

Spatial transcriptomics using combinatorial fluorescence spectral and lifetime encoding, imaging and analysis

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Abstract:

Multiplexed mRNA profiling in the spatial context provides important new information enabling basic research and clinical applications. Unfortunately, most existing spatial transcriptomics methods are limited due to either low multiplexing or assay complexity. Here, we introduce a new spatialomics technology, termed Multi Omic Single-scan Assay with Integrated Combinatorial Analysis (MOSAICA), that integrates *in situ* labeling of mRNA markers in cells or tissues with combinatorial fluorescence spectral and lifetime encoded probes, spectral and time-resolved fluorescence imaging, and machine learning-based target decoding. This technology is the first application combining the biophotonic techniques; Spectral and Fluorescence Lifetime Imaging and Microscopy (FLIM), to the field of spatial transcriptomics. By integrating the time dimension with conventional spectrum-based measurements, MOSAICA enables direct, highly-multiplexed, *in situ* spatial biomarker profiling in a single round of staining and imaging while providing error correction removal of background autofluorescence. We demonstrate mRNA encoding using combinatorial spectral and lifetime labeling and target decoding and quantification using a phasor-based image segmentation and machine learning clustering technique. We then showcase MOSAICA's multiplexing scalability in detecting 10-plex targets in fixed colorectal cancer cells using combinatorial labeling of only five fluorophores with facile error-correction and removal of autofluorescent moieties. MOSAICA's analysis is strongly correlated with sequencing data (Pearson's $r = 0.9$) and was further benchmarked using RNAscopeTM and LGC StellarisTM. We further apply MOSAICA for multiplexed analysis of clinical melanoma Formalin-Fixed Paraffin-Embedded (FFPE) tissues that have a high degree of tissue scattering and intrinsic autofluorescence, demonstrating the robustness of the approach. MOSAICA represents a simple, versatile, and scalable tool for targeted spatial transcriptomics analysis that can find broad utility in constructing human cell atlases, elucidating biological and disease processes in the spatial context, and serving as companion diagnostics for stratified patient care.

Introduction

Cell fate and cell-cell, cell-niche interactions are tightly regulated in space at both genetic and tissue and system level to mediate organ development, tissue homeostasis and repair, and disease appearance and progression. Therefore, spatial transcriptomics that profile gene expression landscape at the single-cell level in tissues in a 3D spatial context as shown in this work represents a new frontier in biological research and precision medicine¹⁻⁸. For instance, spatial transcriptomics techniques can (a) help realize the vision of the human cell atlas in generating “high-resolution and comprehensive, three-dimensional reference maps of all human cells in the body”, (b) determine molecular mechanisms that govern cell fate, state, lineage and cell cooperation in tissue formation in developmental biology and regenerative medicine, (c) investigate the biological changes associated with different diseases in a spatial-dynamic fashion and to uncover disease molecular mechanisms and discover disease biomarkers, and (d) characterize the complexities of tissue biopsy (e.g. tumor) in clinical pathology to inform personalized disease diagnosis and therapeutic intervention in the era of precision medicine. Spatial transcriptomics tools need to be able to assess multiple transcripts within the same cell and sample in a highly multiplexed fashion due to the heterogeneous gene expression and many different cell identities/states exist in a particular tissue. Furthermore, patient derived materials are often available in limited quantity and generating many sections to test for different markers separately is tedious and non-feasible.

A major bottleneck in spatial transcriptomics is the lack of tools that can be both easy-of-use and highly multiplexing⁷⁻¹¹. Conventional tools for *in situ* analysis including fluorescence *in situ* hybridization (FISH) (e.g., LGC Stellaris™) can only detect 3-4 targets at a time because of the limited number of spectral channels in fluorescence microscopes¹²⁻¹⁴. Conventional methods for *in situ* profiling of transcripts are further confounded by the autofluorescent moieties in tissue preparations including clinical biopsies. Recent single-cell RNA sequencing (scRNAseq) methods provide information on the presence and identity of transcripts in single cells but lack the critical spatial context needed to understand complex heterogeneous tissue¹⁵⁻¹⁷. Spatial transcriptomic methods that are based on sequential labeling, stripping, and imaging (e.g. seqFISH, MERFISH), branched amplification (e.g. RNAscope™, SABER), or *in situ* sequencing (e.g. GeoMx™, Slide-seq) are often too complicated, error-prone, time-consuming, laborious and costly to scale up, limiting their broad usage¹⁸⁻²³. Furthermore, repeated processing of the same sample can damage tissue structural integrity and target molecules and are often not feasible for precious samples such as clinical biopsies.

In this work we report a new spatial-omics technology termed MOSAICA (Multi Omic Single-scan Assay with Integrated Combinatorial Analysis) that enables direct, highly multiplexed biomarker profiling in the 3D spatial context in a single round of staining and imaging. MOSAICA employs *in situ* staining with combinatorial fluorescence spectral and lifetime encoded probes, spectral- and time-resolved fluorescence imaging, and AI-based target decoding pipeline (Fig. 1). Fluorescence lifetime is a measure of the time a fluorophore spends in the excited state before returning to the ground state and is an inherent characteristic of the fluorophore and its surrounding environment²⁴. By utilizing both time and intensity domains for labeling and imaging, we were

able to discriminate a large repertoire of spectral and lifetime components simultaneously within the same sample to enable increased multiplexing capabilities with standard optical systems.

In this study, we described the MOSAICA pipeline including automated probe design algorithm, probe hybridization optimization and validation, combinatorial spectral and lifetime labeling and analysis for target encoding and decoding. Particularly, we developed an automated machine learning-powered spectral and lifetime phasor segmentation software that has been developed to spatially reveal and visualize the presence, identity, expression level, location, distribution, and heterogeneity of each target mRNA in the 3D context. We showcased MOSAICA in analyzing a 10-plex gene panel in colorectal SW480 cells based on combinatorial spectral and lifetime barcoding of only five generic commercial fluorophores. Using this model, we illustrated the multiplexing scalability and MOSAICA's ability to correct for stochastic nonbinding artifacts present within the sample. We further demonstrated MOSAICA's utility in improved multiplexing, error-correction, and autofluorescence removal in highly scattering and autofluorescent clinical melanoma FFPE tissues, demonstrating its potential use in tissue for cancer diagnosis and prognosis. The MOSAICA is rapid, cost-effective, and easy-to-use and can fill a critical gap between conventional FISH and sequential- and sequencing-based techniques for targeted and multiplexed spatial transcriptomics.

Results

MOSAICA Workflow

In a typical MOSAICA workflow (Figure 1), primary oligonucleotide probes designed to specifically bind to mRNA targets with a complementary target region (25 to 30 base long) are incubated with fixed cell or tissue samples (Fig. 1A,B). These primary probes also contain an adjacent adaptor region consisting of two readout sequences for modular secondary probe binding. In this study, double ended secondary probes with fluorophores on each end are hybridized to the readout region on the primary probes (Fig. 1C). Through combinatorial labeling, each target is encoded with a dye with a distinct spectrum and lifetime signature. The labeled samples are then imaged using a confocal microscope (Fig. 1D) that is equipped with both spectral and lifetime imaging capabilities. Both spectral and fluorescence lifetime data will be captured and visualized using phasor plots (Fig. 1E). Our automated machine learning algorithm and a codebook then reveals the locations, identities, counts, and distributions of the present mRNA targets in a 3D context (Fig. 1F).

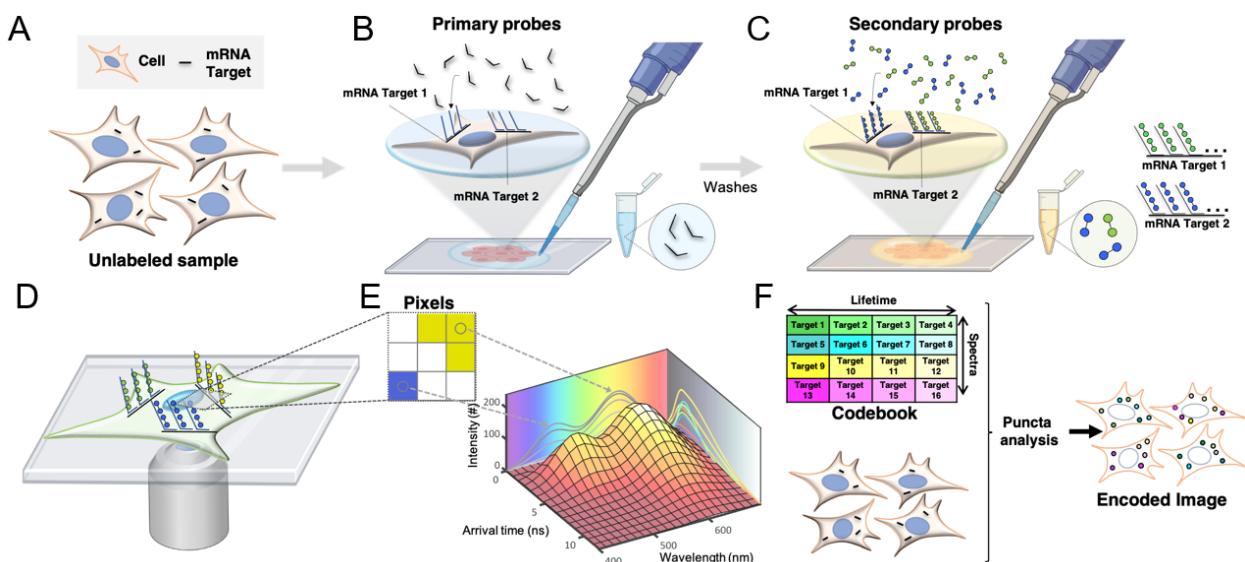


Figure 1. Schematic of the MOSAICA approach for labeling and analysis of spectral and time-resolved components. **A)** Sample(s) can be fixed cells or tissues. RNA transcripts from genes of interest are targeted for detection. **B)** Primary labeling probes are designed to include two functional regions: a target region which is complementary and can bind to the mRNA target and an adjacent readout region which can subsequently bind to fluorescently labeled oligonucleotides. **C)** Secondary fluorescent probes are added to bind to the primary probes to form different combinations (combinatorial labeling) through a “readout” domain. **D)** Labeled targets are measured under a fluorescent microscope to interrogate the spectral and lifetime characteristics of the labeled moieties. **E)** Phasor analysis is used to identify which fluorophore labels are present in each pixel and puncta. **F)** Labeled targets eliciting the encoded intensity-based or time-based signature are decoded to reveal the locations, identities, counts, and distributions of the present mRNA targets in a multiplexed fashion.

Probe design pipeline

To rapidly design oligonucleotide probes for each gene, we modified the python platform, OligoMiner²⁵, a validated pipeline for rapid design of oligonucleotide FISH probes. Briefly, as shown in Supplementary Figure 1A, using the mRNA or coding sequence (CDS) file of the target gene, the blockParse.py script will screen the input sequence and output a file with candidate probes while allowing us to maintain consistent and customized length, GC, melting temperature, spacing, and prohibited sequences. Using Bowtie2, the candidate probes are rapidly aligned to the genome to provide specificity information that is used by the outputClean.py script to generate a file of unique candidates only. The primary probes comprise complementary sequence of typically 27-30 nucleotides (nt) and are designed mostly within the CDS region, which has fewer variation than the untranslated region (UTR)²⁰. We wrote a script, seqAnalyzer.py, to automate the alignment of primary probes to sequencing data (Fig. S1B) so that probes that aligned to regions of lower read counts would be discarded. Furthermore, primary probe “read-out” domains and secondary probes (typically 15 to 20 nt long) are designed to be orthogonal to each other to avoid off-target binding. Libraries and databases of over 200,000 orthogonal sequences are available online and we have simply used those that have been previously validated²⁶. Fluorophores exhibiting distinct spectrum (typically with excitation/emission spectra in the 400-700 nm range) and lifetimes (typically in the 0.3-10 ns range) can be conjugated to oligos which were obtained through commercial vendors (see Methods).

Probe labeling validation and optimization

We first investigated the specificity of our labeling condition using a simple cell mixture model comprising wild-type HEK293T-X cells and HEK293T-X cells engineered with mNeonGreen (Fig. S2A) by detecting mNeonGreen mRNA as the target gene. Since only fluorescent mNeonGreen positive cells can express the corresponding mRNA transcripts, this cell mixture model provides a straightforward tool to assess specificity and nonspecific binding. Using a Nikon epifluorescence microscope to image the samples following staining with primary and secondary probes (all probe sequences used in this study are provided in Table S3), we detected on average 43.5 puncta per mNeonGreen positive cell ($n = 76$ cells) and 0.25 puncta per wild-type cell ($n = 164$) (Fig. S2B,C), indicating minimal nonspecific binding with our probe labeling strategy. To further validate the baseline level of nonspecific binding, we included a negative control with the primary probe designed towards dopachrome tautomerase (DCT), a gene in the mouse genome that is not expressed in our HEK293T-X model system, along with a condition with secondary probes only. Similarly, an average of 43.5 puncta per cell was detected for the mNeonGreen cells while the wild type and negative controls a mean of 2.5 puncta per cell was detected with a lower signal to noise (Fig. S2B,C). We next optimized labeling efficiency by testing the number of primary probes and incubation times of primary probes and secondary probes (summarized in Fig. S3). We determined our optimal condition to comprise a minimal of least 12 primary probes for each target mRNA (Fig. S3A,B) (in practice, we always maximize the number of primary probes per mRNA depending on the size of mRNA. Indeed, 40 primary probes per channel per mRNA were subsequently used in this study) with incubation time of 16 hours for primary probe hybridization and 1 hour for secondary probe hybridization, respectively (Fig. S3C,D), which were used in subsequent experiments.

Imaging and phasor analysis

Lifetime imaging is a tool that measures the spatial distribution of probes with different fluorescence lifetime. Samples are stimulated with modulated or pulsed lasers at a particular frequency, typically around the 40 to 80 MHz, which allows the fluorescence to decay within the stimulated period, typically in the ns range. After acquiring for sufficient time, i.e., after enough laser pulses or periods, one can construct a histogram of photon arrival times at each pixel. The shape of this histogram has a rapid rise, followed by a faster or slower decay which is characteristic of the fluorescent molecule(s) present in the pixel. To model this decay data, an exponential decay model can be fitted or alternatively one can make use of the fit-free phasor approach^{27,28}. We used this second approach because it requires no a priori knowledge of an underlying model (i.e. number of fluorescent species at the pixel) and it is computationally inexpensive in virtue of the Fast Fourier Transform algorithm. The phasor transform extracts two values from the decay curve that characterize the shape (and importantly not the size, so that the transform is independent of the amount of photons) and these two values, namely S and G, correspond to the two coordinates of the pixel on the phasor plot (see equations in the supplemental material). The values are obtained by an integral of the product of the decay of the two trigonometric functions, sine and cosine, fit in the stimulation period, and they correspond to the first order terms of the Fourier Series decomposition of the decay curve.

Similarly, if one uses a spectral detector, i.e., a separate detector for different spectral bands, then for each pixel, one can obtain another histogram, in this case with the number of photons arriving in each channel, i.e., at each wavelength. This curve can also be transformed to an analogous spectral phasor space to map the recorded spectra at each pixel onto the 2D spectral phasor space²⁹. Combining the lifetime measurement with a spectral detector, one effectively has a 5-dimensional space in which to characterize each pixel. On top of the spatio-temporal coordinates (x,y,z,t), each pixel now carries information in 5 additional coordinates: its intensity value (however many photons arrived at that pixel), the two phasor coordinates for the lifetime phasor transform, and the two phasor coordinates for the spectral phasor transform. A typical image, on the order of 10^6 pixels, obtained with this method provides 10^6 points in this 5D space³⁰. If the sample presents different populations of fluorescent molecules at different locations, the pixel phasor data at these different locations map to different positions in this phasor space and a clustering technique can be used to resolve each population.

Figure 2 depicts the spectral/lifetime analogy for fluorescence microscopy using the phasor approach. As an example, it uses a hypothetical experiment where 4 different target genes are targeted with 4 fluorescent species. Of the 4 species, we construct the example so that two fluorescent species emit in one color and the other two in another color. At the same time, within each color, one has a short lifetime and the other has a long lifetime. This hypothetical sample is excited, and the individual photons are detected at each pixel (Fig. 2A). In each pixel, we accumulate enough photons to build a spectral histogram and a lifetime histogram (Fig. 2B). These curves are phasor-transformed to reveal two distinct populations in the phasor space, corresponding to the two colors and the two lifetimes. By means of our previously published automatic clustering using machine learning³¹, we identify these populations and return to the image space to label each pixel depending on the group it belongs to in the phasor space (Fig. 2C). By combining the spectral and lifetime information, we have automatically segmented the image into regions, i.e., identified the pixels that belong to the different species (Fig. 2D). Again, note that in this example in Figure 2, we have chosen the probes to be the most convoluted case possible; one couple shares a similar spectrum and the other couple shares another spectrum. At the same time, one of the members of either couple share a similar lifetime and the other two members of either couple share another lifetime. This is the reason why even if there are four distinct fluorescent probes, only two spectral populations are detected both in the spectral and lifetime phasor space, and the combinations of these two populations yield to the four distinct groups. The four probes cannot be resolved unless both the lifetime and spectral information are accessed.

