	NM_152715.3	0.011212212
TCTN2	TCTN2	NM_001143850.2	-0.043588495
TLR6	TLR6	NM_006068.4	0.023101459
TLR9	TLR9	NM_017442.3	0.007388632
TMEM150B	TMEM150B	NM_001085488.2	0.047516373
TMEM55A	TMEM55A	NM_018710.2	0.092843127
TMEM59	TMEM59	NM_004872.3	-0.01338575
TMEM97	TMEM97	NM_014573.2	-0.017200824
TOMM34	TOMM34	NM_006809.4	0.001075717
TOMM40	TOMM40	NM_001128916.1	-0.016585944
TP53I3	TP53I3	NM_001206802.2	0.008965939
TP53INP1	TP53INP1	NM_001135733.1	0.007065765
TWF2	TWF2	NM_007284.3	0.009791223
TXNRD1	TXNRD1	NM_001093771.2	0.061826237
U4	U4	ENST00000363404.1	-0.054178672
UFC1	UFC1	NM_016406.3	0.030267626
USP10	USP10	NM_001272075.1	2.37E-04
VAMP3	VAMP3	NM_004781.3	0.006474929
VARS	VARS	BC012808.2	-0.022807781
VARS	VARS	NM_006295.2	-0.028171927
VPS37A	VPS37A	NM_152415.2	0.018414112
YBX1P1	YBX1P1	ENST00000445822.1	-0.023116427
ZNF211	ZNF211	NM_001265600.1	-0.037642067
ZNF223	ZNF223	NM_013361.4	-0.018825169
ZNF561	ZNF561	NM_152289.2	-0.005189719
ZNF79	ZNF79	NM_007135.2	-0.011118332

1. Denoted *w* in equation 17

Table 2. Target sequences of the GPS.

Gene Symbol (Probe)	Target sequence
8133549	ATGCACAGCGCGGCTAAATTGGATTCGACAGCACCGGAAACGGCGACTCCCACTTGGGGCGCTGCGGACACACGAGTCGAGGCTGCCTTCCAGGAAGCAA
8140170	AAGATGAAACCAATAGCCTAATTTTAATTCACTCGTGCATCCCGCCTGCTGCGTTTCAGAGCTGACTGTTCAGATGTGTCATGCTTTTTTCATTGGTCCG
8145244	AGAGGCCTGAGCCTGAACAACATGGCTTCCCCCAGCGTGAGACTCGCTTGTCCTCCCACCGCCTGCTCTCTCCTGATGACCAGGTTCCAGGAGTTATCAA
AAMDC	GAAATTGCTTCCTTATCATGGGGGCAAATGAAAGTAAAAGGCTCTAATACAACCTATAAGGACTGCAAAGTATGGCCAGGGGGTAGTCGGACTTGGGATT
ABAT	GTCGACGTTGAATTTGATTATGATGGGCCTCTGATGAAGACGGAAGTCCCAGGGCCTAGATCTCAGGAGTTAATGAAACAGCTGAATATAATTCAGAATG
ABHD5	TATTCCTTATGGATGGGCAAAAAGGCCAATGCTCCAGCGAATTGGTAAAATGCACCCTGACATTCCAGTTTCAGTGATCTTTGGCGCCCGATCCTGCATA
ACER2	TTTAAAAAGGTCCCCTCCTCCTCCCTAATGTGTCTGTGGACCACCTGGATTCCACTGTACAAGGGGAAAAGTGTCTATTCCTTTCCCAAAGATGGAAAAT
ACLY	CGTGTTAAGGGCTTGTTTGGTATCCCACTGAAATGTTCTGTGTTGCAGACCAGAGTCTGTTTATGTCAGGGGGATGGGGCCATTGCATCCTTAGCCATTG
ACTR10	TCATAGGTGGCACTTCTATGTTGCCAGGATTTCTCCACAGATTGCTTGCAGAAATAAGGTATTTGGTAGAAAAACCAAAATATAAAAAAGCACTTGGCAC
ADAM20	CGAGCTTGGTCATAATTTGGGTATGCAACATGACACCCAGTGGTGTGTGTGCGAGCTACAGTGGTGCATAATGCATGCCTATAGAAAGGTGACAACTAAA
ALDH18A1	CAACTGAAAAGAGCCAGGAAAACCCGGGAATTTTCCAAAAGGTCTTCACGTTAAACTTGTCTTATCTCAGGAGAGAGCCCGCTCTTGTCTCCCAGTTCCT
ALDH1B1	GCAAAACTCCTCTGTGGCGGAGAGCGTTTCGGGGAGCGTGGTTTCTTCATCAAGCCTACTGTCTTTGGTGGCGTGCAGGATGACATGAGAATTGCCAAAG
ALKBH6	GTTCCTGCCCCTTTGGGGCTGCTGTGACTCCGCGACCTAGGAACCGTGGGCAAAGGGGGCTCCCCTGGGTTATTTATTTTCCCAATAATTTTGTGTGAGC
ANAPC1	CCCTGCTGTTCAGATGCTGATATGTGTCCTGTGCTTCCTGGATGGCCAGTGGGATCATAAGCTGGTAGAAGCAAGACCTTCATCCACTGACTTCATATTT
ANAPC5	GGCCCAGATGTTGCTGAGCATGAACAGCCTGGAGGCGGTGAATGCGGGCGTGCAGCAGAACAACACAGAGTCCTTTGCTGTCGCACTCTGCCACCTCGCA
ANKRA2	CAGACATTAAAATAGAACATCCACTGGACCCAAATTCAGAAGAAGGGTCAGCTCAGGGTGTTGCCATGGGAATGAAATTCATATTGCCTAACCGATTTGA
ARFGAP3	CAAATCAATACGGTATACAGAGTTAAAGTGGAATGAGGTAAGAAGATACAGCTACAGAAAATAGTTGCGTGTATGGGAGAACAGTCATTGTAATTGGGTA
ARHGAP9	GCTCTGGACCCGCGGAGCTGAGCGCCGGGGAGGACGAAGAAGAGGAGTCGGAGCTGGTGTCCAAGCCGCTGCTGCGCCTCAGCAGCCGCCGGAGCTCCAT
ASB7	ACCACAATGCCAACATCGACATTCAGAATGGTTTCCTGTTGCGATACGCCGTGATCAAAAGCAATCACTCTTATTGCCGAATGTTCCTTCAGAGAGGGGC
ATP6V0D1	ATGTATCGCCCAGCGCCACCGCGCCAAAATCGACAACTACATCCCTATCTTCTAGCGTCCTGGCCCAAGGCTCTCAATTGCACTCTTTGTGTGTGTGTGT
ATP6V0E1	GATGCTGTTCTTCTGAGAGATACGTTACTCTCTCCTTGGAATCTGTGGATTTGAAGATGGCTCCTGCCTTCTCACGTGGGAATCAGTGAAGTGTTTAGAA
ATP6V1H	ACTGAAAGAGAAACTCGCCAAGAATATGCCCTGGCTATGATTCAGTGCAAAGTTCTGAAACAGTTGGAGAACTTGGAACAGCAGAAGTACGATGATGAAG
BCL7A	ATTCACAGTCCTCGATGGAACATTCGATGAACAGCTCAGAGAAAGTAGATCGGCAGCCGTCTGGAGACTCGGGTCTGGCCGCAGAGACGTCTGCAATCTC
BIN2	AGCTACAGTCTCCAGTCCTCTTACCTCACCTACTAGTCCCTCTACACTTTCCTTGAAGAGTGAGAGTGAATCTGTCTCAGCAACTGAAGATCTGGCACCT
BLMH	TGCTCCTTGTTCCTAGAGTAGAGTGGAGGGAGGGTGGCCTAAGAGTTGAGCTCTCGGAACTGCATGCTGCTGGACAGTATCACTGTCTTTCCTAGATGGC
C12orf57	TCCAGGCGTTCTCCGCCCCGGAGAATGCAGTGCGCATGGACGAGGCTCGGGATAACGCCTGCAACGACATGGGTAAGATGCTGCAATTCGTGCTGCCCGT
C19orf54	GATTGACAACAGCCCGGACCCTGCGGCCTGCCTATTCCATCTGAATGTCGCATCGTCTGTTTCTCACTAGGGGCCGCCTCTGTCATCTCACTAGACATTT
C1orf174	ACCATGCCCGGCCAGTGTCCTTTCTTATACACGTACATACATGATGATGGCTTGAGTCAGCTGCAGGGCAGTGGGCTTAATGAGAGGGATCTTTGTAAAG
C20orf24	TGCCATCCATTATGACTGATGGTGTACAGCTCCCAAGTGCTCCCTATCCAGTCCAAAGGACCCTCTTGATTACAGCACAGGAACTTGATCGTTGGGGAAC
C3orf62	GCTATAGCCAGGGCCAAGCTCCAGGAAATCGTGGCCATTCAGGGGTAGTTTGCAGCCTCA

