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PRINCIPAL INVESTIGATORS: Philip W. Kantoff, MD

CONTRACTING ORGANIZATION: Sloan Kettering Institute for Cancer
Research.
New York, NY 10065

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14. ABSTRACT Mortality from prostate cancer (PC), an estimated 30,000 deaths in 2019, is associated with development of aggressive and treatment-insensitive metastatic castration-resistant prostate cancer (mCRPC). We will investigate the status and role of Y chromosome (ChrY) genes in regulating drug sensitivity and mCRPC development and progression. Though ChrY loss in men is associated with increased risk of disease and mortality, the role of ChrY genes in regulating PC progression is poorly understood. To investigate the clinical impact of ChrY gene expression, we developed new methodology to analyze mutational variants of ChrY genes in PC patient cohorts, previously unsuccessful due to the high number of repetitive sequences and paralog families. Using a custom reference for each paralog family, our method increased ChrY read depth coverage to be on par with whole-exome sequencing allowing for normal/tumor variant calling. We also generated the first CRISPR/Cas9 library targeting human ChrY to further understand the role of individual ChrY genes in regulating antiandrogen treatment sensitivity and mCRPC development in PC models in vitro and in vivo. This multifaceted approach will potentially identify predictive markers for treatment sensitivity based on ChrY. These markers will allow for development of tailored therapies and serve as targets for drug development.					
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MUTATIONAL LANDSCAPE OF THE Y CHROMOSOME AND PROSTATE CANCER

1. INTRODUCTION

Prostate cancer (PC) is the most common cancer and leading cause of death among men in the United States with an estimated 30,000 deaths in 2019. PC associated mortality is attributed to the development of metastatic castration-resistant prostate cancer (mCRPC) which is characterized by its aggressiveness and poor response to treatment. Though loss of the Y chromosome (ChrY) in men has been associated with increased risk of disease and mortality, the role of ChrY genes in disease progression is poorly understood.¹⁻³ Our team presented the first report of a ChrY gene, *KDM5D*, which regulates tumor growth and docetaxel sensitivity through epigenetic modification of key cell cycle regulators and androgen receptor signaling.^{4,5} The study also reported the loss of *KDM5D* to be associated with increased mortality and aggressive disease in patient cohorts suggesting its role as a potential biomarker for mCRPC. Together, these studies highlight the urgency to further explore the role of ChrY genes in PC progression and further determine its mutational landscape to develop therapeutic targets as well as biomarkers and gene expression signatures which will allow physicians to predict drug response in patients and thereby prescribe effective treatment regimens. This multidisciplinary approach will facilitate determination of the clinical impact of ChrY genes on PC progression and treatment resistance.

2. KEYWORDS

Prostate cancer, metastatic castration-resistant prostate cancer, Y chromosome, antiandrogen therapy, drug insensitivity, docetaxel, epigenetics, biomarkers, tumor suppressor, precision medicine, mutations, CRISPR/Cas9 library screening

3. ACCOMPLISHMENTS

What were the major goals of the project?

The major goals of the project as outlined in the SOW are:

SPECIFIC AIM 1: To determine the mutational landscape of the Y chromosome (ChrY) in men with prostate cancer in the SU2C/PCF, TCGA, and other cohorts

Major Task 1: Structural analysis of the Y chromosome (ChrY). This goal is 10% complete, in accordance with the SOW (1–36 months, responsible PIs and sites: Schultz, MSK; Van Allen, DFCI).

Major Task 1, Subtask 1: Identify the samples with ChrY loss. This goal is 10% complete, in accordance with the SOW (1–36 months, responsible PIs and sites: Schultz, MSK; Van Allen, DFCI).

Major Task 1, Subtask 2: Quantify the focality of ChrY loss. This goal is 10% complete, in accordance with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 1, Subtask 3: Assess mutual exclusivity of ChrY loss with genomic lesions in prostate cancer pathways. This goal is 0% complete. Work will begin in month 18 which is in line with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 1, Milestones: Define the extent of ChrY loss in metastatic prostate cancer and evaluate the association with clinically actionable signaling pathways. This goal is 10% complete, in accordance with the SOW (At 36 months).

Major Task 2: Determine functional features associated with ChrY mutations. This goal is 20% complete, in accordance with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 2, Subtask 1: Identify the putative tumor suppressors that are inactivated on ChrY. This goal is 30% complete, in accordance with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 2, Subtask 2: Assess differential AR activity between samples that show ChrY loss and samples without alterations on ChrY. This goal is 10% complete, in accordance with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 2, Subtask 3: Correlation of ChrY loss with Gleason score and sample type. This goal is 10% complete, in accordance with the SOW (1–36 months, responsible PI and site: Schultz, MSK).

Major Task 2, Milestones: Define the mutational landscape of ChrY and determine if the LOY is significantly associated with disease risk. This goal is 20% complete, in accordance with the SOW (At 36 months).

SPECIFIC AIM 2: To perform genetic screening by CRISPR to identify ChrY genes that are of importance in the development of castration-resistant prostate cancer (CRPC) or resistance to androgen receptor (AR)–targeted therapies.

Major Task 3: Forward genetic screening of ChrY genes. This goal is 20% complete, in accordance with the SOW (1–12 months, responsible PIs and sites: Kantoff and Schultz, MSK).

Major Task 3, Subtask 1: Establish barcoded cell line model systems. Cell lines used: LNCaP, VCaP, LAPC4, LNCaP-Abl, and RWPE-1 (Kantoff Lab). This goal is 50% complete, in accordance with the SOW (1–12 months, responsible PI and site: Kantoff, MSK).

Major Task 3, Subtask 2: Construct and optimize ChrY CRISPR/Cas9 library. This goal is 50% complete, in accordance with the SOW (1–12 months, responsible PI and site: Kantoff, MSK).

Major Task 3, Subtask 3: Screening of ChrY CRISPR/Cas9 library. Cell lines used: LNCaP, VCaP, LAPC4, LNCaP-Abl, and RWPE-1 (Kantoff Lab). This goal is 0% complete.

Work will begin in month 12 which is in line with the SOW (1–24 months, responsible PI and site: Kantoff, MSK).

Major Task 3, Subtask 4: Sequencing analysis of sgRNAs and barcodes to identify target genes. This goal is 0% complete. Work will begin in month 12 which is in line with the SOW (1–24 months, responsible PIs and sites: Kantoff and Schultz, MSK).

Major Task 3, Milestones: Identify ChrY candidate genes that are of importance for development of CRPC and drug resistance and generate hypothetical models for further functional validations. This goal is 20% complete, in accordance with the SOW (At 24 months).

SPECIFIC AIM 3: To characterize the functional significance of genes involved in resistance in cell culture and animal models. We will confirm the functional importance of *KDM5D* and *UTY* in progression to CRPC. The clinical significance of these genes will be corroborated with an evaluation of the ChrY landscape in prostate cancer specimens.

Major Task 4: Perform functional validation of candidate genes including *KDM5D* and *UTY* in cell line models. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (1–36 months, responsible PIs and sites: Kantoff and Schultz, MSK; Gerke, MCC).

Major Task 4, Subtask 1: Apply specific gene silencing and/or over-expression (as relevant) in a broader panel of prostate cancer cell lines to assess the impact of the expression of a specific candidate gene on cell growth, invasiveness, and drug sensitivities with or without androgen treatment. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (1–36 months, responsible PI and site: Kantoff, MSK).

Major Task 4, Subtask 2: To identify the pathways/mechanisms that a specific gene involved in leading to the observed phenotypes by RNA-seq, ChIP-seq, or phospho-kinase screening. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (1–36 months, responsible PIs and sites: Kantoff and Schultz, MSK).

Major Task 4, Milestones: Determine molecular mechanisms/pathways underpinning the involvement of ChrY genes in prostate cancer progression. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (At 36 months).

Major Task 5: Perform functional validation of candidate genes in mouse xenograft model. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (1–36 months, responsible PI and site: Kantoff, MSK).

Major Task 5, Subtask 1: Generate mouse xenografts using stable cell lines with inducible knockdown or overexpression of candidate genes. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (1–36 months, responsible PI and site: Kantoff, MSK).

Major Task 5, Subtask 2: Treat mouse xenografts with drug or vehicle and measure tumors. 10 NOD/SCID IL-2 gamma null mice will be used in each experimental or control arm [10 mice per group X 2 groups = 20 mice per experiment]; the number of experiments will be determined by the number of candidate genes identified in Specific Aim 2. This goal is 0% complete. Work will begin in month 24, which is in line the SOW (1–36 months, responsible PI and site: Kantoff, MSK).

Major Task 5, Milestones: Determine the impact of gain and loss of a specific candidate gene on tumor growth in the absence of androgen or in response to a specific drug treatment in vivo. This goal is 0% complete. Work will begin in month 24 which is in line with the SOW (At 36 months).

Major Task 6: Clinical validation of the role of target genes on PC progression within PC cohorts. This goal is 0% complete. Work will begin in month 12 which is in line with the SOW (12–36 months, responsible PIs and sites: Kantoff and Schultz, MSK; Gerke, MCC).

Major Task 6, Subtask 1: Assess the clinical impact of *KDM5D* and *UTY* expression on prostate cancer outcomes in four different cohorts. This goal is 0% complete. Work will begin in month 12, which is in line with the SOW (12–24 months, responsible PIs and sites: Kantoff and Schultz, MSK; Gerke, MCC).

Major Task 6, Subtask 2: Validate the clinical impact of newly identified target genes on prostate cancer outcomes in four different cohorts. This goal is 0% complete. Work will begin in month 12 which is in line with the SOW (24–36 months, responsible PIs and sites: Kantoff and Schultz, MSK; Gerke, MCC).

Major Task 6, Milestones: Characterization of ChrY-associated genes that impact prostate cancer clinical outcome in the context of treatment with androgen deprivation therapy or AR-targeted drugs. This goal is 0% complete. Work will begin in month 12 which is in line with the SOW (At 36 months).

What was accomplished under these goals?

Major progress has been made towards the aims outlined in the original application following the timeline indicated in the SOW.

SPECIFIC AIM 1: To determine the mutational landscape of the Y chromosome (ChrY) in men with prostate cancer in the SU2C/PCF, TCGA, and other cohorts

Major Activities

The landscape of somatic copy-number alteration and somatic mutation of the ChrY in prostate cancer were supervised by the Schultz and Van Allen groups at Memorial Sloan Kettering Cancer Center (MSK) and Dana-Farber Cancer Institute (DFCI), respectively. Due to the presence of numerous paralogs and pseudogenes, somatic variant calling of most ChrY genes is challenging. To circumvent this problem, we have developed a new method to specifically call mutations in these genes. We have completed somatic mutation calling in ChrY in prostate cancer from The Cancer Genome Atlas (TCGA). The same methodology will be applied in other datasets such as the Stand Up To Cancer/Prostate Cancer Foundation Dream Team “Precision Therapy for Advanced Prostate Cancer” (SU2C/PCF) data.

Specific Objectives

The specific objectives proposed in the SOW were to: 1) identify the samples with ChrY loss; 2) quantify the focality of ChrY loss; 3) assess mutual exclusivity of ChrY loss with genomic lesions in prostate cancer pathways; 4) identify the putative tumor suppressors that are inactivated on ChrY; 5) assess differential androgen receptor (AR) activity between samples that show ChrY loss and samples without alterations on ChrY; 6) correlate ChrY alterations with Gleason score and sample type; 7) define the mutational landscape of ChrY and determine if the loss of ChrY is significantly associated with disease risk.

Significant Results or Key Outcomes

In a first attempt of reporting the mutational landscape of the ChrY in prostate cancer, we have performed all current analysis using the TCGA dataset and developed a new method to specifically call mutations in paralogs that are known to be difficult to analyze. This proof of concept will be applied to the SU2C-PCF cohort that includes 444 mCRPC patients with available whole-exome sequencing of tumor/normal pairs samples.

From the 498 patients with available tumor/normal pairs in the TCGA cohort, we excluded patients with metastasis sample only and patients with available normal tissues other than blood. A total of 426 patients were included in the subsequent analysis. First, we investigated the mutational status of the 44 reported protein-coding genes present in ChrY and found 11 non-silent mutations in 6 genes (**Figure 1**). The top ChrY mutated gene was *PCDH11Y* (n=5, 1.2%) followed by *KDM5D* (n=2, 0.5%). A total of 11 patients (2.6%) had at least one non-silent mutation.