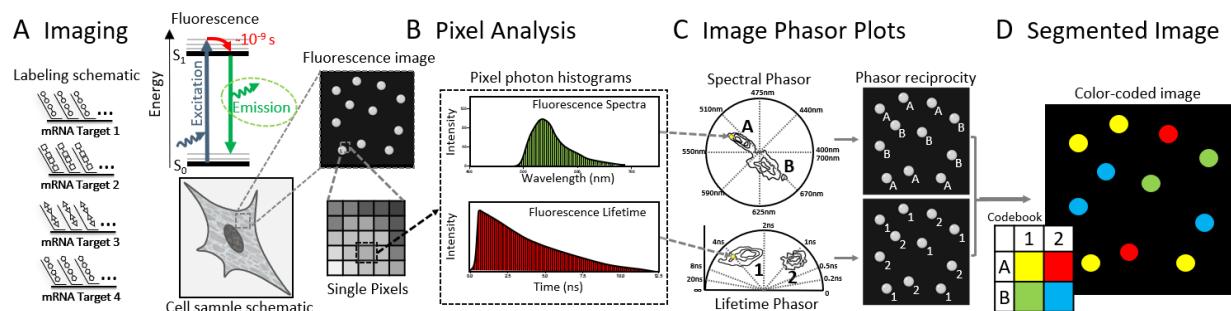


Figure 2. Image and phasor analysis with spectrum and lifetime analysis in MOSAICA. **A)** As an example, four different probes are used to target four different genes. The fluorescence is collected using the spectral and FLIM instrument to form images where each pixel carries information of the spectra and lifetime. **B)** At each pixel we compute the photon distribution in the spectral and temporal dimension. The phasor transform maps these distributions in each pixel to a position on the phasor space. **C)** The phasor plots reveal the presence of different populations. These populations are identified and then mapped back to the original image. **D)** We color code the pixels based on the combination of the two properties. This allows us to separate by lifetime probes that were emitting with similar spectra and vice-versa, separate by spectra probes that fluoresce with similar lifetimes.

Combinatorial target spectral and lifetime encoding and decoding

In the previous section, we showed how by combining the time dimension with the spectral dimension, we can increase the number of possibilities and therefore enhance the multiplexing capabilities squaring the number of targets that can be resolved. To further increase multiplexing and improve detection efficiency, we employ combinatorial labeling, a method in which targets are labeled with two or more unique fluorophores, to greatly increase the base number of targets we can label with a given number of fluorophores/probes. To illustrate this concept, here we demonstrate a minimal exemplary working example of combinatorial labeling where two probes are used to label three targets. In this situation, each probe labels one target and the third target is labeled with both probes simultaneously. Figure 3 shows a real case with such configuration, both for spectra and for lifetime. In Figure 3A, the cartoon represents the case of using two probes with distinct spectra. When imaging this sample, we can use two spectral channels, Figure 3B/C, where some targets appear in only one channel, other targets appear in only the other channel and the target that is labeled with both probes appears in both channels. All targets are then detected and color-coded depending on their presence in one channel, the other or the two simultaneously (Fig. 3D) and the overall counts of each combination in the field of view can be provided (Fig. 3E).

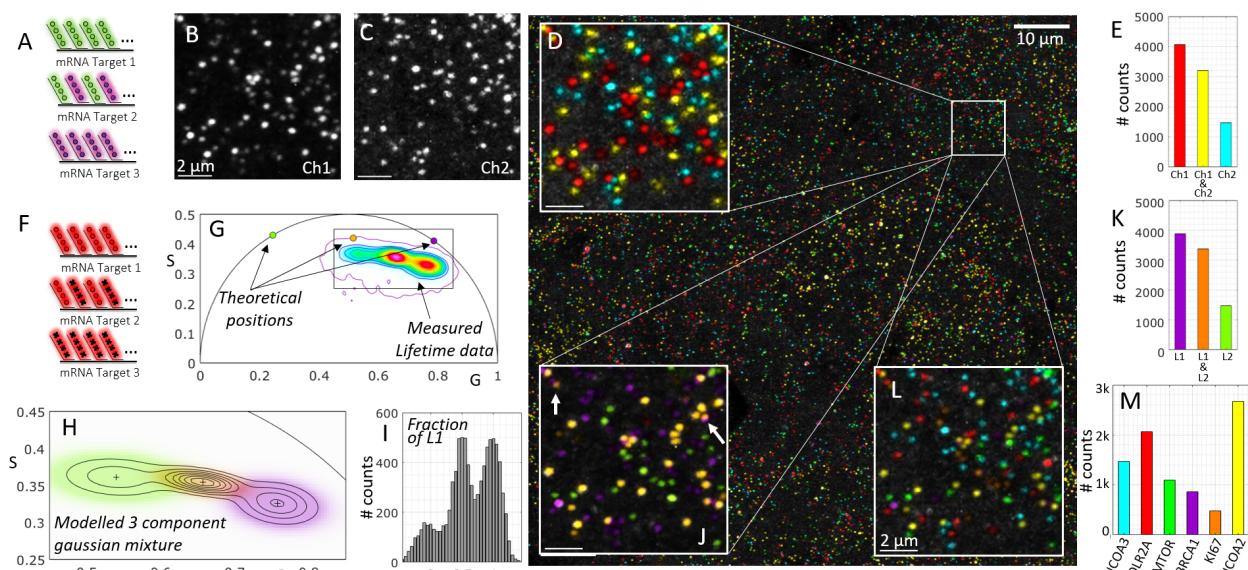


Figure 3. Working example of combinatorial labelling of three mRNA targets with two probes. **A)** Three different target genes are tagged using two probes with different spectra. Targets 1 and 3 are tagged each with one probe, Target 2 is tagged with both simultaneously. **B,C)** The fluorescence is collected in the two expected spectral channels for the known emission of the two probes. **D)** The maximum projection of the two channels is shown and pseudocolored depending on the presence in the respective channels (as an inset within the whole field of view). **E)** The actual counts of each target within the whole field of view. **F)** As a parallel example, three different target genes are tagged using two probes with different lifetime. Targets 1 and 3 are tagged each with one probe, Target 2 is tagged with both simultaneously. **G)** The phasor plot presents three populations, corresponding to the pixels with the three combinations; the two components by themselves plus the linear combination falling in the middle. **H)** Machine learning clustering technique is used to identify the groups (Gaussian mixture model). **I)** The multicomponent method is used to extract the fraction of one of the components in each detected puncta. **J)** The same inset is shown with the pseudocoloring now depending on the lifetime clustering. **K)** The counts for each lifetime cluster in the whole field of view. **L)** The combination of the information in both the spectral and the lifetime dimension yields a final 6-plex. **M)** The overall counts for the 6-plex detection including POLR2A (Alexa647 & ATTO565), MTOR (ATTO647 & ATTO565), K167 (Alexa647 & ATTO647), BRCA1 (Alexa647), NCOA2 (ATTO647), NCOA3 (ATTO565) with the appropriate genes that correspond to each combination. Experiments were conducted with cultures of mNeon green cells.

Similarly, we show a case in which the targets are now labeled with two probes that have similar spectra but different lifetimes (Fig. 3F). In this case, we also introduce the use of the phasor approach to reveal the three expected populations, the pixels that contain both probes appear in the midpoint between the phasor positions of the pixels that contain only one of the probes. Figure 3G shows the phasor distribution obtained from the same field of view as in the spectral example, in which we also show the theoretical locations of the probes (corresponding to Alexa647 and ATTO647 with respective lifetimes of 1 ns and 3.5 ns). As is expected in real experimental conditions, there are additional fluorescent components in the sample. We broadly refer to the bulk of these additional components as autofluorescence, which pulls the data away from the expected positions and converges to the mean phasor position of the autofluorescent components. We have previously shown that the Gaussian Mixture Models is the most optimal machine learning clustering algorithm to model phasor data³¹, and we use this machine learning technique to infer the phasor locations of the probe combinations (Fig. 3H). We can now successfully classify each pixel of the original image into one of the clusters and obtain a probability of belonging to each, i.e., the posterior probability of the model. This allows us to

color-code the transcripts depending on their assignment to one of the 3 clusters (Fig. 3J) and obtain the counts of the three lifetime components (Fig. 3K). Additionally, we apply our lifetime multicomponent analysis technique³² in which for each detected puncta, we estimate the presence of one of the lifetime components, in this case lifetime1 (Alexa647, purple in the figure), to obtain the expected result; that there are clearly three populations with respective fractions centered around [0, $\frac{1}{2}$ and 1] (Fig. 3I).

In the general case, we combine the lifetime and spectral dimensions, and we perform the clustering of the data in a 4D spectral/lifetime phasor space. The clustering technique has the power to not only identify which puncta belong to each cluster but also to assign a probability of belonging to that cluster, which can be used to quantify the certainty of the labeling. For example, in the inset in Figure 3J, we show two cases of puncta that have relatively low confidence in the cluster assignment; they are depicted with blended colors because they fall in the regions of the phasor space where the two clusters are merging.

In this combinatorial example in Figure 3, the three clusters in the lifetime domain multiplexed with the channel-based in the spectral domain yield a 6-plex image using only 3 probes (Fig. 3L,M). The specific genes targeted for this experiment with the combined probes were POLR2A (Alexa647 & ATTO565), MTOR (ATTO647 & ATTO565), KI67 (Alexa647 & ATTO 647), BRCA1 (Alexa647), NCOA2 (ATTO647), NCOA3 (ATTO565). In the general combinatorial experiment using couples of N probes the total number of possible target genes grows quadratically:

$$\binom{N}{2} = \frac{N!}{2(N-2)!} = \frac{N^2 - N}{2} \quad (1)$$

Simultaneous 10-plex mRNA detection in fixed colorectal cancer SW480 cells using MOSAICA

We next applied MOSAICA to a 10-plex panel of mRNA targets in colorectal cancer SW480 cell culture samples. This cell line was chosen because its xenograft model exhibits spatial patterns of heterogeneity in WNT signaling³³, which will allow us to study tumorigenesis in the spatial context and potentially identify cancer stem cell populations in colorectal cancer in future. Here, we selected this model as a validation platform to demonstrate the multiplexing scalability and error correction capabilities of our approach. We began by first identifying a set of 10 genes with known expression levels from our bulk sequencing data. Using the aforementioned probe design pipeline, we designed 80 probes (two pairs of 40 probes) for each gene: BRCA1, BRCA2, CENPF, CKAP5, KI67, MTOR, NCOA1, NCOA2, and NCOA3. These genes were chosen due to their housekeeping status or involvement in tumorigenesis in colorectal cancer. By encoding each gene with a distinct combination of two fluorophores, we generated a codebook of 10 labelling combinations from only five fluorophores following Equation 1: $\binom{5}{2} = 10$ (Fig. 4A) (see Table S2 for the probes used for each target). To assess the baseline nonspecific binding events of our assay, we included a negative probe control sample which was labelled with primary probes not targeting any specific sequence in the human genome or transcriptome but still containing readout regions for secondary fluorescent probes hybridization (Fig. 4A right). Matching numbers

and concentrations of primary and secondary probes that were used in the 10-plex panel were used in this sample.

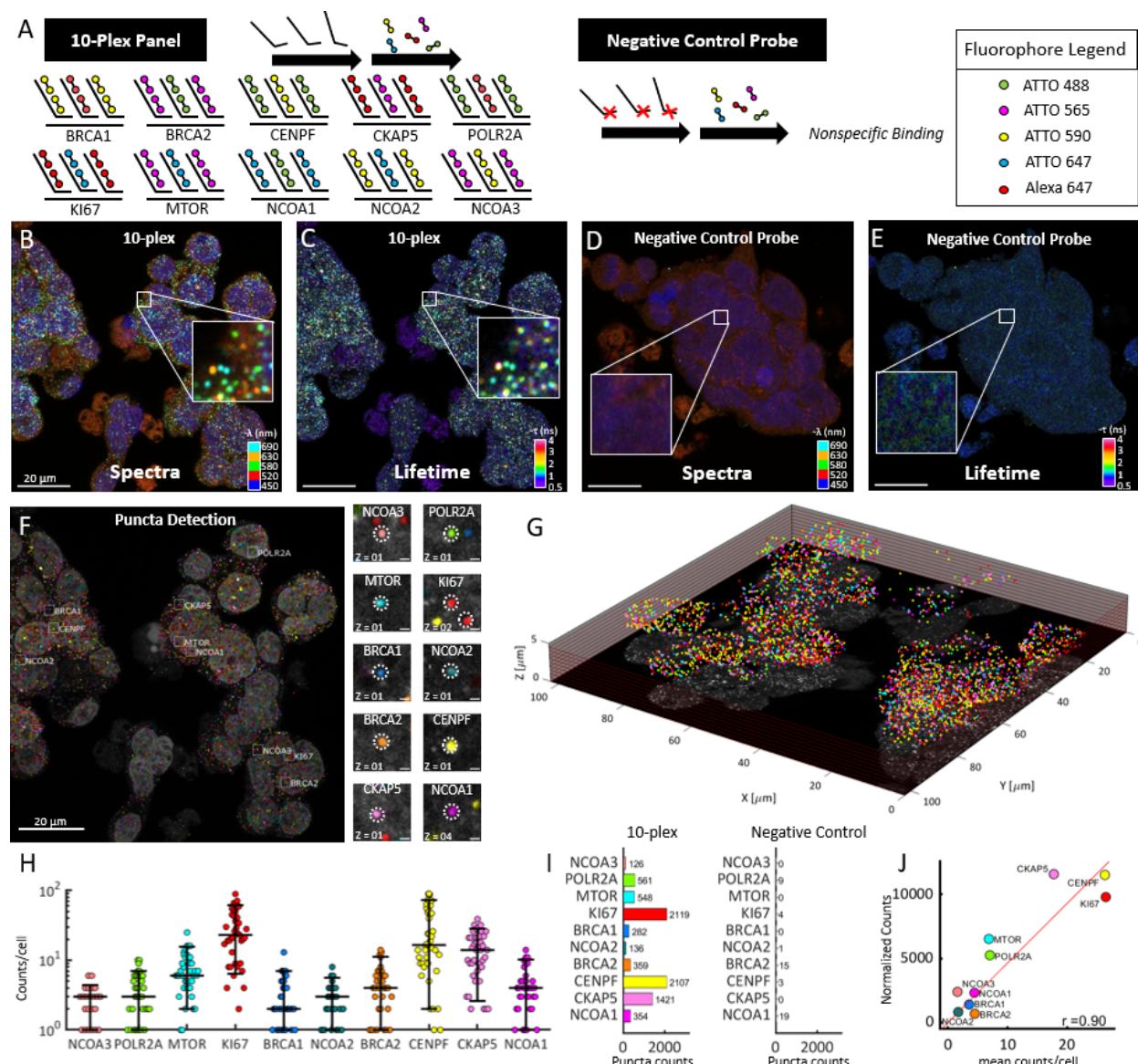


Figure 4. Simultaneous 10-plex detection of genes in colorectal cancer SW480 cells in a single round of labeling and imaging. **A)** 10 different types of gene transcripts are labeled with primary probes followed by respective and complementary fluorescent secondary probes. Each gene is labeled with a combination of 2 different fluorophores for 10 combinations. Negative control probes (*m*NeonGreen, DCT, TYRP1, and PAX3) targeting transcripts not present in the sample were used with their respective secondary fluorophore probes. **B)** Spectral image (max-projection in z) of a field of view of the labeled 10-plex sample (5-channel pseudo coloring). **C)** Lifetime image (max-projection in z) of a field of view of the labeled 10-plex sample (phasor projection on universal circle pseudo coloring). **D)** Spectral image of the labeled negative control probe sample. **E)** Lifetime image of the labeled negative control probe sample. **F)** Final puncta detection after being processed in our analysis software showing highlighted example puncta of each target (insets, right). Scale bar 20 μm in main image and 1 μm in insets. **G)** 3D representation of the field of view for the 10-plex sample. **H)** Number of puncta detected for each gene expression target in each cell for the labeled 10-plex sample (N=80 cells). **I)** Overall puncta count of each transcript in the 10-plex sample (left) and negative control

probe sample (right). J) Correlation of detected puncta (mRNA puncta count) vs. RNA-bulk sequencing (normalized counts) is shown for each target with Pearson r of 0.9.

Figure 4B depicts a spectral image overlay (five fluorescent channels including DAPI) of the labeled 10-plex SW480 sample. Additionally, in the same measurement, the orthogonal lifetime information attained by interrogating each pixel for their lifetime components. These pixels were phasor-transformed and pseudo-colored based on their projected phasor coordinates on the universal circle, creating the image depicted in Figure 4C. In doing so, both dimensions of data can now be simultaneously accessed to determine which cluster of pixels meet the appropriate and stringent criteria for puncta classification. Similarly, Figure 4D/E depict the merged composite spectral and lifetime images of the corresponding negative control probe sample. Figure 4F depicts the now detected pseudo-colored clusters which were successfully classified as one of the RNA markers. A representative inset image for each marker and its targeted detection is provided on the right. With 40 Z-stack images, we generated a 3D spatial distribution of the field of view to visualize the spatial analysis in a 3D context (Fig. 4G).

MOSAICA employs an error-correction strategy by gating for specific and pre-encoded fluorophore combinations and rejecting any fluorescent signature which do not meet these criteria. Specifically, in addition to the population of pixels that represents the decoded puncta as mentioned above, there was a population of pixels of various shapes and sizes which did not fit the criteria. Simulations to look into overlapping and inconsistent signals were run (Fig S4A,B). Plotted in Supplementary Figure 4C are the total detected puncta in this experiment, separated into populations depending on our classification criteria. Of the total detected puncta ($n = 13,521$), a considerable fraction $n = 4,488$ (33%), were observed emitting fluorescence only in a single channel and was indicative of nonspecific binding events and/or autofluorescence moieties. As previously characterized by several groups, nonspecific binding events is an inherent issue with smFISH which arises from the stochastic binding of cDNA probes towards cellular components such as proteins, lipids, or nonspecific regions of RNA and follow a random distribution¹⁴. When combined with native autofluorescence moieties which can also exists as diffraction-limited structures that emits a strong fluorescent signal in any single channel, this group represents a confounding problem for standard intensity-based measurements and analysis because they share similar SNR and intensities to real labeled puncta and cannot be differentiated. This is the main benefit of implementing the combinatorial encoded criteria which rejects this large amount (around 33%) of stochastic and nonspecific binding labeling events as well as any event eliciting a lifetime signature that deviated from the utilized commercial fluorophores. Finally, we also observed a relatively small group of puncta emitting fluorescent signal across more than two spectral channels but still eliciting the same spectral and lifetime signatures as the utilized fluorophores, $n = 880$. To characterize this population, we performed a simulation running 20,000 iterations of various puncta densities and fitted the corresponding exponential model that characterizes the probability of puncta overlap (described in Methods section and Supplementary Figure 4A and B). We attained an interval for the fraction of lost puncta due to optical crowding ranging from 2.1% to 6.6% which accounts for the 880 puncta or 6% of the total detected puncta. We name this group the overlapped in Supplementary Figure 4C.