	TTTGTAACATTATTGTGTTGTCCTGTGCATTTCCAATGCA
C9orf89	CCTGGTGCAGGACACGCCTTTCCTGACAGGCCATGGGCGCTTGAGTGAGCAGCAGGTGGACAGGATCATCCTCCAGCTGAACCGTTACTACCCACAGATC
CARM1	GACGACCAGGCCTCGGTCACAACGGACGTGACATGCTGCTTTTTTTAATTTTATTTTTTTATGAAAAGAACCAGTGTCAATCCGCAGACCCTCTGTGAAG
CD33	GATCCACATCCTCTACAGGTCGGGGACCAAAGGCTGATTCTTGGAGATTTAACACCCCACAGGCAATGGGTTTATAGACATTATGTGAGTTTCCTGCTAT
CD86	AGTATTTTGGCAGGACCAGGAAAACTTGGTTCTGAATGAGGTATACTTAGGCAAAGAGAAATTTGACAGTGTTCATTCCAAGTATATGGGCCGCACAAGT
CD93	TGGGATCCAACGAGCCCTCCTATTTTCACAGTGTTCTGATTGCTCTCACAGCCCAGGCCCATCGTCTGTTCTCTGAATGCAGCCCTGTTCTCAACAACAG
COX20	GGAAGAAAGTGTGACCCGTTCGACGGAACAAAGGACATGACAGCCCGGCCCCGTGCGGCCACTGCGGAGCGTTAGGAACATTCCCTAAAATGGCGGCCGG
COX7A2L	CTGATTTCCCTGGAGGTTCTGGATGAAGGCTGAACACAGGCTTGTTAATGTCAGTCTGTGCTGAGGACCTCAGGGACTTGAGGTTGCATTTTTGAGCATG
CRHBP	TGGAAAACACGTAAATCGTGTGACTTTTGAGTATCGTCAGCTGGAGCCGTACGAGCTGGAAAACCCAAATGGAAACAGTATCGGGGAATTCTGTTTGTCT
CSGALNACT2	AGAAGATGCGGTCACTGCAAGAAAGAAGGAATGTAGGGGCTAATGGCATAGGCTATCAGAGCAACAAAGAGCAAGCACCTAGTGATCTTTTAGAGTTTCT
CYP51A1	GTGACAGGCGGCAACCTCTTGTCCATGCTGCTGATCGCCTGCGCCTTCACCCTCAGCCTGGTCTACCTGATCCGTCTGGCCGCCGGCCACCTGGTCCAGC
DDRGK1	GTGTGATTGACGACCGGGGCAAGTTCATCTACATAACCCCAGAGGAACTGGCCGCCGTGGCCAACTTCATCCGACAGCGGGGCCGGGTGTCCATCGCCGA
DDX19A	TCTCTCGGTTGCTCCCTCTGCCTAGGCCCCTGGTACTCAGTCACGGCAGCCAGGAGACCCCAGGTGAGTTTCTGAGCGCATACGTAGTTGGTTCTTACCC
DDX21	AGAAAGAGGAGCCATCTCAAAATGACATTTCTCCTAAAACCAAAAGTTTGAGAAAGAAAAAGGAGCCCATTGAAAAGAAAGTGGTTTCTTCTAAAACCAA
DHCR24	CCAGCCAGGCCTAGTGCACCCCAAAGGAAATGAGGCAGAGCTCTACATCGACATTGGAGCATATGGGGAGCCGCGTGTGAAACACTTTGAAGCCAGGTCC
DHCR7	CCTTTCAGGTGTAGGCAGGTGGGCTCTGCTTCCCGATTCCCTGTGAGCGCCCACCCTCTCGAAAGAATTTTCTGCTTGCCCTATGACTGTGCAGACTCTG
DHX33	TGAGTTGGGAGCCGTTAGGCTGAATGTTACTGCTTGCCATATGATGTGAAGTACAGCAATATCCCAAGTTCTTGTGACTGAGGGAGATTTTCTGGAAGGG
DNAJB4	GCTGCTCAATTAATGTACCAACACTGGATGGAAGAAACATACCTATGTCAGTAAATGATATTGTGAAACCCGGAATGAGGAGAAGAATTATTGGATATGG
DNAJB9	GGGCCCAAGCTGCCGACCCGAGCCGATCGTCAGGGTCGCCAGCGCCTCAGCTCTGTGGAGGAGCAGCAGTAGTCGGAGGGTGCAGGATATTAGAAATGGC
DNAJC5	CCTTCCGAGGTTGACACCGTGTCCTCCGCGGTGTTTCTCGCCTGGTCGTCTCGTCGTGTGGACGCTGCCGTTCTGGTTCTCGGAGGTGTGTCCTTCGCCG
DNAJC9	GCGGCTGCTTCCTCCGGGGTCGTATCTCCGCCCGGCATGGGGCTGCTGGACCTTTGCGAGGAAGTGTTCGGCACCGCCGACCTTTACCGGGTGCTGGGCG
DRAM2	AGCTGTGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTCTTCTGG
DTD1	TTTCTACCACATCTTGGCTTGCTTTTGGAACAGGCTGGCCCAGCATCATTTGTCATCAAGTCCACTGTGGTGTATTCTGCGTGTCCATGGCGGGGGTTCT
EDEM2	AACCGCATGGAGTCGTTCTTCCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACG
EEF2KMT	CGGGTCCTTGAGCAGCTCCGAGGGAATGTCCTTCTCAATGGCCTCTCATTAGAGGCAGACATCACTGCCAAGTTAGACAGCCCCAGGGTGACAGTGGCCC
EMC7	CAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTT
EVI2B	AACACCAAACAACCAACACCAATAGCCAACACCTCCTCCCAGCAAGCCGTGTTCACCTCTGCCAGACAACTACCATCTGCCCGTACTTCTACCACACAAC
FAM212B	CCTTGTTGGGAGGGTGGCAGAGGTCCTGCCAGGCCCACAGTCTGTTCCCCCTCCAGTCAACCTTCTCTTGGCAGCAGCACCAAGTTTCCATCCCATAGGA
FAS	TATCGTCCAAAAGTGTTAATGCCCAAGTGACTGACATCAACTCCAAGGGATTGGAATTGAGGAAGACTGTTACTACAGTTGAGACTCAGAACTTGGAAGG
FASN	GCCAGGACCTGGCTTTCCTGAGCATGCTGAACGACATCGCGGCTGTCCCCGCCACCGCCATGCCCTTCCGTGGCTACGCTGTGCTGGGTGGTGAGCGCGG
FBXO10	CCAGTTTGACAACTGCAACTTTGAGAACGGGCACATCCAGGTCCATGGCCCGGGTACTTGCCAAGTGAAGTTCTGTACCTTCAAAAACACCCATATCTTC
FDPSP2	TAACAATATGTGAGAAACCCATCTGATCACTGCAGACCTGCTGAAATCTGTTACAACTAATCCTTCAATCCTCACCAGAATGCTGGCTGTCCTGCCTCTG
FDXR	GTTTTAGCTTTCAGCAACTGAGGTAACCTTAGGGACAGGTGGAGGTGTGGGCCGATCTAA