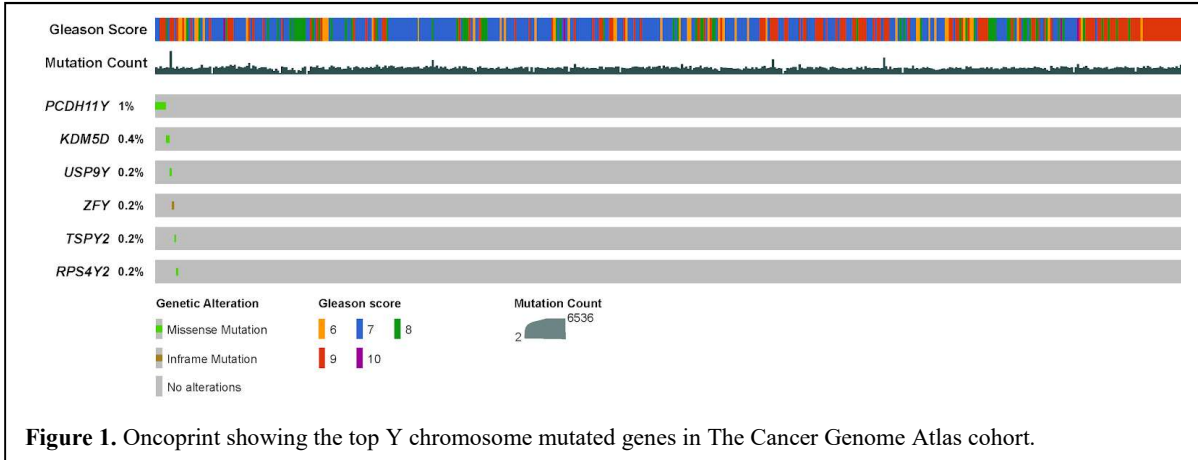
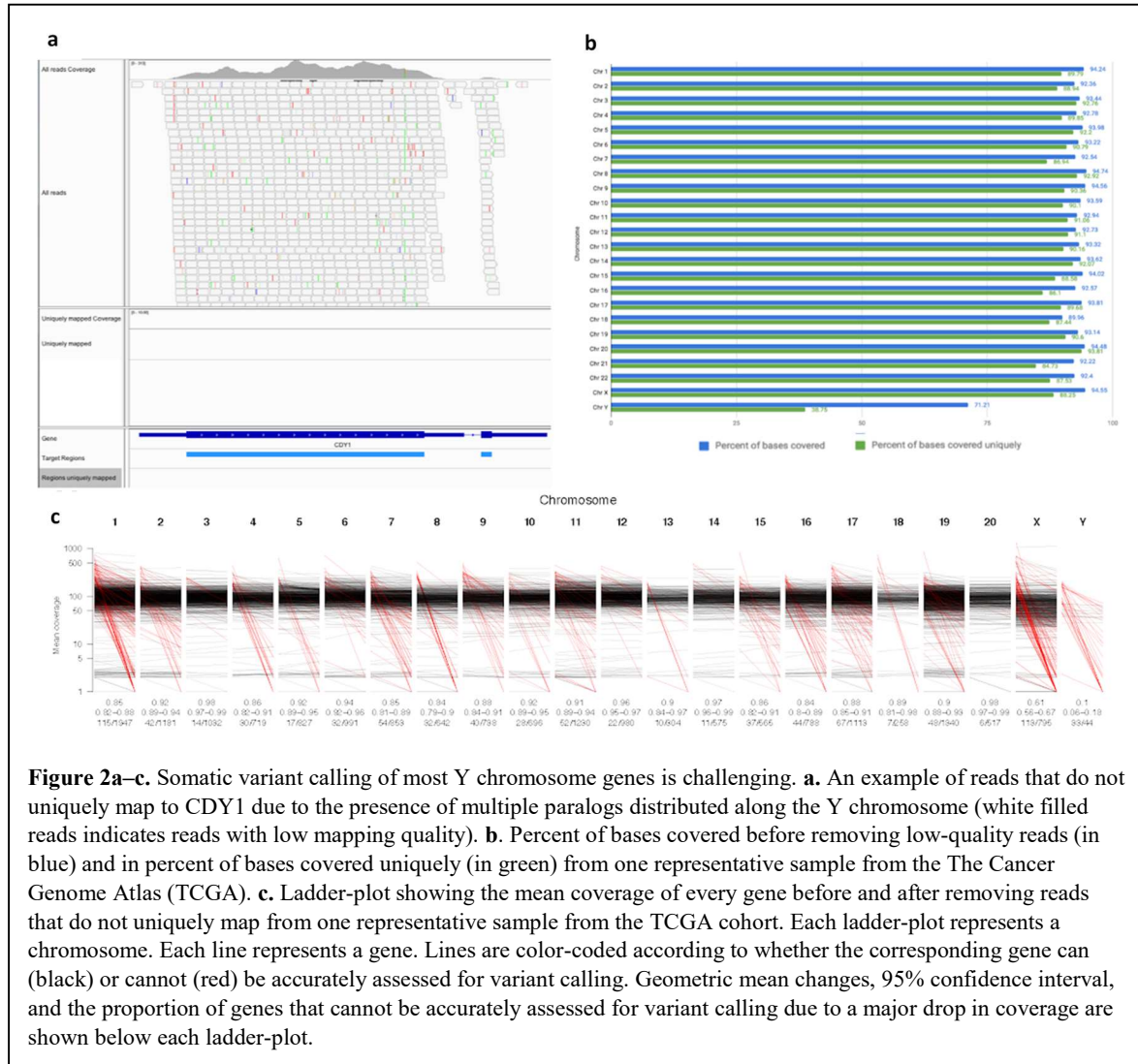
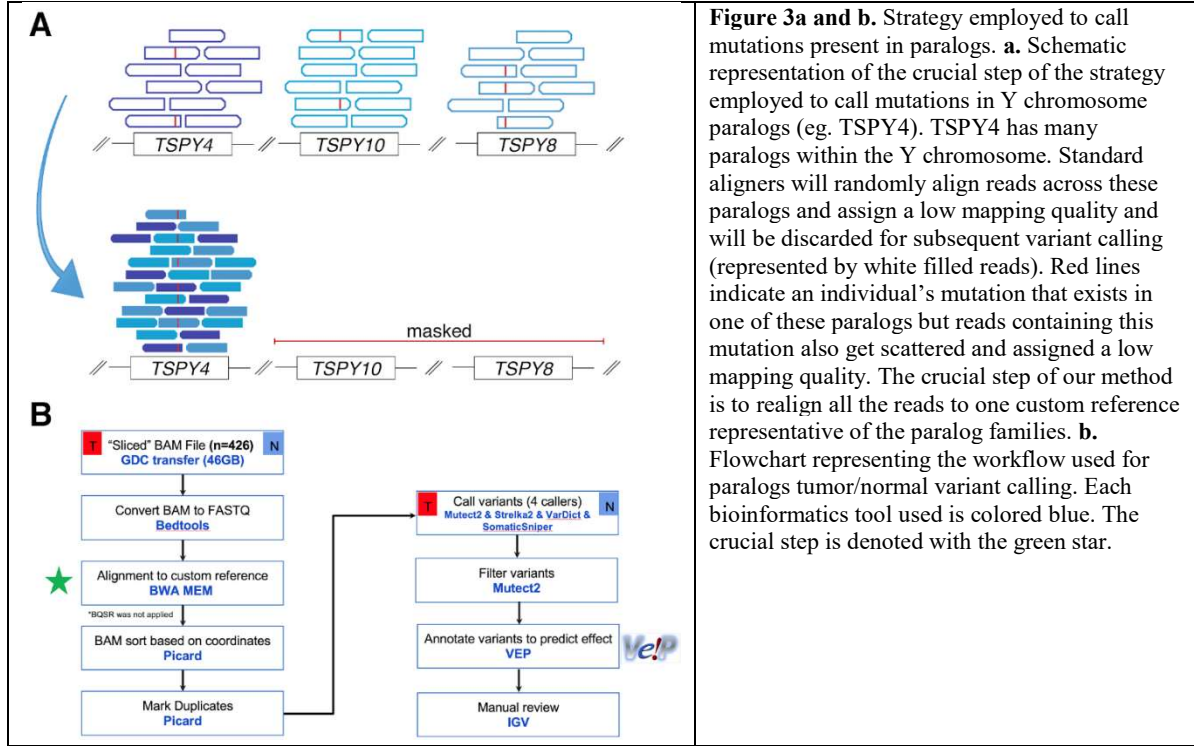


Figure 1. Oncoprint showing the top Y chromosome mutated genes in The Cancer Genome Atlas cohort.

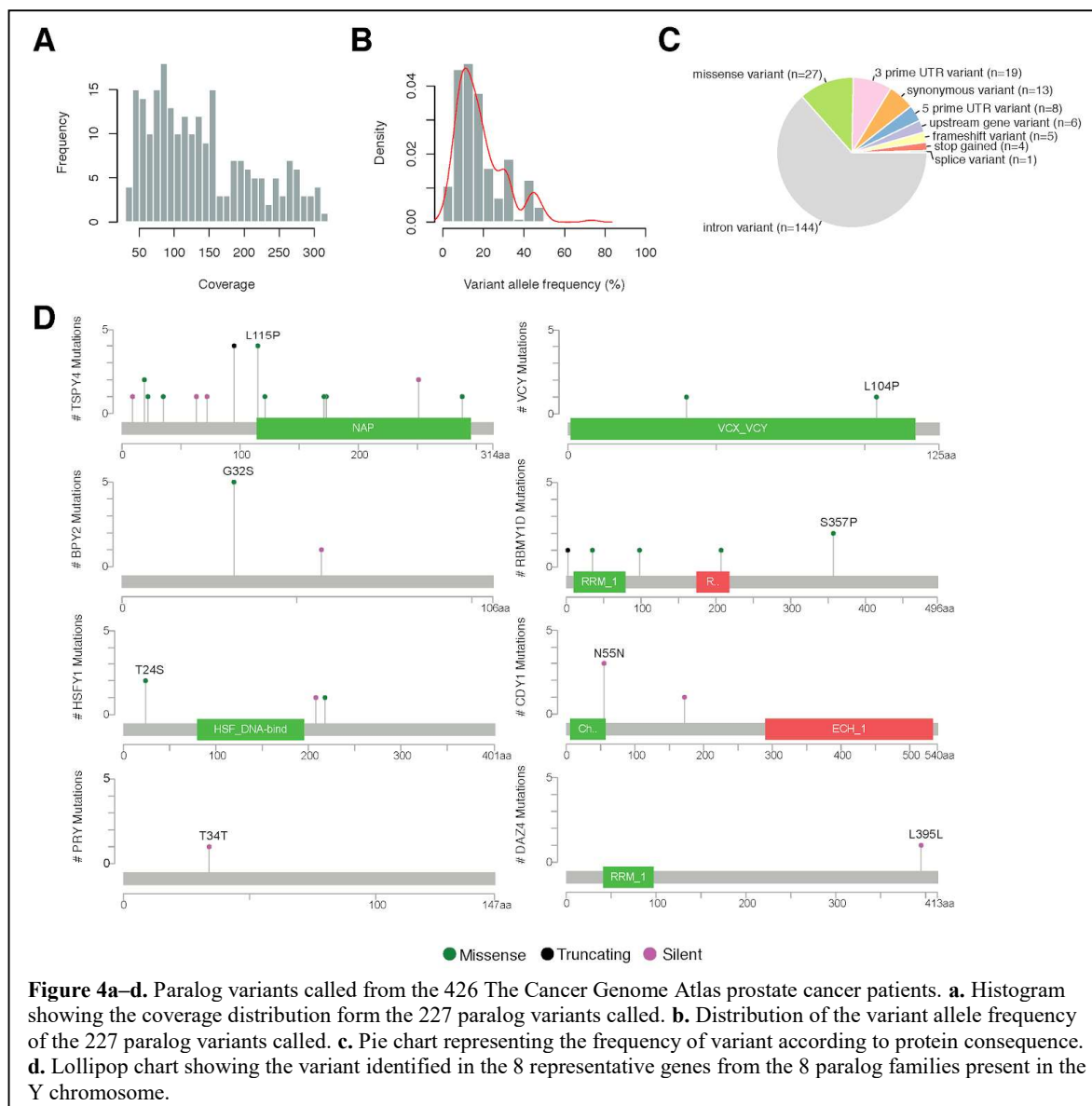
Among the 44 reported genes in the ChrY, 29 belong to a paralog family. From the six mutated genes, only one belongs to a paralog family (*TSPY2*), which was lower than expected by chance ($p = 0.018$, Monte-Carlo test). The numerous ChrY genes belonging to paralog families are known to be challenging for aligning with the use of short-read sequencing technologies. Many genes in the human genome were duplicated during evolution and are still transcriptionally and translationally active. These duplicated regions distributed along the genome pose a problem for short-reads alignment. For example, the ChrY gene *CDY1* has 99% homology with *CDY1B*, *CDY2A*, and *CDY2B* making variant calling impossible (**Figure 2a**). We first sought to investigate the extent of the problem at the nucleotide and gene level across chromosomes. As shown in **Figure 2b and c**, ChrY is the

most impacted by the drop in coverage due to non-uniquely mapped reads. Only approximately 38% of the ChrY region is covered uniquely, making variant calling problematic as aligners will map the read randomly to one of these regions and the mapping quality (MAPQ) of the read will be assigned as 0, which are then ignored by mappers. To avoid this problem, we have developed a new method to specifically call mutations in paralogs. Briefly, for each paralog family, we realigned the reads using a custom reference, which is the longest representative gene from its paralog family while masking the other genes of the family (**Figure 3**).





In ChrY, there are eight paralog families representing a total of 29 genes. For each family, we selected eight representative genes and employed our tailored strategy for variant calling. After filtering the variants that passed, we retrieved a total of 227 paralog variants (**Figure 4**). The observed read depth coverage and the variant allele frequency distribution was in the range of whole-exome sequencing technologies (**Figure 4a and b**). We found a majority of intronic variant in RBMY1D ($n = 73$) and TSPY4 ($n = 42$) that include large intronic regions (**Figure 4c**). We found 27 missense variants and 9 truncating variants in 34 patients (34/426, 8%), two of which were previously identified bringing the total number of patients with ChrY mutations to 43 (43/426, 10%). Of note, we found several hotspot mutations (defined as present in at least two patients) in TSPY4, BPY2, RBMY1D, HSFY1, and CDY1 as shown in the lollipop charts (**Figure 4d**).



The comparison between patients with or without ChrY mutations is ongoing and the same strategy will be applied in the metastatic setting in the SU2C-PCF dataset.

Other Achievements

In order to determine copy-number alterations in prostate cancer, we plan to use the FACETS method. Our laboratory spent the last year getting familiar with the method, and we are now ready to start using it on multiple prostate cancer data sets, including those from MSK, TCGA, and PCF/SU2C.

SPECIFIC AIM 2: To perform genetic screening by CRISPR to identify ChrY genes that are of importance in the development of castration-resistant prostate cancer (CRPC) or resistance to androgen receptor (AR)–targeted therapies.

Major Activities

Genetic screening by CRISPR will be conducted in the Kantoff group at MSK. As proposed in the SOW, we have completed design and generation of the ChrY CRISPR/Cas9 library. Optimization of library infection in target cell lines is underway.

Specific Objectives

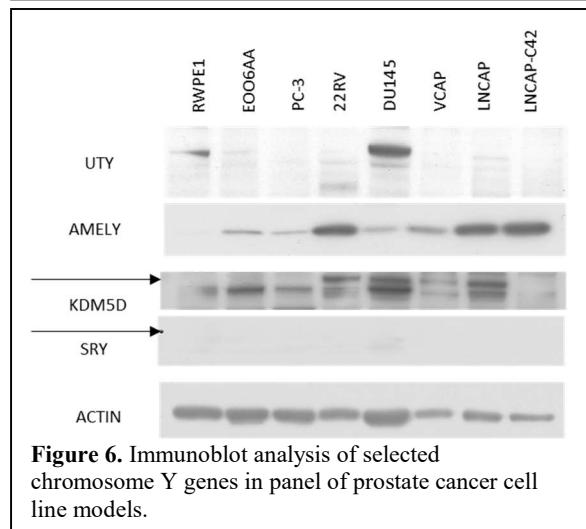
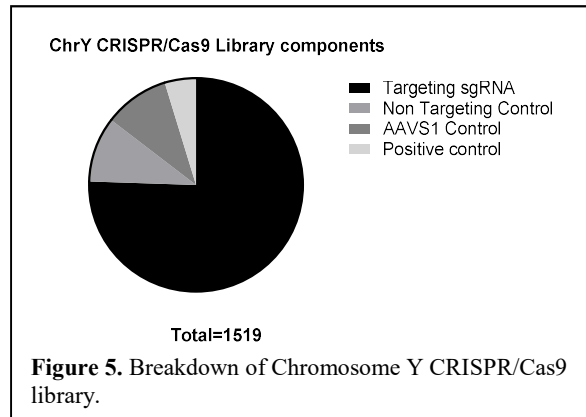
The objectives proposed in the SOW were to: 1) establish barcoded cell line model systems; 2) design and construct ChrY CRISPR/Cas9 library; 3) optimize the CRISPR/Cas9 library in target cell lines; and 4) conduct positive selection screens with the ChrY CRISPR/Cas9 library to identify genes responsible for mCRPC development and antiandrogen resistance.

Significant Results or Key Outcomes

We have successfully generated a ChrY CRISPR/Cas9 library. The pooled library is constructed to be used in a lentiviral system allowing high transduction efficiency. The library (attached as Appendix 1) contains 4 sgRNAs/gene and targets 45 protein coding genes, 53 non-coding genes, and 188 pseudogenes. In addition, we have included 150 Adeno-Associated Virus Integration Site 1 (AASVI) controls, 150 negative controls, and 72 positive controls resulting in a total of 1,519 sgRNAs (**Figure 5**). This pool will allow us to effectively analyze the impact of loss of ChrY genes, including non-coding and pseudogenes, in subsequent screens to identify regulators of drug sensitivity and mCRPC disease progression. We will optimize the library in target cell lines (LNCaP, VCaP, LAPC4, LNCaP-Abl, and RWPE-1) followed by positive genetic screens to identify regulators of antiandrogen therapy resistance.