The number of puncta detected for each target gene in each cell for the labeled 10-plex sample was plotted (Fig. 4H). Figure 4I plots the total number of detected puncta for the labeled 10-plex sample split into the different genes classified using MOSAICA phasor analysis with combinatorial labeling. In comparison, we also show the MOSAICA pipeline results with the negative control sample obtaining counts of less than five per thousand mainly due to noise in the images. To validate these puncta count, we compared them to matching RNA-seq data from the same cell type. Shown in Figure 4J is a scatter plot of the average mRNA puncta count for each cell plotted against the normalized counts from DESeq2 of our bulk RNA-sequencing data for each gene. When fitting with a straight line we obtained a Pearson correlation of $r = 0.904$, indicating a significant positive association between the two methods. The number of counts per cell was obtained by simply dividing the total number of detected genes into the number of cells obtained by 3D segmentation of the individual nuclei stained with DAPI. The individual cell edges were estimated by growing the edges of the nuclei until convergence (see Methods section). A total of 80 cells were analyzed for this experiment.

To further evaluate the detection efficiency, we performed benchmarking tests with our method against LGC StellarisTM and RNAscopeTM which are commercial gold standard FISH methods (Fig. S5). Using the housekeeping gene, POLR2A, as an exemplary target, we found a significant association between the number of detected puncta by our method and LGC StellarisTM (t -test p -value = 0.4). When compared to RNASCOPETM, we observed that for this cell type and target, both our assays and LGC StellarisTM did not correlate significantly ($p = 7.8 \times 10^{-4}$ and $p = 3.4 \times 10^{-4}$), indicating a discrepancy in detection efficiency between the two methods. We attribute this difference to MOSAICA and LGC StellarisTM utilizing a direct labeling and amplification-free method while RNASCOPETM utilizes a tyramide signal amplification reaction which generates thousands of fluorophore substrate per transcript and can lead to overlapping puncta or undercounting of detected puncta. Together, these data show MOSAICA can robustly detect target mRNAs of broad dynamic range of expression levels from single digit to hundreds of copies per cell.

Multiplexed mRNA analysis in clinical melanoma skin FFPE tissues

We next investigated whether MOSAICA can provide multiplexed mRNA detection and phasor-based error-correction to clinically relevant and challenging sample matrices. Assaying biomarkers *in situ* in tissue biopsies has great clinical values in disease diagnosis, prognosis and stratification including in oncology³⁴⁻³⁶. Specifically, we applied a mRNA panel consisting of KI67 (indicative of cell proliferation), POLR2A, BRCA1, MTOR, NCOA2, and NCOA3 to highly scattering and autofluorescent human melanoma skin biopsy FFPE tissues obtained from and characterized by the UCI Dermatopathology Center. Using the same probe design pipeline, primary probes were encoded with a combination of two fluorophores for each gene to exhibit a unique fluorescent signature (Fig. 5A left).

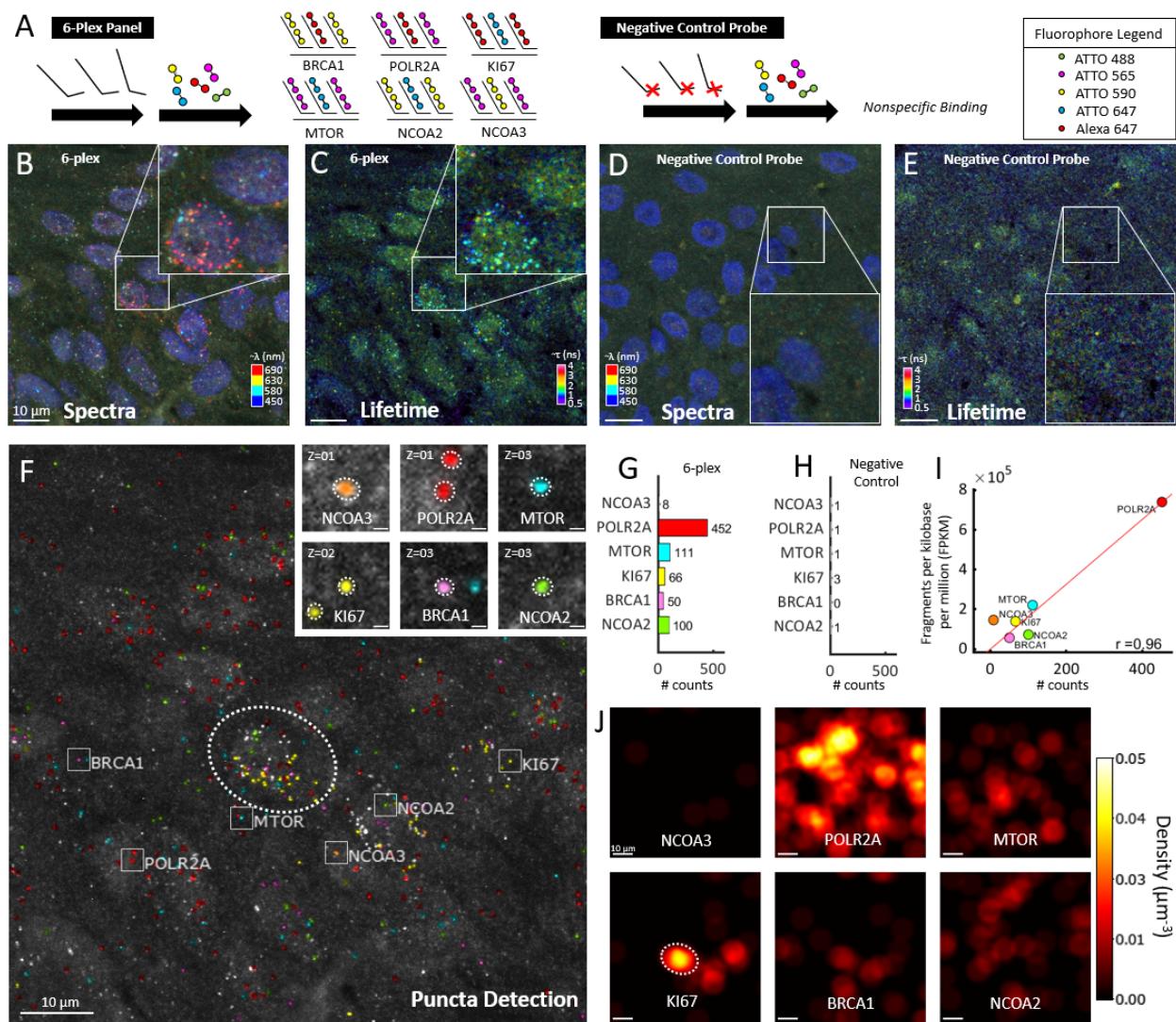


Figure 5. Multiplexed mRNA detection in epidermis region of human skin melanoma FFPE tissue. A) 6 different types of gene transcripts were labeled with primary probes followed by respective and complementary fluorescent secondary probes. Each gene was labeled with a combination of 2 different fluorophores for 10 combinations. Negative control probes targeting transcripts not present in the sample were used with their respective secondary fluorophore probes. **B)** Spectral image (max-projection in z) of a field of view of the labeled 10-plex sample (3 channel pseudo coloring). **C)** Lifetime image (max-projection in z) of a field of view of the labeled 10-plex sample (phasor projection on universal circle pseudo coloring). **D)** Spectral image of the labeled negative control probe sample is depicted. **E)** Lifetime image of the labeled negative control probe sample. **F)** Final puncta detection of the 6-plex field of view after being processed in our analysis software showing highlighted example puncta of each target (insets, right). Scale bar is 10 μm in the main image and 1 μm in insets. **G)** Overall puncta count of each transcript in the 6-plex sample. **H)** Puncta count for the negative control probe sample. **I)** Correlation of detected puncta (mRNA puncta count) vs. bulk sequencing (fragments per kilobase per million (FPKM)) is shown for each target. **J)** Transcript density in the field of view for each of the genes reveals clustering of specific genes, as an example KI67 appears highly expressed in three cells, one of them marked with a dotted ellipse that corresponds to location in F.

Figure 5B depicts a spectral image overlay (four fluorescent channels including DAPI) of the epidermis region of a labeled 6-plex skin tissue sample. Similarly, as in the previous section, the orthogonal lifetime image was attained after using phasor analysis to create the image depicted

in Figure 5C. Figure 5D/E depict the merged composite spectral and lifetime images of the corresponding negative probe sample also in the epidermis region. Figure 5F depicts the pseudo-colored puncta which were successfully classified and identified as their assigned mRNA markers. A representative inset image for each marker and its targeted detection is provided on the right. Using this approach, we observed that a population of puncta consisting of nonspecific, autofluorescent, or unknown sample artifacts were rejected from analysis, ($n = 438$) or 29% of total detected clusters (Fig. S4D). In addition to this group, we observed MOSAICA rejecting a small group of puncta that emitted fluorescence in multiple spectral channels ($n = 168$). Since, this fraction (11%) exceeded the optical crowding range (2.1% to 6.6%) our simulations and model permits, we attribute this discrepancy to autofluorescence moieties which had fluorescent signatures that spans a broad emission spectrum and elicits a multispectral response. With conventional intensity-based measurements and analysis, both contaminating groups are inherent image artifacts that compromise the integrity of puncta detection unless complicated quenching steps or additional rounds of stripping, hybridization, and imaging are utilized^{14,37}. With MOSAICA, these contaminating artifacts can be accounted for with the integration of spectral, lifetime, and shape-fitting algorithms.

Figure 5G/H plots the total number of detected puncta for the labeled 6-plex sample and the negative control probe sample to highlight the final counts obtained using MOSAICA. We observed MOSAICA platform results with the negative control sample obtaining counts of less than five per thousand. To validate these puncta counts and their relative expressions, we examined the relationship between the decoded puncta with matching bulk RNA-sequencing obtained from The Cancer Genome Atlas (TCGA) database (see Methods section). Shown in Figure 5I is a scatter plot of mRNA puncta count for each cell plotted against fragments per kilobase per million (FPKM). We observed a Pearson correlation of $r = 0.959$ for this 6-plex sample, indicating a significant positive association between the two methods and the capability for MOSAICA to capture a wide range of differentially expressing markers. Lastly, as shown in Figure 5J, the density map of the detected transcripts provides a visual method to identify spatial localization of clusters of genes, such as KI67 (indicative of proliferating tumor cells) being more prevalent in the dermis region while POLR2A is dispersed throughout the region. Overall, *in situ* profiling biomarkers such as KI67 and their spatial clustering can have diagnostic and prognostic values in malignant diseases and MOSAICA provides a robust platform to profile these markers³⁸.

Discussion

MOSAICA provides a new solution that fills a major gap in the spatialomics field (Fig. S6) by simultaneously achieving both simplicity and multiplexing by enabling direct *in situ* spatial profiling of many biomarkers in a single round of staining and imaging. This solution contrasts existing approaches such as conventional direct labeling approaches (e.g., LGC Stellaris™, RNAscope™, etc.) which can only analyze 3 - 4 targets due to limited spectral channels as well as recent spatial transcriptomic approaches (e.g., seqFISH) which can provide greater multiplexing capabilities but at the expense of many iterations of sample re-labeling, imaging, indexing, and error-prone image registration. MOASICA accomplishes this by uniquely integrating the lifetime dimension with the conventional spectral dimension, employing combinatorial fluorescence

spectral and lifetime target encoding, and exploiting machine learning- and phasor-based deconvolution algorithms to enable high-plex analysis and error-correction. This enables MOSAICA to simultaneously access both spectral and lifetime dimensions to achieve higher plex detection without sacrificing assay throughput as well as correcting for autofluorescent moieties and stochastic nonspecific binding artifacts, which are inherent challenges associated with existing intensity-based measurements.

Compared to existing sequential hybridization and imaging approaches, MOSAICA significantly reduces the number of hybridization and imaging rounds required to profile larger multiplexed panels of RNA biomarkers. By imaging every fluorophore and labeled transcript simultaneously rather than sequentially, the need to relabel probes or reimaging samples is precluded which is often the bottleneck for these complex and lengthy assays. For a 10-plex panel, this drastically shortens assay time by at least of factor of 4 – 5x and scales up even more as the panel becomes more multiplexed, making these assays more practical, effective, and affordable for routine laboratory or clinical usage. This is particularly important in clinical settings, where biopsy samples are limited in quantity and the need to avoid repetitive stripping, rehybridization, and image registration to preclude damage to the tissue structure integrity and target molecules is highly critical. In terms of cost, compared to existing commercial platforms where assay ranges from several hundred dollars to thousand dollars per batch of samples, MOSAICA utilizes inexpensive DNA primary probes which can be purchased in batch or as microarrays for a minimal price. Fluorescently conjugated secondary probes can also be used and shared as a common set among many different genes, scaling down costs to several dollars per assay or 10 – 20x less than commercial vendors. Compared to indirect spatial transcriptomic methods that analyze barcoded regions of interest (ROIs) using downstream sequencing (e.g., GeoMx® Digital Spatial Profiler, 10x Genomics Visium), the direct, imaging-based MOSAICA would be advantageous for targeted mRNA profiling with higher spatial resolution (subcellular features or single molecules), simpler workflow, lower cost, and potentially higher throughput (number of tissue sections analyzed per day) with a camera-based system (below). Moreover, the MOSAICA platform utilizes standard fluorescent probes and fluorescence microscopy (several commercial instruments capable of acquiring both spectral and lifetime information are available, e.g., Leica SP8 FALCON, PicoQuant rapidFLIM, ISS FastFLIM, etc., and already exist in many shared core facilities in academia and industry). Fluorescence imaging remains the most familiar and widely used technique in biological research and its minimal requirements of MOSAICA will permit quick and broad adoption in the scientific community.

As a complementary tool to existing spatial-omics methods, MOSAICA broadly enables scientists and clinicians to better study biology, health, and disease and to develop precision diagnostics and treatments. Gene expression is heterogeneous and many different cell identities/states exist in a particular tissue. To fully characterize cells *in situ*, we need to be able to assess multiplexed panels of genes within the same cell, which can be readily addressed by MOSAICA. As such, MOSAICA can help accelerate spatiotemporal mapping experiments to construct 3D tissue cell atlas maps. Additionally, MOSAICA represents a powerful tool for targeted *in situ* validation of RNA sequencing data. scRNAseq returns cell identities in the form of “differentially expressed gene lists” that “define” cell types. However, the clustering process is subjective, variable and

error-prone. Multiplex spatial transcriptomics using MOSAICA can validate whether a pattern of gene expression really defines a cell type or conflates multiple cell types. Furthermore, we are currently developing MOSAICA to serve as a clinical companion diagnostic tool for stratified care. Of particular interest is the spatial profiling of the organization and interactions between tumor cells, immune cells and stromal components in tumor tissues that can inform cancer diagnosis, prognosis, and patient stratification^{39,40}. With MOSAICA's ability to analyze numerous markers in a single round, we believe this feature will be particularly attractive for clinicians or researchers working with precious patient derived materials.

Further ongoing work for this platform includes improving multiplexing by scaling up the number of fluorophores and their combinations using our combinatorial-based labeling approach. For instance, Equation A and our simulation (Fig. S4) predict that with different combinations of 10 fluorophores using triple labeling strategy, MOSAICA can barcode and detect 120 mRNA targets. Our immediate next step is to scale our multiplexing capability to about 60-plex, which will bridge the gap between conventional FISH and sequential- and sequencing-based methods and can be rapidly employed to numerous applications in targeted spatial transcriptomic analysis in basic and translational research. In the future, we will further expand our codebook by implementing a Förster resonance energy transfer (FRET)-based barcoding method⁴¹ by using different FRET fluorophore pairs and tuning the distance between fluorophore donor and acceptor. We can utilize the FRET phenomena as an additional error correction mechanism at the nanometer level to resolve multiple transcripts in the same voxel. Moreover, we will improve imaging throughput with our recently developed camera-based light-sheet imaging⁴² and hyperspectral imaging³⁰. Indeed, MOSAICA is versatile and can be further integrated with other imaging modalities such as super-resolution, expansion microscope and multi-photon imaging techniques⁴³⁻⁴⁵ to increase subcellular resolution and enable imaging large highly scattering tissues.

Additionally, we will further develop our image analysis software with a user interface which enables classification and visualization of single-cell phenotypes, spatial organization and neighborhood relationship. Our current software platform's puncta detection and puncta classifier algorithm can also be improved using modern image processing techniques such as convolutional neural networks with clinical training sets to optimize true and false positive detection of biomarkers. We anticipate on benchmarking these sets with experimental data with stripping methods to determine fidelity of labeled targets. Lastly, we will implement multi-omics analysis enabling codetection of mRNA, protein and other omics markers. In particular, simultaneous detection of protein and transcript levels within the same sample can reveal the genotypic and phenotypic heterogeneity and provide enriched information for biology and disease diagnosis.

Methods

Primary probe design

A set of primary probes were designed for each gene. A python code was used to rapidly design the primary probes while controlling various aspects of the probes such as GC content, length, spacing, melting temp, and prohibited sequences. To begin, probes are designed using exons

within the CDS region. However, if that region does not provide over 40 probes, the exons from the CDS and UTR regions are used. The candidate probes are then aligned to the genome using Bowtie2, an NGS aligner, to determine if these probes are specific. Probes that are determined specific are then aligned to the RNA sequencing data on the UCSC Genome Browser, further eliminating probes that do not align to regions with an adequate number of reads. While mapping the probes to the genome on the UCSC Genome Browser, the probes are aligned with BLAT (BLAST-like alignment tool). A local BLAST query was run on the probes for the genes in the panel to eliminate off-target hits. For this experiment, each gene had the maximum number of probes that could be designed with our pipeline and requirements. The final primary probe design included 2 assigned readout sequences of secondary probe with a “TTT” connector in between, another connector, then one of the probes specific for the gene. The primary probes were ordered from Sigma Aldrich and pooled together for each gene. The sequences of all probes used in this study are listed in Table S3.