	CCCCTTACCCATCTCTCTACTGCTGGACTGTGGAGGGTCA
FOXO4	TTATGCAGGGGGTGTCCCTCCCACCCTCAATGAAGGTCTAGAGCTGTTAGATGGGCTCAATCTCACCTCTTCCCATTCCCTGCTATCTCGGAGTGGTCTC
FTH1P2	GAAAAAAGTGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATA
FTH1P5	GATCACTTGAATCCAGGAGGCAGAGGCTGCAGTCAGCCAAAATTACTCCACTGCCCTCCAGCCTAGGCAACAGAGTGAGAATCTGTCTCAAAAATAAAAA
FUCA2	CTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGGTCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAG
GAS2L3	CTGGGCTCTATGTCAGTCCGTTCTAAATTGCCAAATTCTCCAGCAGCATCTTCTCATCCCAAGCTCAAGTCTTCAAAAGGCATAACGAAGAAACCGCAGG
GDAP2	CTCTCTACTTCCCAAGGTCATTAAAAGAGGAGAATCGATCATTGCCCTACCTACCTGCAGATATTGGAAATGCAGAAGGGGAGCCTGTGGTACCTGAACG
GDF11	TTGGCAGAGCATCGACTTCAAGCAAGTGCTACACAGCTGGTTCCGCCAGCCACAGAGCAACTGGGGCATCGAGATCAACGCCTTTGATCCCAGTGGCACA
GLRX	CAGTCAATTGCCCATCAAACAAGGGCTTCTGGAATTTGTCGATATCACAGCCACCAACCACACTAACGAGATTCAAGATTATTTGCAACAGCTCACGGGA
GNL3L	GAGAATTACGTACTTGTTGAGTACAAACTGCACCAAGCCCTGGAGACCCATTACCACCGTTAACCCTCAATACAGCTCTGCTAGTAAGGGATTCGTCTCC
GNPNAT1	AGTTGGCTTTCCAAAACAACAGAAATCCTTCACCAATAGAGTGCACTACTTACCTGCTTATAGCCTATACAGACGAACTGATCTGTCCTTCGTGAAACGC
GSR	GCAACGAAGGCAGACTTTGACAACACAGTCGCCATTCACCCTACCTCTTCAGAAGAGCTGGTCACACTTCGTTGAGAACCAGGAGACACGTGTGGCGGGC
GTF3C2	GGTAACCATCATGTATGCCCACGAGGGTGATAGTAATTCGTGAGACTGAAGTTGCTTAGAGTACTTCTTTGACCAAGGAATACCACAGACACCCTACCGA
HBP1	CTTGTGGAGGACCTGGTGGTCAAGACTTTGCAAGATCTGGATTCAGTAAAAACTGTGGCTCACCTGGATCATCACAGCTCTCTTCCAATTCTTTGTATGC
HIST1H1C	TTAAAAAGGCGGGCGGAACCAAACCTAAGAAGCCAGTTGGGGCAGCCAAGAAGCCCAAGAAGGCGGCTGGCGGCGCAACTCCGAAGAAGAGCGCTAAGAA
HIST1H1E	CCCCGGTGTCCGAGCTCATTACTAAAGCTGTTGCCGCCTCCAAGGAGCGCAGCGGCGTATCTTTGGCCGCTCTCAAGAAAGCGCTGGCAGCCGCTGGCTA
HIST1H2AE	ACTAGTCAAATCCGTCAGTGATCCCGAGTCCCAGAAACCAAAGGCTCTTTTCAGAGCCACCCACCTTTTCTGTAAAGTGCTGGAATACACATACGATGCC
HIST1H2BE	GCCAAGCACGCTGTGTCAGAGGGCACCAAGGCCGTTACCAAGTACACCAGCTCCAAGTAAACTTGTCCCTGCAACTGCCTTAGTAAACCCAAAGGCTCTT
HIST1H3G	CGAGTGACTATCATGCCCAAGGACATTCAGCTCGCTCGCCGCATTCGTGGGGAGAGAGCGTAGAGGTTTCCGGGCAGTAATTCTATCCAACTTAAAAAGG
HIST1H3J	CTAAGGACATCCAGCTTGCGCGTCGTATCCGTGGCGAGCGAGCATAATCCCCTGCTCTATCTTGGGTTTCTTAATTGCTTCCAAGCTTCCAAAGGCTCTT
HIST1H4A	CAAGCGCCACCGCAAGGTGTTGCGTGACAACATCCAGGGCATCACCAAGCCGGCCATCCGGCGTCTGGCCCGGCGTGGCGGTGTGAAGCGGATCTCTGGT
HIST2H2AA3	ACGACGAGGAACTGAACAAGCTGCTGGGCAAAGTCACCATCGCCCAGGGCGGCGTCTTGCCTAACATCCAGGCCGTACTGCTCCCTAAGAAGACGGAGAG
HIST2H2AA3	AGGCAGGAGTTTCTCTCGGTGACTACTATCGCTGTCATGTCTGGTCGTGGCAAGCAAGGAGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCCCGCG
HIST2H2BF	TCTTGGTGAAAGCTGAGCACTTCATAGGCTGTTTACAGGTCCTTCTCCACAGGAAAATACTTCCTCCAGGACAAGAACCCTGTCTTGGTTCCAAACTTTC
HMGB3	TATTAGTGGGTAGTGTAACATTTTATCCAGGTTGGGGTGAGGGGAGATGGCCACAGTAGCAAGTGGTGACACTAAATACCATTTTGAAGGCTGATGTGTA
HMGCR	GATATCAGAGCTCTTAATGTTGCTTAGATGAGGGTGACTGTCAAGTACAAGCAAGACTGGGACCTTAGAAATCATTGTAGAAACACAGTTTTGAAAGAAA
HMGCS1	GGCTTCTGCACAGATAGAGAAGATATTAACTCTCTTTGCATGACTGTGGTTCAGAATCTTATGGAGAGAAATAACCTTTCCTATGATTGCATTGGGCGGC
HMOX1	AGAGGGAAGCCCCCACTCAACACCCGCTCCCAGGCTCCGCTTCTCCGATGGGTCCTTACACTCAGCTTTCTGGTGGCGACAGTTGCTGTAGGGCTTTATG
HNRNPL	GCCATCATGCCTGGTCAGTCATACGGGTTGGAAGACGGGTCTTGCAGTTACAAAGACTTCAGTGAATCCCGGAACAATCGGTTCTCCACCCCAGAGCAGG
IRS2	GCGCCGAAACGGGTGATCGCTCTCGACTGCTGCCTGAACATCAACAAGCGCGCCGACGCCAAGCACAAGTACCTGATCGCCCTCTACACCAAGGACGAGT
ISCU	CCACACCAGCTGTTTCCCACCTGCTGTGCAGTCACCTTAGATGTTCAGAAGCCGCTTCCTCTCCACTGAAGAGCTATGAGATACGCACAATACTTGCTGT
ISG20L2	TGTCCTGTGTCTGGTTAAGTGTCCCATGGAAGGGGAAAGCCTTCACGTCAGAACCCAACCCTATACCTTTTACTTCTTAAATGGTGCTAACCACAGGTGT
KCNE3	TGAATTCAGAAACTATCCCAGATCTCAGCTAGAACCATCCACTGTTCTGTTTGTCCAGTTT

	CAACTTAAGGGATCTCCATGCGGTCCCTGGAAGTACCCA
KGFLP1	CACCAGGAGCACACTTATATCATGGAAATCAGGACAGTGGCAGTTCGGATTGTGGCAATCAAAGGGGTGGAAAGTGAATTCTATCTTGCAATGAACGAGG
KIAA0226L	CCTGGGAAGGGATCAGCGATCACTCTGGCATTATTGATGGTTCGCCCAGACTCCTGAACACTGACCATCCTCCTTGCCAATTAGACATCAGGCTCATGAG
LINC00987	TCAGAGCAGCCAGTGGGGCAGGACAATGTTTTTCATCAAATGTCCTTAGATTTGGAGGAGGTTTCCCCAGTGTATCCAGTGGTTGTCTTCCTCTTGATTA
LPAR1	TCTAGACGTGTGCTGTCCACAGTGCGACGTGCTGGCCTATGAGAAATTCTTCCTTCTCCTTGCTGAATTCAACTCTGCCATGAACCCCATCATTTACTCC
LRPPRC	ATGTTGGCACTAGGAGTCATCAGATCTAGGCTTCATCATTTTCCAGTGAGAAGCAGAGACCCAAAGGGCCTGTTACTTGTGCTTGGTCAGGGGACTGTCT
LY96	AGAAGTTATTTGCCGAGGATCTGATGACGATTACTCTTTTTGCAGAGCTCTGAAGGGAGAGACTGTGAATACAACAATATCATTCTCCTTCAAGGGAATA
MAP2K1	CAGAAGCAGAAGGTGGGAGAACTGAAGGATGACGACTTTGAGAAGATCAGTGAGCTGGGGGCTGGCAATGGCGGTGTGGTGTTCAAGGTCTCCCACAAGC
MAPK13	CCTCACCCATCCCTTCTTTGAACCCTTCCGGGACCCTGAGGAAGAGACGGAGGCCCAGCAGCCGTTTGATGATTCCTTAGAACACGAGAAACTCACAGTG
METTL2A	ATTGGCTTTTTACCGAATTCCCTGAGCTGGCACCTAGCCAAAATCAAAATCATTTGAAGGACTGGTTCTTGGAGAACAAGAGTGAAGTACCTGAATGTAG
MGST3	CAAAGTGGAGTATCCTATCATGTACAGCACGGACCCTGAAAATGGGCACATCTTCAACTGCATTCAGCGAGCCCACCAGAACACGTTGGAAGTGTATCCT
MRPL30	GCAACAATGACATTGTCATGCTTATTGTCCCAATATCCATCCTGTCGTAGATCTTAATGTTTTTGATCGTTGCGTTAAAGTGGAAGTGCCACCCACAGTG
MRPL4	AAGTTACTACTACATGCTGCCCATGAAGGTGCGGGCGCTGGGTCTCAAAGTGGCACTGACCGTCAAGCTGGCCCAGGACGACCTGCACATCATGGACTCC
MRPS17	CTGTTCCACGAGCAAAGCATGTGAAACATGAACTGGCTGAGATCGTTTTCAAAGTTGGAAAAGTCATAGATCCAGTGACAGGAAAGCCCTGTGCTGGAAC
MSANTD2	ATCCAGATGCCGCCGTCAGACTCTTCATGGAAACCCTTTCTTCAATTGGGCCAGTACGACTTCTAAGGAATCATAGTAGACTTGGGCCAGAAAAAACAGA
MTR	TGAGTGAACTACAGCTATACCTCACAATAAGAATGAATCTCAGAAAATATTAAGGAAAAAAGCAAGTTTGAAGAGACCACATGGGGCGTACTATTTTTAT
MYBBP1A	CAGCAGCAGCTCCAAACAGGAGCAGGACCTTCTGCACAAGACGGCGCGCATCTTCACGCACCACCTGTGCCGTGCCCGGCGCTACTGCCACGACTTGGGT
NBR1	CCTGGATGAGGAAAATGAAGAGGTATCCATCAACAGTCAAGGAGAATATGAAGAAGCGCTTAAGATGGCAGTTAAACAGGGAAACCAACTGCAGATGCAA
NIP7	CAGACGGCTGTATGGAAAGGCCGAGCTTTGTTTCCTGTGTTTGTGTGGACTCCACCATCATGTTGAATTTTGTCAACACTCTGGCCTCTTCAGGGACTTC
NLRP12	GGACCTGAATAAAATGACCCACAGTAGGTTGGCAGCGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGAATGGTCCTATCTGCTGGCTCTCCC
NOL6	AGGAGGAGAATGCTGCCTCCTTTCAGTCTGGTCTACACCCACTTTCTGGTAGCCTCTCTGCTTCCTGTAATTCTGGCTGTTTTTCCAGACTCAGCTCAAA
NQO1	CCGAATTCAAATCCTGGAAGGATGGAAGAAACGCCTGGAGAATATTTGGGATGAGACACCACTGTATTTTGCTCCAAGCAGCCTCTTTGACCTAAACTTC
NRBP1	AGAGACCTTGAACAAGTTCAATTTTGCCAGGAACAGTACCCTCAACTCAGCCGCTGTCACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCCTGATCTG
NUBPL	ATGTGTATGGACCTTCAGTTCCAAAGATGATGAATCTGAAAGGAAATCCGGAATTATCACAGAGCAACCTAATGAGGCCTCTCTTGAATTATGGTATTGC
NUDT14	AGACCCTCGGCGTCATCTTTGGTGTCTCATGGTTCCTCAGCCAGGTGGCCCCCAACCTGGATCTCCAGTGAGACTCCAGGGTTCTAGACAGAGGCCAGTC
NUFIP1	GAAGGTCCACCGGAGGCAAATGCAGATCCTCTTGGTGTTTTGATAAACAGTGATTCTGAGTCTGATAAGGAGGAGAAACCACAACATTCTGTGATACCCA
NUP153	GAACTTCATTCTCTGGTCGCAAGATAAAGACTGCTGTTAGACGCAGGAAATAAAGGTCACATTGGTGTTGTACTCAATTTTAACAACAGCTGGTGCCCTG
OR5B21	AGTTCTTCTTCTTTGTGGGGTTTGCCACTGTTGAGTGCTACCTCCTGGCCTCCATGGCCTATGATCGCCATGCAGCGGTATGTAGGCCTCTTCATTACAC
OSER1	GATGATGTGACCATTGAGGACCTGTCAGGCTACATGGAGTATTACTTGTATATTCCCAAGAAAATGTCCCACATGGCAGAAATGATGTACACCTGATAGC
OTTHUMT00000400136	GAGGAGGAAGAAGGTGATGGTGAGGAAGAGGACGGAGATGAAGATGAGGGAGCTGAGTCAGCTACGGGCAAGCGGGCAGCTGAAGATGATGAGGATGACG
PASK	TTTGGTGTCCTCTGAGCATTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCCTTCCACGTTGGATGCTGGCCCTGAGGACACGTGCCCATCAGCA
PAWR	ATGAAGCAGGGCAGAAAGAGCGGAAACGAGAAGATGCAATTACACAACAGAACACTATTCAGAATGAAGCTGTAAACTTACTAGATCCAGGCAGTTCCTA
PDAP1	TGAAGGGCTCATCGACATCGAGAACCCCAACCGGGTGGCACAGACAACCAAAAAGGTCA