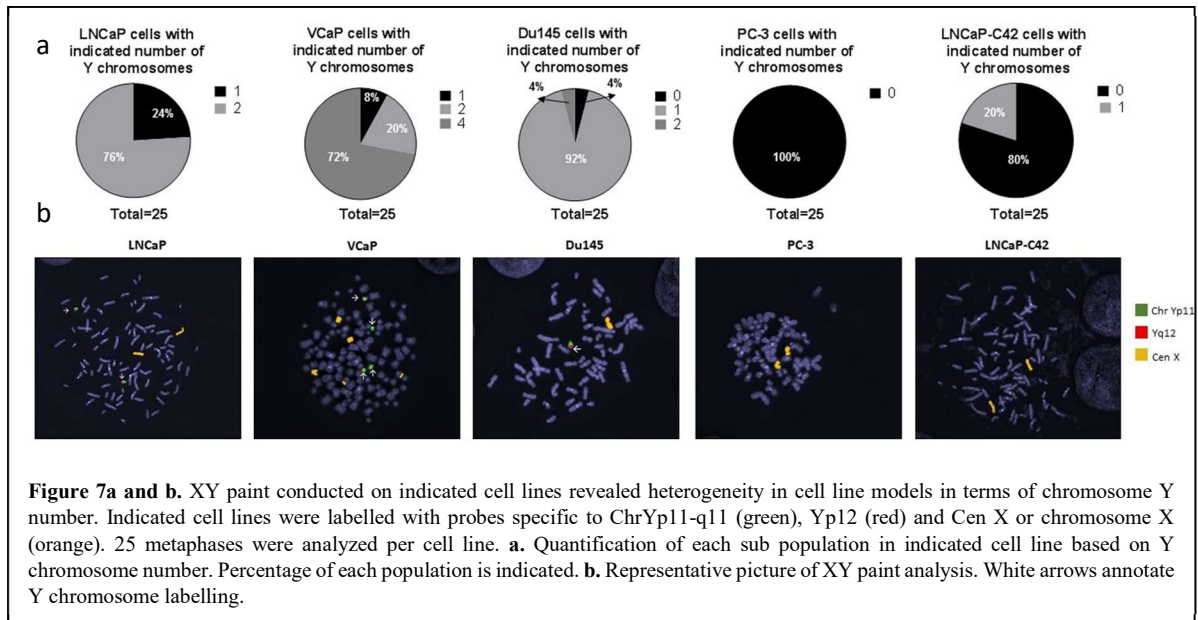
Other Achievements

To assess baseline expression of ChrY genes, immunoblotting of selected genes (*Sry* and *Amely* located on p-arm, *Uty* and *Kdm5d* located on q arm) was conducted in a panel of PC cell lines (**Figure 6**). Minimal expression of ChrY genes was detected in cell lines lacking ChrY: PC-3 and E006AA. The analysis provided an understanding of basal expression of ChrY genes in cell line model



systems. The target cell lines LNCaP-Abl and LAPC4 will be added to the analysis during the next reporting period.

Spectral karyotyping was performed on target cell lines to determine the status of X and Y chromosomes. Whole chromosome fluorescence in situ hybridization (FISH) probes were used to successfully label X and Y chromosomes, also called XY paint. As shown in **Figure 7a-b**, this allowed quantification of the heterogeneity in cell line models in terms of ChrY number. The target cell lines LNCaP-Abl, LAPC4, and RWPE-1 will be added to the analysis during the next reporting period.



SPECIFIC AIM 3: To characterize the functional significance of genes involved in resistance in cell culture and animal models. We will confirm the functional importance of *KDM5D* and *UTY* in progression to CRPC. The clinical significance of these genes will be corroborated with an evaluation of the ChrY landscape in PC specimens.

Major Activities

As per the timeline in the SOW, work on Specific aim 3 will begin in month 24 following identification of candidate genes from Specific aim 2.

Specific Objectives

The specific objectives described in the SOW were to: 1) Perform functional validation of candidate genes including *KDM5D* and *UTY* in cell lines models; 2) identify pathways/mechanisms that a specific gene is involved in leading to the observed phenotype by RNA-seq, CHIP-seq, or phosphor-kinase screening; 3) generate mouse xenografts using stable cell lines with inducible knockdown or overexpression of candidate genes and treat them with drug or vehicle to measure tumors followed by molecular characterization, and 4) assess the clinical impact of *KDM5D*, *UTY*, and candidate gene expression on PC outcomes in clinical datasets from the following patient cohorts: SUC2/PCF cohort, TCGA cohort, Harvard Prostate Tumor cohorts (Health Professionals Follow-Up and Physician's Health

Studies), and Specialized Programs of Research Excellence (SPOR) in Prostate Cancer Biorepository, and Clinical Research Information System (CRIS) database at Dana-Farber Cancer Institute.

Significant Results or Key Outcomes

Nothing to report.

Other Achievements

Nothing to report.

What opportunities for training and professional development has the project provided?

Nothing to report.

How were the results disseminated to communities of interest?

Nothing to report.

What do you plan to do during the next reporting period to accomplish the goals?

The project is currently underway in accordance with the timeline outlined in the SOW. Barcoded cell line models will be established to track subpopulations and model heterogeneity during the development of antiandrogen resistance.

The ChrY CRISPR/Cas9 library has been generated. We will optimize the library in target cell lines (LNCaP, VCaP, LAPC4, LNCaP-Abl and RWPE-1) followed by positive genetic screens to identify regulators of antiandrogen therapy resistance. We will also finalize our mutation calling on ChrY in prostate cancer and apply the FACETS method to identify copy-number changes. As outlined in Specific Aim 3, functional validation of candidate genes and xenograft studies will be conducted in the Kantoff and Schultz groups at MSK. Clinical validation of candidate genes in patient cohorts will be conducted by the Kantoff and Schultz groups at MSK and the Gerke group at Moffit Cancer Center.

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4. IMPACT

a. What was the impact on the development of the principal discipline(s) of the project?

Nothing to report.

b. What was the impact on other disciplines?

In cancers that affect both sexes, men have an increased risk of disease and mortality compared with women. This indicates that ChrY may potentially play a role in overall disease progression in men and not only in gender-specific cancers such as prostate and testicular cancers. The generated ChrY CRISPR/Cas9 library will facilitate exploring the role of ChrY genes in disease progression in other cancers such as urothelial, skin, lung, colon, and hematologic malignancies. The XY-specific FISH probes designed and generated to analyze the status of the X and Y chromosomes in target cell lines may also be utilized to investigate their state in disease progression in disciplines other than prostate cancer. In summation, both generated materials have the potential to significantly advance our understanding of the role and significance of sex-chromosomes in disease.

c. What was the impact on technology transfer?

Nothing to report.

d. What was the impact on society beyond science and technology?

Nothing to report.

5. CHANGES/PROBLEMS

a. Changes in approach and reasons for change

The initial narrative proposed 10 single-guide RNAs (sgRNAs)/gene in the ChrY CRISPR library. A high number of repetitive sequences and gene paralogs in the human Y chromosome required a change in library design due to increased potential off-target effects of sgRNAs. This was resolved by using 4 sgRNA sequences per gene family opposed to 10 sgRNAs/gene. For genes with no off-target effects, the library contains 4 sgRNAs/sequence. This method will decrease the number of false positives from cell death due to increased DNA damage resulting from off-target effects.

Even though we are generating cell line models with barcoding to track cell populations through antiandrogen treatment, these assays will be conducted separately from the

CRISPR library. We will instead use the barcoding approach as a part of the functional validation to assay the importance of candidate genes in specific cell populations during antiandrogen and chemotherapy treatments. The barcoded cells will also be used to assay heterogeneity in parent cell lines with and without antiandrogen and docetaxel treatment. This change in research strategy is to decrease loss of cell viability from DNA damage due to the combined load of the barcode and CRISPR libraries in the cell line models. This is still in line with the original goals of the project to track the importance of ChrY genes in specific cell populations involved in the development of mCRPC. If the barcoded cells do not have significant loss of viability, we can potentially attempt to optimize the CRISPR library, but it will still be a concern if the results are of physiological relevance.

b. Actual or anticipated problems or delays and actions or plans to resolve them

Initial methodology requiring design of 10 sgRNAs/gene was modified to 4 sgRNAs/gene or gene family in cases of high homology to decrease off-target effects and the subsequent number of potential false positives. The required revision of the library design strategy due to the high number of repetitive sequences on ChrY led to unanticipated delays; however, the timeline is back in accordance with the SOW.

c. Changes that had a significant impact on expenditures

Nothing to report.

d. Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents.

Nothing to report.

e. Significant changes in use or care of human subjects.

Nothing to report.

f. Significant changes in use or care of vertebrate animals.

Nothing to report.

g. Significant changes in use of biohazards and/or select agents.

Nothing to report.

6. PRODUCTS

a. Publications, conference papers, and presentations

Journal publications.

Nothing to report.

Books or other non-periodical, one-time publications.

Nothing to report.

Other publications, conference papers, and presentations.

Nothing to report.

b. Website(s) or other Internet site(s)

Nothing to report.

c. Technologies or techniques

Nothing to report.

d. Inventions, patent applications, and/or licenses

Nothing to report.

e. Other Products

The first CRISPR/Cas9 library targeting human Y chromosome genes was generated. Following publication, the library will be shared via the Addgene repository.

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

a. What individuals have worked on the project?

Name:	Philip Kantoff
Project Role:	Initiating Principal Investigator
Researcher Identifier (e.g. ORCID ID):	0000-0001-7275-0597
Nearest person month worked:	2
Contribution to Project:	Dr. Kantoff oversees all aspects of this project.
Funding Support:	NIH, DoD, Prostate Cancer Foundation, Movember Foundation

Name:	Sai Harisha Rajanala
Project Role:	Research Fellow
Researcher Identifier (e.g. ORCID ID):	0000-0002-7096-3756
Nearest person month worked:	5
Contribution to Project:	Dr. Rajanala has replaced Yuki Yoshikawa, MD. She will generate the cell line models with the CRISPR/Cas9 library and conduct genetics screens to identify regulators of antiandrogen therapy sensitivity. Dr. Rajanala will also conduct functional validation of candidate genes following positive genetic screens.
Funding Support:	Institutional

Name:	Rahim Hirani
Project Role:	Research Technician
Researcher Identifier (e.g. ORCID ID):	0000-0002-9304-9916

Nearest person month worked:	0-1
Contribution to Project:	Mr. Hirani has replaced Mohammad Atiq, MD. He will assist Dr. Rajanala with the functional validation of candidate genes.
Funding Support:	DOD

Name:	Nikolaus Schultz
Project Role:	Collaborating Principal Investigator
Researcher Identifier (e.g. ORCID ID):	N/A
Nearest person month worked:	1
Contribution to Project:	Dr. Schultz oversees all efforts related to this proposal in close collaboration with Dr. Van Allen
Funding Support:	NIH, DOD, POETIC

Name:	Bastien Nguyen
Project Role:	Research Fellow
Researcher Identifier (e.g. ORCID ID):	N/A
Nearest person month worked:	11
Contribution to Project:	Dr. Nguyen will collaborate with Dr. Van Allen's (DFCI) laboratory on sequence analysis.
Funding Support:	DoD

Name:	Subhiksha Nandakumar
Project Role:	Bioinformatics Engineer
Researcher Identifier (e.g. ORCID ID):	N/A
Nearest person month worked:	2
Contribution to Project:	Ms. Nandakumar will assist Dr. Nguyen with bioinformatics analysis.
Funding Support:	NIH, DoD

Name:	Eliezer Van Allen
Project Role:	Principal Investigator
Researcher Identifier (e.g. ORCID ID):	vanallen81
Nearest person month worked:	1
Contribution to Project:	Dr. Van Allen oversees all efforts related to this proposal in close collaboration with Dr. Schultz
Funding Support:	NIH, DOD, Damon Runyon Cancer Research Foundation, Novartis, Prostate

	Cancer Foundation, Bristol Myers Squibb, Movember Foundation, Brown Performance Group, Leidos Biomedical Research, Inc, Starr Consortium
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Name:	Eric Kofman
Project Role:	Computational Biologist
Researcher Identifier (e.g. ORCID ID):	N/A
Nearest person month worked:	2
Contribution to Project:	Dr. Koffman's focus is on the analysis, method development, and application pertaining to identifying genomic features that correlate with mutational signature analysis of prostate cancers.
Funding Support:	Starr Consortium

b. Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period?

There have been the following changes to active support:

KANTOFF, PHILIP

New Grants Since Last Submission

Title: W81XWH-14-1-0515 SLCO2B1 and SLCO1B3 as new targets for enhancing androgen deprivation therapy for prostate cancer

Role: Principal Investigator

Sponsoring Agency: CDMRP

Effort: 0.60 calendar

Level of Funding: \$245,515

Dates: 11/12/2018–12/31/2020*

Agency Contact: Nrusingha Mishra

Agency Contact Information: (Email) Nrusingha.Mishra.civ@mail.mil

Goals/Aims: The proposed aims of this project are 1) We will determine the impact of statins and estrogens on the uptake of DHEAS or T through SLCO2B1 and SLCO1B3 and their effects on PCa cell lines; 2) We will determine the impact of expression levels of SLCO2B1 and SLCO1B3 on prostate tumor progression to CRPC in the presence or absence of statins or estrogens in animal models; 3) We will determine the association between PCa survival and the use of statins and tumor expression levels of SLCO2B1 and SLCO1B3 in men with different genotypes of SLCO2B1 and SLCO1B3 in the Health Professionals Follow-up Study and ADT PCa cohorts; 4) We will identify and optimize small molecule inhibitors of SLCO2B1 and SLCO1B3 and test these inhibitors in cell based and animal models of PCa.

Overlap Statement: No overlap

*Note the change in dates.

Title: GC232671 Prostate Cancer Outcomes: An International Registry to Improve Outcomes in Men with Advanced Prostate Cancer (IRONMAN Registry)

Role: Principal Investigator

Sponsoring Agency: Movember Canada

Effort: 0.60 calendar

Level of Funding: \$43,076

Dates: 11/30/2016–11/29/2019

Agency Contact: Paul Villanti

Agency Contact Information: (Email) info.us@movember.com

Prostate Cancer Outcomes: An International Registry to Improve Outcomes in Men with Advanced Prostate Cancer (IRONMAN Registry)

Goals/Aims: The overarching mission of the Prostate Cancer Outcomes: An International Registry to improve outcomes in men with advanced prostate cancer is to provide an evidence basis for improving the patient management, experiences, and outcomes among men with advanced prostate cancer internationally.

Overlap Statement: No overlap

Title: W81XWH1810330 Cholesterol Synthesis and Statin Therapy in Prostate Cancer

Role: Mentor

Sponsoring Agency: CDMRP

Effort: 0.60 calendar

Level of Funding: \$107,564

Dates: 7/1/2018–6/30/2020

Agency Contact: Jennifer Shankle

Agency Contact Information: (Email) Jennifer.e.shankle.civ@mail.mil

Goals/Aims: To assess cholesterol biosynthesis as a prognostic biomarker in metastatic prostate cancer and as a predictive biomarker for statin therapy.

Aim 1: To validate intratumoral cholesterol biosynthesis as a prognostic factor for lethality among patients with localized prostate cancer.

a) To validate IHC for HMGCR protein expression in archival prostate cancer tissue. We will generate HMGCR quantification cut-offs and compare with SQLE mRNA measured in a subset of patients.

b) To define the risk of lethal prostate cancer associated with HMGCR protein expression in tumor tissue at cancer diagnosis. We will quantify the risk of metastasis and cancer death after prostatectomy (HPFS, PHS cohorts) and in a watchful waiting setting (SWWS cohort) to establish HMGCR as a protein biomarker.

Aim 2: To assess cholesterol biosynthesis as a predictive biomarker for ADT resistance.

a) To quantify the risk of development of CRPC on ADT associated with HMGCR protein expression. We will test whether HMGCR expression at cancer diagnosis predicts duration of response to ADT (SWWS). **Aim 3:** To assess cholesterol biosynthesis as a prognostic biomarker in metastatic prostate cancer and as a predictive biomarker for statin therapy.

a) To assess the prognostic value of SQLE mRNA expression in metastatic CRPC. We hypothesize that high SQLE mRNA expression is associated with poor overall survival in mCRPC (SU2C/PCF cohort).

b) To assess the predictive value of SQLE mRNA for the association of statin therapy and overall survival in metastatic CRPC (SU2C/PCF cohort).