Secondary probe design

Secondary probe structures were based on the design from the Zhuang group⁴⁶. In short, the 20-nt, three-letter readout sequences were designed by generating a random set of sequences with the per-base probability of 25% for A, 25% for T, and 50% for G. Sequences generated in this fashion can vary in their nucleotide content. To eliminate outlier sequences, only sequences with a GC content between 40% and 50% were kept. In addition, sequences with internal stretches of G longer than 3 nt were removed to eliminate the presence of G-quadruplets, which can form secondary structures that inhibit synthesis and binding. To remove the possibility of significant cross-binding between these readout sequences, algorithms from previous reports were used to identify a subset of these sequences with no cross-homology regions longer than 11 contiguous bases⁴⁶. Probes were then checked with BLAST to identify and eliminate sequences with contiguous homology regions longer than 11 nt to the human transcriptome. From the readout sequences satisfying the above requirements, 16 were selected.

Cell culture

Human embryonic kidney (HEK293T) cells (632180; Takara) were cultured in DMEM (10-013-CV; Corning) supplemented with 10% FBS (1500-500; Seradigm) and 1% penicillin (25-512; GenClone). Human colorectal adenocarcinoma (SW480) cells were cultured in DMEM with high glucose (SH30081.02; HyClone) supplemented with 10% FBS (1500-500; Seradigm), 1x L-Glutamine (25-509; GenClone), and 1% penicillin (25-512; GenClone). The cells were plated into 8-well chambers and then fixed. The 8-well plates (155409; Thermo Scientific) for HEK293-T and SW480 cells were coated with fibronectin bovine plasma (F1141-2MG; Sigma Aldrich) before seeding cells onto the 8-well plates. All cultures were grown at 37°C with 5% CO₂.

mNeonGreen cell engineering

A mNeonGreen construct was transfected into HEK293T-X cells with FuGENE HD Transfection Reagent (E2311; Promega). The cells were then selected with puromycin (NC9138068; Invivogen) and Zeocin (AAJ67140XF; Alfa Aesar) 3 days after transfection.

Preparation of fixed cells in cell chambers

When the cells reached 70% confluence, cells were fixed for 30 minutes using 4% paraformaldehyde (15710; Electron Microscopy Science), then washed with PBS 3 times. The cells were then incubated with sodium borohydride (102894; MP Biomedicals) for 5 minutes and washed with PBS 3 times. 0.5% Triton X-100 (T8787-100ML; Sigma-Aldrich) in PBS was incubated in each well for 5 minutes and cells were washed with 2x SSCT (2x SSC with 0.1% TWEEN® 20 (P9416-100ML; Sigma-Aldrich). For storage, cells were left in 70% ethanol at 4°C.

Preparation of FFPE tissues

The University of California Irvine IRB approved this study for IRB exemption under protocol number HS# 2019-5054. All human melanoma cases were de-identified samples to the research team at all points and therefore considered exempt for participation consent by the IRB. Fully characterized human patient skin melanoma FFPE tissues with an immune cell score of brisk were obtained from the UCI dermatopathology center then sectioned to 5 µm slices using a rotary microtome, collected in a water bath at 35°C, and mounted to positively charged Fisher super frost coated slides. The tissue sections were then baked at 60°C for 1 hour. For antigen unmasking, slides were deparaffinized, rehydrated then followed by target retrieval (with citrate buffer).

Primary probe hybridization

Blocking buffer containing 100 mg/ml Dextran sulfate sodium salt (D8906-100G; Sigma-Aldrich), 1 mg/ml Deoxyribonucleic acid from herring sperm (D3159-100G; Sigma-Aldrich), 0.01% Sodium Azide (S2002-100G; Sigma-Aldrich), 0.01% tween, and 15% ethylene carbonate (AC118410010; Fisher Scientific) in 2x sodium saline citrate (SSC) was added to the fixed cells or tissues and incubated at 60°C for 8 minutes and then at 37°C for 7 minutes. Following this pre-block step, primary probes with 5nM of each probe in blocking buffer were added to the samples and incubated at 60°C for 30 minutes and then overnight at 37°C.

Secondary probe hybridization

Once the primary probe solution is removed, the sample is washed with 2x Saline-Sodium Citrate Tween (SSCT) twice. Wash buffer (2xSSCT with 10% ethylene carbonate (EC)) is used for 3 washes and incubated in 60°C for 5 minutes each time. Blocking buffer is added and incubated at room temperature for 5 minutes. The sample is then incubated in a solution with 5 nM of the secondary probes in blocking buffer at 37°C for an hour. The sample is washed with 2x SSCT twice before using wash buffer to wash 3 times and incubated in 42°C for 5 minutes each time. For the first wash, 10 mg/mL Hoechst (H3570; Invitrogen) is diluted 1:1000 in PBS and added to cells. Later, the wash buffer is then removed and replaced with glycerol mounting media and ready for imaging.

LGC Stellaris™

LGC Stellaris™ RNA FISH probes (Biosearch Technologies, CA, USA) were used, with 48 × 20 mer fluorophore conjugated oligos tiling the length of the target transcript. The POLR2A probe set

were supplied as predesigned controls conjugated to Quasar 570 fluorophores. Labeling/staining was carried out as described in the LGC Stellaris™ protocol for adherent mammalian cells. The POLR2A probe sets were used at 50 nM.

RNAscope™

The FFPE tissue sections were deparaffinized before endogenous peroxidase activity was quenched with hydrogen peroxide. Target retrieval was then performed, followed by protease plus treatment. The fixed cells pretreatment included treatment with hydrogen peroxide and protease 3. The RNAscope™ assay was then performed using the RNAscope™ Multiplex Fluorescent V2 kit and Akoya Cy5 TSA fluorophore. The positive control (POLR2A) and negative control (dapB) were in C1.

Microscopy Imaging

Our samples can be imaged with any instrument provided that it has spectral and lifetime acquisition capabilities. Our measurements were taken on two separate instruments; a generic FLIM instrument is depicted in Supplementary Figure 7. For validation of fluorophores and their spectral and lifetime signatures, measurements were taken on a 2-channel ISS Alba5 STED platform. This system is equipped with a pulsed white laser (NKT SuperK EXTREME) system where the excitation wavelength(s) can be selected with an acousto-optic tunable filter (NKT SuperK SELECT). Single photons were detected with avalanche photodiode detectors (Excelitas Technologies) and their arrival times with respect to the stimulating frequency (78MHz) were measured with a FPGA-based electronic board (ISS FastFLIM). Imaging was achieved by fast beam scanning with galvo mirrors and 3D stacks of images were acquired with a z-piezo mount on the objective.

For measurements of multiplexed/combinatorial labeling and detection experiments (Figures 4 and 5), we utilized a Leica SP8 with the Falcon module. This platform employs a white light laser and an acoustic optic beam splitter dichroic, and the Leica hybrid detectors with excitation band selectable by means of a prism. 3D measurements of cells and tissue samples were taken with a 100x plan apochromat oil objective with a numerical aperture of 1.40, yielding images with an x-y resolution of 100 nm and z-spacing of 500 nm.

For epifluorescence measurements (Supplementary Figures 2 and 3), images of labeled mRNA transcripts were taken on an inverted Ti-E using a 100x plan apochromat oil objective with a numerical aperture of 1.40. Samples were illuminated with a Spectra-X (Lumencor) LED light source at the 395 nm, 470 nm, 555 nm and/or 640 nm excitation wavelengths. Images were acquired with an Andor Zyla 4.2 sCMOS camera at 4K resolution with 6.5 μm pixels.

Image Processing

A custom set of scripts were written in MATLAB to process the acquired image stacks, identify individual transcripts and assign each of them to each gene. After reconstructing the images out of the digital list of photons, the analysis runs in parallel a 3D blob detection pipeline on the intensity image stacks to identify each transcript and on the other a clustering pipeline on the

phasor-transformed lifetime/spectral phasor data to detect distinct spectral/lifetime populations. A classifier then assigns pixels as belonging to a particular gene. The whole pipeline is depicted in Supplementary Figure 8.

Briefly, the intensity 3D stacks are run through a blob detection algorithm that was developed in order to identify each transcript. The images can be seen as a 3D space where the transcripts appear as spherically symmetric locations with a radial increase in intensity, namely puncta. The algorithm first computes the low frequency background noise by means of a median filter with a kernel 10 times the size of the expected puncta (the diffraction limit of the instrument, in our case around 250 nm). This low frequency background is subtracted from the high-pass filtered data obtained by convolving by a gaussian filter of the expected size of the puncta. This on one hand enhances the puncta in the image by giving a prominence value at each pixel with respect to the surrounding regions and on the other suppresses noise in the images. A search for local maxima is performed by finding the locations where the gradient goes to zero and the divergence of the gradient is negative. Once the centers in the 3D coordinate space are obtained the size, absolute brightness and prominence of each puncta is measured.

In parallel, the raw photon counts are used to construct the photon arrival time histogram and photon spectral histogram at each pixel. Phasor transforms are applied to each pixel in each image of the 3D stack in order to construct the stacks' phasor plot. This phasor data is in general a 4-dimensional, each pixel in the intensity image has four additional coordinates; two for the spectral phasor transform plus two for the lifetime phasor transform. The phasor coordinates are clustered using Gaussian Mixture Models⁴⁷. We used an initial experiment tagging house-keeping genes in order to guarantee that all expected populations were present and we trained the Gaussian Mixture Model using this initial experiment. This pretrained model is then applied to the new sets of data in order to classify each pixel into one of the clusters allowing for the presence of empty clusters. The number of clusters N intuitively should be the number of distinct fluorescent probes or different combinations of probes used to tag the sample, but one must allow for additional populations in the sample, e.g., autofluorescent species. For this reason, in the training of the Gaussian Mixture Models we allowed for one additional cluster to account for autofluorescence and noise.

Finally, by computing the mean phasor coordinates of the pixels within each detected puncta, we can compute the phasor position of each puncta and assign a gene label to it by a priori knowing the expected positions of each combination of probes depending on the spectra and lifetime of the probes.

DAPI image stacks are segmented by means of simple thresholding, estimating the threshold value by hard splitting of the histogram of photon counts in the channel. The 3D segmented nuclei are then iteratively grown by convolution by a minimal 3x3x3 kernel. This convolution is applied at each pixel of the edge of the segmented volume until no available space is left in between the segmented volumes. This yields a division of the imaged volume into a number of polyhedra where each face is exactly in the plane bisecting the two closest nuclei edges. This process is analogous to a Voronoi tessellation using the surface of the nuclei instead of points.

Simulations

In order to test the detection and classification pipeline, we wrote a set of scripts to simulate spectral/lifetime data which provided a ground truth towards detection and accurate classification debugging. This data generation script allows randomly distributing N diffraction-limited transcripts in an arbitrarily big 3-dimensional space, each with a gaussian intensity profile. We simulated our transcript gaussian profile with a X-Y standard deviation of 200 nm and a Z standard deviation of 500 nm, a peak intensity of 1 ± 0.3 (the intensity becomes relevant when simulating background noise). In the simulation run that we used to test the crowding limitations of the system we simulated tagging genes with couples out of a total of 12 fluorescent probes; 4 distinct spectral probes and 3 distinct lifetimes in each, yielding a total of $\binom{12}{2} = 66$ possible genes.

We generated the simulated images in a cubic space of $10 \times 10 \times 10 \mu\text{m}$, discretized as an image stack of 33 images of 1000×1000 pixels (yielding a voxel resolution of $100 \times 100 \times 300 \text{ nm}$). This volume was generated containing increasing densities of transcripts, ranging from a single transcript of each gene (66 transcripts) up to 2,000 transcripts of each gene (132k transcripts) and for each possible value of density a total of 10 iterations each time. These 20k simulated image stack sets were individually processed by our image processing pipeline and the transcript position and labelling obtained by the pipeline was compared to the known ground truth of the generated data. This simulation provided a benchmark of the density limitations of the method but at the same time giving an idea of the underestimation of the number of transcripts as a function of local density. The simulations allowed us to model the estimated number of overlapping transcripts as a function of density.

A similar set of simulations was run by emulating the conditions in the 10-plex experiment (Figure 4) where the genes are tagged with combinations of 2 out of 5 probes. The 20k iterations for different densities allowed to plot the density of the classification obtained after detection compared to the real number of transcripts in the simulations. This simulation was fit to the probabilistic model obtained from calculating the number of transcripts that are not overlapped in space (see next section), from which the true number of puncta was extracted (see Supplementary Figure 4).

Overlapping Probability

The fraction of puncta that do not overlap with any other puncta depends on the total number of puncta present in the volume of study and the relative proportion between said total volume and the volume of each individual puncta. The following expression is obtained as the product of $N-1$ times the fraction of available space having removed the volume occupied by one transcript:

$$\frac{n}{N} = \left(1 - \frac{v_i}{V_T}\right)^{N-1} \quad (2)$$

where n is the number of isolated puncta, N is the total number of puncta, v_i is the volume of each puncta and V_T is the total volume (simulated or scanned). The real number of transcripts N cannot be analytically isolated from the previous equation, but one can graphically obtain it. Due to the fact that the transcripts are sub-diffraction limit, the value of v_i depends on the point spread function of the instrument. Using the detected number of counts $n=13.5k$ and the estimated cellular volume $68 \text{ k}\mu\text{m}^3$, both obtained from the two image stacks shown in Figure 4, we proceeded to estimate the real number of transcripts present in the sample using the previous expression. Assuming an interval of possible volumes for the transcripts between 0.1 and $0.3 \mu\text{m}^3$ we obtained an estimated percentage of overlapping puncta in the interval [2, 6.6]%, which accounts for the number of puncta detected in more than 2 channels in the 10-plex experiment (6%). See Supplementary Figure 4.

Sequencing Data

Colorectal cancer SW480 cell bulk RNA sequencing (unpublished data) was analyzed with DESeq2. Average expression is then obtained for comparison to the MOSAICA puncta count for each gene. For the human skin melanoma FFPE tissue, the patient sample did not have corresponding sequencing data. RNA sequencing data was obtained from The Cancer Genome Atlas (TCGA), available on the National Cancer Institute (NCI) Genomic Data Commons (GDC) data portal, from 5 human skin melanoma FFPE biopsy thigh punch samples [Entity ID: [TCGA-EE-A2GO-06A-11R-A18S-07](#), [TCGA-EE-A20C-06A-11R-A18S-07](#), [TCGA-YG-AA3N-01A-11R-A38C-07](#), [TCGA-DA-A95Z-06A-11R-A37K-07](#), [TCGA-GN-A26C-01A-11R-A18T-07](#)]. The sequencing data were analyzed with HTseq and normalized for sequencing depth and gene length using Fragments Per Kilobase Million (FPKM). The average of the 5 patient samples for each transcript were used for correlation graphs with Spectral-FILM puncta count.

Statistical Analysis

When comparing distributions of puncta counts, signal-to-noise ratios, and intensity values, Student t-tests were performed for against the probability that the measured distributions belong to distributions with equal means. The reported probability values in the figures are symbolized with (*) for $p<0.05$, (**) for $p<0.01$, (***) for $p<10^{-3}$ and (****) for $p<10^{-4}$). Pearson correlation coefficient was computed to determine the correlation between the average expression level to the puncta count of each transcript.

Author Contribution

T.V., A.V. and J.G. designed, conducted and analyzed the experiments. T.V., A.V., J.G. and W.Z. wrote the manuscript. K.L., Q.X., J.F., J.Z. and C.D. conducted experiments. J.S., L.H., J.W., M.W., A.G., P.H. and E.G. provided technical support and consulted on the study. E.G. and W.Z. designed and directed the project.

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Conflict of interest

T.V and J.G are shareholders of Arvetas Biosciences Inc. A.V. and K.L recently joined Arvetas Biosciences Inc as employees. W.Z. is a cofounder of Velox Biosystems Inc., Amberstone Biosciences Inc, and Arvetas Biosciences Inc.

Data Availability

Scripts and algorithms used for the image manipulation, puncta detection and gene classification are available at request. Raw images and data used for figures 3, 4 and 5 are also available at request. Probe sequences used for labeling are included in the supplementary material section.