	CACAACTGGATCTGGACGGGCCAAAGGAGCTTTCGAGGAGA
PDE1B	CGGTCTCTGCTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAACATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAG
PFAS	TACACTGCACTGAATGTAAGGAATTGTTGCTTGTGGAAGTTTCTCAGCGTTTCTGGCTGTCTTAGGGCTGGCCTCAGAACCCAGCATTCCTGTTATTTGC
PHLDA3	CCCAAGGAGCTCAGCTTCGCCCGCATCAAGGCCGTGGAGTGCGTGGAGAGCACCGGGCGCCACATCTACTTCACGCTGGTGACCGAAGGGGGCGGCGAGA
PIK3AP1	CGAGAAGGTTGTTTCCTACTCGAAGCAGCAGAACCTGCCGACGGTGACTTCACCTGGGAACCTGATGGTGGTGCAGCCGGACCGCATTCGCTGTGGGGCA
PINK1	TGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTT
PMM2	CGTGTCTTGTAAGGTGCGGCTAGAAACTGGGGACATGGCAGCGCCTGGCCCAGCGCTCTGCCTCTTCGACGTGGATGGGACCCTCACCGCCCCGCGGCAG
PNO1	CAGTGGTCGGTCACAAGAAACCAGCTGAACAATTTCAGTCATTTGAAGCCTCCGTCCCTTCTTCCATTCTCAGCCAGAAGCATAAACAGAAAAGAAAGAT
POLR2E	GGTGTACTGCCAGCGCATGCAGGAGGAGAACATCACACGGGCTCTCATCGTGGTGCAGCAGGGCATGACACCCTCCGCCAAGCAGTCCCTGGTCGACATG
POLR3E	GCAAACACTAAACTAGCATCATGGTGCTATCTTCAAATGGTTACAGGAAGGCGATCTTGTTGGGCTCAGCGTTACGTGTATCTAGAGGGAACGGAGCTAA
PPM1D	CCAATGGCATTATTAGGTCTTAAAGTAGTTACTCCCTTCTCGTGTTTGCTTAAAATATGTGAAGTTTTCCTTGCTATTTCAATAACAGATGGTGCTGCTA
PREX1	CGGGTTAGAGGGTCACTGGGAAACACCGGGCGGTGGCTTCTGTGATTTATTTTCTTGATGGTAACTTCTCAGAGCAGGGCGATTGGGACATCACCAGCCA
PSTPIP1	CCCCCAGCACTGTCCCCACCTTGCTAGGGCCCAGAACCAAGCGTCCCCCAGCCCCGAGAGGGAGCCTGTCGTCTCCCAGGGAATAAAGGAGTGCGTTCTG
RAB33B	TTGGAAATAAATGTGACTTGAGAAGTGCCATACAGGTACCCACAGACTTGGCACAAAAATTTGCTGACACACACAGTATGCCTTTGTTTGAAACGTCTGC
RENBP	ATGCCCGGGTGGCACCTCCTGGCAAGAAGTGTGCCTTTGTGCTGACTCGGGACGGCCGCCCGGTCAAGGTGCAGCGAACCATCTTCAGTGAGTGTTTCTA
RFC2	GCTCACTTGTGGCATCTGGGCTACTCACCAGAAGATATCATTGGCAACATCTTTCGAGTGTGTAAAACTTTCCAAATGGCAGAATACCTGAAACTGGAGT
RNASEH1	AGCCAGCGGCTGTCTTGCTGCCTGTACTTACTGGTGTGGAAAATAGCCTGCAGGTAGGACCATTGCAGTGATGGGCAGATGCGTCTTTCACACGGAATCA
RNF146	ATTTGTCTGCAAACATGTGTTCATCCAGTCAGTCTGCCCTGTAAGCACGTTTTCTGCTATCTATGTGTAAAAGGAGCTTCATGGCTTGGAAAGCGGTGTG
RNF24	GGTCTCTTACTAACTCCATTACACTCTCTCTCCTGGAGCCTCATCTCCATGTCAAGCAGGAGGGTAAAGAAGGGAACTAAGAGCAGGTCTTTCAAGCCAC
RNF26	TCCCCAGCTTTTGCGGCCACAACACATCAGTGTCATTTGGGTGTTTTGGCAACTCAGGGGCCTTCGGATGATCTTAAACCTTTGTGTTCAGCCAGAGCCC
RPF2P1	AAGAAGCGGCCAAATAATCTAGTAATAGGTCATATGTATGACTACCATGTGCTGGATATGATTGAATTAGGTATTGAGAATTTTGTCTCTCTAAAAGACA
RPSA	GGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTC
RPUSD2	CGTAAGGTGCGGCCCTATTACTTTGACTTCCGGACCTACTGCAAAGGTCGCTGGGTGGGCCACAGCTTGCTGCACGTCTTCAGTACCGAGTTCCGAGCTC
RRP12	CTCATTCCTCGCCACGGCTTAGTCAACATGGGTCGCTCGGGAAAGTTGCCTTCTGGTGTCTCAGCTAAGTTGAAGCGCTGGAAGAAAGGCCACAGCAGCG
RXRA	CTTGTAGTTGTACAGTGCTGTTGGTTTGAAAAGGTGATGTGTGGGGAGTGCGGCTCATCACTGAGTAGAGAGGTAGAATTTCTATTTAACCAGACCTGTA
SCARB2	ACCAGAAGCAGAGACACCACTTTTCAAAGGACTTCTTGGTTTCAGCATAACCTAAGACAGGGAATTGGGAGCCATCATATGTCACAGTGTTCAGAATTCA
SERBP1	TACCAGCGAGATCTTCAGGTTAACTAAGAAAAGCCCAGAAACTTCATTATTTACTGTGCTTTGTATGGCATAACTGGTAACAAGGCAGTAAAATGATACA
SFPQ	TTTAAATGGTTATGTAAGCAAAGCTGAACTGTAAATCTTCAGGAATATGTATTAAGATTGTGGAATGGGTGTAAGACAATTGGTAGGGGGTGAAAGTGGG
SLC25A32	ACCTTAGAGAAAAGAGAAAGTAAGCTCAAAGAGGACAATTCCAGTATATCTGCCCAAGGCAGCAACAAGCTCTTTTGTGTTTAAGGCATAAAAGAAGAAT
SLC35B3	AATATATTTCTATCACTGTGCCATCCAAAACCCAAACAATGTCACCACACATCAAGTCAGTTGACGACGTTGTGGTACTTGGCATGAATCTCAGCAAGTT
SLC37A4	CTGGCGCAGCACGCTGGCCCTATCTGGGGCACTGTGTGTGGTTGTCTCCTTCCTCTGTCTCCTGCTCATCCACAATGAACCTGCTGATGTTGGACTCCGC
SLC5A6	CGTGGGCATGTCTACCTTCTCCATCATGGACTATGTGGTGTTCGTCCTGCTGCTGGTTCTCTCTCTTGCCATTGGGCTCTACCATGCTTGTCGTGGCTGG
SMPD4	GGAGCTGCAGCCCATCCGGAGCTATGAGATCGCCAGCTTGGTCCGCACACTCTTTAGGCTG