Overlap Statement: No overlap

Title: (Challenge Award) The Impact of DNA Damage Repair Abnormalities in Prostate Cancer

Role: Principal Investigator

Sponsoring Agency: Prostate Cancer Foundation **Effort:** 0.30 calendar

Level of Funding: \$200,000

Dates: 10/12/2018–10/12/2020

Agency Contact: Howard R. Soule

Agency Contact Information: (Email) hsoule@pcf.org

Goals/Aims: The specific aims are: 1) to determine the association between pathogenic variants in DDR genes in the germline genome and long-term risk of lethal PC in 3,000 men with high-risk, localized PC. We will perform whole exome sequencing of known DDR pathway genes in germline DNA in clinically well characterized cohorts of men with localized high-risk disease followed for decades after diagnosis. 2) to estimate incremental effectiveness, cost-effectiveness and cost-utility ratios for DDR germline mutation screening and risk-tailored management compared to no screening and standard management for men with, or at risk for, high-grade/locally advanced PC.

Overlap Statement: No overlap

Title: (Challenge Award); Clonal Hematopoiesis in Prostate Cancer

Role: Principal Investigator

Sponsoring Agency: Prostate Cancer Foundation **Effort:** 0.30 calendar

Level of Funding: \$350,000

Dates: 12/31/2018–12/31/2020

Agency Contact: Howard R. Soule

Agency Contact Information: (Email) hsoule@pcf.org

Goals/Aims: Our results will define how CH influences outcomes of prostate cancer patients. We will define how CH evolves and how cancer therapies affect its progression. This knowledge will guide the way for better treatment selection among conventional therapies, both for primary and advanced disease. It may inform us about the need to intervene with anti-inflammatory agents.

The specific aims are: 1) We will estimate the excess risk of cancer-specific, cardiovascular, and all-cause mortality due to CH among prostate cancer patients in the HPFS and PHS cohorts. We hypothesize that CH status is associated with worse outcomes, particularly in men treated with XRT. 2) We will determine the impact of cancer therapies on CH among men with advanced prostate cancer in order to increase safety and tolerability of effective therapy for advanced disease. A) We will determine how therapies for advanced prostate cancer impact CH and its evolution over time in IRONMAN and IMPACT patients. B) We will determine how CH predicts occurrence of cytopenias in IMPACT patients. C) We will determine how CH predicts 1. shortened time on prostate cancer-directed treatment and 2. acceleration of cardiovascular disease in IRONMAN patients. 3. We will assess which patients with advanced prostate cancer have systemic inflammation due to CH, and if antiinflammatory treatment mitigates the consequences of CH. A) We will determine which circulating biomarkers of inflammation are associated with specific CH mutations (IMPACT and HPFS patients). B) We will explore if the anti-inflammatory drug aspirin specifically benefits men who have CH (PHS patients).

Overlap Statement: No overlap

SCHULTZ, NIKOLAUS

Grants Terminated Since Last Submission

Title: A113642 (PI: Butowski) Ivy Foundation Early Phase Clinical Trials Consortium

Role: Collaborator

Sponsoring Agency: Ben and Catherine Ivy Foundation **Effort:** 0.36 calendar

Level of Funding: \$55,000 **Dates:** 12/1/2014–11/30/2018

Agency Contact: Michelle Stevens

Agency Contact Information: CGAwardTeam@ucsf.edu

Goals/ Aims: The team will be responsible for the screening, enrollment, and treatment of glioma patients in the context of Ivy Consortium Clinical Trials.

Overlap Statement: No overlap

Title: 3 P30 CA008748-52 S1 (PI: Thompson) Cancer Center Support Grant

Role: Project Co-Leader

Sponsoring Agency: NIH/NCI

Effort: 1.20 calendar

Level of Funding: \$254,562

Dates: 1/20/1997–12/31/2018

Agency Contact: Funmi Elesinmogun

Agency Contact Information: elesinmf@mail.nih.gov

Goals/Aims: The objective of the proposed study is to create a comprehensive survey of cancer education and healthcare access, history, and intentions around prostate cancer (PCa) and colorectal cancer (CRC) screening behaviors, knowledge of cancer trials, and use of internet/mHealth technologies among residents of and BS/BW neighborhoods with these 3 specific aims: 1. Develop appropriate survey instruments and sampling

methodology to conduct a community-level population health assessment of Bedford-Stuyvesant and Bushwick. 2. Implement the survey instrument and web survey/content. 3. Survey data integration and aggregation with other local secondary sources, data analysis and matching with HINTS, and other cancer control surveillance data for NYC and nationally.

Overlap Statement: No overlap

New Since Last Submission

Title: 1U24 CA233243-01 (PI: Cerami) Human Tumor Atlas Network: Data Coordinating Center

Role: Principal Investigator

Supporting Agency: NIH/NCI

Effort: 1.20 calendar months

Level of Funding: \$211,038

Dates: 9/30/2018–6/30/2023

Agency Contact: Justin Birken

Agency Contact Information: birkenjg@mail.nih.gov

Goals/Aims: MSK will perform all work related to the proposed HTAN instance of the cBioPortal for Cancer Genomics. MSK will build, maintain and run automated pipelines that transfer data from Synapse into cBioPortal, maintain all user logins, and will develop all new features proposed in the application. Members of the MSK team will work closely with the collaborators at Emory to incorporate the Cancer Digital Slide Archive software into cBioPortal. MSK will also be involved in user support & outreach.

Overlap Statement: No overlap

VAN ALLEN, ELIEZER

Grants Terminated Since Last Submission

Title: 5 P50CA090381-13 SPORE in Prostate Cancer

Role: Project Co-Leader

Supporting Agency: NIH/NCI

Effort: *Effort subsumed under K08

Level of Funding: \$161,731

Dates: 9/23/2013–6/30/2018

Agency Contact: N/A

Agency Contact Information: N/A

Goals/Aims: Project 3. Genomic determinants of resistance to primary androgen deprivation therapy and aggressive disease. The specific aims of the project are as follows: Aim 1. Whole genome sequencing of CaP that shows de novo or acquired resistance to ADT. Aim 2. Targeted genomic profiling of CaP cohorts to identify somatic determinants of clinical aggressiveness and progression to CRPC. Aim 3. Characterization of resistance to ADT by systematic ORF screening.

Overlap Statement: No overlap

Title: Movember Foundation PCF Challenge Award

Role: Co-Principal Investigator

Supporting Agency: Prostate Cancer Foundation

Effort: 0.12 calendar

Level of Funding: \$280,000

Dates: 7/31/2015–7/30/2018

Agency Contact: Howard Soule

Agency Contact Information: applications@pcf.org

Goals/Aims: Aim 1. Determine the frequency of heritable (germ-line) genomic aberrations encoding DNA damage/repair proteins in men with metastatic CRPC. Aim 2. Conduct a Phase 2 clinical trial to ascertain response rates to FDA-approved genotoxic therapeutics in patients with germ-line or somatic alterations in DNA repair pathways. Aim 3. Develop minimally invasive biomarkers capable of distinguishing patients for therapeutics targeting DNA repair pathways.

Overlap Statement: No overlap

Title: MO Internal Grant – Single cell dissection of prostate cancer bone metastases

Role: Principal Investigator

Supporting Agency: DFCI

Effort: 0.12 calendar

Level of Funding: \$50,000

Dates: 12/31/2016–12/29/2018

Agency Contact: N/A

Agency Contact Information: N/A

Goals/Aims: 1) To perform characterization of cell populations isolated from prostate bone metastasis by single-cell transcriptome analysis. 2) To identify compounds that eliminate treatment-resistant prostate bone metastasis via a single cell functional screen.

Overlap Statement: No overlap

Title: PCF Challenge Award - Neoadjuvant intense androgen deprivation therapy for men with localized high risk prostate cancer

Role: Co-Investigator

Supporting Agency: Prostate Cancer Foundation

Effort: 0.12 calendar

Level of Funding: \$500,000

Dates: 12/31/2016–12/29/2018

Agency Contact: Howard Soule

Agency Contact Information: applications@pcf.org

Goals/Aims: The aims of this project are to utilize clinical trial data to study the biologic basis of exceptional responses for men with localized high risk prostate cancer, as well as the mechanisms of resistance. We will analyze data to provide a predictive biomarker to select men for androgen deprivation therapy (ADT) treatment approach and provide valuable data.

Overlap Statement: No overlap

New Since Last Submission

Title: R01CA227388 Integrative Somatic and Germline Computational Biology to Redefine Clinical Actionability in Solid Tumors

Role: Principal Investigator

Supporting Agency: NIH/NCI

Effort: 3.0 calendar

Level of Funding: \$1,143,750

Dates: 6/1/2018–5/31/2024

Agency Contact: Jacquelyn Saval

Agency Contact Information: Jacquelyn.saval@nih.gov

Goals/Aims: Aim 1. To determine inherited cancer risk in solid tumors through integrative computational biology. Aim 2. To evaluate the impact of somatic and germline interactions on DNA repair defects and response to platinum--based chemotherapies in solid tumors. Aim 3. To identify somatic and germline features that coordinate to alter the immune microenvironment and impact selective response to immune checkpoint blockade in solid tumors.

Overlap Statement: No overlap

Title: U01CA233100 Molecular and immune drivers of immunotherapy responsiveness in prostate cancer

Role: Principal Investigator

Supporting Agency: NIH

Effort: 1.32 calendar

Level of Funding: \$3,263,125*

Dates: 9/1/2018–8/31/2023

Agency Contact: Min-kyung H Song

Agency Contact Information: songm@mail.nih.gov

Goals/Aims: Aim 1. To define the systemic and infiltrating immune responses in prostate cancer associated with response to checkpoint blockade. Aim 2. To determine the immunologic impact of chromatin dysregulation and inhibition in prostate cancer. Aim 3. To establish the impact of existing DNA damaging agents for sensitizing prostate cancer to immune checkpoint blockade.

Overlap Statement: No overlap

*Total direct costs include subaward agreement

Title: U2CCA233195 The Cellular Geography of Therapeutic Resistance in Cancer: Biospecimen Unit

Role: Co-Leader

Supporting Agency: NIH

Effort: 1.20 calendar

Level of Funding: \$24,269

Dates: 9/24/2018–8/31/2023

Agency Contact: Yantian Zhang

Agency Contact Information: yantian.zhang@nih.gov

Goals/Aims: Aim 1. Create an adaptive power analysis paradigm for tumor cell atlases. Aim 2. Develop a pre-processing and analysis computational workflow for each data modality. Aim 3. Determine the cell intrinsic and extrinsic features relevant to tumors

Overlap Statement: No Overlap

Title: Characterizing and overcoming genomic mechanisms of resistance to PD-1 inhibitors in melanoma

Role: Co-Principal Investigator

Supporting Agency: Novartis

Effort: 0.30 calendar

Level of Funding: \$322,852

Dates: 1/1/2018–12/31/2020

Agency Contact: N/A

Agency Contact Information: N/A

Goals/Aims: Aim 1. To characterize acquired and intrinsic resistance to standard of care immune checkpoint inhibitors. Aim 2. To identify genomic drivers of acquired resistance to immune checkpoint inhibitors in GU/melanoma.

Overlap Statement: No overlap

Title: Movember GAP5 Award – Testicular cancer translational research project

Role: Principal Investigator

Supporting Agency: Movember Foundation

Effort: 0.06 calendar

Level of Funding: \$15,554

Dates: 3/1/2018–2/28/2020

Agency Contact: Sam Gledhill

Agency Contact Information: sam@movember.com

Goals/Aims: Aim #1. To establish a secure platform for identifying, collecting and analysing clinical and biospecimen data to answer the above clinical question and to ensure this resource is available for future translational use. Aim#2. To determine if there are germline genetic features associated with resistance to cisplatin-based chemotherapy. Aim #3. To determine the association between putative molecular tumour tissue markers (DNA, mRNA, miRNA) and resistance to cisplatin-based chemotherapy.

Overlap Statement: No overlap

Title: Deep learning models to accelerate translational cancer genomics

Role: Principal Investigator

Supporting Agency: Brown Performance Group **Effort:** 0.18 calendar months

Level of Funding: \$200,000 **Dates:** 6/4/2018–6/3/2020

Agency Contact: Audrey Cook

Agency Contact Information: acook@brownperformance.com

Goals/Aims: Aim 1. To develop a biologically informed machine learning model for outcome prediction and hypothesis generation using cancer genomics. Aim2. To apply P-net to translational and clinical cancer genomics challenges and identify novel predictive markers.

Overlap Statement: No overlap

Title: W81XWH-18-1-0480 Predictive biomarkers for nivolumab treatment in metastatic renal cell carcinoma

Role: Co-Investigator

Supporting Agency: DoD/KCRP TRPA **Effort:** 0.30 calendar

Level of Funding: \$25,835 **Dates:** 9/1/2018–8/31/2021

Agency Contact: Jamie Shortall

Agency Contact Information: jamie.a.shortall.civ@mail.mil

Goals/Aims: AIM 1 will focus on the validation of blood-based biomarkers of response to nivolumab in metastatic ccRCC. Aim 1a: To validate the impact of nivolumab therapy on kynurenine, and to examine whether changes in kynurenine levels correlate with nivolumab benefit. Aim 1b. To validate the negative predictive value of serum adenosine in patients treated with nivolumab. Aim 2 will focus on the validation of tissue-based biomarkers of response to nivolumab in metastatic ccRCC. Aim 2a: To validate the predictive value of biomarkers expression by immunostaining assays in patients treated with nivolumab. Aim 2b: To validate the predictive value of tumor genetic alterations in patients treated with nivolumab. Aim 2c: To investigate the predictive value of T-effector- and myeloid-associated gene signatures in patients treated with nivolumab (Exploratory Aim).

Overlap Statement: No overlap

Title: Phase II: Broad Institute Cancer Model and Development Center

Role: Investigator

Supporting Agency: Broad Institute/NCI **Effort:** 0.60 calendar

Level of Funding: \$12,134 **Dates:** 12/1/2018–5/31/2020

Agency Contact: David Hoffman (Broad Institute)

Agency Contact Information: hoffmann@broadinstitute.org

Goals/Aims: The Broad CMDC has three goals: 1) Achieve industry scale: Produce 100 patient-derived models per year with a focus on cancer types currently lacking precision therapies Gastroesophageal, Pancreas, Glioblastoma and Pediatric Solid Tumors); 2) Innovate to maximize efficiency: Iteratively optimize and refine workflows to improve success rates, maximize efficiencies and reduce costs; 3) Succeed for rare cancers: Demonstrate proof-of-concept for how to overcome key bottlenecks in rare and underrepresented cancers.

Overlap Statement: No overlap

c. What other organizations were involved as partners?

1. **Organization Name:** Dana-Farber Cancer Institute
2. **Location of Organization:** Boston, MA
3. **Partner's contribution to the project:**
 - a. **Financial support:** None
 - b. **In-kind support:** None
 - c. **Facilities:** MSK and MCC staff will use the facilities resources at their respective institutions for this project. Dr. Van Allen and his team will use the facilities and resources available to them at DFCI.
 - d. **Collaboration:** Dr. Van Allen oversees all efforts related to this proposal in close collaboration with Dr. Schultz. Personnel from both the Schultz and Van Allen groups will collaborate on sequencing analysis for the project.
 - e. **Personnel exchanges:** None
 - f. **Other:** None
1. **Organization Name:** Moffit Cancer Center
2. **Location of Organization:** Tampa, FL
3. **Partner's contribution to the project**
 - a. **Financial support:** None
 - b. **In-kind support:** None
 - c. **Facilities:** MSK and DFCI staff will use the facilities resources at their respective institutions for this project. Dr. Gerke will use the facilities and resources available to him at MCC.
 - d. **Collaboration:** Dr. Gerke will work with the MSK study team to integrate findings from the Health Professionals Follow-up Study (HPFS) and Physicians' Health Study (PHS) into the broader scope of the project. Dr. Gerke will also assist in the epidemiologic and statistical interpretation of findings from the study.
 - e. **Personnel exchanges:** None
 - f. **Other:** None

8. SPECIAL REPORTING REQUIREMENTS

a. COLLABORATIVE AWARDS

Drs. Kantoff and Schultz are submitting duplicative reports with tasks clearly marked with the responsible PI and research site.

b. QUAD CHARTS

Not applicable.