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Supplementary Material:

Table S1. List of Fluorophores Used

Fluorophore	Detection Channel	Excitation Max (nm)	Emission Max (nm)	Extinction Coefficient (M-1cm-1)	Quantum Yield	Brightness	Lifetime (ns)
ALEXA 647	1	650	668	270,000	0.33	89,100	1.04
ATTO 647N	1	646	664	150,000	0.65	97,500	3.5
ATTO 590	2	593	622	120,000	0.8	96,000	3.7
ATTO 565	3	564	590	120000	0.9	108,000	4
ATTO 488	4	500	520	90,000	0.8	72,000	4.1

Table S2. List of Genes Used and their Assigned Fluorophore Combination

Gene	Fluorophore 1	Fluorophore 2	No. of Probes per Gene	Present in Channel(s)	Used in Figure(s)
NCOA3	ATTO 565	ATTO 590	80	2, 3	4
POLR2A	ATTO 488	ALEXA 647	80	1, 4	4
MTOR	ATTO 565	ATTO 647	80	1, 3	4
MKI67	ATTO 647	ALEXA 647	80	1	4
BRCA1	ATTO 590	ALEXA 647	80	1, 2	4
NCOA2	ATTO 590	ATTO 647	80	1, 2	4
BRCA2	ATTO 488	ATTO 565	80	3, 4	4, 5
CENPF	ATTO 488	ATTO 590	80	2, 4	4, 5
CKAP5	ATTO 565	ALEXA 647	80	1, 3	4, 5
NCOA1	ATTO 488	ATTO 647	80	1, 4	4, 5

Table S3. List of Sequences Used

Gene	Probe Number	Codebook	Target Region	Readout 1	Readout 2	Full Sequence
MNEONGREEN	1	1	CTGGACCTTCCTCTTCTGGGCT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	2	1	GAACCTCGGCATCGCTTCTCT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	3	1	CTGGCCAGACGGCAGCACAGCA	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	4	1	GCCCCATGTCAGCTCGCATCGCA	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	5	1	GTCTGGAAAGCTTCTCTGGCATCTT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	6	1	GTTCAGCTTGCTCTGGACATGGCTC	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	7	1	GGTCCTGGGAAACACGGATAGCGTC	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	8	1	CTTCAGTAGTTGGCGGCGATGGTTT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	9	1	GAAGGTGTTGGCTGGCGGCGGTG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	10	1	GTACCTGGCTTCATTCGGCTGTGTA	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	11	1	CTGCACCTTCCTCTCTGGGCT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	12	1	GAACCTCGCCATCGCGCTTCTCT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	13	1	CTGGCCAGACGGCAGCACAGCA	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
MNEONGREEN	14	1	GCCCCATGTCAGCTCGCATCGCA	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
NCOA3	1	2	TTCACTGAAACAGATAATGGCG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGGATTTTCGACCTTCTTCCTCTGGGCT
NCOA3	2	2	GTGTCGAAACAGAACGAGAACAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	3	2	CCATACATTAAATCTGGCTGTGTA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	4	2	ACACCATGATCTTCTGGAAACATA	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	5	2	TCAGCTGGCTTGGCGCTCTGCAC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	6	2	CTGGCTTGAAGATAATACTCGGA	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	7	2	AAAAGGAAACACTTCTGGGCAAC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	8	2	AAATGATCGAACATGGCTTCTCA	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	9	2	GATTAGGACACCTTGTGGCTGTC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	10	2	GTTCGGATGGCGGCTGATGATGTC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	11	2	GGCCGTATGCTTGGCACGCTTCAG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	12	2	CAGGGCATGAGTGGAGCTAGGTG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	13	2	GGGCCAGGAGTCAATCACCT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	14	2	CCAGAACAAACACTTCTGGGCAAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	15	2	ACACCGAGAATATGATATTCTCT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	16	2	ATCTGGGGAGGCTTACAGAACGCTC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	17	2	GCCCTGGAAACCATGCTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	18	2	CCCAAATTGATAACTCTCCAATATG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	19	2	TTCAAGGACTCTGGCTTCTGTTT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	20	2	ACCAAAATCGAGGAGTCACT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	21	2	CAAAAGGAACTAAGGAGCAGCTT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	22	2	AATTACTGAGCTTACCTCTTCT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	23	2	CTGTTACAGAGAACGACGGCTT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	24	2	CAAGTTGCTCGAGATGGATTC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	25	2	ACTGGGAAAGACACCGACGATATA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	26	2	GGGGAGGAAAGTCTGGCAAGGAG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	27	2	CAAGAGAAAACCTTAAATAGGAC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	28	2	ATTCACCTTACCTAAATGGTACTCAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	29	2	CCCCTGTTAAACCAAGAACCTT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	30	2	TGGAACTTGTGAAATTCACATCGG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	31	2	CTCGACTGGCTTCATCTTCTCA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	32	2	GCTCTCTGGTCTTAACTGATCATCA	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	33	2	GCACAGACAGTCAGCACGGCTGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	34	2	AAACAGATGCTTCCAGGGCAAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	35	2	ATATGGACAGACATACCGACAGAC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	36	2	CTTCAAGTAAAGGAGGCTTCTTCAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	37	2	AGATGAGGACAGAACGAGCAATTTC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	38	2	CCCAAGAACCTTAACTGGTCTTC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	39	2	CAACATGCAACAGCTTCCGGCA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	40	2	CAACAGATGCTTCCGGCTTGGCG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	41	2	CAACCCGGACAGCTTCCATCCAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	42	2	GTCTCCAGAACTTGGGGCTGCC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	43	2	CATGTTGGCAGCTGGCTACAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	44	2	CACCAAGCTTCAAGAACAAAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	45	2	GAATCTGTTCTTCTGTTAGTGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	46	2	AGAAAGGACAGCTTGGGCTAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	47	2	GATTGAGGACAGGAACTTATTC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	48	2	CTCTCTCTGGTCTGTTAGTGT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	49	2	TTCTGGACAGCTTGGGTTACTG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	50	2	TTTCCTGCTTCTGTCAGGAAAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	51	2	AATATCTGTTCTTCTGTTAGTGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	52	2	AGAGCTGGCTTGGGGCTTCTTC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	53	2	TTCTGTTGTTGGCTTCTTCT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	54	2	TTGTGCTTCTGGCTTCTTCT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	55	2	GTCTGGTCTGGTCTTCTGTT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	56	2	GTAGCAACTTCTACATGTAATG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	57	2	TTTAACTGAGTCTGGGTTACCTG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	58	2	AAAATACTTAACTGAAACGGAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	59	2	GGCTTACAGTGGAGAACGACTCT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	60	2	GGGTAGCTTGGGGCTTCTTCT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	61	2	AAGAACGATTTGGGTTAACTGAGTC	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	62	2	TAATGACCTTCTGGGCTGTTG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	63	2	GCTAAAGCCTGAATCCATTGAGA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	64	2	GAGTAGGAACTTCCTGGTGTGTT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	65	2	TTGAGCTCTGGTGTGTTAGTGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	66	2	CTCCCTGTTCTGGGTTAACTTGGT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	67	2	CTGTAATGCTGGGCTTCTGCTCA	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	68	2	TGGTATCATTCCTGGGTTAACTGAG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	69	2	CTCTGGCTTCTGGGCTTCTG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	70	2	TAATCCGAAACTTCTGGGTTACCTG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	71	2	ACAGGAGAACGACGGCTTCTG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	72	2	TTTCGACTCTGGTGTGTTAGTGG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	73	2	TTTTAGGTTCTGGGTTAACTTGGT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	74	2	TTTCACCACTGGGTTCTGGGTT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	75	2	GGGTAGGGTATTACAGGAACTATGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	76	2	TGTCAGCTGGGTTCTGGGCTAC	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	77	2	CCAGTCATGGTCTGGGGCTTCT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	78	2	TTGGCAAGGCTTGGGGCTTCTG	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	79	2	TTGTTAGTATCTGGGTTAACTGGG	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGAT	AGGGATGTAGTACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
NCOA3	80	2	TTAATAACGACGGCTTCTGGGTT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGAT	TGTGTGAAAGTAACTGGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	1	3	ACTGGACTCTTGTGATGGCGCAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	2	3	TTGATGGCAACTTCTGGGCTACAGAC	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	3	3	AGGGGAGGACGGCTTCTGGGCTAC	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	4	3	CACAGCAGTGGAGAACGAGAAC	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	5	3	GGATGATCTGTTGTTAGTGGT	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	6	3	TGCAAGGCTTGGGGCTTCTGGG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	7	3	ACGGCACTTGTGCTATCTCC	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	8	3	CATACAGCTTGTGATGGCGCAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	9	3	AGAGTCCTTACATGGCTTCT	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	10	3	AGATGAGCTTGGGGCTTCTGGG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	11	3	CATGCCAGACAACTCTGGCT	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	12	3	TTCAAGGCTTGGGGCTTCTGGG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	13	3	GCTCTGGGGCTTGGGGCTTCTGG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	14	3	CAACCGCTTGGGGCTTCTGGG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	15	3	TCTTGGGGCTTGGGGCTTCTGG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAG	AGGGTGTGTTTGGGTTAACTGAGGTTTGGGATGTTAAGGAGAACGAGAACAT
POLR2A	16	3	CAAACTGGCTTGGGGCTTCTGG	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGAT	GGGGATGTATTGAAGGAGGATTTGGGATGTTAAGGAGAACGAGAACAT

POLR2A	17	3	TGATGTACTTGGCGCTGGTACTGG	AGGGTGTGTTGTAAGGGT	AGGGTGTGTTGTAAGGGT	AGGGTGTGTTGTAAGGGT
POLR2A	18	3	TAGCCGGTCAGCTGGAGGACTCAGT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	19	3	CTGGCGGTAAAGATTAACATTCGG	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT
POLR2A	20	3	TAGACCCATTGGGAAGATGGCGGCCA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	21	3	TGGCAGGTCAAGTCATCTCATCG	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT
POLR2A	22	3	CAATACCATGAGCAGCGGATGTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	23	3	TTTGCAGTCAGTGAGTCGTC	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT	AGGGTGTGTTGAAAGGGAT
POLR2A	24	3	GGAACATCAGGAGGTACTACCTCA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	25	3	ACAATGAGTGGACAGGATGAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	26	3	GGAGGAGTCGCTGAGGAGGCCT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	27	3	CTTACAGCATGAGTCATGACT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	28	3	GACAGTCATGATGTTGAGAAGA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	29	3	TGACCTCTGAGGAGGCGAGT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	30	3	GCCCTTAATAGTCTGAACTCTG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	31	3	TCAAACTGCTCCGGAGAGTTTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	32	3	CTCGAGGAGGAGGAGCTTGTCTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	33	3	ACTTGAAGTATTGATCACAGAGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	34	3	CAAATGAACTGCTTGGCTGACG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	35	3	GAAGTGGAGGAGCTGGGCTGCTG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	36	3	CGCTAGTAGGAGTCATCCACAA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	37	3	ACTTCACATGACTACCTGAGAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	38	3	AGGTTCTGAACTTCACTGTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	39	3	CTTCAGCAGGCTTCATCGAGATG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	40	3	CGATCCTGCAAACTTGGCTTCA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	41	3	AGATGACCTGAGCACTCCGATCC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	42	3	GTGGGATGTTGAGAAGTTCTGA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	43	3	TCAACATCAGGCTTCTCTCAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	44	3	ATGTTGAGGAGCAGCTGGTACCTT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	45	3	CCACTGAGGCAAACTTCCTGCTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	46	3	TCTGGGAGGAGCTTCAAGGAGAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	47	3	ACCAGATGTTGAGAAGTTCTAAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	48	3	AAATGTTGATGAGCTTCAAGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	49	3	ATGAGGAAAGGAGCTTGGCTCT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	50	3	TATGCCAGCAGGCCAGAACATTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	51	3	TGTTGAGCAGCTTCCTTCAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	52	3	CAAATGAGGAGCTTACATGAGAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	53	3	AGTCATGCTTCTCGAGCTGTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	54	3	GCATGTCATCAATTAGATGAGCTCA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	55	3	TGATGCCAGTACAGGCCAGCCTG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	56	3	TCATCTGTTCTGACCACTTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	57	3	ATGTTGAGCTGAGTCAGCAGGAGAA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	58	3	CACTCTGAGGAGCTTGAATCCC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	59	3	CTTACAGCAGGCCAGTTCATGAGCT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	60	3	AGATGAGCTGAGCTCCGCTC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	61	3	TCGGTAGTACGATAGGACGATCA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	62	3	TCATGAGTCGCTCTGCTGCTGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	63	3	CCGCAAGCATGATATTGAGACAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	64	3	CCCTGTTCAAGGTCAGTCAGCAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	65	3	GTGAGCTGGAGCTTGAAGGAGAC	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	66	3	GGGTGATGTTGGAGACTAGTGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	67	3	GAGTAGCTGGAGGAGCTGGAGA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	68	3	CGAGTAGCTGGAGGAGCTGGAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	69	3	GAAGTGGAGAAGATTCGGTGAAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	70	3	TAGTTGGCTGCTGGTGGTGAAGT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	71	3	GATGTCGGCTGAGTCGGTGTAG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	72	3	TGGGCTAGTGAAGGGAGCTGGT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	73	3	GGTAGATGTTGGAGACTAGTGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	74	3	TGGGACTGTTAGAACGGCTGG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	75	3	GAATAGGCTGGAGCTGGAGGAGTA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	76	3	GATAGCCGGCTTGTGAGCTAGTGA	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
POLR2A	77	3	CAGTTCTCTGCTACGTCATCCG	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT	AGGGATGTGTTGAAAGGGAT
MTOR	1	4	ACTGCAACATGCTGAGCCGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	2	4	TGGTTCTCTTCAGCTGGTTGAGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	3	4	CCATGACAACTGGCTTGAAGGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	4	4	GGCAAGCAGCCAACTTCCTGG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	5	4	TTCCAGGCTGGCTCTCCATCCAAT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	6	4	TGTCAGGAAAGAACAGGGTACGAG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	7	4	ATCAGCAGCAGGAGAACGGGCTCA	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	8	4	CTCTTCGTCAGCTGGCTGGTTG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	9	4	AGGCTACAGCCAGCACAGAGGCC	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	10	4	ATTTCAGGACAGCTTCAGTGG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	11	4	TCCTGGAGCTACTGGTCTGAGCA	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	12	4	ACAGGAACTTGGTCAAGGCTTCA	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	13	4	TGAGCTTCTGGAGGAGCTGAGTC	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	14	4	CCAGGCTGGACTTGGTCTGGAG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	15	4	TCTGACAGCTGGTCTGGAGCTT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	16	4	ACCTACAGCCAGCACAGAGGCC	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	17	4	CTTGGTCTGGAGCTTGGTGTAGT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	18	4	CATTCTGGAGCTTCAAGGCTTCA	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	19	4	ATTCAGGCTTCAAGGCTTCA	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	20	4	GTTCAGGAAATGTCAGCACAGG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
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MTOR	22	4	GCTTACAGCTGGAGCTGGAGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	23	4	GTGATCAAGCAGCTGGAGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	24	4	CAAGGCTGGCTAGCTGGAGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	25	4	CATGGGGCTACTGGTCTGGTATT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	26	4	GGGCTTACACTAGCAGCTGGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	27	4	TCTGCTGAGCTTCAAGGATCA	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	28	4	TTTGCTGTTAAGGCTAACAGGCC	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	29	4	CTGACAGCTGGAGCTGGAGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	30	4	TTGACCTGGAGCTTCAAGGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	31	4	ATCAGGACAGCTGGAGCTGG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	32	4	AGAGAGTGTGAGCTGGAGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	33	4	ATGCTGGAGGAGCTTCAAGGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	34	4	TTAACAGGCTGGAGCTGGAGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	35	4	GCTCAATGAGAAGATGTCGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	36	4	GGGCTGAGCTGGAGCTTCAAC	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	37	4	GTCAGGGCTTCAAGGCTTCTAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	38	4	GGCATGATGAGTGTGAACTGGAC	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	39	4	TCCATGGCTGGAGGAGCTGTC	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	40	4	TCAAAGGATGTCCTCTCATCG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	41	4	ACTGTCCTCTGAGCTACATCG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	42	4	GTGCACTTCAAGGCTGGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	43	4	GCGCTGGCTGGAGCTGGAGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	44	4	GCGGATGAGCTGGAGCTGGAGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	45	4	GAGGGCTGAGCTGGAGCTGGAGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	46	4	GTGTCAGCTGGAGCTGGTCTG	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	47	4	GGCAGCTCTCACCGAGCACAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	48	4	GTAGTCTGGAGCTGGAGCTGGCA	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	49	4	GTCAAGGCAAGGAGCTGGCTCC	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG
MTOR	50	4	GTTGCTGAGCTGGAGCTGGCT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT	ATAGGAAATGGTGTGAGTGT
MTOR	51	4	TGCAAGGAGCTGGAGCTGGCT	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG	AGAGTGAATGAGTGTGAG

BRCA1	4	6	CCACATGAACTTGAAGAACAGACTAC	GGGTGATTTAAGGGAGGAT	GGGTGATTTAAGGGAGGAT	GGGTGATTTAAGGGAGGAT	GGGTGATTTAAGGGAGGAT
BRCA1	5	6	AGTAACTAAGTCGTTCTCGTGTGA	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	6	6	CAGCCTTTCATACATTCTTCCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	7	6	GCCCCATCTGATGTCGCTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	8	6	CCGGCTCATTCATCTGCTCTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	9	6	CTGCTATTGTTATCCTAACAGAACATC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	10	6	TCTGGAAAACCCTAACATTCATTCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	11	6	ACTTGGGATTGATTGACACTCC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	12	6	TCTACCTTCTTAAAGCCTAACATC	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	13	6	TTTCAGTTACATGGCTTAAAGTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	14	6	TGGCTCATCAGAACTCTCTTATAAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	15	6	TCTCAGGATGAGGCTGATGATG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	16	6	GAACCTGAACTTCCTTCTGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	17	6	ATCTACCTGACCTTCTCTGGTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	18	6	TGGAGGCTTCTATGGGGTAGATT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	19	6	GTTCAGGCCTAAATGGCTGTGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	20	6	AGTGGGGCTTAACTGACTACT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	21	6	CTGACTGCTTAACTGGTGTACTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	22	6	CTTCAGTCTGAGTTGGCTCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	23	6	TTTACTCTGCTTCTGCTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	24	6	AGCTTGGAACTTCTGCTCT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	25	6	TGGAGGCTTCTGGATGAACTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	26	6	GGCTCTCAGTAACTGACCTTACT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	27	6	GCTACTCTACAGCTTCTCTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	28	6	CCATACTGACCTAGGATCAATGAA	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	29	6	AACAACTGATTAAGTCTCTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	30	6	TGGACTTAACTGCTTCTGCT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	31	6	GGGGTAACTTAACTGATGATCAA	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	32	6	CTGGATTAACTGAACTGGCAAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	33	6	TTTCTTCTTAACTGGGAGGTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	34	6	AGCTGCTGATTAACCTACTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	35	6	GCTCTTCTTACATCTTCTGCTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	36	6	CTCTCTGAGTAACTGATGACACT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	37	6	GGGGTGTATGAACTATGGTTTAAAG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	38	6	CCATTCTTCTGGATCACATGAA	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	39	6	CACTTCTATGACTGAACTTACTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	40	6	CTGTTCTACTCTGCTGTAATG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	41	6	ACTTGTCTTAACTGACCTGGTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	42	6	ATTCAGGATGCTTACAACTTACT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	43	6	GAACAACTGAGTGGATCATGACT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	44	6	CATCTACAACTGGCTCACAGTGT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	45	6	CTCTTCTTGGAGCTTCTGCTAA	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	46	6	GTGAAAGGGCTAGGCTCTGCTAA	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	47	6	TTCTGAGGACTTAACTTCTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	48	6	GAAGGCTTCTTACCTCTACTAGAATG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	49	6	TCTAGACGACCTGGCTGACAC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	50	6	GTGACTGCTGAGTAACTGATCTTCA	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	51	6	AGAACATTCTTCTCTTCAACTAGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	52	6	TCACTGACTGCTGAAAGAACAAACG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	53	6	GTGGAAAGGACCAAACTGGAGGAT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	54	6	TCCCTGGTCTTCTGACGATGCTTC	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	55	6	CAATTCTCTGGAGCTTCTTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	56	6	TGCTGTTCTGATGAGCTTCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	57	6	CTCAAGGCGAGGAGGACTCTATG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	58	6	AGGGATTACATCTTCTTCTGATGAA	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	59	6	AACTATGCGACAGACCTTAAAC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	60	6	ACCTTCTACCTCTGCTTCTTCTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	61	6	CTCTGAGATGAGTGGTCTTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	62	6	CTCTCTGAACTTAACTCTTAACTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	63	6	CTCTGGAACTAGATTTCTGCTC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	64	6	GCTGTTCTGAGTAACTGGAGGAGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	65	6	GGTGGCAACAGGGCTACCTGGTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	66	6	ACTTCATGACGAGGAGTGGAGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	67	6	ATCTGAGTATGGAGCAGCTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	68	6	CACTTCTTCTGTTCTGTTACAC	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	69	6	CACCCTCTGGCTGGCACCACTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	70	6	GGCTGCTGAGTCTGGCTGG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	71	6	CAGATTCTTAAAGGAGGACTAAC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	72	6	TCATTGTTGGCTTAACTGGTTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	73	6	TGAGGCCAAGGCACTCTGCTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	74	6	AGGAATCTGAACTTGGGGACCTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	75	6	CCCCAGCTTCTGTTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	76	6	CCAACTTCTGAACTTCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	77	6	GGAAATGATTAACTACGGCTAAC	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	78	6	ATTCAGGATGCTACAGAACAGCTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
BRCA1	79	6	ACAGCTCTGAACTTCTGGTTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
BRCA1	80	6	GTCCTCATCTGGCTTCTGCTT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	1	7	TCACATCTCTGCTTCTGCTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	2	7	TCAGCTCTCTGTTCTGTTACATG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	3	7	CGACAGTAACTGGATGCTGCTT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	4	7	GCGGAAGCTGACTGATGCTTCT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	5	7	CAAGAGTCTGCTACAGAACAGGAA	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	6	7	GATGAGTCTGCTTCTGTTGIG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	7	7	ATTTGCTACTGGCTTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	8	7	TCTTCTGGCTTCTTGGGGAAAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	9	7	TCATGGCTGGCTTCTGTTGGGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	10	7	TGAAAGATCTGGCTGTTGAGTGT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	11	7	GGGAGCTGTTGTTACATGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	12	7	GCCAACAGTCTGCTTCTGAGAC	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	13	7	CAAGCTTCTGAACTTCTGAGGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	14	7	CGAGTTCATCTGCTTCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	15	7	CGCTGCTCTGCTTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	16	7	GCCCCCTTCTGCTTCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	17	7	ACCAAGAACAGGAGGACTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	18	7	CTTCCTGCTTCTGAGGCTTCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	19	7	TGTTCACTTCTGGCTTCTGAGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	20	7	TGGCTGAGTCTCTGCTTCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	21	7	GCGGAAGCTGACTGCTTCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	22	7	TACTGCTCTGCTTCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	23	7	GCTCATCTCTGCTTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	24	7	CTATTCTGAACTCATCCTTCT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	25	7	TGTCATGCTGACTGAGGCTGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	26	7	GTGAGTCTGACTGAGGCTGG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	27	7	TCTGTTCTGGCTTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	28	7	GCTTCTGCTTCTGCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	29	7	TCCCTGCTTCTGCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	30	7	TGACTCTCTGCTTCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	31	7	TTCCGATCATCTCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	32	7	CTGAAGCTTCTGGCTTCTGAGG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	33	7	TAAGCTTCTTCTGCTTCTGAGG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT
NCOA2	34	7	CTCTCTGCTTCTGCTGCTG	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT	GGGGATGATTAAGGGAGGAT
NCOA2	35	7	GAATAGCTTCTGCTGCTG	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT	TGTGATGAACTGAGGGGT