	TCGTCTGCCATCAACCACAGATTTGCAGGACAGATGGCG
SNHG1	ACCTTTTCACAGACCTGTACTGAGCTCCGTGAGGATAAATAACTCTGAGGAGATGGGCCCTGCAAGCCTCTTGCTTAGCCGTCTGTTCAGAAAATAGCGT
SNHG12	CTGTCCTCATTTGTGACTATGGACCTATGGAGTTGGGACAATCTCTATGGGAAGCAGAAGGCAAGGACCCCGGTCATTTTAGGTAGAAACAACAGCATGC
SNORA45B	GCCGAGACTAGAGTCACATCCTGACACAACTCTTGTCCTGGTGTGCTAGAGTACTCGAAGAGAATCTACTGGTCTTGATTCACTGGTGGGGGCAGTCGGT
SNX27	TTTTTTAAATCAGATCACCCTCCATGTTGTTCCTGACCCACAGGGGAAGCTGTCCTCAGTTGTAGCCGTCTTGACTGGATGAGTCCTGGCAGTCTTTCTA
SPRY2	GCCGTTTTAACTGATATGCTTGTTAGAACTCAGCTAATGGAGCTCAAAGTATGAGATACAGAACTTGGTGACCCATGTATTGCATAAGCTAAAGCAACAC
SQLE	TAAATCTTTAGGTTGGGGCTGCATTGCCCTGGAGCCGCACTCTTGAGTCCGAGGCCATCTTTTGTTGGAGAAGGCGTCGGCGTTGGCGTTTTCCCGAGGT
SREBF2	GCCTCCAGCCTTCCTGAGTTTCTCTCTCCTGAACCCTACTCTCTCCTTTTTGCTTCCTCAGTTTTTATCAGGCTTTCTCTGGGGGACAGCAGTCTCTGAG
SRP72P2	CCAGAGAAAGGCACAGCTCTTAGTAAACATTTGCCATCATCAGATAGTATGTCTCTAAAAGTAGATGTTGAGGCTCTTGAAAATTCTCCTGGTGCTACAT
ST3GAL6	AGCAGCTCTTTTTGAAGGACATTATAGAAAAAAACCTCGTAATCAACTTGACTCAAGATTGACTCTACAGACTCAGAAGATGATGCTAACAGTGTTAGTT
STK17B	GAGCAGCATATACCCTCTCGGGGACATTAAAATAGTAGATTTTGGAATGTCTCGAAAAATAGGGCATGCGTGTGAACTTCGGGAAATCATGGGAACACCA
TAPT1	TTGACTGAATCTGTGGCTTCATGCGCTGAAGAAGCTGGGTCCTGGGGCAACAAGTGCTGTGTTGCCAGGACAAATAGATGCTAAACATGGCACTTAAATA
TAS2R5	GGATCAGAAAATTCAACTGGTCCTCATATAACCTCATTATCCTGGGCCTGGCTGGCTGCCGATTTCTCCTGCAGTGGCTGATCATTTTGGACTTAAGCTT
TBCEL	CATGCTTCTCTACTATTTTGACCATGAAGCACCCTTTGGCCCAGAGGAAATGAAGTACAGCTCTCGGGCATTGCATTCCTTTGGCATTAGGGATGGAGAT
TCTN2	TGGGTTCTAATGAGGGCGCGGTTCTGCTGTGCCCGGCCCGCGAGGTCTAAGGCATGGGCTTCCAGCCTCCGGCCGCTCTTCTTTTGAGGCTTTTCCTTCT
TLR6	AAAAGACCTACCGCTGAAAACCAAAGTCTTAGATATGTCTCAGAACTACATCGCTGAGCTTCAGGTCTCTGACATGAGCTTTCTATCAGAGTTGACAGTT
TLR9	TGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGG
TMEM150B	GCGAGTGGGTCGTGGCCATGCTGCTGTTCGCGCTCTTCGGTCTCTTAGCCGTTGACTTCTCCGCCCTGGAGAGCTGCACCCTGTGTGTTCAGCCGTGGCC
TMEM55A	GGGAGCCATAAGAGTCAGTTATCCAGAACACAGTTTTGCATAAGCTTGTTTATGATTCAGTAATGCAGGTGAGAGTGTCTAGCAGTTCTTGGTAAGCTAC
TMEM59	ACCATGGCCTTGGCCGGAGGTTCGGGGACCGCTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCT
TMEM97	TCATCTACTCTGTTCACACCATGACAACCTTAATTCCGATACTCTCCACATTTCTGTTTGAGGATTTCTCCAAAGCCAGTGGTTTCAAGGGACAAAGACC
TOMM34	AGACCCCAACTCACTGCAGTTCATCTGAACAACCTGAGCTCCTGGGCCGGGGTGGAAGGAGGGGGATAAACCTAAGGCCCTGATCCAAAGCAGCCTGTTG
TOMM40	CCACCCTGCCCCGTCCACTTTCCCATCTCCTCGGTATAAATCATGTTTATAAGTTATGGAAGAACCGGGACATTTTACAGAAAAAAAACAAAAAACAACA
TP53I3	GCACTTTGACAAGCCGGGAGGACCGGAAAACCTCTACGTGAAGGAGGTGGCCAAGCCGAGCCCGGGGGAGGGTGAAGTCCTCCTGAAGGTGGCGGCCAGC
TP53INP1	CAGGTGGATTAACCACTATCAAGGTGGAAACAAGTCCTATGGAAAACCTTCTCATTGAACATCCCAGCATGTCTGTCTATGCTGTGCATAACTCCTGCCC
TWF2	CAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTGCTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGC
TXNRD1	ATCTTTTCTCCTTGCCTTACTGCCCGGGTAAGACCCTGGTTGTTGGAGCATCCTATGTCGCTTTGGAGTGCGCTGGATTTCTTGCTGGTATTGGTTTAGA
U4	TGTGCAGTGTCAGTGTTGTCGCCAGTGAGGTTTACCCAAGATGTGATTATTGCTGATTGAAAACTTTTCCCACTACCCCACCATGATGACTTGAAATATA
UFC1	ACAAACACACACCAAACAGTACTGCTACTTAGTTTCTAAGGCTGCACAGGGAAGGGAAAGACTGGGCTTTGGACAATCTAGAGGTAATTTATATCCGCCC
USP10	TCGGCTAATGAATGAGTTCACTAATATGCCAGTACCTCCAAAACCCCGACAAGCTCTTGGAGATAAAATCGTGAGGGATATTCGCCCTGGAGCTGCCTTT
VAMP3	AGCTGAGGCGCACCAGGACACAGCTTCCATTTCTTTAACGTCTGTTCCCTTAACATCGCTGAAATGATTTACTGTTGAAGAGATGCCTTGCGGTGTGGCC
VARS	AAGGTGGATGAGGCCATCGCCCTATTCCAGAAGATGCTGTGATCCACCACCCAGCTTCACCCCTCACCCCCAGCGGCTCACCATGGGGATGGCAGCAATA
VARS	CCCAGGGGGCAGCCGGGCGGCTGTCCTTGTCCAACAGTGGGTCAGTTACGCCGACACGGA

	GTTAATACCAGCTGCCTGTGGAGCAACGCTGCCGGCCCTG
VPS37A	AAGCCTGCCGCTCCTTCATTTGGTGTCCTTTCAAATCTGCCATTACCCATTCCCACAGTGGATGCTTCAATACCGACAAGCCAAAATGGTTTTGGGTACA
YBX1P1	CCTCACATCGGCGGCGCCTGCCGGCGGGCACAAAAAGGTCATCGCAACGAAGGTTTTGGGAACGGTAAAATGGTTCAATGTAAGGAACGGATATGGTTTC
ZNF211	ACACACTTGTTCAGGACCAGAGAATCCTCACTAGAGAAGGACTTTTTGAGTGCAGTAAATGTGGGAAAGCATGTACGCGAAGATGTAACCTCATTCAGCA
ZNF223	ACCTTCCAATTGTGGGAAGTGTAAACAATCCTTCAGTGATATGTCCATCTTTGATCTTCCTCAGCAAATACGCTCAGCAGAGAAGTCTCATTCCTGTGAT
ZNF561	GCAAGCCTTGATAATCATATGGGAATCCACACTGATGAGAAACTCTGTGAATTTCAGGAATATGGGAGAGCTGTCACAGCTTCTTCACACCTAAAGCAGT
ZNF79	GTTGCCAGTTGCCAGTTGCCAGTCGTTTTTCGGAAAGCTGGCAGCGGCTTTTTCACCGGGTTCTGCTTGAGGCCGAGCCAAAGAGTGGCTGTGACTCGGG

Table 3. Fixed parameters derived from equations 2, 4 and 16. Note that values have been rounded.