9. APPENDICES

Appendix 1: ChrY CRISPR/Cas9 Library

Gene	gRNA label	gRNA	Tool	Gene Type
AMELY	AMELY_1	CAGGCATCAGTGCTTGCT GG	Brunello	Coding
AMELY	AMELY_2	CGTAACCATAGGAAGAG TAC	Brunello	Coding
AMELY	AMELY_3	GATGTGGTGATGAGACTG CA	Brunello	Coding
AMELY	AMELY_4	GCACCACCAAATCATCCC CG	Brunello	Coding
BPY2	BPY2_1	ATATGTCAGCAAGCCCAC TA	Brunello	Coding
BPY2	BPY2_2	CAATAGTACCTGTGAAAA TC	Brunello	Coding
BPY2	BPY2_3	GCCCTCTGTAAGCAGCAC CT	Brunello	Coding
BPY2	BPY2_4	TGACGCTTGTCCCCAGAG CC	Brunello	Coding
BPY2B	BPY2B_1	ATGAGATTATGCTGTATC AC	Brunello	Coding
BPY2B	BPY2B_2	CATAATCTCATTTGTATG CT	Brunello	Coding
BPY2B	BPY2B_3	GCACAATTACTTCTGTGA TC	Brunello	Coding
BPY2B	BPY2B_4	GTGAAGTGACTCTTCTGA CT	Brunello	Coding
BPY2C	BPY2C_1	AAGCTTGATCATCATACC TT	Brunello	Coding
BPY2C	BPY2C_2	AATAGTACCTGTGAAAAT CT	Brunello	Coding
BPY2C	BPY2C_3	AGCCAGGACACGTGCAG GAC	Brunello	Coding
BPY2C	BPY2C_4	GTGATGTTAATATTCTGC AT	Brunello	Coding
CDY1	CDY1_1	TACAATGTCTCTGTATGT GC	Brunello	Coding
CDY1	CDY1_2	TCTGCACCAGGACGTGAC AA	Brunello	Coding
CDY1	CDY1_3	TGCTGGCAGCAAATAACT TG	Brunello	Coding

CDY1	CDY1_4	TTTGACCACAAAACACTGTG AG	Brunello	Coding
CDY1B	CDY1B_1	ACAGGTTTCAGCTACCCGA AA	Brunello	Coding
CDY1B	CDY1B_2	AGAAGATGCACTTCACCA TA	Brunello	Coding
CDY1B	CDY1B_3	CAGGACGTGACAAAGGG TCC	Brunello	Coding
CDY1B	CDY1B_4	TTGCTGCCAGCAAGAACG TT	Brunello	Coding
CDY2A	CDY2A_1	AATATTACTGATGACAGC AG	Brunello	Coding
CDY2A	CDY2A_2	CAGTGACTGATAAACACC AC	Brunello	Coding
CDY2A	CDY2A_3	GACCACAAGAAAACACTGT GAG	Brunello	Coding
CDY2A	CDY2A_4	TCTGCACCAGGATGTGAC AA	Brunello	Coding
CDY2B	CDY2B_1	ATAGACCCATTAGCAGCC AA	Brunello	Coding
CDY2B	CDY2B_2	ATGACAAACAGGATGAC ACT	Brunello	Coding
CDY2B	CDY2B_3	CTGCACCAGGATGTGACA AA	Brunello	Coding
CDY2B	CDY2B_4	TACAATGTCTCTGTATGT GA	Brunello	Coding
DAZ1	DAZ1_1	ACGTGCTGAGTTACAGGA TT	Brunello	Coding
DAZ1	DAZ1_2	CACAGTTTCAGAACGTCT GG	Brunello	Coding
DAZ1	DAZ1_3	CGCCAGACGTTCTGAAAC TG	Brunello	Coding
DAZ1	DAZ1_4	TCATCAGCTGCAGCTAGC CA	Brunello	Coding
DAZ2	DAZ2_1	GGATTAACCTACCAAAGG ACG	Brunello	Coding
DAZ2	DAZ2_2	TCAGCATTTTCAGGTCACC AC	Brunello	Coding
DAZ2	DAZ2_3	TCTGCTTATCCACATTCA CC	Brunello	Coding
DAZ2	DAZ2_4	TGTTTCGTTTGTTAATGA CG	Brunello	Coding
DAZ3	DAZ3_1	ATGACCTGACCTGGTGAA TG	Brunello	Coding
DAZ3	DAZ3_2	GTGACCTGAAATGCTGAA TC	Brunello	Coding

DAZ3	DAZ3_3	GTGACCTGAAATGGTGAT CT	Brunello	Coding
DAZ3	DAZ3_4	TTACCTGATAATTGTATA CA	Brunello	Coding
DAZ4	DAZ4_1	ACAGGATTCGGCGTGATT TG	Brunello	Coding
DAZ4	DAZ4_2	CAGACGTTCTGAAACTGT GG	Brunello	Coding
DAZ4	DAZ4_3	CATCCAGTGATGACCTGA CC	Brunello	Coding
DAZ4	DAZ4_4	CATGGTAAAAAGCTGAA GCT	Brunello	Coding
DDX3Y	DDX3Y_1	AGGACGAACTCTAGATCG GT	Brunello	Coding
DDX3Y	DDX3Y_2	CGTGGACGGAGTGACTAT GA	Brunello	Coding
DDX3Y	DDX3Y_3	CTTACATTCTCAATATGT GG	Brunello	Coding
DDX3Y	DDX3Y_4	TCAACTATACGACGTATC TG	Brunello	Coding
EIF1AY	EIF1AY_1	AAGAGGTTATGCCATATC AG	Brunello	Coding
EIF1AY	EIF1AY_2	GATTACCTGAGCATACTC TG	Brunello	Coding
EIF1AY	EIF1AY_3	GGAGGTAAAAACAGGCG CAG	Brunello	Coding
EIF1AY	EIF1AY_4	TGAATCTGAAAAAAGAG AGT	Brunello	Coding
HSFY1	HSFY1_1	ACAGAAGATTCCCTTGTT AG	Brunello	Coding
HSFY1	HSFY1_2	AGAATCGTCTGTCTTAAG CA	Brunello	Coding
HSFY1	HSFY1_3	GTAAGAGTGAAGAGAAG AAT	Brunello	Coding
HSFY1	HSFY1_4	TTCACACAATGGAGACCT AG	Brunello	Coding
HSFY2	HSFY2_1	ACACAATGGAGACCTAGT GG	Brunello	Coding
HSFY2	HSFY2_2	GTAACTTGGACTTTCTAA CA	Brunello	Coding
HSFY2	HSFY2_3	TATAATCCAAATTTCAAG CG	Brunello	Coding
HSFY2	HSFY2_4	TTTAAATATGCCTCTAAC AA	Brunello	Coding
KDM5D	KDM5D_1	AGTGCATTGAACACTACC GC	Brunello	Coding

KDM5D	KDM5D_2	CAAACAAAACCTTATCTCC TG	Brunello	Coding
KDM5D	KDM5D_3	GGTGGAGGCCTATCAAGC TG	Brunello	Coding
KDM5D	KDM5D_4	TTGCCAAGTATGCTCCCG TG	Brunello	Coding
NLGN4Y	NLGN4Y_1	ACTGGACCCAAGATCTCA CT	Brunello	Coding
NLGN4Y	NLGN4Y_2	AGTGACTATCTTTGGCTC GG	Brunello	Coding
NLGN4Y	NLGN4Y_3	CAGACATTCTACCATGTC CG	Brunello	Coding
NLGN4Y	NLGN4Y_4	TGTTATGGTCTATATCCA TG	Brunello	Coding
PCDH11Y	PCDH11Y_1	GAAGTGCATAGTAGTTGT CA	Brunello	Coding
PCDH11Y	PCDH11Y_2	GATATGCTGCATTCTCCA GG	Brunello	Coding
PCDH11Y	PCDH11Y_3	GTGCAACGGATGCAGAC AGT	Brunello	Coding
PCDH11Y	PCDH11Y_4	TCATAAGAATAGTTGTAA GG	Brunello	Coding
PRORY	PRORY_1	AGAAGGCTTTCTGGATCC CG	Brunello	Coding
PRORY	PRORY_2	AGGAGAAGTCCGATATG GAG	Brunello	Coding
PRORY	PRORY_3	GGCCTCCGGAGAGAGCA ATG	Brunello	Coding
PRORY	PRORY_4	TGCTGCTGTGGACGATAT CG	Brunello	Coding
PRY	PRY_1	CAGGCGGTCATCTCACGA AG	Brunello	Coding
PRY	PRY_2	TCTCCATTCTAGATATGG GA	Brunello	Coding
PRY	PRY_3	TGGAAAATCTCTGAAATT TG	Brunello	Coding
PRY	PRY_4	TTTCCAAGGCTACCACCA GA	Brunello	Coding
PRY2	PRY2_1	AAAATCTCTGAAATTTGG GG	Brunello	Coding
PRY2	PRY2_2	CATTCTAGATATGGGAAG GT	Brunello	Coding
PRY2	PRY2_3	GGCCTCAAGACCTCTGTT CA	Brunello	Coding
PRY2	PRY2_4	TTATACTTCTCTGAGACT AC	Brunello	Coding

RBM1A1	RBM1A1_1	AATGCTGCCAAAGATATG AA	Brunello	Coding
RBM1A1	RBM1A1_2	AGATCTGCAAGAGGAAG CCG	Brunello	Coding
RBM1A1	RBM1A1_3	ATCCAAGTTGCCAAGAAA CG	Brunello	Coding
RBM1A1	RBM1A1_4	GACGAGAATGACCATAA TCA	Brunello	Coding
RBM1B	RBM1B_1	CGCATGTCAACAAGACAT GA	Brunello	Coding
RBM1B	RBM1B_2	GATCGAACCAGCAAATCC AG	Brunello	Coding
RBM1B	RBM1B_3	GGTGGCTTCCCTCACAAG AA	Brunello	Coding
RBM1B	RBM1B_4	TGATTATGGTCATTCTCG TC	Brunello	Coding
RBM1D	RBM1D_1	GAAGCCGTGGAGGAACA AGA	Brunello	Coding
RBM1D	RBM1D_2	GATGGTTATGCAACTAAC GA	Brunello	Coding
RBM1D	RBM1D_3	TATCCATGGCCTCTAGAT GG	Brunello	Coding
RBM1D	RBM1D_4	TGCCAAAGATATGAATGG AA	Brunello	Coding
RBM1E	RBM1E_1	GAGTATGCTCCACCATCT AG	Brunello	Coding
RBM1E	RBM1E_2	GCCACCCTCTTGTTCTC CA	Brunello	Coding
RBM1E	RBM1E_3	TATGCATAGCCTCTAGAT GG	Brunello	Coding
RBM1E	RBM1E_4	TGACATGCGATCATTTCT CC	Brunello	Coding
RBM1F	RBM1F_1	ATGGTTATGCAACTAACG AT	Brunello	Coding
RBM1F	RBM1F_2	GAAGATATTGTCGCTCTG CG	Brunello	Coding
RBM1F	RBM1F_3	GAAGCAGTGGAGGAACA AGA	Brunello	Coding
RBM1F	RBM1F_4	TGCGAAAGATATGAATG GAA	Brunello	Coding
RBM1J	RBM1J_1	AATGCTGCGAAAGATATG AA	Brunello	Coding
RBM1J	RBM1J_2	CGGGATGAAAGTTATTCT AG	Brunello	Coding
RBM1J	RBM1J_3	GATATTGTCGCTCTGCGT GG	Brunello	Coding

RBM1Y1J	RBM1Y1J_4	TCTGCAAGAGGAAGCAG TGG	Brunello	Coding
RPS4Y1	RPS4Y1_1	AGTGAAGGGAATCCCTCA CC	Brunello	Coding
RPS4Y1	RPS4Y1_2	CCTTGGTGTCATAGACCA GG	Brunello	Coding
RPS4Y1	RPS4Y1_3	TGCTGTTACCCGCATCAC AG	Brunello	Coding
RPS4Y1	RPS4Y1_4	TTGGATGCTTGACAAACT AA	Brunello	Coding
RPS4Y2	RPS4Y2_1	CCGCCTGGTCTATAATAC CA	Brunello	Coding
RPS4Y2	RPS4Y2_2	GACAAAGGGAATTCCAC ACC	Brunello	Coding
RPS4Y2	RPS4Y2_3	TCACCTTGATGAGAGGAT CT	Brunello	Coding
RPS4Y2	RPS4Y2_4	TTCCTGAGGAAGACTATC AG	Brunello	Coding
SR1Y	SR1Y_1	AAGAGAATATTCCCGCTC TC	Brunello	Coding
SR1Y	SR1Y_2	CCATGAACGCATTCATCG TG	Brunello	Coding
SR1Y	SR1Y_3	GCAAGCAGCTGGGATAC CAG	Brunello	Coding
SR1Y	SR1Y_4	TAAGTATCGACCTCGTCG GA	Brunello	Coding
TBL1Y	TBL1Y_1	AAATCCTCCAAAGAACCG AG	Brunello	Coding
TBL1Y	TBL1Y_2	AGGCTAGCAAATCACTGA CA	Brunello	Coding
TBL1Y	TBL1Y_3	GACATTGTATACGAGAAG GG	Brunello	Coding
TBL1Y	TBL1Y_4	GGGACAGGGACTCTATA GGG	Brunello	Coding
TGIF2LY	TGIF2LY_1	AGACCAATTTGTCTTTGT TG	Brunello	Coding
TGIF2LY	TGIF2LY_2	GCGACTGGATGTATAAGC AT	Brunello	Coding
TGIF2LY	TGIF2LY_3	GCGGAGGATCTTAACGG ACT	Brunello	Coding
TGIF2LY	TGIF2LY_4	GTTATTTCTCGACATGAT TG	Brunello	Coding
TMSB4Y	TMSB4Y_1	CATGTCTGACAAACCTGG TA	Brunello	Coding
TMSB4Y	TMSB4Y_2	GCAGCCATGTCTGACAAA CC	Brunello	Coding

TMSB4Y	TMSB4Y_3	TCGCAGCTATCGAACAGG AG	Brunello	Coding
TMSB4Y	TMSB4Y_4	TTCTCGATCTCAGCCATA CC	Brunello	Coding
TSPY1	TSPY1_1	CTTGGTGTGTGCGAGTGC CA	Brunello	Coding
TSPY1	TSPY1_2	GACCCCAGAGTCTGCACC GG	Brunello	Coding
TSPY1	TSPY1_3	GGAGGGCCTCGTGGAGC GGC	Brunello	Coding
TSPY1	TSPY1_4	GGCGCCTCTGCGGTCTAG GT	Brunello	Coding
TSPY10	TSPY10_1	AAGCCCCACCTAGACCGC AG	Brunello	Coding
TSPY10	TSPY10_2	AGGCTGCGGCAGGGTTTC TG	Brunello	Coding
TSPY10	TSPY10_3	CTCCTCCAGTGCAGACTC TG	Brunello	Coding
TSPY10	TSPY10_4	CTGTACAGCCTCCATCCT GA	Brunello	Coding
TSPY2	TSPY2_1	AGGCTGCGGCAGGGTTCC TG	Brunello	Coding
TSPY2	TSPY2_2	CTGCACAGCCTCCATCCT GA	Brunello	Coding
TSPY2	TSPY2_3	GCTGTTGGATGACATAAT GG	Brunello	Coding
TSPY2	TSPY2_4	TCTGGATGACGGCGCCTC TG	Brunello	Coding
TSPY3	TSPY3_1	GACCCCAGAGTCTGCACT GG	Brunello	Coding
TSPY3	TSPY3_2	GCGCCTCTGCGGTCTAGG TG	Brunello	Coding
TSPY3	TSPY3_3	GGCGGAGGAGGAGGGCC TCG	Brunello	Coding
TSPY3	TSPY3_4	GTGTGTGCGAGTGCCAAG GA	Brunello	Coding
TSPY4	TSPY4_1	AGCGGGAAAAGATGGAG CGG	Brunello	Coding
TSPY4	TSPY4_2	CAGGATGGAGGCTGTAC AGG	Brunello	Coding
TSPY4	TSPY4_3	CGGCAGGGTTTCTGTGGC GT	Brunello	Coding
TSPY4	TSPY4_4	GTTGGATGACATAATGGC GG	Brunello	Coding
TSPY8	TSPY8_1	AGGAGGAGGGCCTCGTG GAG	Brunello	Coding