NCOA2	36	7	TGGTGTGAAAGTTGGATCTGGAT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGTGAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	37	7	AAGATCGTGGGACGATTCTTC	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	38	7	TCTGTGTCGATGTCATTTCTC	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	39	7	CATGTCGTGTCATTTCAACCT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	40	7	ATAGTGTGTCGATCAGTGGAG	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	41	7	GGACTCTGTGATGTCATCTGG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	42	7	CTGGTGGCCGAGACTGTCAT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	43	7	CTGTCATGCCACTGTTGTCG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	44	7	TGCTGTGTCGTCATCTGGTT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	45	7	ACTGGAATGGTTGCAAGCTG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	46	7	GGGTGAACAAATAGCACAGCT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	47	7	CTGTCGTGTCGACTGTCAGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	48	7	AAGGTGAATGCAGTCAGACTA	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	49	7	TGACAGGTTGATAAATTTGCT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	50	7	ACAAAGGCTGATTCCTTCAACAT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	51	7	CCCCAAATCAGGTTCTTCAACAT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	52	7	GCTGTCGCGGTCGTCCT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	53	7	AGAGATACGACTGTCATTTGG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	54	7	TCCTTCAACATGTCATTTAGAC	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	55	7	AAATTGTCATTAACCTACGCCCTC	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	56	7	AGGGTACAGGTTGTTTAAACAA	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	57	7	CTGACAGGAGAACAGATGTCGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	58	7	GCTTCACTGTTGTCATGTCATTT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	59	7	GCTGATTGTTGATCACCTTACCTT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	60	7	GCTCATTTAAACACCTCGGGCTC	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	61	7	TTGGCTTGACTGACGACTCTTA	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	62	7	CTCTGTAGTACAGTCATCTCTAACG	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	63	7	CTTGGTGTGATCTCTCTATTC	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	64	7	GCACATTTCAGACTGTCATACCT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	65	7	ACTGGTGGCCACTGAAAGTGTGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	66	7	GGAAAAAGTAGGAGCTTGGAGGG	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	67	7	TTGTATCCACATGCGCTACGGG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	68	7	GTGCTGTTGAGGAACTGACTCTTA	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	69	7	AGATGTTGGTACGGCTGTGAGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	70	7	AAATACCGGGCAGATGATTTAA	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	71	7	CCCTAAAACAGCAATGATCAGAA	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	72	7	ACCTGATTGAAACCGTAAGAACATTTC	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	73	7	CAAGCCAGAATAGACATACATAGGG	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	74	7	TGCAAGTGTGATCTGCCACCTT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	75	7	TTGTGAGGAGGATGTCCTCTTC	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	76	7	GCTTAAAGAACACCGGGAGAAACATT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	77	7	GGACAGTATGTAAGGAACTACAGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	78	7	AGCTTCTCTGAAGGAACTGTTA	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
NCOA2	79	7	AATAACAACTCATGCGGTAACA	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT	TGTGTGAAAGTAGGGGT
NCOA2	80	7	CTACTTGTGATTCAGCTGCAAC	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT	ATAGGAATGGTGGTAGTGT
BRCA2	1	8	GTGGAGTTTAAATAGGTTGTC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	2	8	AGCCAGGTTGATTAAGATGTTCTC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	3	8	TGGTCCCTACAGATTAAGAATGAG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	4	8	GGCTCTGTTGAGGATTCATTTGCT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	5	8	TTCACAGGGCAGATGTCACACT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	6	8	ATTAGACGTTAACAGGGTTGAGT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	7	8	GTGGCAAGGAAATTCATGGTAAAGA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	8	8	GCTCTCTGTTGAGGTTGAGT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	9	8	ATATGCTGCTTCACTGTTGAGT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	10	8	AGTTGTCATGACTGACCTGAA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	11	8	CCAGCTTCATTCAATTAATTGGAC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	12	8	GGGGCTACAGGATTTAGTGTGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	13	8	TGTAATGTTGAGGTTGAGGAT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	14	8	GCTGCTCTTACATAAACATGCTGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	15	8	TGTCCTGAGGAAATTCATGAGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	16	8	CTTGGTCTGTTGAGGTTTACATTGAT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	17	8	CTTGTGAGGATGTCATCTCTGTA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	18	8	CTTGTGAGGATGTCATCTCTGTA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	19	8	TTGAGGTTGGGATTTAGTGTGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	20	8	TGTGTCATCTACAACTGGTGTG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	21	8	CTCTGCTGTTGAAATTCATCTGAG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	22	8	CTTGGTCTGTTGAGGTTTACATTGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	23	8	CTTGTGAGGATGTCATCTCTGTA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	24	8	ATCTGTTGAGGTTGAGGTTTACATT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	25	8	GCATTCTGTTGAGGTTGAGGTTTAC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	26	8	TGTCGTCATCTGTTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	27	8	CACTGCTCATTAACCTTACATTGAG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	28	8	CAGTAACTGAGCACTGGCTTCT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	29	8	CTTGGTCTGTTGAGGTTTACATTGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	30	8	TTCTGAGGTTTACATTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	31	8	GGAAATCTGGTTGAGGTTTACATT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	32	8	TCTGTTCTCATTAACCTGAGGTTA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	33	8	CTTCTGTTGAGGTTTACCTGAGGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	34	8	GCTGTGAGGAAATTCATGAGTTGAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	35	8	AGGTGTTGGCTTCACTGTTGAGGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	36	8	CCACAGTCATTAACCTAACAGGTTA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	37	8	GGCTGAATTTCATGACTGAAATGG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	38	8	GTTCAGGTTGGCTTCACTTACATT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	39	8	ACGTTTACCTGGCTTCACTTACATT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	40	8	CTCTGATCATCTGAGGTTTACATT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	41	8	TTCTTCATCATGAGGTTTACATTGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	42	8	TTTCCATGAGGTTTACATTGAGGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	43	8	GACTCTGTTGAGGTTTACATTGAGG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	44	8	GCTGTCGAGTGTGTTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	45	8	AACTGTCCTGGTTGAGGTTTAC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	46	8	GTGAAGACTGTTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	47	8	GGTTGTTGTTACATTGAGGTTTAC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	48	8	TTCTGTTGAGGTTTACATTGAGGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	49	8	CACCTGTTGAGGTTTACATTGAGGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	50	8	GTCATCATCTTCACTAACAGGTTA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	51	8	CATTCTCTTGGGAGGATGAAAGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	52	8	CGGTGTTGTTGAGGTTTACATTGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	53	8	CTGCAACTGGTAACTTACATTGAA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	54	8	TGCGCTGTTGAGGTTTACATTGTT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	55	8	CACTGTTGAGGTTTACATTGAGGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	56	8	ATCATGAGGCTCATGTCATCACT	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	57	8	ACAGACTGCTGGCTGTCAGGAGAC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	58	8	ATCCACCATGCGCAACTGTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	59	8	TGCTGTTGAGGTTTACATTGTT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	60	8	AGAAAGTTTACATTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	61	8	ATCTAACCTGGCTTCACTAACGTC	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	62	8	GCCATTCTTCAAGACGTCAGGG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	63	8	TCTAGGGTCAAGGAAATCACTGG	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	64	8	AAAAGGAGTAACTGGGAGGAGGAAA	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	65	8	CAAGACGACACTGGCTGTTGAGT	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA
BRCA2	66	8	CAAGGTTTACATTGAGGTTTAC	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG	AGAGTGTAGTGTAGGTAG
BRCA2	67	8	CATGGCTTCACTTCACTGGCTA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA	TGTGTGAGGGATTGAGGATA

BRCA2	68	8	AAACCTTGTCTTTGGTCAGCAGA	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	69	8	GCTTCCATACAAAATTCTTGGCATAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	70	8	ATTGGATTCTGGTCGCTTACGAGG	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	71	8	CTCTTGTGACTGAGAACAAACAG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	72	8	GTTTCTGCTCATGGAAATGATTCG	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	73	8	AGACAGGTGGAAACGACTCTCT	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	74	8	CAGTCTTGTGCTCATCACTCTTCT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	75	8	GCAGCGGGAAACAAATGACAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	76	8	CTTATGGGTGCTTGTGTTTGTC	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	77	8	TCTCTGTGCTCATGTTACCTTC	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	78	8	AACAAAGGACTTGTATTATCACTG	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
BRCA2	79	8	GAGATGTAGTACAAGCTGTTCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
BRCA2	80	8	GGCTGGGAACTCTGCTTCTG	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT	AGAGTGTAGTAGTGGGAGT
CENPF	1	9	CTTCTGGATTGTTGGCTTGTGTTT	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	2	9	CTGGAATTAATCTTCTGCTTCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	3	9	GCATCTTCTTCTGAAATGAAAGT	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	4	9	CTGCTTGTGAACTTGTGAACTCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	5	9	GAAACTTATCACTTGGCTTCTC	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	6	9	TCATCCTTCACTTGTGAACTTCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	7	9	TGTGGAGGAAACGACTGGCTGAC	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	8	9	GCCTCTGGATTGACTCTGCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	9	9	GATCTGACTGGCTTGGAACTCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	10	9	TGTTCTGTTGCTTGTCTTCACTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	11	9	CCAGATCAGCACAGCACTTCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	12	9	ACTCTTCTCCTGCTGCTCATCTA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	13	9	CGTTCTGCTTCTCTGTTGATCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	14	9	CTGGCTTCTACCTCTGCTTAC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	15	9	CATATGGCTGAGGACCTGTTGAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	16	9	GCTGTAACTTACCAAGGACTTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	17	9	TCAACTTATTTGTAGATGCCAGAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	18	9	TTTGAGGCTGCTGATCTGTTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	19	9	CTGTCCTGCTTCTGATGTTCTC	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	20	9	AGTCTCTGCTTCTGTTGATCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	21	9	GCATTAATTCTTCAAGGCTTCTT	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	22	9	CTTCATCTTCTGAAATGACTCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	23	9	ACTAGTGTGATTCTTCAAGGATC	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	24	9	CTTCCTGCTTCTGCTTCAACTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	25	9	CATCGCTGCTTCTGCTTCAACTAGT	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	26	9	AGAGTCTTCAATTGTTGCTTCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	27	9	CCAACTGCTGAACTTACATCTGAGAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	28	9	TCTAGGCCCCTGAAATTTCTTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	29	9	CATTGTTTGTGAGGAGGACTGAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	30	9	GAGGTCTTCTGCTGCTGCTGAG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	31	9	CTCTGGTGTACTCTTCAACTCTA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	32	9	CTCTGGTCTTCAAGGAAACAGACAG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	33	9	CCAAATTCTTGGCTTCAACTGACTA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	34	9	CTTGAAGGTTCTGATCTGCTTCA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	35	9	TGCTAACTGAGCTGCTGAGCACCA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	36	9	GGTTTCTTCTGCTGCTGATCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	37	9	CAAGCTCTGGCTTCTTCACTTAA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	38	9	TTCTGACAAATACTGCTTCAACG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	39	9	CAGTCTTCTGCTTCTTCTCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	40	9	ACCGAAGACTTAACTGAGCTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	41	9	TGTTGTTCTCTGTTCTGTTCTG	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA	TGTGGAGGATTGAAGGATA
CENPF	42	9	CTGAGGCTTCAATTGTTGATCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	43	9	GCATTAGGACGAAATACTTCACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	44	9	TCTCTGTTGATCTTCTTCCCG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	45	9	TGAGGCCCTGAGGACTTCTACTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	46	9	ACGCTGATTTCTGCTGATCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	47	9	CTTGTGACCTGAGGACTTCTCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	48	9	CTAACTTCAAGGCTGAGCTTCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	49	9	GTTCCTTCTTCAATTGTTGTTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	50	9	GATTCTTCTGAACTTCTTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	51	9	TTTCTGCTGCTTCTTCTGCTGAT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	52	9	TTTCATCTGCTTCAACTGACTA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	53	9	ATTCCTGCTTCAAGGAACTTCAACTTAC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	54	9	TAGTCCTGCTTCTTCTGACAT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	55	9	CTTGGCTTCTTCTTCAATTGTTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	56	9	CTTGTGCTTCTTCTTCAACTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	57	9	TGTCCTGCTTCTTCAATTGTTCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	58	9	GCCTCTGGCTTCTTCTGCTGAG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	59	9	CTCTGGTGTACTTCTGAGGACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	60	9	CTTGAAGGTTCTGAGCTGATCTAC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	61	9	GCATCTGCTTCTTCTGCTGCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	62	9	CTAACTGAACTTCTGCTTCTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	63	9	CTCTGCTTCTTCTTCAACTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	64	9	CTACIAAGGACTCTGCTTCTCTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	65	9	CTGCTGCTTCTTCTGCTGCTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	66	9	TTTGATGTTCTGACTGTTCTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	67	9	CATTCTGACTTCTGAGCTGACTTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	68	9	CAGTCTTCTGAGCTTCTGATCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	69	9	TTTCCTAGTGTGAGCTCTCAATTG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	70	9	GCATCTGAGCTTCTTCTACTAC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	71	9	GTTGTTCTGCTTCTTCAACGAG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	72	9	CTCTGGTGTCTGCTTCTTCTACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	73	9	GCTCTGGTGTCTGAGGACTTCTCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	74	9	TGTTGAACTCTGAGCTTGTATCA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	75	9	TGTCGCTTCTACATCTTCTGTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	76	9	TAGCAAAAGGACGCTTCTGAGAT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	77	9	TTTGGCTTCTGCTGAGCTTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	78	9	TCTACATCTTCTTCTGCTGCT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	79	9	GCTCTGGCTTCTGCTGCTGTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CENPF	80	9	GGATGCCCTGACTTCTGCTGAG	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	1	10	CACTGCTTCTGACTTCTTCAACTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	2	10	AGTCGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	3	10	GCTTCTGACTTCTTCAACTTAC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	4	10	AGATCTGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	5	10	CAAGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	6	10	GGCTACCTGACTTCTTCTGCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	7	10	GCTCTGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	8	10	CCATCTGCTTCTTCAACGAACTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	9	10	TTGGAAAGAACTTCAAGGACTGTC	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	10	10	TATTTGTTGCTTCTTCAACTCAT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	11	10	GTCTACATCTTCTTCAACTTCAAA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	12	10	GGGGCTTCTGCTGAGCTTCTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	13	10	TGCGAAAGGACCACTTCAACTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	14	10	CCAAACGCTTCTGACTTCTTCA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	15	10	TTGTCCTGACTTCTTCAACTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	16	10	AAGATGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	17	10	AGTGGCGGAACTTCTTCAACTTCA	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	18	10	CAAGCTTCTGACTTCTTCAACT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT
CKAPS	19	10	TGACTCTGACTTCTTCAACTT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT	TGTGTGGAAATTTAGGGGAGT