Gene symbol / probe	Mean value	Standard deviation	Right singular vector 1	Right singular vector 2	Right singular vector 3	Right singular vector 4
8133549	4.5182e-04	1.4283e-04	2.5097e-03	-1.8536e-03	-4.0248e-03	-0.00611348
8140170	1.4554e-04	1.7121e-05	3.3305e-05	-2.6032e-04	-4.8457e-04	-0.00292602
8145244	2.5377e-05	3.4990e-06	-1.8773e-05	-6.1729e-05	5.4388e-05	-0.00053173
AAMDC	5.7515e-04	3.0824e-05	2.5539e-04	-1.2146e-04	-7.2408e-04	-0.00578902
ABAT	1.1132e-04	1.5357e-05	1.5956e-04	-1.6347e-04	-1.2759e-03	-0.00187114
ABHD5	4.4036e-04	4.0876e-05	1.5973e-04	-6.2015e-04	1.7325e-03	-0.00664016
ACER2	1.0304e-04	1.8318e-05	-7.2403e-06	-3.8645e-04	3.1910e-04	-0.00247865
ACLY	5.8438e-03	7.1846e-04	-1.4984e-03	1.6132e-02	-3.6265e-02	-0.07425802
ACTR10	1.7216e-03	1.6686e-04	1.5182e-03	-1.1284e-03	-9.0431e-03	-0.02793668
ADAM20	3.0110e-05	9.2212e-06	-6.1850e-05	-2.3875e-04	2.6973e-04	0.00006436
ALDH18A1	1.7187e-03	2.8662e-04	-1.6811e-03	7.3199e-03	-5.6015e-03	-0.01560509
ALDH1B1	6.2342e-04	9.9871e-05	-4.6288e-04	2.6254e-03	-2.6511e-03	-0.00389216
ALKBH6	3.6617e-04	4.2550e-05	2.1501e-04	-2.0706e-04	-2.4232e-03	-0.00791079
ANAPC1	5.8934e-04	9.3208e-05	-2.8313e-04	2.2395e-03	-3.0259e-03	-0.00864778
ANAPC5	9.7778e-04	1.2951e-04	-4.8783e-04	3.2077e-03	-4.1662e-03	-0.01010754
ANKRA2	7.3498e-04	8.4449e-05	9.1143e-05	-1.4841e-03	8.0872e-04	-0.01369242
ARFGAP3	1.4149e-03	2.0153e-04	2.6887e-03	-2.4875e-03	-8.0766e-03	-0.02436383
ARHGAP9	9.3590e-04	1.3215e-04	8.0938e-04	-6.8467e-04	-8.9417e-03	-0.02322168
ASB7	4.2643e-04	2.5881e-05	-7.9959e-05	1.9377e-05	2.6747e-04	-0.00535931
ATP6V0D1	1.5623e-03	2.0275e-04	1.4196e-03	-1.7720e-03	-1.2392e-02	-0.03413852
ATP6V0E1	5.3751e-03	3.5481e-04	2.2555e-03	-3.3230e-04	-1.5169e-02	-0.06804218
ATP6V1H	8.5822e-04	5.9376e-05	5.2995e-04	4.4525e-04	-1.7338e-03	-0.01051003
BCL7A	8.9467e-05	1.2148e-05	-6.5984e-05	3.0626e-04	-3.2382e-04	-0.00075268
BIN2	2.1399e-03	4.5842e-04	5.7509e-03	-6.7488e-03	-1.2883e-02	-0.05512667
BLMH	3.5911e-03	5.7786e-04	-3.2699e-03	1.5297e-02	4.5448e-03	-0.01830570
C12orf57	1.3322e-03	7.9132e-05	1.1578e-03	-1.3011e-03	4.1489e-03	-0.00380043
C19orf54	2.2205e-04	3.0565e-05	-3.8857e-05	5.9354e-04	-1.3457e-03	-0.00423594
C1orf174	7.1349e-04	9.2504e-05	-4.2843e-04	2.4263e-03	-2.9243e-03	-0.00319425
C20orf24	7.6027e-03	7.5924e-04	1.2587e-02	-4.2479e-03	-8.9831e-03	-0.09035502
C3orf62	4.8631e-04	1.3566e-04	3.4463e-04	-2.2843e-03	-1.0043e-02	-0.01816866
C9orf89	8.1689e-04	1.7591e-04	1.5913e-03	-3.3817e-03	-1.1481e-02	-0.01524311
CARM1	3.2134e-04	5.6379e-05	-1.2756e-04	1.3701e-03	-2.6915e-03	-0.00442977
CD33	2.4101e-03	2.1373e-04	-1.0621e-03	3.3595e-04	2.0098e-03	-0.04341797
CD86	3.8308e-04	1.0104e-04	4.5752e-04	-2.4880e-03	-4.1463e-03	-0.00695299
CD93	1.0297e-03	1.8719e-04	-4.9983e-04	-1.2500e-03	-9.2628e-03	-0.03581670
COX20	1.8061e-04	1.8701e-05	-5.3495e-05	4.8015e-04	-8.0640e-04	-0.00097030
COX7A2L	3.7763e-03	1.5097e-04	-3.3834e-04	3.9696e-03	5.5893e-03	-0.00680108
CRHBP	3.1396e-05	6.3543e-06	6.4461e-06	-1.6468e-04	-2.8891e-04	-0.00030849
CSGALNACT2	8.4655e-04	1.7205e-04	1.5286e-03	-3.4852e-03	-5.4415e-03	-0.01811495
CYP51A1	2.9692e-04	3.3620e-05	-1.3282e-04	7.7324e-04	-1.2006e-03	-0.00341559
DDRGK1	3.7388e-04	2.9532e-05	2.0836e-04	2.6678e-04	-2.9976e-04	-0.00546238
DDX19A	7.6103e-04	1.1000e-04	-3.9899e-04	2.6084e-03	-4.9038e-03	-0.00949823
DDX21	8.0496e-03	1.1317e-03	-7.1875e-03	2.8252e-02	-3.5932e-02	-0.06123340
DHCR24	1.8164e-03	3.6410e-04	-1.6158e-03	9.5178e-03	-4.8583e-03	-0.02008720
DHCR7	4.8980e-04	7.9845e-05	-3.0788e-04	2.0026e-03	-2.1867e-03	-0.00598937
DHX33	3.9725e-04	6.4334e-05	-2.8816e-04	1.3876e-03	-3.4839e-03	-0.00663468
DNAJB4	3.3196e-04	1.6946e-04	2.1940e-03	-3.2759e-03	-6.7924e-03	-0.00947064
DNAJB9	3.9883e-05	6.6337e-06	7.4773e-05	-1.2812e-04	-1.7370e-04	-0.00062447
DNAJC5	4.0796e-04	4.6428e-05	2.6339e-04	-2.6442e-04	-1.6502e-03	-0.00890540
DNAJC9	3.3037e-04	3.0646e-05	-1.2866e-04	7.5332e-04	-1.3369e-03	-0.00211743
DRAM2	1.0966e-03	4.9586e-05	-3.1451e-04	-1.4886e-04	1.7470e-03	-0.00958195
DTD1	1.3773e-03	2.2068e-04	-1.1536e-03	5.8709e-03	-5.7999e-03	0.00047618
EDEM2	8.0818e-04	8.6814e-05	4.0182e-04	1.8608e-04	-3.7547e-03	-0.01701617
EEF2KMT	2.2969e-04	2.8551e-05	-4.9810e-05	5.7753e-04	-1.6640e-03	-0.00346659
EMC7	1.7741e-03	6.5825e-05	9.6569e-05	-8.2368e-05	-5.2211e-03	-0.01195038
EVI2B	2.3101e-03	2.4299e-04	7.6136e-04	-2.8472e-03	4.1407e-03	-0.04532218
FAM212B	2.3839e-04	6.4469e-05	1.3881e-04	-1.3777e-03	3.5563e-04	-0.00856900
FAS	6.4123e-04	1.2536e-04	3.5232e-04	-2.7344e-03	4.8343e-03	-0.01470100