TSPY8	TSPY8_2	CGGCGCCTCTGCGGTCTA GG	Brunello	Coding
TSPY8	TSPY8_3	GCTCCTCCAGTGCAGACT CT	Brunello	Coding
TSPY8	TSPY8_4	GGTGTGTGCGAGTGCCAA GG	Brunello	Coding
USP9Y	USP9Y_1	GTAACGGGTGAACTACA GAC	Brunello	Coding
USP9Y	USP9Y_2	TAACAATACTCATCGCCT AG	Brunello	Coding
USP9Y	USP9Y_3	TGATGGTCCCAATCTAGA GG	Brunello	Coding
USP9Y	USP9Y_4	TGGTACAGACCCCATAAC AC	Brunello	Coding
UTY	UTY_1	AGGATTCATAGAGAGTAC CT	Brunello	Coding
UTY	UTY_2	AGTAGAAGTAGACCAAA CCA	Brunello	Coding
UTY	UTY_3	TCAGAACTTCTGTTGAAC TG	Brunello	Coding
UTY	UTY_4	TGACTGTCAGCATCCCCC TG	Brunello	Coding
VCY	VCY_1	AGTCCAAAGCCGAGAGC CTC	Brunello	Coding
VCY	VCY_2	CCCCAGTGGCCCGAAGA AGA	Brunello	Coding
VCY	VCY_3	CCGGCCAAGGCCAAGGA GAC	Brunello	Coding
VCY	VCY_4	GAGAAGGGAGAAGCAGT TCG	Brunello	Coding
VCY1B	VCY1B_1	AAGGGAGAAGCAGTTCG TGG	Brunello	Coding
VCY1B	VCY1B_2	AGGCCAAGGAGACAGGA AAG	Brunello	Coding
VCY1B	VCY1B_3	CCTTCTTCTTCGGGCCAC TG	Brunello	Coding
VCY1B	VCY1B_4	TTCTCCCTTCTCGGCCAC CT	Brunello	Coding
ZFY	ZFY_1	CAGTCAAAGGATGACCAT CA	Brunello	Coding
ZFY	ZFY_2	GAAACTATGTCACTCGTC AG	Brunello	Coding
ZFY	ZFY_3	GATAAGTTTACATAACCA CC	Brunello	Coding
ZFY	ZFY_4	GCATGAGCAGCAAATTG ATG	Brunello	Coding

FAM197Y2	FAM197Y2_1	CAGCGGTTCTGGGATCAC GA	BROAD	Non Coding
FAM197Y2	FAM197Y2_2	TGCATGTTCTCCTCATGT GG	BROAD	Non Coding
FAM197Y2	FAM197Y2_3	CTGCATGTTCTCCTCATG TG	BROAD	Non Coding
FAM197Y2	FAM197Y2_4	AAAGCAGCATCAGCAGG CAG	BROAD	Non Coding
FAM197Y3	FAM197Y3_1	GGGGGAAAAACAGCATC AGC	BROAD	Non Coding
FAM197Y3	FAM197Y3_2	AAAACAGCATCAGCAGG CAG	BROAD	Non Coding
FAM197Y3	FAM197Y3_3	TTATAAAAAATTCTGTGC CT	BROAD	Non Coding
FAM197Y3	FAM197Y3_4	TCAGCCATCCCGGTTACC GG	BROAD	Non Coding
FAM197Y4	FAM197Y4_1	GGGGGAAAAGCAGCATC AGC	BROAD	Non Coding
FAM197Y4	FAM197Y4_2	TCAGCAATCCTGCCAAAA CC	BROAD	Non Coding
FAM197Y4	FAM197Y4_3	ACAGCTGAATGAGCTCAG GT	BROAD	Non Coding
FAM197Y4	FAM197Y4_4	CCTTCATGATGATTTTAC TG	BROAD	Non Coding
FAM197Y5	FAM197Y5_1	GTGGAGGAACTCAGCCAT CC	BROAD	Non Coding
FAM197Y5	FAM197Y5_2	AAAAAATTCTGTGCCTGG GT	BROAD	Non Coding
FAM197Y5	FAM197Y5_3	TTGGCAGGATTGCTGAGG TG	BROAD	Non Coding
FAM197Y5	FAM197Y5_4	CCACAGTGAAATCATCAT GA	BROAD	Non Coding
FAM197Y6	FAM197Y6_1	AAAGGAAATCATCCTGCC AC	BROAD	Non Coding
FAM197Y6	FAM197Y6_2	CCAAACAGCTGAATGAG CTC	BROAD	Non Coding
FAM197Y6	FAM197Y6_3	GCAGAGGAATCCTTTGAA GC	BROAD	Non Coding
FAM197Y6	FAM197Y6_4	GAGGAATCCTTTGAAGCT GG	BROAD	Non Coding
FAM197Y7	FAM197Y7_1	GCTGAATGAGCTCAGGTA GG	BROAD	Non Coding
FAM197Y7	FAM197Y7_2	GTCTGCATGTTCTCCTCA TG	BROAD	Non Coding
FAM197Y7	FAM197Y7_3	CCAGAACCGCTGGACTGC AG	BROAD	Non Coding

FAM197Y7	FAM197Y7_4	CTCATTCCACTGCAGTCC AG	BROAD	Non Coding
FAM197Y8	FAM197Y8_1	ATCATGAAGGAGCACTGT GT	BROAD	Non Coding
FAM197Y8	FAM197Y8_2	CCTGCCACCGGTAACCGG GA	BROAD	Non Coding
FAM197Y8	FAM197Y8_3	CAGCAATCCTGCCAAAAC CC	BROAD	Non Coding
FAM197Y8	FAM197Y8_4	CTGTGTTGGCATCCTCGG TA	BROAD	Non Coding
FAM197Y9	FAM197Y9_1	TGCAGGTTCTCCTCATGT GG	BROAD	Non Coding
FAM197Y9	FAM197Y9_2	CTGCAGGTTCTCCTCATG TG	BROAD	Non Coding
FAM197Y9	FAM197Y9_3	TCTGCAGGTTCTCCTCAT GT	BROAD	Non Coding
FAM197Y9	FAM197Y9_4	GTCTGCAGGTTCTCCTCA TG	BROAD	Non Coding
FAM224A	FAM224A_1	TTCATTCTGAATAAGAAC TG	BROAD	Non Coding
FAM224A	FAM224A_2	AGTCTCATGATAGATAGA CA	BROAD	Non Coding
FAM224A	FAM224A_3	GATGACATCTTATGGACC CA	BROAD	Non Coding
FAM224A	FAM224A_4	GGAAC TTTATCACACCAA GC	BROAD	Non Coding
FAM224B	FAM224B_1	GGTGTGATAAAGTTCCAA CT	BROAD	Non Coding
FAM224B	FAM224B_2	CTGGGTCCATAAGATGTC AT	BROAD	Non Coding
FAM224B	FAM224B_3	GTCTCCTTCTGTGCGCAA GG	BROAD	Non Coding
FAM224B	FAM224B_4	CCTTAACAATCCCAAGTT GA	BROAD	Non Coding
FAM41AY1	FAM41AY1_1	TATGAACCAGCATTGAAG GG	BROAD	Non Coding
FAM41AY1	FAM41AY1_2	AATAATTGAACCGGGTCA CA	BROAD	Non Coding
FAM41AY1	FAM41AY1_3	AGGAGGCAGAACGAGTC TCA	BROAD	Non Coding
FAM41AY1	FAM41AY1_4	AGCTAAAGAGTTGACAC GCA	BROAD	Non Coding
FAM41AY2	FAM41AY2_1	CTGACCACGTTCTACCC TG	BROAD	Non Coding
FAM41AY2	FAM41AY2_2	GAGCCTGAAATAATTGAA CC	BROAD	Non Coding

FAM41AY2	FAM41AY2_3	CATGAACGTATGGATGCC CT	BROAD	Non Coding
FAM41AY2	FAM41AY2_4	CAGCTAAAGAGTTGACAC GC	BROAD	Non Coding
LINC00278	LINC00278_1	CTGCTGTTGAGAGCGCCA CT	BROAD	Non Coding
LINC00278	LINC00278_2	CAGGACAACCTCAACCCG AG	BROAD	Non Coding
LINC00278	LINC00278_3	ACAGCACAACAGAACCT AAG	BROAD	Non Coding
LINC00278	LINC00278_4	TGTGCTACAGGACCTCGG TA	BROAD	Non Coding
LINC00279	LINC00279_1	TAGTTCCATGATCTTAGT AG	BROAD	Non Coding
LINC00279	LINC00279_2	GCAAGTCTTCTCATTAGG AG	BROAD	Non Coding
LINC00279	LINC00279_3	CTGATGAGCATTTCATGAA GC	BROAD	Non Coding
LINC00279	LINC00279_4	GGAGGTGTTTCAAGACAG TG	BROAD	Non Coding
LINC00280	LINC00280_1	ATGGTGATAAGTGGTGAG TT	BROAD	Non Coding
LINC00280	LINC00280_2	TCTTCTTAATGCCTGAAC GC	BROAD	Non Coding
LINC00280	LINC00280_3	CTGCTACAGGAAGAAAG TGG	BROAD	Non Coding
LINC00280	LINC00280_4	TCACCTTAATTCAGCACT CA	BROAD	Non Coding
NLGN4Y- AS1	NLGN4Y-AS1_1	GAAAAAAATATATAGC CGG	BROAD	Non Coding
NLGN4Y- AS1	NLGN4Y-AS1_2	GAGTGAGAAAATTGTTAG CA	BROAD	Non Coding
NLGN4Y- AS1	NLGN4Y-AS1_3	ATAATACACTTGATCACC TA	BROAD	Non Coding
NLGN4Y- AS1	NLGN4Y-AS1_4	AACTTTCATCAAGGCAG AA	BROAD	Non Coding
TTY1	TTY1_1	CCACTGTGGGACCATAAG TG	BROAD	Non Coding
TTY1	TTY1_2	CCTCCGTGGAGAAGTGTC AG	BROAD	Non Coding
TTY1	TTY1_3	TCACCTGTGAATATAACC TG	BROAD	Non Coding
TTY1	TTY1_4	GGTGGGGATACAATCTTG TG	BROAD	Non Coding
TTY10	TTY10_1	TTACTAGATGACAGATCG TG	BROAD	Non Coding

TTY10	TTY10_2	TGGTAACAGGTAGCAATC AG	BROAD	Non Coding
TTY10	TTY10_3	TTCTGTACTTCTGCATAC GT	BROAD	Non Coding
TTY10	TTY10_4	ACTACTGACCACCAAGAC AG	BROAD	Non Coding
TTY11	TTY11_1	CATTCTGCAACAACCAGC CG	BROAD	Non Coding
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TTY11	TTY11_3	TTGTAACAGGAATAGTCA GG	BROAD	Non Coding
TTY11	TTY11_4	TCTTGTGGTCATGAGAAC AT	BROAD	Non Coding
TTY12	TTY12_1	GAAGCACTGTGACATAA GGG	BROAD	Non Coding
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TTY12	TTY12_3	CATCATAGTGATATATCA CT	BROAD	Non Coding
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TTY13	TTY13_1	TCTAATGGTAGCTACGAT GG	BROAD	Non Coding
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TTY13	TTY13_3	GCAACAATAAGGTCAGA CAG	BROAD	Non Coding
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TTY14	TTY14_1	TGGACCGAGATCTTCAGT TG	BROAD	Non Coding
TTY14	TTY14_2	CAGGGACTGAGCAAGTT ATG	BROAD	Non Coding
TTY14	TTY14_3	ATGGACTAAGAAAACAC CAG	BROAD	Non Coding
TTY14	TTY14_4	TGAAACCTACCCCAATGT GT	BROAD	Non Coding
TTY15	TTY15_1	AATGGTACTAGTAATAAG TG	BROAD	Non Coding
TTY15	TTY15_2	AACTTAGAATGATGACA CA	BROAD	Non Coding
TTY15	TTY15_3	AAAATCCCCCATAACACC CA	BROAD	Non Coding
TTY15	TTY15_4	ACTCACCTTGAATCACCC AA	BROAD	Non Coding

TTY16	TTY16_1	CCCAGCCGTTGGGAAACA TG	BROAD	Non Coding
TTY16	TTY16_2	GGCACAACAAAGGTGCT CCC	BROAD	Non Coding
TTY16	TTY16_3	GAAACATGAGGACATGG CCA	BROAD	Non Coding
TTY16	TTY16_4	TCTATAGCAAAAAGACAC TT	BROAD	Non Coding
TTY17A	TTY17A_1	TGGTTCACCTTGACTCAC AT	BROAD	Non Coding
TTY17A	TTY17A_2	ACACAACCTACCCCATAA TG	BROAD	Non Coding
TTY17A	TTY17A_3	ATGTGCTTCAAAGCTCAA CA	BROAD	Non Coding
TTY17A	TTY17A_4	CATTGGAAAATACTTGAA CT	BROAD	Non Coding
TTY17B	TTY17B_1	TGAAATCCTTCCTCATTA TG	BROAD	Non Coding
TTY17B	TTY17B_2	TGAACCAAAATTTTCAGGC TC	BROAD	Non Coding
TTY17B	TTY17B_3	CAGGTGTGTTTCAGGCTGC TG	BROAD	Non Coding
TTY17B	TTY17B_4	TTCCTGTTACAGGTGTGT TC	BROAD	Non Coding
TTY17C	TTY17C_1	AACTTACCCCATATGAG GA	BROAD	Non Coding
TTY17C	TTY17C_2	CCAGTGAAAATCTTGAGA AT	BROAD	Non Coding
TTY17C	TTY17C_3	CCACACTGAACCAAAATT TC	BROAD	Non Coding
TTY17C	TTY17C_4	ACATTGGAAAATACTTGA AC	BROAD	Non Coding
TTY18	TTY18_1	TGTTGCCATACATCAAAC TG	BROAD	Non Coding
TTY18	TTY18_2	CGGAGGCCCAAAATGAA GAG	BROAD	Non Coding
TTY18	TTY18_3	CGACAAAGGCATGTCCA AAG	BROAD	Non Coding
TTY18	TTY18_4	GCAAGTTCTTGAGACAGA CT	BROAD	Non Coding
TTY19	TTY19_1	AGCAGGTGATGCATCTTG TG	BROAD	Non Coding
TTY19	TTY19_2	GGTGAAGATACAGTCTGT TG	BROAD	Non Coding
TTY19	TTY19_3	AATTTGGTTCCCAACTGA GC	BROAD	Non Coding