CKAP5	20	10	AGTACCCAACTGTTCAATGGCGCAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	21	10	GTTGGACCATCAGCTGGAAAGGG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	22	10	CAGGGACAGGATTCCTTCCTTCA	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	23	10	AGAGGTCTGGTTGGTGAGAAAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	24	10	GTTTCACTGGTCCGGCTCTCG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	25	10	ACAGCACCGCTTCCTTCAGATC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	26	10	CTCTGGCTGCGATTAGCTGGCTC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	27	10	ACAACCTGCCTGACCTTGGAAA	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	28	10	CTTCAACTGTCGAAACAGGCACT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	29	10	TTTGGGATTTCTTGGAAAGAAC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	30	10	TACAGATACTACGCCAAGCAGGT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	31	10	TCATCTGGTCACTCTTCCTC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	32	10	GAAACAAAGGAAAGGATCTGGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	33	10	GGAAAGATCAGACATGGCTC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	34	10	ATATCTTGGTGCACCTTCAGGA	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	35	10	CCAAAGCTTACAGCTGGTAGGAG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	36	10	AGCCATTCTTCATGGCTGCTG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	37	10	GGTGTGTTCTAGCGCCAGCCCAG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	38	10	GAACAAAGAAGGAAAGGATCTGGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	39	10	TCTGGCCCTTCTTCAGACATTC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	40	10	CTTAACTGATCATGAAGAAGGAC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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CKAP5	42	10	TGCTTCTAGGGTGGACGAGCTTGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
CKAP5	43	10	TGCTCTTCTTCACTTGGAAACAA	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
CKAP5	44	10	GTGTCCTAAGTATTCTCCGGGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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CKAP5	52	10	TCTTAACTGTTGAAACACTGATCC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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CKAP5	74	10	AAATCTTACCTGGCTTCTTGTGAA	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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CKAP5	80	10	CTCCGGACAGCTGGAGGTTGGTGT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	1	11	GGGATCTTCTCTTGTGAGGATCT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	2	11	TTTATTTCTTCTTGTGAGGATCT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	3	11	ACTACGACTGTCAGTCACTGACT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	4	11	CGACTGTTTCTTCAACTTGTGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	5	11	TGTCATGCTGACTGTTGTGATTC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	6	11	CTTCTGACTGCTTCACTGGCTG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	7	11	ATTCCTCTTCATGAGGAACTTAC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	8	11	AGCTGTTGACTCTTGTGACAAAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	9	11	TTCTCAGGAACTTCTGATGTC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	10	11	TAGCTGCTGAGTTGGTGTGAGT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	11	11	TACTTCAGCTTCACTGGCTT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	12	11	TTGGCTTCTGAGGACAGCTGGGACT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	13	11	GTAGTACCTCTGGTCTGATGAC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	14	11	TCTCAGGAACTGATCATAGAGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	15	11	GGTGTGGCTTGTGAGGTTGGTGTG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	16	11	TTCTCAGGTTGGCTTCTTCAGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	17	11	ATGTCGTTGACTTGGTGTGAGT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	18	11	CGATGATGATTAACCTGGTGTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	19	11	GGGAATGAACTTCAGGAGAAATTG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	20	11	GATACTGGATTGACGGAGGTTAC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	21	11	ATGTCGTTGTTGGTGTGAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	22	11	CTGCTGGGGCTTCTGGTGTGAGT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	23	11	AAACTCTTCTGGCTTCTGGTGTG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	24	11	TAACTCTGACTTCTGGCTTCTGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	25	11	AAAGGGCTTACCTGGTGTGAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	26	11	TGTCCTTCTAGGAGAAATTGAGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	27	11	GGATGCTTCTGGCTGAGGAGGCTT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	28	11	GGAGGACTTACGTTAGGAAATGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	29	11	CTGGGTTGAGGTTGAGGTTGAGG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	30	11	GTTCTTCTGGCTTCTGGTGTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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NCOA	32	11	TGCTGTTGTTTATTTCTGGTGTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	33	11	GAGCTGTTGAGGTTGAGGTTAC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	34	11	CCCTGAGGAGGAGGTTGGCTAC	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	35	11	TGTCAGGTTGAGGTTGAGGTTAC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	36	11	CGAGCTGTTGAGGTTGAGGTTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
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NCOA	38	11	AGAGGGCAACGACTCTGGTGTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	39	11	CCCTCTGAGGAGGTTGGCTGAGG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	40	11	CAGCACAGGTTGAGGTTGAGGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	41	11	TTCTGAGGTTGAGGTTGAGGAGG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	42	11	GGAGCTGTTGAGGTTGAGGTTGAG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	43	11	CCACTTACCTTCACTCATCCAGG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	44	11	TGTTACATGCTGACTTCTGGTGTG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	45	11	ACTGGCTGGGGCTTCTGGTGTGAG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	46	11	TGATCACTGAGCTGGCTGAGGCTG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	47	11	ACCGCACCATCTGGCTG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	48	11	GGATGCTGAGGTTGAGGTTGAGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	49	11	GATGCGCTTCTGGTGTGTC	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT
NCOA	50	11	GTCGTCAGTCTGGCTGAGGAGG	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT	GGGTGATTGAAAGGAGGAT
NCOA	51	11	CCAGCTTCTGGCTGAGGAGGCTG	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT	TGTTGGGGATTGAAAGGAT

NCOA	52	11	GTTTCACTTGGCCAAGGAAGG	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGTATAGGAAATGGTGTAGTGTGTTTACATTTGCCACTAAGGAAGG
NCOA	53	11	ATCTCTGTATAAACATCTAACCCCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTATCTCTGTATAAACATCTAACCCCC
NCOA	54	11	AAAGGTGGCTGTCTGTGGTGTG	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAAAGGGCTGTGTGTTG
NCOA	55	11	TGCGTTGAAAGGGCTAGGGAGATT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGCTTGAAGGATAATTITGGCTTGAAGGAGATTGAGGAGATT
NCOA	56	11	GTGTTACTTGAACAGGCATGTCCC	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTACTITGACAGGCCATGTCCC
NCOA	57	11	GCGGAGGAGTCTTAAAGGTGTTGCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	58	11	ATAGTTAAAGTCGAAGCTGGTAAAGGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	59	11	AAGATAGCTTCCGATTTTGTTGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	60	11	TGTTGATCCTGCTCATATTGAT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	61	11	CTGTTGACTGTACAGTCCTGGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	62	11	GCTGCTGTTAGTACCTGTCTGTG	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	63	11	AGATGAGGGAGGGAGGTGTTTCCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	64	11	TGTGGAGACCCCTAGGGAGACGGG	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	65	11	AAACGGCTGTAGAACGGCTGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	66	11	ATGCTCAGGATTGCTGTAGTGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	67	11	ACTGCTCCATGTTCTGTCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	68	11	TGCACTGAGGATTGATTCCAGGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	69	11	GGAGCAAAGTGGCTCACCTGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	70	11	CACCATGGCTCCAGGGCTTAA	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	71	11	GGGGCAGTGGAGTTGCTGGAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	72	11	GGCCTTCACTGCTGTAGTGTAC	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	73	11	TGTTCTGGACAGCTGTACA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	74	11	GTATACCTGGCTGTGGAGGGCTG	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	75	11	CTCATCTGGACATCTGGCCATTC	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	76	11	TGAGGAGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	77	11	TTCAGTAGAGGCCATGTGTCTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	78	11	TTTGAAGAAGGTCACTGGATGAGAGC	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT
NCOA	79	11	CCAGGCTGGTCAGGTAAAGGTCCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATAATTITGGAGGGATTGAAGGATA
NCOA	80	11	TGACGGGGCTTGTAGTCCCAGT	ATAGGAAATGGTGTAGTGT	ATAGGAAATGGTAGTGT	ATAGGAAATGGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGTATTITAGGAAATGGTGTAGTGT

Phasor Transform Expressions

The first-order phasor transform of the lifetime intensity photon histogram $I(t)$:

$$S = \frac{\int_0^T I(t) \sin(\omega t) dt}{\int_0^T I(t) dt} \quad (1)$$

$$G = \frac{\int_0^T I(t) \cos(\omega t) dt}{\int_0^T I(t) dt} \quad (2)$$

Where T is the period between excitation pulses (or modulation period), and $\omega = \frac{2\pi}{T}$ the pulsation frequency such that the period of trigonometric functions matches the excitation period T .

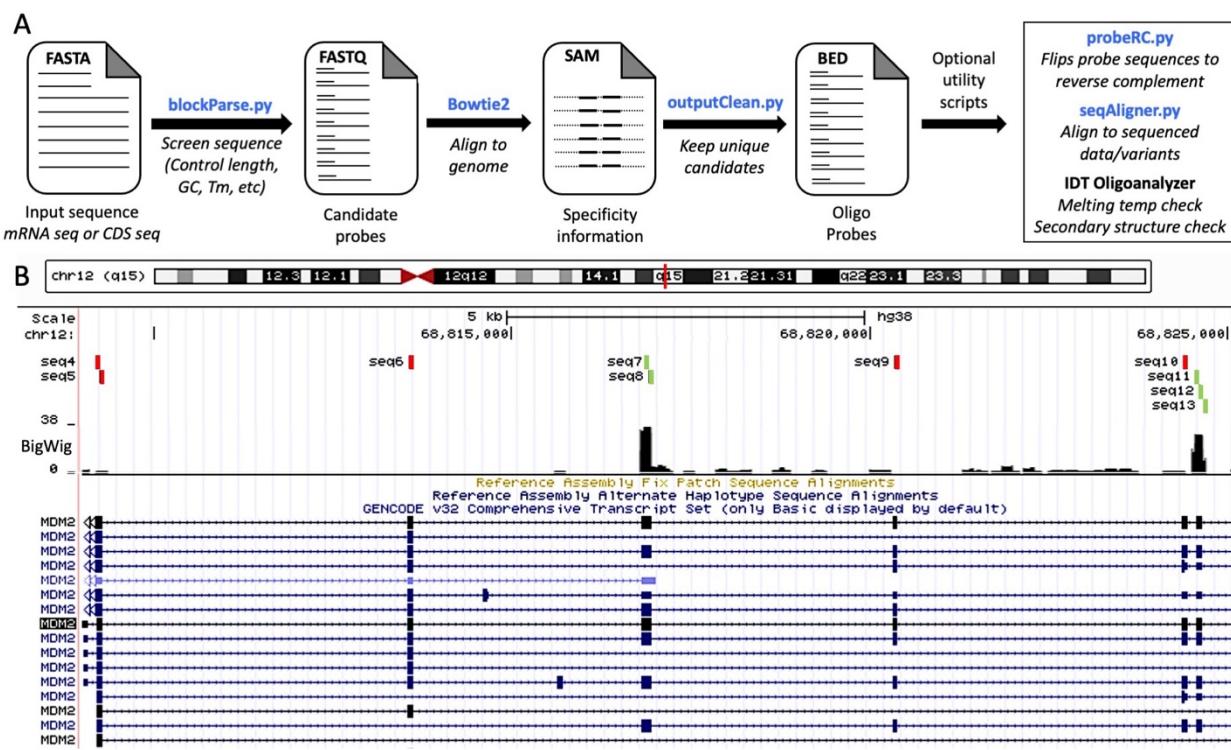
The first-order phasor transform of the spectral intensity photon histogram $I(\lambda)$:

$$S = \frac{\int_{\lambda_0}^{\lambda_f} I(\lambda) \sin(\omega\lambda - \omega\lambda_0) d\lambda}{\int_{\lambda_0}^{\lambda_f} I(\lambda) d\lambda} \quad (3)$$

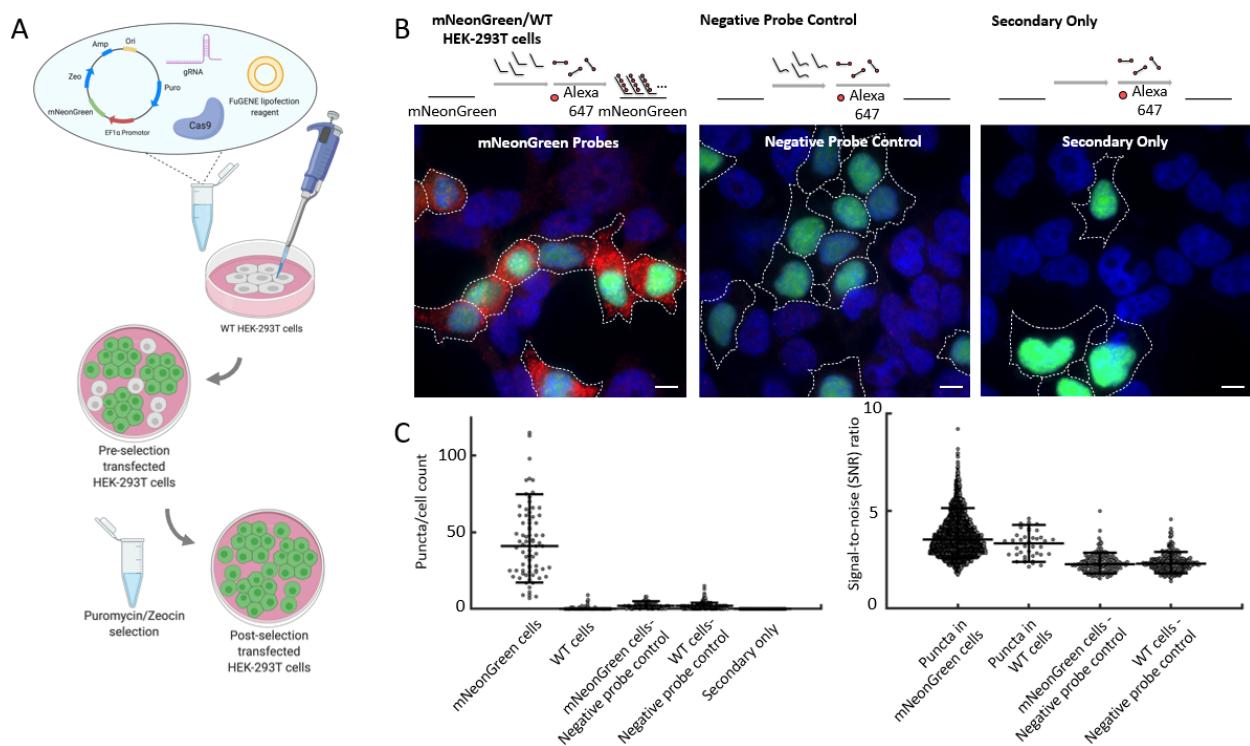
$$G = \frac{\int_{\lambda_0}^{\lambda_f} I(\lambda) \cos(\omega\lambda - \omega\lambda_0) d\lambda}{\int_{\lambda_0}^{\lambda_f} I(\lambda) d\lambda} \quad (4)$$

Where λ_0 and λ_f are the limits of the spectral band of the detector, and $\omega = \frac{2\pi}{\lambda_f - \lambda_0}$ the pulsation frequency such that the period of trigonometric functions matches the spectral bandwidth.

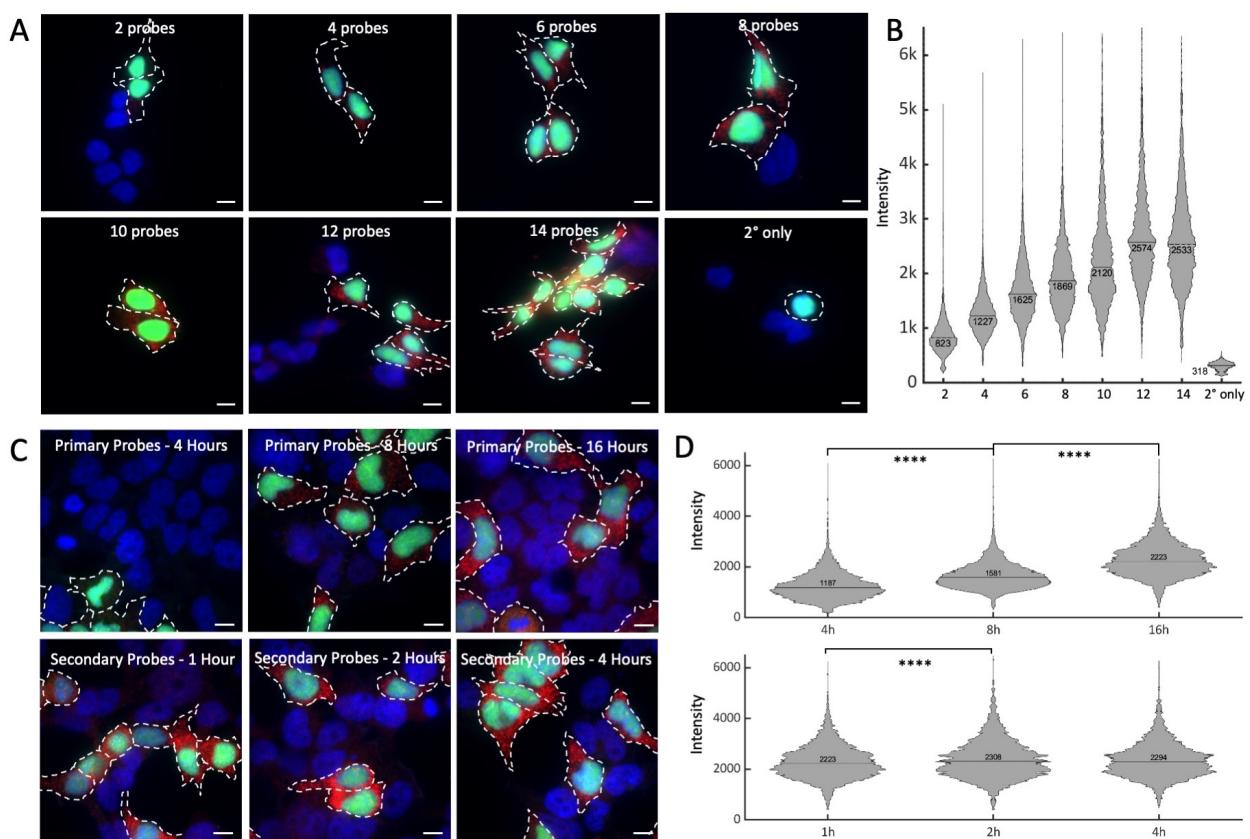
Figures



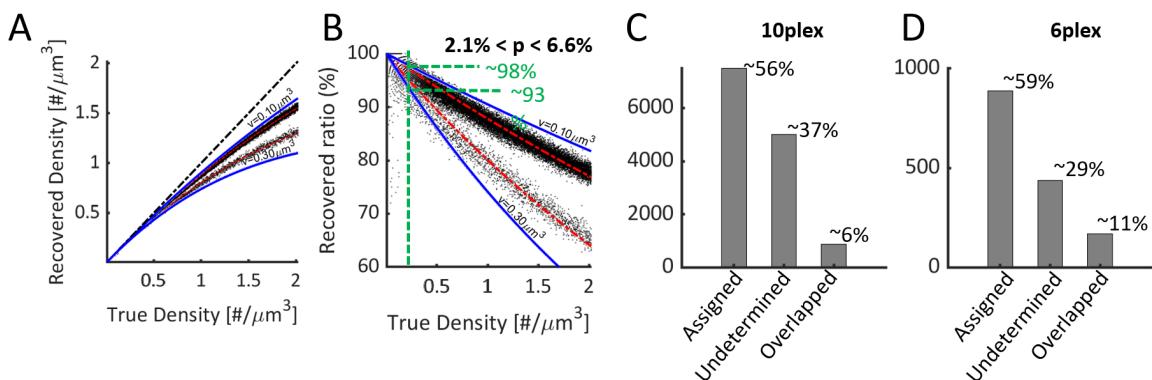
Supplementary Figure 1. Schematic overview of probe design process. A) A modified version of Oligominer was used to design primary probes. **B)** In the seqAligner.py script, the probes (labeled “seq#”) go through BLAT and are aligned to the RNA sequencing data, as seen on the UCSC Genome Browser. The BigWig browser track shows a histogram of the read counts and probes are aligned and compared to the read counts of the region they overlap with. Probes that overlapped with more than 5% of the highest read count were used (green) and those that aligned with regions considered as “low read count” (5% or less) were removed from the final probe list (red).