FASN	9.0628e-05	1.6959e-05	1.7107e-05	2.9458e-04	-1.3803e-03	-0.00211110
FBXO10	1.3960e-04	1.8663e-05	4.6233e-05	-2.5583e-04	-1.4194e-03	-0.00282219
FDPSP2	1.9827e-05	4.0921e-06	9.1471e-07	-1.0757e-04	-1.3609e-04	-0.00022447
FDXR	2.1800e-03	2.6398e-04	-2.4264e-03	2.4238e-04	2.1269e-02	-0.04115244
FOXO4	1.5579e-04	3.9761e-05	5.7620e-04	-5.5038e-04	-2.2638e-03	-0.00316527
FTH1P2	4.5798e-02	4.0771e-02	7.6550e-01	-4.9018e-01	2.5669e-01	0.25549954
FTH1P5	2.7674e-03	6.7324e-04	-6.0133e-04	-1.7567e-02	-1.1753e-02	-0.04703638
FUCA2	3.5319e-04	3.6215e-05	2.3266e-04	2.4245e-04	-1.5945e-07	-0.00699774
GAS2L3	1.3947e-04	1.6665e-05	-5.1309e-05	3.2876e-04	-1.7637e-03	-0.00071262
GDAP2	6.5238e-04	5.3254e-05	2.4577e-04	-5.8718e-04	-1.4576e-03	-0.00978013
GDF11	3.1094e-04	6.4860e-05	-4.9132e-04	1.6097e-03	-1.7414e-03	-0.00297424
GLRX	3.0651e-03	3.0275e-04	4.6262e-03	-4.6688e-04	1.1617e-02	-0.04029299
GNL3L	2.7790e-03	3.7467e-04	-7.4548e-04	8.7157e-03	-1.1060e-02	-0.04019007
GNPNAT1	9.8218e-04	1.2745e-04	4.2477e-05	3.4008e-03	-3.4261e-03	-0.00633684
GSR	4.9648e-04	1.9163e-04	3.1836e-03	-2.5710e-03	-7.7123e-03	-0.01063721
GTF3C2	9.9819e-04	1.2489e-04	7.0357e-05	2.5587e-03	-5.8276e-03	-0.01604800
HBP1	1.0250e-03	7.3891e-05	-1.6652e-04	-1.5965e-03	5.7876e-04	-0.00963194
HIST1H1C	1.9775e-02	5.9216e-03	-2.6144e-02	1.4621e-01	-1.4668e-01	0.47711392
HIST1H1E	3.1671e-03	9.4168e-04	-4.7869e-03	2.3085e-02	-3.6106e-02	0.06569297
HIST1H2AE	1.2063e-04	1.4763e-05	-1.8444e-04	2.8563e-04	-7.6644e-04	0.00072179
HIST1H2BE	4.0402e-05	3.9040e-06	2.4163e-05	-6.5732e-05	-3.8644e-04	-0.00033357
HIST1H3G	9.3671e-03	3.2665e-03	-1.3101e-02	8.2165e-02	-5.9871e-02	0.25315102
HIST1H3J	3.7997e-04	1.5972e-04	-9.4117e-04	3.8345e-03	-4.6857e-03	0.01278548
HIST1H4A	7.6318e-04	2.0265e-04	-1.1187e-03	5.1851e-03	-3.9055e-03	0.01153801
HIST2H2AA3	1.6830e-02	4.6136e-03	-2.3381e-02	1.1302e-01	-1.5212e-01	0.34491738
HIST2H2AA3	2.6997e-02	7.6662e-03	-3.6535e-02	1.8995e-01	-2.3296e-01	0.56275120
HIST2H2BF	8.8239e-05	6.3817e-06	-7.6076e-05	-6.5892e-05	-3.5414e-04	-0.00086378
HMGB3	5.8493e-04	9.2812e-05	-7.0989e-04	2.2947e-03	1.6585e-03	0.00503650
HMGCR	1.6613e-03	1.9991e-04	-1.3122e-03	4.9721e-03	-2.2765e-03	-0.01328650
HMGCS1	1.1521e-03	1.6022e-04	-7.3833e-04	3.7712e-03	-7.5671e-03	-0.01310609
HMOX1	6.8970e-04	3.2122e-03	6.1978e-02	-1.5028e-02	8.2658e-02	0.20103196
HNRNPL	6.3236e-03	7.3197e-04	-1.8179e-03	1.7027e-02	-3.3481e-02	-0.07015847
IRS2	1.7547e-04	4.0153e-05	2.3983e-04	-9.4543e-04	-1.9437e-03	-0.00284235
ISCU	1.5406e-03	8.5983e-05	-9.6074e-04	5.1070e-04	4.9671e-03	-0.01322872
ISG20L2	2.5348e-03	3.0626e-04	-7.0767e-04	7.0391e-03	-1.4017e-02	-0.03061880
KCNE3	2.1541e-03	2.1983e-04	3.2379e-03	-1.3050e-03	1.0432e-02	-0.02797126
KGFLP1	4.4151e-05	5.2796e-06	2.3824e-05	-1.2879e-04	-2.4936e-04	-0.00035227
KIAA0226L	7.3878e-05	9.6308e-06	1.2805e-04	-1.2309e-04	-3.2883e-04	-0.00117442
LINC00987	2.1777e-05	3.2647e-06	3.3359e-05	-5.4467e-05	-1.5949e-04	-0.00038076
LPAR1	4.0991e-04	1.2243e-04	1.5745e-03	-2.2347e-03	-4.1959e-03	-0.00978784
LRPPRC	8.4634e-04	1.3222e-04	-5.7166e-04	3.2522e-03	-4.7577e-03	-0.00995254
LY96	9.5864e-05	5.1539e-05	6.0207e-04	-8.8031e-04	-4.1122e-03	-0.00270925
MAP2K1	1.0697e-03	9.3007e-05	7.2346e-04	-6.5655e-04	-8.1276e-03	-0.01379365
MAPK13	1.6037e-04	3.5155e-05	5.2021e-04	-4.4255e-04	7.1153e-04	-0.00387732
METTL2A	1.5774e-03	1.7606e-04	-6.6014e-04	4.1765e-03	-6.4694e-03	-0.01616961
MGST3	4.2260e-03	3.8684e-04	3.4929e-03	-2.9687e-03	-2.5260e-02	-0.06133234
MRPL30	1.8462e-03	2.0920e-04	-1.4049e-03	5.3439e-03	-5.5660e-04	-0.01046705
MRPL4	3.6029e-03	5.3786e-04	-2.0515e-03	1.3713e-02	-2.3091e-02	-0.02738792
MRPS17	1.8735e-03	2.4661e-04	-1.8014e-03	6.3051e-03	-6.4317e-03	-0.00520824
MSANTD2	1.1648e-04	2.1106e-05	2.3159e-04	-4.5166e-04	-5.4317e-04	-0.00145663
MTR	9.7805e-04	1.4014e-04	-3.9227e-04	3.1214e-03	-5.3582e-03	-0.01576247
MYBBP1A	2.5274e-04	4.7423e-05	-1.5006e-04	1.0212e-03	-3.4613e-03	-0.00414286
NBR1	1.2933e-03	2.6486e-04	4.5049e-03	-3.4564e-03	-7.8736e-03	-0.01576903
NIP7	1.8952e-03	2.6479e-04	-1.1303e-03	6.9899e-03	-6.8964e-03	-0.01048136
NLRP12	1.5523e-04	4.6611e-05	7.5407e-04	-5.2514e-04	-6.9034e-04	-0.00464704
NOL6	6.4989e-04	9.5458e-05	-1.6010e-04	2.0906e-03	-5.5005e-03	-0.00996760
NQO1	2.4362e-03	2.4267e-03	4.1341e-02	-3.8247e-02	-1.8951e-02	-0.05082434
NRBP1	1.3653e-03	1.1856e-04	8.7936e-04	1.1014e-04	-7.5060e-03	-0.02105981
NUBPL	3.7564e-04	5.2941e-05	-1.4982e-04	1.3485e-03	-2.2319e-03	-0.00310388
NUDT14	1.0583e-04	1.3355e-05	8.0360e-05	-1.4906e-04	-4.2942e-04	-0.00237240
NUFIP1	6.0570e-04	8.6748e-05	-4.2978e-04	2.2717e-03	-4.2555e-04	-0.00448637
NUP153	1.1603e-03	9.9910e-05	2.5765e-04	2.4809e-03	-3.1149e-03	-0.00823033
OR5B21	1.4907e-05	2.7126e-06	5.2862e-07	-7.0948e-05	-3.1701e-05	-0.00019308
OSER1	6.0852e-04	4.7353e-05	7.1053e-04	-7.6571e-04	-8.7228e-04	-0.00361331