TTY19	TTY19_4	ATGAAATAGTCTAGATTC CC	BROAD	Non Coding
TTY1B	TTY1B_1	ACACGTGCTTCACATCAT GA	BROAD	Non Coding
TTY1B	TTY1B_2	TAGGATCATGAGACTATC TG	BROAD	Non Coding
TTY1B	TTY1B_3	CTGCCTGTGAAATCCCAC TG	BROAD	Non Coding
TTY1B	TTY1B_4	ACACCGCTGACACTTCTC CA	BROAD	Non Coding
TTY2	TTY2_1	CAGCTGACATGCCTACAG CG	BROAD	Non Coding
TTY2	TTY2_2	TGTGGATAAGAACTCCGT GG	BROAD	Non Coding
TTY2	TTY2_3	ATGATGGTCTTCTGTGAA CA	BROAD	Non Coding
TTY2	TTY2_4	TTACCTGAGAACCCAGAA GT	BROAD	Non Coding
TTY20	TTY20_1	TAGTCTTAGTAAATGAAG AG	BROAD	Non Coding
TTY20	TTY20_2	GGACGATTGAAGGTTACT TA	BROAD	Non Coding
TTY20	TTY20_3	ATTTACATCCAACCTCTTC AC	BROAD	Non Coding
TTY20	TTY20_4	AAAAAAAAACTGGACGAT TGA	BROAD	Non Coding
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TTY21	TTY21_2	AACCCACTGCCTTACCCA AA	BROAD	Non Coding
TTY21	TTY21_3	AATCATTCATGAGTCTGC AG	BROAD	Non Coding
TTY21	TTY21_4	GTAAGGCAGTGGGTATC TC	BROAD	Non Coding
TTY21B	TTY21B_1	TGGTCAGGTCCAACCTGAA AG	BROAD	Non Coding
TTY21B	TTY21B_2	GAGTCTGCTCTCTTGGGG AT	BROAD	Non Coding
TTY21B	TTY21B_3	GCTCTAGAGTCTAGACCT TT	BROAD	Non Coding
TTY21B	TTY21B_4	GACCATGGAGACTGCCCA AA	BROAD	Non Coding
TTY22	TTY22_1	AGAACCATTTCATGACTG TG	BROAD	Non Coding
TTY22	TTY22_2	AGTGGGTGCTTCATGTTG TG	BROAD	Non Coding

TTY22	TTY22_3	GACTCCTATGACCATCAC CA	BROAD	Non Coding
TTY22	TTY22_4	AGGATCATGGGACTATAC TG	BROAD	Non Coding
TTY23	TTY23_1	CAGCAATCCTACCAAAAC CC	BROAD	Non Coding
TTY23	TTY23_2	TCTACACAGATATCCACC TG	BROAD	Non Coding
TTY23	TTY23_3	CAGTTGTTCTGGGATCAT GA	BROAD	Non Coding
TTY23	TTY23_4	CCTCCCTGGACACATACT GA	BROAD	Non Coding
TTY23B	TTY23B_1	ATAAGACAGTCCACTTCA CA	BROAD	Non Coding
TTY23B	TTY23B_2	AAACAGAACATGACAGA CCT	BROAD	Non Coding
TTY23B	TTY23B_3	GAATGAGATACCCTGTAC CC	BROAD	Non Coding
TTY23B	TTY23B_4	TCAGCAATCCTACCAAAA CC	BROAD	Non Coding
TTY2B	TTY2B_1	TTCTTATCCACAAAGTCA CA	BROAD	Non Coding
TTY2B	TTY2B_2	AGTCTCATGATCCTACAA GA	BROAD	Non Coding
TTY2B	TTY2B_3	GAACAGGGAAGAGTTTA GTG	BROAD	Non Coding
TTY2B	TTY2B_4	CCTTGTGTCTAAGAGTAT GC	BROAD	Non Coding
TTY3	TTY3_1	CATGATGTAGTCCCTTGA AG	BROAD	Non Coding
TTY3	TTY3_2	TCTTCTGCAGGATGATTG GG	BROAD	Non Coding
TTY3	TTY3_3	TGCAGAAGATTCTTCAAA TG	BROAD	Non Coding
TTY3	TTY3_4	GCTACAAGCAGATCAAA ACC	BROAD	Non Coding
TTY3B	TTY3B_1	ATTGGGAGGTCATTAGAA AC	BROAD	Non Coding
TTY3B	TTY3B_2	CTTTAAGGTTGCCACTTC AA	BROAD	Non Coding
TTY3B	TTY3B_3	CCATTTGAAGAATCTTCT GC	BROAD	Non Coding
TTY3B	TTY3B_4	GTTGTCTCATTACTGTAC TG	BROAD	Non Coding
TTY4	TTY4_1	GAATGAATTGTGACATAC GA	BROAD	Non Coding

TTY4	TTY4_2	ACACCCTCTATTCAACAC AA	BROAD	Non Coding
TTY4	TTY4_3	AAAGGAGGTTTCAGACAA ATG	BROAD	Non Coding
TTY4	TTY4_4	GTGTGAGAACCACCCTCA TG	BROAD	Non Coding
TTY4B	TTY4B_1	TGATTCAAGACTGAGAAC AC	BROAD	Non Coding
TTY4B	TTY4B_2	TACGACGGAGTACAAAA CCT	BROAD	Non Coding
TTY4B	TTY4B_3	CTATCGCATAATGCCTCT TG	BROAD	Non Coding
TTY4B	TTY4B_4	TGCTATTGTGACATACAC CT	BROAD	Non Coding
TTY4C	TTY4C_1	TCACAGACTGCCTCACAC AA	BROAD	Non Coding
TTY4C	TTY4C_2	CCACACTCTTCACTGAAA GG	BROAD	Non Coding
TTY4C	TTY4C_3	GGTGTATGTCACAATAGC AC	BROAD	Non Coding
TTY4C	TTY4C_4	GCCTGGACATTGTCCACA AG	BROAD	Non Coding
TTY5	TTY5_1	CACTTACCACTAAGCCAC GT	BROAD	Non Coding
TTY5	TTY5_2	TGACACACTCCTTAACCC GG	BROAD	Non Coding
TTY5	TTY5_3	GACCTGAAATGACATCCG GA	BROAD	Non Coding
TTY5	TTY5_4	GGATTCACTTCACCACAC CT	BROAD	Non Coding
TTY6	TTY6_1	ATGAATGCCACAATTCCC TG	BROAD	Non Coding
TTY6	TTY6_2	TGCAAGAATTGAGTCCCA GG	BROAD	Non Coding
TTY6	TTY6_3	ACAATGAAGGAGTGACG TGA	BROAD	Non Coding
TTY6	TTY6_4	ATAAAGGTGAGGATACA AGC	BROAD	Non Coding
TTY6B	TTY6B_1	GTGCAAGAATTGAGTCCC AG	BROAD	Non Coding
TTY6B	TTY6B_2	GAGATGTCTAGACTGTGA TG	BROAD	Non Coding
TTY6B	TTY6B_3	GTGTATCCCACAAAGAAG AC	BROAD	Non Coding
TTY6B	TTY6B_4	ATTCTCCAGTGTACATCC CA	BROAD	Non Coding

TTY7	TTY7_1	CTGCCTGCAATAATGCAC TG	BROAD	Non Coding
TTY7	TTY7_2	CAGGCAAGAGTCCACCA CCA	BROAD	Non Coding
TTY7	TTY7_3	AAATGCACATGCACGCCT CA	BROAD	Non Coding
TTY7	TTY7_4	ATTCAAGGGACCCTGCGG AC	BROAD	Non Coding
TTY7B	TTY7B_1	CACTAGCAGTCCGGTCCA CA	BROAD	Non Coding
TTY7B	TTY7B_2	GTATACAATCTGGTGAAA GG	BROAD	Non Coding
TTY7B	TTY7B_3	CAGGACCTCCACACCGTG AG	BROAD	Non Coding
TTY7B	TTY7B_4	ATGAATGTCACAATTCCG TG	BROAD	Non Coding
TTY8	TTY8_1	GCCAGCCCGAAGGAACA TCA	BROAD	Non Coding
TTY8	TTY8_2	CAGTGTTTCACGCTAACC CA	BROAD	Non Coding
TTY8	TTY8_3	ACACACCCCTAAGCACAC AA	BROAD	Non Coding
TTY8	TTY8_4	AACCAAACCTCAGGAGCT ACC	BROAD	Non Coding
TTY8B	TTY8B_1	AATGAACCGTGAAATCCC TA	BROAD	Non Coding
TTY8B	TTY8B_2	GTTGACTTTAAGCACCTG CT	BROAD	Non Coding
TTY8B	TTY8B_3	TTCTTCAGGAAGACCCAC CT	BROAD	Non Coding
TTY8B	TTY8B_4	GTAGATGTGAGCCAGCCC GA	BROAD	Non Coding
TTY9A	TTY9A_1	CAAAATCTAGGACACTCT AG	BROAD	Non Coding
TTY9A	TTY9A_2	AAATAGTACAATATTGCC TG	BROAD	Non Coding
TTY9A	TTY9A_3	AATACAGTGTCTCTAAT GG	BROAD	Non Coding
TTY9A	TTY9A_4	TGTGATAGAATTAAAAAG TG	BROAD	Non Coding
TTY9B	TTY9B_1	TGTGTGATAGAATTAAAA AG	BROAD	Non Coding
TTY9B	TTY9B_2	GTAGAAAACAGAAATAT GCT	BROAD	Non Coding
TTY9B	TTY9B_3	TCTGGAGTGTGATTAGAG CT	BROAD	Non Coding

TTY9B	TTY9B_4	AATGAGATCAATTGTAAA GG	BROAD	Non Coding
ZFY-AS1	ZFY-AS1_1	CATCTTGGAAACCCTAAG TG	BROAD	Non Coding
ZFY-AS1	ZFY-AS1_2	CTGTGATAACATTACCTG CA	BROAD	Non Coding
ZFY-AS1	ZFY-AS1_3	AGAAATGGGTTCCAAAA ACA	BROAD	Non Coding
ZFY-AS1	ZFY-AS1_4	GCTGGACTCTTCTACTGT GA	BROAD	Non Coding
ACTR3BP1	ACTR3BP1_1	AATCTATGTATGCCACAA AG	BROAD	Pseudogene
ACTR3BP1	ACTR3BP1_2	GGGAGTGAAAGAATGAG GAG	BROAD	Pseudogene
ACTR3BP1	ACTR3BP1_3	GTCTCCAGTGACGTTCAA GA	BROAD	Pseudogene
ACTR3BP1	ACTR3BP1_4	TGATGTGGATCCCTGGAA GT	BROAD	Pseudogene
AGKP1	AGKP1_1	TTGTAAGAAGAGACAGA CAC	BROAD	Pseudogene
AGKP1	AGKP1_2	TGTGATGGATAGTTCAAT GG	BROAD	Pseudogene
AGKP1	AGKP1_3	TCAGTCCAGAAATGTATA TG	BROAD	Pseudogene
AGKP1	AGKP1_4	AGGTTATGAGGGATAAGT CA	BROAD	Pseudogene
ANKRD20A6 P	ANKRD20A6P_1	TCCATAGAACATGTCTAC AT	BROAD	Pseudogene
ANKRD20A6 P	ANKRD20A6P_2	GCTCAAGAGCCAGAGGTT GG	BROAD	Pseudogene
ANKRD20A6 P	ANKRD20A6P_3	ATTCGGCTTCGGGAGCTG CA	BROAD	Pseudogene
ANKRD20A6 P	ANKRD20A6P_4	AGACATGTTCTATGGAGC CG	BROAD	Pseudogene
ANKRD36P1	ANKRD36P1_1	TACCATTCTGGTTGGAC AG	BROAD	Pseudogene
ANKRD36P1	ANKRD36P1_2	CATCATGATACGTCGACA GA	BROAD	Pseudogene
ANKRD36P1	ANKRD36P1_3	ACAGGCTGTACAAC TAGG GC	BROAD	Pseudogene
ANKRD36P1	ANKRD36P1_4	TGAAAAATTGACCCTTAC AT	BROAD	Pseudogene
ANOS2P	ANOS2P_1	CTGACATAAGACCCAACT GA	BROAD	Pseudogene
ANOS2P	ANOS2P_2	ACATAGCCGATTGTATAC AG	BROAD	Pseudogene

ANOS2P	ANOS2P_3	CTTCCAAGTAAAGTGACT GG	BROAD	Pseudogene
ANOS2P	ANOS2P_4	GTTCTCAAATACACCCT GT	BROAD	Pseudogene
ARSDP1	ARSDP1_1	AAGTCATCATGACTTATA CG	BROAD	Pseudogene
ARSDP1	ARSDP1_2	ATAGCTGAGAGAGATCA CCT	BROAD	Pseudogene
ARSDP1	ARSDP1_3	TGTGAATTGTGCATTCCG CG	BROAD	Pseudogene
ARSDP1	ARSDP1_4	AAAACACAAGAAGCCCA TGC	BROAD	Pseudogene
ASS1P6	ASS1P6_1	CAAATGGGCACCTACGTG AG	BROAD	Pseudogene
ASS1P6	ASS1P6_2	CTATGCTCATTTACACAT CG	BROAD	Pseudogene
ASS1P6	ASS1P6_3	CAGCCACACAAGCATGC AGG	BROAD	Pseudogene
ASS1P6	ASS1P6_4	CCTCATGTGTATCAGCTA TG	BROAD	Pseudogene
ATP5PFP1	ATP5PFP1_1	GGATCTTCAAATTTGAAG TG	BROAD	Pseudogene
ATP5PFP1	ATP5PFP1_2	TCCATAAAGAGTTTCTGT AG	BROAD	Pseudogene
ATP5PFP1	ATP5PFP1_3	CTTATTAAATGCCACTGC AG	BROAD	Pseudogene
ATP5PFP1	ATP5PFP1_4	TGAAGTCATTGAAAAACC CC	BROAD	Pseudogene
BCORP1	BCORP1_1	GGGAATCCTCCTACTCTA CG	BROAD	Pseudogene
BCORP1	BCORP1_2	GATTACTTAAATGACCTA CA	BROAD	Pseudogene
BCORP1	BCORP1_3	TTAACGAAGCATGTTTAC AC	BROAD	Pseudogene
BCORP1	BCORP1_4	AAGTACAACACTTCTGT GG	BROAD	Pseudogene
BPY2DP	BPY2DP_1	TGCATACTGGGTCTAGTC AG	BROAD	Pseudogene
BPY2DP	BPY2DP_2	GTATAATTGACACAACAC TT	BROAD	Pseudogene
BPY2DP	BPY2DP_3	GTCATTGCCTCACAAGAA CA	BROAD	Pseudogene
BPY2DP	BPY2DP_4	AATGTCACATCCGATCAC CT	BROAD	Pseudogene
C2orf27AP1	C2orf27AP1_1	GAGGCCGGTGGCTGTACA TG	BROAD	Pseudogene

C2orf27AP1	C2orf27AP1_2	ATGGAGATTTGCCCTCAC CT	BROAD	Pseudogene
C2orf27AP1	C2orf27AP1_3	AGTGTGGCAGGAGCTAG AGG	BROAD	Pseudogene
C2orf27AP1	C2orf27AP1_4	TCTTCTTGACAGGCAGAC AG	BROAD	Pseudogene
CD24P4	CD24P4_1	GCTGCCGAAACAATACGT TG	BROAD	Pseudogene
CD24P4	CD24P4_2	TCTGCCCATGTCCCCTAC GT	BROAD	Pseudogene
CD24P4	CD24P4_3	GAGTACTTCCAACACTGG GT	BROAD	Pseudogene
CD24P4	CD24P4_4	TGGCGTCTGGAAGTCCAA TG	BROAD	Pseudogene
CDC27P2	CDC27P2_1	GCGACCTGTTCTTACTAC CC	BROAD	Pseudogene
CDC27P2	CDC27P2_2	GATGACACATCAATTACA GA	BROAD	Pseudogene
CDC27P2	CDC27P2_3	GTACGCAACCAGAATTGT AG	BROAD	Pseudogene
CDC27P2	CDC27P2_4	CTGAATCTCAGGTGTGAT TG	BROAD	Pseudogene
CDY3P	CDY3P_1	CAGAACAACCTGGATTACA TG	BROAD	Pseudogene
CDY3P	CDY3P_2	TAAAGAAAGAGACCGAT TTG	BROAD	Pseudogene
CDY3P	CDY3P_3	GCACTACACCAGAGTAG GAG	BROAD	Pseudogene
CDY3P	CDY3P_4	TAACATATATTGTATCCC AT	BROAD	Pseudogene
CSPG4P1Y	CSPG4P1Y_1	TTGCTGAAGGCCATGTTG TG	BROAD	Pseudogene
CSPG4P1Y	CSPG4P1Y_2	GTGCACACAGACAGTGC ACA	BROAD	Pseudogene
CSPG4P1Y	CSPG4P1Y_3	CGGCCATATTGATGGTAC CC	BROAD	Pseudogene
CSPG4P1Y	CSPG4P1Y_4	CCATGATACTGCCAGACA GG	BROAD	Pseudogene
CTBP2P1	CTBP2P1_1	GCAATTCATCCAGTCATC GT	BROAD	Pseudogene
CTBP2P1	CTBP2P1_2	TGGAGTAAACTATTTGCC TG	BROAD	Pseudogene
CTBP2P1	CTBP2P1_3	AAATAGTAGTGAATGCCG GA	BROAD	Pseudogene
CTBP2P1	CTBP2P1_4	GGGACTCAAGTGACAAG ATG	BROAD	Pseudogene