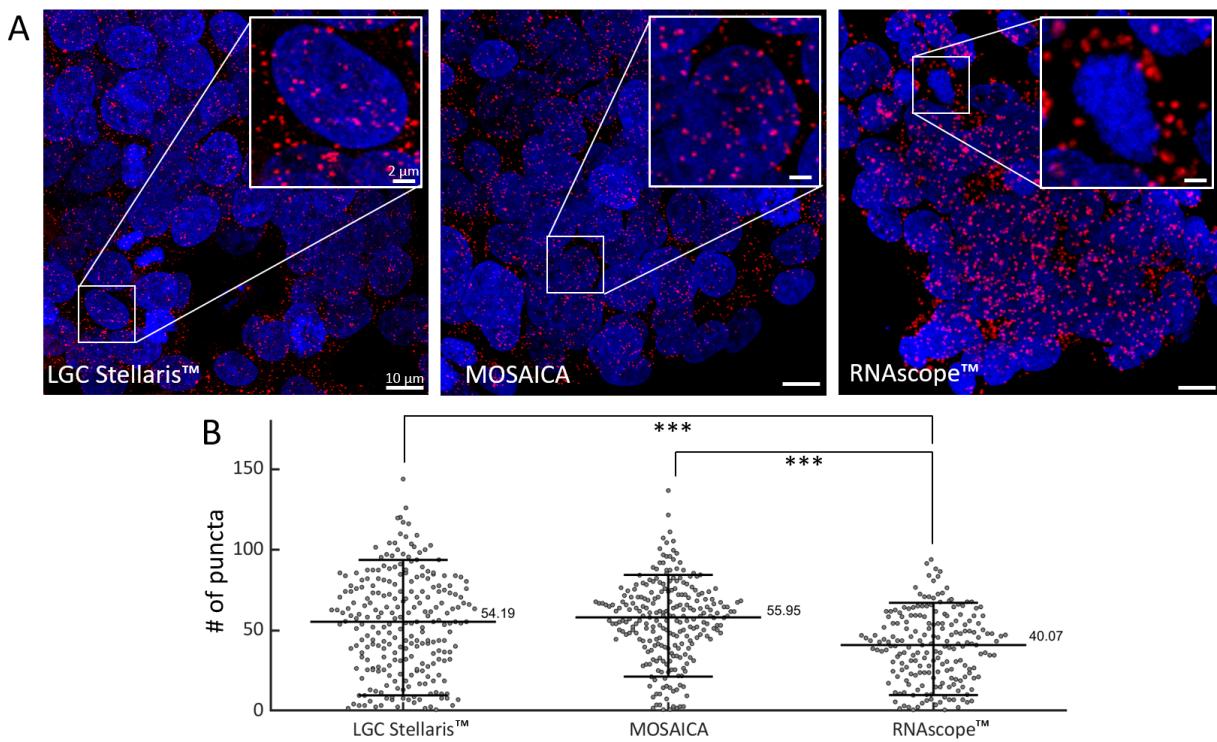
Supplementary Figure 2. Validation of probe hybridization in mNeonGreen cells. **A)** Schematic of engineering of mNeonGreen HEK293T-X cells. Engineered mNeonGreen plasmids were transfected into HEK293T-X cells with FuGENE HD Transfection Reagent. Three days after transfection, the cells were then selected with Puromycin and Zeocin. **B)** Schematic and representative images of each condition. The primary probes were designed to be complementary to mNeonGreen transcripts. A dopachrome tautomerase (DCT) primary probe negative control, which uses primary probes targeting sequences not present in the mNeonGreen HEK-293T-X cells but can still bind to secondary fluorescent oligonucleotides, was used to indicate any nonspecific binding which can occur with primary probe labeling. A negative control where only secondary probes were added but no primary probes were added was used as a reference for nonspecific binding from secondary probes alone. For each condition, the concentration of each primary probe (14 in total) was 1 nM and the secondary probe was 5 nM. Scale bar = 10 μ m. **C)** Plots to quantify the detected puncta per cell and signal-to-noise (SNR) ratio under different conditions. Left, scatter plot showing puncta number per cell ($n=755$ cells). Right, signal-to-noise ratio (SNR). SNR=each signal intensity/the mean of background noise ($n=3,860$ puncta).



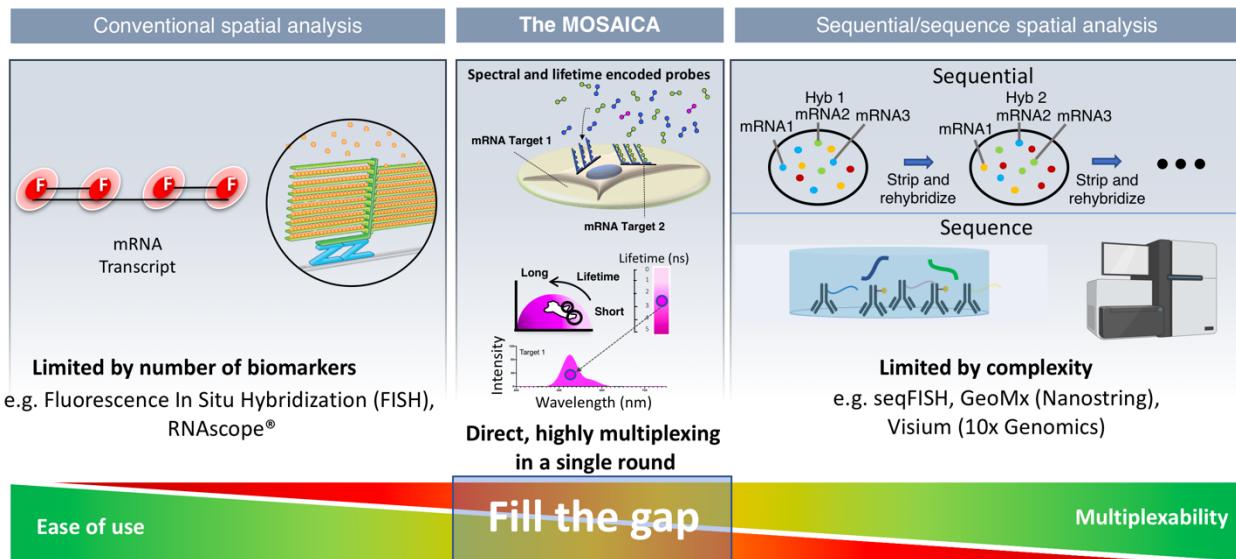
Supplementary Figure 3. Optimization parameters of in situ hybridization conditions. **A)** Representative images of mNeonGreen cells with different numbers of primary probes. Conditions included 2, 4, 6, 8, 10, 12, and 14 mNeonGreen primary probes to the HEK293T-X mNeonGreen and WT model. The concentration of each primary probe is constant (5 nM). Scale bars are 10 μ m. **B)** Intensity distribution of detected puncta shows the effects of the number of primary probes on signal intensity (total $n \approx 64k$ puncta). **C)** Representative images of mNeonGreen cells with different incubation time of probes. The primary probes hybridization incubation times consisted of 4, 8, and 16 hours. For secondary fluorophore probes, incubation times tested were 1, 2, and 4 hours. Scale bars are 10 μ m. **D)** Intensity distribution of detected puncta as a function of incubation time. Top, primary probe incubation time (total $n \approx 26k$ puncta). Bottom, secondary probe incubation time (total $n \approx 20k$ puncta). Pairwise t-test resulted in p -values $<10^4$ for conditions marked with ***.



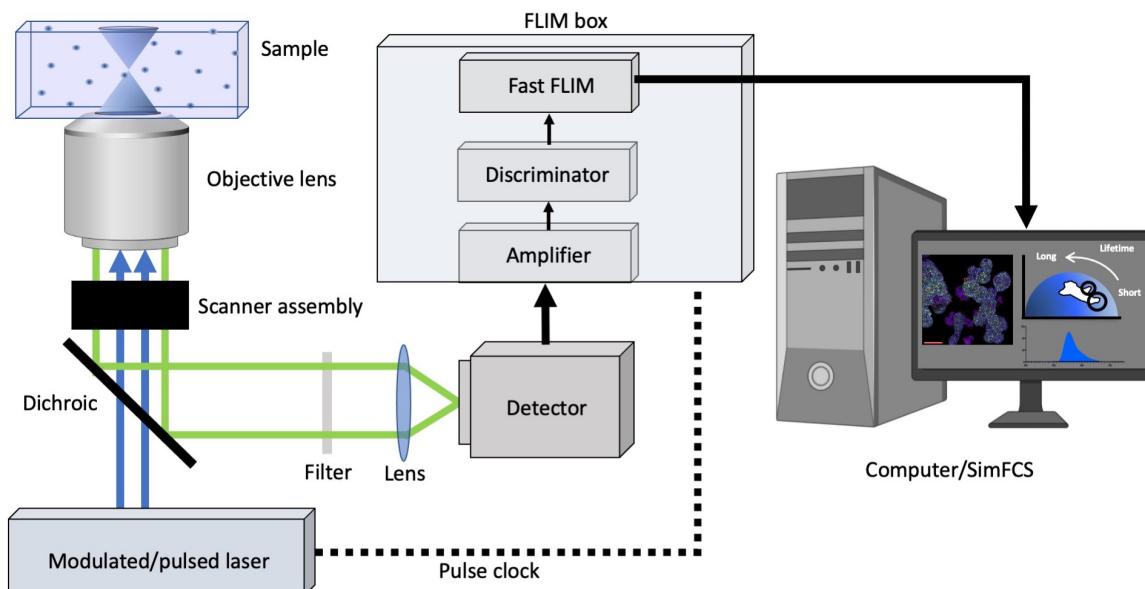
Supplementary Figure 4. Overlapping and inconsistent signal simulations. Simulations are run at different densities to generate 3D image stacks and puncta are detected using our image processing pipeline. **A)** Recovered density by our system as a function of the true density for the limit considered puncta volumes (blue) and simulation trends (top trend for 1plex bottom trend for 10-plex). **B)** Percentage of recovered puncta for the 1plex (top trend, depicting ratio of underestimated due to overlap) and 10-plex (bottom trend, depicting ratio of inconsistent signal due to overlap), again between the limit considered puncta volumes (blue). **C,D)** Number of puncta assigned to a particular gene, undetermined puncta and overlapped puncta for the 10-plex experiment (Figure 4 in the paper) and 6-plex experiment (Figure 5 in the paper).



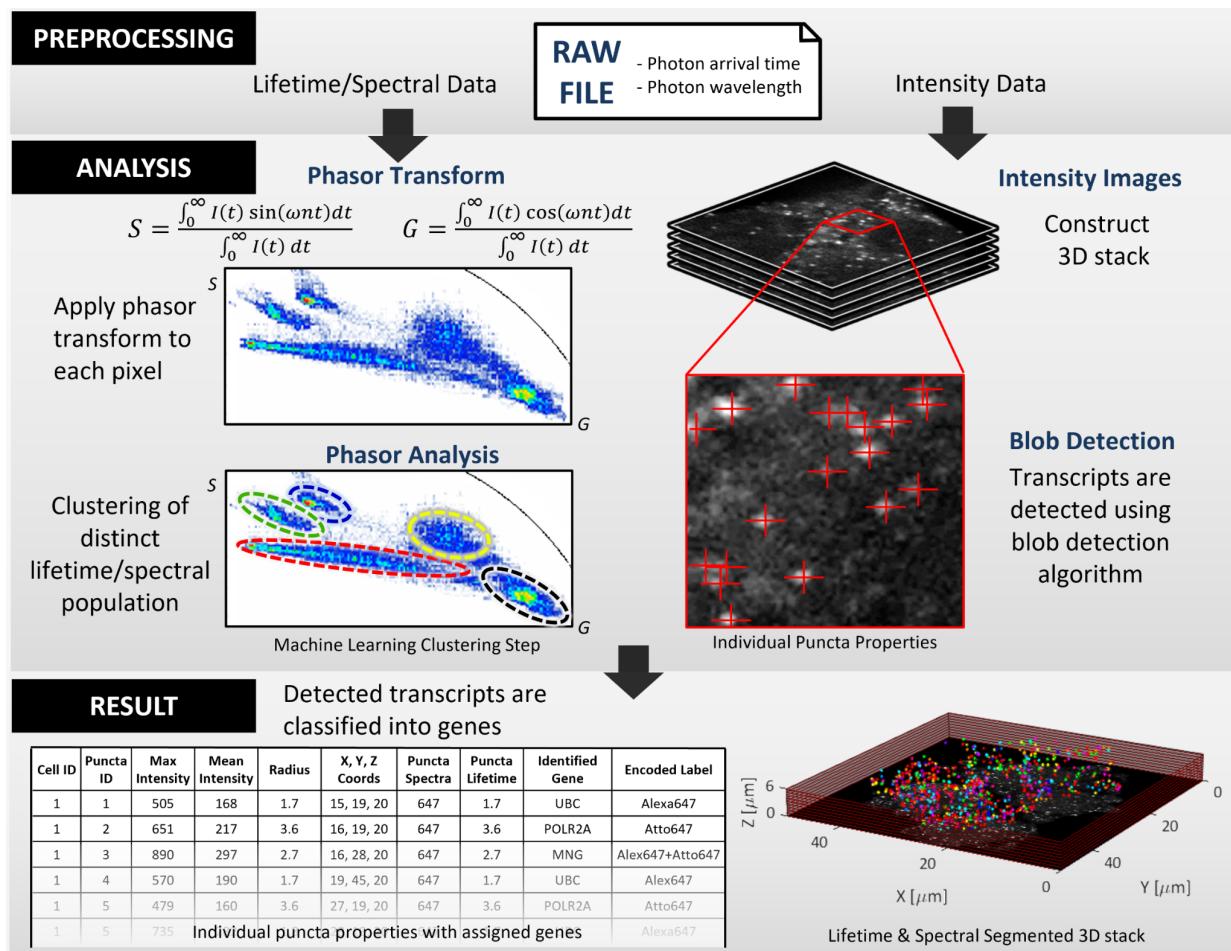
Supplementary Figure 5. Benchmarking MOSAICA against RNAscope™ and LGC Stellaris™. **A)** POLR2A gene expression on colorectal cancer SW480 cells following RNAscope™, LGC Stellaris™ and MOSAICA protocols. Scale bars are 10 μm . **B)** Puncta counts per cell volume between three platforms. MOSAICA exhibited comparable puncta per cell count compared to benchmark LGC Stellaris™, whereas RNAscope™ was undercount. Pairwise t-test against null hypothesis that values belong to distributions of equal means were $p = 0.4$ (LGC Stellaris™ vs MOSAICA), $p = 3.4 \times 10^{-4}$ (LGC Stellaris™ vs RNAscope™) and $p = 7.8 \times 10^{-4}$ (MOSAICA vs RNAscope™). A sliding volume of $3000 \mu\text{m}^3$ was used throughout the image stacks and the number of puncta counts per volume was obtained. This number was then divided into the average number of cells per volume depending on the 3D segmentation of DAPI nuclei.



Supplementary Figure 6. Multiplexed spatial transcriptomics with MOSAICA, which is rapid, cost-effective, and easy-to-use, can fill a critical gap between conventional FISH and sequential- and sequencing-based techniques.



Supplementary Figure 7. Generalized spectral-FLIM Microscopy setup. A pulsed/modulated light source is used to illuminate the sample and the fluorescence of the sample is collected by a spectral detector (current resolution around 10 nm). The repetition rate can either be supplied by or delivered to the laser which is used by the electronics in the digital frequency domain to obtain a single photon arrival time using the heterodyne principle (current resolution around 50 ps)



Supplementary Figure 8. Automated pipeline of the processing and analysis. Raw data consists of a list of detected photons with their times of arrivals. Using the acquisition parameters, dwell time, number of pixels, number of repetitions per image etc. the image stacks are reconstructed. Knowing the laser frequency, a photon histogram for each voxel is built and the phasor transform is applied. The two custom made algorithms work in parallel, one identifying clusters in the phasor space, the other identifying puncta in the intensity space. The two then recombine to result in each transcript being identified, assigned to a particular gene and its morphological properties measured.