OTTHUMT00000400136	1.5314e-02	2.9951e-03	-2.3415e-02	7.7141e-02	-1.6579e-02	0.04483399
PASK	2.1961e-04	4.2636e-05	-2.2616e-04	1.0705e-03	-2.3870e-04	-0.00314459
PAWR	1.9237e-03	1.9840e-04	-7.6421e-04	4.6507e-03	-3.2777e-03	-0.02076843
PDAP1	1.0888e-03	1.1556e-04	-5.0387e-04	2.8022e-03	-3.1834e-03	-0.01001634
PDE1B	8.5428e-05	1.5634e-05	-5.6911e-05	-3.2221e-04	-5.2020e-04	-0.00202344
PFAS	5.8928e-04	1.2098e-04	-4.7105e-04	3.1001e-03	-5.6377e-03	-0.00482516
PHLDA3	5.5104e-04	1.2393e-04	5.1128e-05	-2.8382e-03	3.7148e-03	-0.01401531
PIK3AP1	1.2690e-03	3.9721e-04	5.1673e-03	-6.6581e-03	-2.0828e-02	-0.03141707
PINK1	5.0202e-04	6.1417e-05	7.2143e-04	-8.2260e-04	-4.9602e-05	-0.00866381
PMM2	1.3339e-03	1.3692e-04	-7.5063e-04	2.4706e-03	-9.4436e-03	-0.01643319
PNO1	1.4160e-03	1.8089e-04	-6.6261e-04	4.4098e-03	-1.1309e-02	-0.00871518
POLR2E	1.6011e-03	2.1907e-04	-1.2445e-03	5.6690e-03	-5.6407e-03	-0.00905997
POLR3E	5.5138e-05	5.4544e-06	1.8796e-05	1.8484e-05	-5.3474e-04	-0.00087464
PPM1D	7.8608e-04	8.5265e-05	-3.6703e-05	-1.8964e-03	1.0958e-03	-0.01069473
PREX1	4.0742e-04	4.9562e-05	1.4704e-04	-4.2908e-04	-1.7915e-03	-0.00949222
PSTPIP1	1.3934e-03	1.6429e-04	1.0006e-03	-3.8580e-06	4.1269e-03	-0.03253404
RAB33B	7.5138e-04	7.2380e-05	-2.1430e-04	-1.2194e-03	2.7147e-03	-0.01137027
RENBP	1.5765e-04	2.1428e-05	1.6101e-04	-3.7807e-04	-4.2608e-04	-0.00303179
RFC2	1.7060e-03	2.6441e-04	-1.5346e-03	7.0314e-03	-8.6332e-04	-0.00624848
RNASEH1	4.5122e-04	5.6169e-05	-5.0775e-05	1.4892e-03	-1.4556e-03	-0.00307611
RNF146	1.0194e-03	7.2414e-05	2.5049e-04	-1.7000e-04	-1.1500e-03	-0.01485885
RNF24	2.5279e-04	3.9122e-05	6.2928e-04	-3.6270e-04	-2.8515e-04	-0.00443522
RNF26	1.1181e-03	1.6334e-04	-4.6579e-04	4.2035e-03	-5.0431e-03	-0.01043286
RPF2P1	1.5036e-03	2.0024e-04	-8.7530e-04	5.3257e-03	-6.8123e-03	-0.00154366
RPSA	1.5113e-01	1.5689e-02	-1.5672e-01	3.5071e-01	8.9051e-01	0.15611101
RPUSD2	3.1732e-04	4.3775e-05	-1.9041e-04	1.1739e-03	-1.2111e-03	-0.00039793
RRP12	4.1710e-04	6.6389e-05	-2.1478e-04	1.5095e-03	-3.8471e-03	-0.00591840
RXRA	7.6577e-04	1.5822e-04	2.5930e-03	-6.7199e-04	2.7150e-03	-0.01956232
SCARB2	6.1337e-04	1.5695e-04	1.5798e-03	-2.2031e-03	-1.0635e-02	-0.01905517
SERBP1	1.1797e-03	1.4719e-04	-8.8677e-04	3.5890e-03	-6.3518e-03	-0.00870158
SFPQ	2.6924e-03	3.8594e-04	-2.1885e-03	9.7856e-03	-9.2041e-03	-0.02249951
SLC25A32	1.0191e-03	1.4114e-04	-5.3889e-04	2.9280e-03	-1.0105e-02	-0.01368467
SLC35B3	8.9866e-04	7.6810e-05	6.5454e-04	-4.6803e-04	-3.3679e-03	-0.01358739
SLC37A4	2.1752e-04	3.8812e-05	-1.3774e-04	1.0474e-03	-1.0416e-03	-0.00065803
SLC5A6	1.1915e-03	1.8754e-04	-5.0919e-04	4.5420e-03	-9.2197e-03	-0.01444607
SMPD4	4.8959e-04	6.3467e-05	-1.7017e-04	1.4935e-03	-2.1520e-03	-0.00634247
SNHG1	2.5865e-03	4.3767e-04	-3.2941e-03	1.1102e-02	-1.0095e-02	0.01345041
SNHG12	1.5465e-03	2.3293e-04	-7.4091e-04	4.6182e-03	-1.2386e-02	-0.02938228
SNORA45B	4.7222e-01	3.9607e-02	-6.1495e-01	-7.3587e-01	1.2574e-01	0.21773827
SNX27	3.1147e-04	3.5126e-05	1.7064e-04	-8.1100e-05	-2.1970e-03	-0.00653877
SPRY2	3.5101e-04	3.3199e-05	-2.2879e-04	4.7878e-04	-2.4430e-03	-0.00447489
SQLE	5.4091e-04	7.9671e-05	-6.9748e-04	1.7101e-03	-3.1681e-03	-0.00688509
SREBF2	5.5673e-04	7.1950e-05	-1.2573e-04	1.3648e-03	-4.0541e-03	-0.00963133
SRP72P2	4.6518e-03	5.4365e-04	-2.0373e-03	1.4502e-02	-1.1193e-03	-0.02614572
ST3GAL6	7.2716e-04	1.2418e-04	1.2182e-03	-1.8004e-03	-6.5347e-03	-0.01649096
STK17B	5.5895e-04	8.1655e-05	4.7262e-04	-1.8056e-03	3.4429e-04	-0.00928462
TAPT1	1.1898e-03	1.3171e-04	9.9847e-04	-1.0689e-03	-6.5876e-03	-0.02289105
TAS2R5	6.8331e-05	1.4195e-05	8.5899e-05	-2.3892e-04	-1.0962e-03	-0.00168321
TBCEL	2.3760e-04	2.3327e-05	1.0363e-04	-2.7615e-04	-7.0944e-04	-0.00420745
TCTN2	6.0862e-05	6.8146e-06	-6.1846e-05	1.2406e-04	-2.9930e-04	-0.00079524
TLR6	2.6550e-04	1.0886e-04	1.2130e-03	-2.0154e-03	-4.9339e-03	-0.01004769
TLR9	1.0008e-05	1.5584e-06	3.5424e-06	-3.3527e-05	-8.1098e-06	-0.00020478
TMEM150B	3.7840e-05	8.9124e-06	1.1141e-04	-1.4047e-04	-1.0661e-04	-0.00105030
TMEM55A	7.0809e-04	6.8116e-05	1.0028e-03	-5.0913e-04	3.8786e-03	-0.00786813
TMEM59	2.7755e-03	1.6905e-04	-8.9890e-04	-2.1435e-03	4.6768e-04	-0.03027478
TMEM97	1.3851e-03	2.6784e-04	-1.8918e-03	7.0164e-03	1.3075e-03	0.00238881
TOMM34	9.1247e-04	1.1261e-04	-2.7906e-04	2.9628e-03	-7.5092e-04	-0.00724332
TOMM40	2.3298e-03	3.8325e-04	-1.4442e-03	1.0114e-02	-1.1187e-02	-0.01581883
TP53I3	7.3415e-04	1.3224e-04	-1.0957e-03	-1.0924e-03	9.8641e-03	-0.02035033
TP53INP1	9.1693e-04	2.1773e-04	5.5621e-05	-4.9110e-03	2.9415e-03	-0.02659310
TWF2	1.3442e-03	1.0276e-04	3.1464e-04	1.3121e-03	-4.1829e-03	-0.01810204
TXNRD1	5.4517e-03	2.0934e-03	3.8205e-02	-2.6062e-02	-4.4558e-02	-0.05576321
U4	8.1576e-05	9.1943e-06	-7.2823e-05	8.6080e-05	-6.7844e-04	-0.00140610
UFC1	6.3446e-03	3.5702e-04	-1.1416e-03	8.4286e-03	2.1950e-02	-0.02514677

USP10	3.5065e-03	2.9938e-04	-5.8838e-04	7.1091e-03	-4.9630e-03	-0.03175341
VAMP3	1.7708e-03	1.5156e-04	-2.9361e-04	7.8977e-05	5.8016e-05	-0.03167155
VARS	2.2490e-03	4.0593e-04	-1.1506e-03	9.0495e-03	-2.2314e-02	-0.04039696
VARS	7.7263e-04	1.2714e-04	-4.5955e-04	2.7679e-03	-7.5048e-03	-0.01265274
VPS37A	1.6532e-03	1.3601e-04	1.1385e-03	-9.6400e-04	-7.0247e-03	-0.02337178
YBX1P1	2.6074e-02	2.8348e-03	-2.1503e-02	7.2717e-02	-2.2145e-02	-0.08214784
ZNF211	1.9701e-04	9.6319e-06	-7.2915e-05	-1.7703e-04	-1.7174e-04	-0.00131234
ZNF223	3.3005e-04	2.5239e-05	-1.7384e-04	-7.2849e-05	-1.3736e-04	-0.00496679
ZNF561	1.0094e-03	1.0111e-04	-5.9602e-04	-1.0210e-03	2.2199e-03	-0.01862486
ZNF79	1.6946e-04	2.0581e-05	5.8157e-05	-4.5212e-04	-9.3092e-04	-0.00229174

Table 4. Fixed parameters derived from equation 6. Note that values have been rounded.

	C1	C2	C3	C4
Reference value	-0.016642	0.016181	-0.0010846	-0.00044008

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