CYCSP49	CYCSP49_1	TGGTACATAGAGTGGGAC AT	BROAD	Pseudogene
CYCSP49	CYCSP49_2	AAGACTGGGCCTAAACTC CA	BROAD	Pseudogene
CYCSP49	CYCSP49_3	TTATTTGCCACTTAAAGG CA	BROAD	Pseudogene
CYCSP49	CYCSP49_4	ACAGGGAATTCTAATTAC AA	BROAD	Pseudogene
DPPA2P1	DPPA2P1_1	TGTTGACAGCAATCCCAC AA	BROAD	Pseudogene
DPPA2P1	DPPA2P1_2	GCAACGTTTCGAGGAAAC GCA	BROAD	Pseudogene
DPPA2P1	DPPA2P1_3	GAAGTGGTAACTTAAGCG CA	BROAD	Pseudogene
DPPA2P1	DPPA2P1_4	AGAAAACAGAAGTTAGT CTG	BROAD	Pseudogene
DUX4L16	DUX4L16_1	GTGGTTCCCACGCCGCAT CG	BROAD	Pseudogene
DUX4L16	DUX4L16_2	TTGGACCCGGAGCCAAA GTG	BROAD	Pseudogene
DUX4L16	DUX4L16_3	CTGCGTCACCGGATCCCA GA	BROAD	Pseudogene
DUX4L16	DUX4L16_4	CGGTATACTTCCTCGCTG AG	BROAD	Pseudogene
DUX4L17	DUX4L17_1	ACAACCAGGCATAAGCC AGG	BROAD	Pseudogene
DUX4L17	DUX4L17_2	ATGGAGGAATTTAGGTCG CG	BROAD	Pseudogene
DUX4L17	DUX4L17_3	TCCTAGAAATGGAGGCC CG	BROAD	Pseudogene
DUX4L17	DUX4L17_4	TCATCCAGTATCAGGCCG GA	BROAD	Pseudogene
DUX4L18	DUX4L18_1	TGGGAAAGCGTTCCTTAC GG	BROAD	Pseudogene
DUX4L18	DUX4L18_2	CAGGCTGTCCCCTGCAC AA	BROAD	Pseudogene
DUX4L18	DUX4L18_3	GTTTCGGGGTCTTGTGAC GG	BROAD	Pseudogene
DUX4L18	DUX4L18_4	TGTTCCAAACACGCTAGT GT	BROAD	Pseudogene
DUX4L19	DUX4L19_1	AGGCAGGCGAAAGCGGA CCG	BROAD	Pseudogene
DUX4L19	DUX4L19_2	CCACGTGCCCTGCACGAC TG	BROAD	Pseudogene
DUX4L19	DUX4L19_3	AGTTGTCGGGAAGGCCAT CG	BROAD	Pseudogene

DUX4L19	DUX4L19_4	AGAATACCGGACTCTGCT GG	BROAD	Pseudogene
EEF1A1P41	EEF1A1P41_1	GAATAAGTCCACATTAC AG	BROAD	Pseudogene
EEF1A1P41	EEF1A1P41_2	ACTTATTCTAACTATCCT CT	BROAD	Pseudogene
EEF1A1P41	EEF1A1P41_3	CTGATTAAAACTGGGGTA GC	BROAD	Pseudogene
EEF1A1P41	EEF1A1P41_4	GTGTATTATGGGTCACTG GT	BROAD	Pseudogene
EIF4A1P2	EIF4A1P2_1	GGAGCAAGACGTGATCA TGA	BROAD	Pseudogene
EIF4A1P2	EIF4A1P2_2	GGGCACCAATATGCGTGC TG	BROAD	Pseudogene
EIF4A1P2	EIF4A1P2_3	TCAACGTGGAACAAGAG GAG	BROAD	Pseudogene
EIF4A1P2	EIF4A1P2_4	AAAATGACAAGTCTATCC CT	BROAD	Pseudogene
FAM8A4P	FAM8A4P_1	GTGCCACCATCCCTGCAC AT	BROAD	Pseudogene
FAM8A4P	FAM8A4P_2	TGGACTGATGGCTACACA TG	BROAD	Pseudogene
FAM8A4P	FAM8A4P_3	TGCTCTCCCAGTCATGAC AA	BROAD	Pseudogene
FAM8A4P	FAM8A4P_4	AGATATCATTTATCCCAC TG	BROAD	Pseudogene
GOLGA2P2Y	GOLGA2P2Y_1	CCAGTACCGAGAACTAGC AG	BROAD	Pseudogene
GOLGA2P2Y	GOLGA2P2Y_2	CTCATCCCAGAAAAAGCC AG	BROAD	Pseudogene
GOLGA2P2Y	GOLGA2P2Y_3	GCCCATGCTGAACATTCC AG	BROAD	Pseudogene
GOLGA2P2Y	GOLGA2P2Y_4	AGCTCCTCAAAGCTGCTG TG	BROAD	Pseudogene
GOLGA2P3Y	GOLGA2P3Y_1	ACAATGAGGAGGAGGCA CCT	BROAD	Pseudogene
GOLGA2P3Y	GOLGA2P3Y_2	AGAGTGCACTGCAGTTGG AG	BROAD	Pseudogene
GOLGA2P3Y	GOLGA2P3Y_3	TATTGCGGAGCTTGAGTG CA	BROAD	Pseudogene
GOLGA2P3Y	GOLGA2P3Y_4	AGTGCCAAAGACGCAGC ACT	BROAD	Pseudogene
GOLGA6L16 P	GOLGA6L16P_1	CAGAGGGCGGAGTCACA CAG	BROAD	Pseudogene
GOLGA6L16 P	GOLGA6L16P_2	GCACGTTCGCACATCGAA GG	BROAD	Pseudogene

GOLGA6L16P	GOLGA6L16P_3	AGCAGCAGGTATCTACAGGG	BROAD	Pseudogene
GOLGA6L16P	GOLGA6L16P_4	GGGAGCAGGATGAGAGACTG	BROAD	Pseudogene
GYG2P1	GYG2P1_1	GTCACGAACCCGCAGAACAG	BROAD	Pseudogene
GYG2P1	GYG2P1_2	TACTCACCCGACATGGTCCTG	BROAD	Pseudogene
GYG2P1	GYG2P1_3	AAGATCACTTGGGCCAGTGA	BROAD	Pseudogene
GYG2P1	GYG2P1_4	CTGGCAGTAGATGTCATCTG	BROAD	Pseudogene
HSFY3P	HSFY3P_1	GCCGATGTATCAAATGTCTAT	BROAD	Pseudogene
HSFY3P	HSFY3P_2	GAGACACAACTGTGTAAACG	BROAD	Pseudogene
HSFY3P	HSFY3P_3	TGCAGGCTTGAAAACCATGC	BROAD	Pseudogene
HSFY3P	HSFY3P_4	ACAAAATGGAGACCTAGTGG	BROAD	Pseudogene
KRT18P10	KRT18P10_1	GGTGGAGAAGGTAGACCGAG	BROAD	Pseudogene
KRT18P10	KRT18P10_2	GATGAGCTGCACCATCTGAA	BROAD	Pseudogene
KRT18P10	KRT18P10_3	AGAGATTGAAGCTCTCAGGG	BROAD	Pseudogene
KRT18P10	KRT18P10_4	TGAGGCCGTGCTGAACATCA	BROAD	Pseudogene
LINC00266-2P	LINC00266-2P_1	CAGTTCAAGATGATGACTCA	BROAD	Pseudogene
LINC00266-2P	LINC00266-2P_2	CCTGCAGTTGAAGATCCATG	BROAD	Pseudogene
LINC00266-2P	LINC00266-2P_3	AAAAGAAGGTGTGTGCAATAG	BROAD	Pseudogene
LINC00266-2P	LINC00266-2P_4	GCATCTTAAAATGATTCAATGC	BROAD	Pseudogene
LINC00266-4P	LINC00266-4P_1	TGGAGCAGCCCACAAGGCTG	BROAD	Pseudogene
LINC00266-4P	LINC00266-4P_2	CACACAAACCTTGGAAGAGA	BROAD	Pseudogene
LINC00266-4P	LINC00266-4P_3	GCCGCTGGGAGCTGCTGCAT	BROAD	Pseudogene
LINC00266-4P	LINC00266-4P_4	CAGTTGGGGGGTGGTCCAGT	BROAD	Pseudogene
MXRA5Y	MXRA5Y_1	GATAGTAGGAGTCTAACAACG	BROAD	Pseudogene

MXRA5Y	MXRA5Y_2	GGGGCAGACCATATCAC GGT	BROAD	Pseudogene
MXRA5Y	MXRA5Y_3	CTCAACTTGAATCCCACC GG	BROAD	Pseudogene
MXRA5Y	MXRA5Y_4	GTTGCACACTCCATGGAC CA	BROAD	Pseudogene
NAP1L1P2	NAP1L1P2_1	TCAAATCACGTATCAAAT AG	BROAD	Pseudogene
NAP1L1P2	NAP1L1P2_2	GGGTTCTACAGGGTGCCA GA	BROAD	Pseudogene
NAP1L1P2	NAP1L1P2_3	ACTTAAATGTGCACAGAC AG	BROAD	Pseudogene
NAP1L1P2	NAP1L1P2_4	GCATTCTCAGAACTTCAG GC	BROAD	Pseudogene
PARP4P1	PARP4P1_1	CAATCATTGTGAAACAAC GA	BROAD	Pseudogene
PARP4P1	PARP4P1_2	GAAGCCCAGTCAGAGTA CCG	BROAD	Pseudogene
PARP4P1	PARP4P1_3	TGTCTTCTGGACGAATCA GT	BROAD	Pseudogene
PARP4P1	PARP4P1_4	TTCACATCAACTTTGGAA CG	BROAD	Pseudogene
PCMTD1P1	PCMTD1P1_1	TGATTACCCACAAATACG TG	BROAD	Pseudogene
PCMTD1P1	PCMTD1P1_2	CAGTGAAGCGATGAAGC CAG	BROAD	Pseudogene
PCMTD1P1	PCMTD1P1_3	AGGCCAAGGGTATTCCTC AA	BROAD	Pseudogene
PCMTD1P1	PCMTD1P1_4	GGAAGAAGATAGTAAAG AAG	BROAD	Pseudogene
PRKY	PRKY_1	ATGATCTATAGGATGTGA GT	BROAD	Pseudogene
PRKY	PRKY_2	TTATTACATAAATTAGAC AG	BROAD	Pseudogene
PRKY	PRKY_3	TGGGGGAATAAGATATCC GG	BROAD	Pseudogene
PRKY	PRKY_4	TACCTGGAACTGCCCAT GG	BROAD	Pseudogene
PRRC2CP1	PRRC2CP1_1	CCATTTAAAAAATGGCG GG	BROAD	Pseudogene
PRRC2CP1	PRRC2CP1_2	CAACTCAACACAGTAAAC TG	BROAD	Pseudogene
PRRC2CP1	PRRC2CP1_3	G TTCAGATGACCGCAGAA CC	BROAD	Pseudogene
PRRC2CP1	PRRC2CP1_4	TTAGCTTCTGAATCATCA TG	BROAD	Pseudogene

PSIP1P2	PSIP1P2_1	CATTGTATGGTTGACCCA CT	BROAD	Pseudogene
PSIP1P2	PSIP1P2_2	AGTCTGTACATTGATGTG TA	BROAD	Pseudogene
PSIP1P2	PSIP1P2_3	ATAACAGAATGGGTATAT AC	BROAD	Pseudogene
PSIP1P2	PSIP1P2_4	TTTAACAGCATAGAACT TG	BROAD	Pseudogene
PSMA6P1	PSMA6P1_1	ATATTTCTCAGGTCTACA CA	BROAD	Pseudogene
PSMA6P1	PSMA6P1_2	ACAACAAACAAATATCAT GG	BROAD	Pseudogene
PSMA6P1	PSMA6P1_3	GGGTGTAAAGCCACTGCA GT	BROAD	Pseudogene
PSMA6P1	PSMA6P1_4	GATCACACTTACATACCT GA	BROAD	Pseudogene
RBMY1A3P	RBMY1A3P_1	GAAGCAGTGGAGGAACA GGA	BROAD	Pseudogene
RBMY1A3P	RBMY1A3P_2	CATTACAGCACAATGGT AG	BROAD	Pseudogene
RBMY1A3P	RBMY1A3P_3	CCCTCACATGAAGGACAC CT	BROAD	Pseudogene
RBMY1A3P	RBMY1A3P_4	AAATATGGTCCCATATCA GA	BROAD	Pseudogene
RBMY2EP	RBMY2EP_1	GGTGGCTACGACGAAAC CCG	BROAD	Pseudogene
RBMY2EP	RBMY2EP_2	GATCATTCTGATCGTACA AG	BROAD	Pseudogene
RBMY2EP	RBMY2EP_3	GTGTATTGTTATAATCAG GG	BROAD	Pseudogene
RBMY2EP	RBMY2EP_4	TGCCAAAGATATGAATGG AG	BROAD	Pseudogene
RBMY2FP	RBMY2FP_1	ACACACATTCTCAGACAT GG	BROAD	Pseudogene
RBMY2FP	RBMY2FP_2	TAATCCCAACTACTCAGC TG	BROAD	Pseudogene
RBMY2FP	RBMY2FP_3	GATAATACAAGTTAACCG AT	BROAD	Pseudogene
RBMY2FP	RBMY2FP_4	AAATGTAAAGATGGAAC CAT	BROAD	Pseudogene
RBMY2HP	RBMY2HP_1	CGATATGCATAGTCTCAA GG	BROAD	Pseudogene
RBMY2HP	RBMY2HP_2	GTGTATTATTATAATCAT GG	BROAD	Pseudogene
RBMY2HP	RBMY2HP_3	GGTCACCACAAGGCCAA CTG	BROAD	Pseudogene

RBMV2HP	RBMV2HP_4	GGCATCTATAGGAGATGA TG	BROAD	Pseudogene
RBMV2KP	RBMV2KP_1	AGAGATCATTCTGAACAC CA	BROAD	Pseudogene
RBMV2KP	RBMV2KP_2	AGAAGCAATAGTTGTATG GG	BROAD	Pseudogene
RBMV2KP	RBMV2KP_3	ATATGGTAGCTCAAGATA TG	BROAD	Pseudogene
RBMV2KP	RBMV2KP_4	GAAGTCGTGAGAGTTACT CA	BROAD	Pseudogene
RBMV2MP	RBMV2MP_1	CTTCCACCGTAAGACAAC TG	BROAD	Pseudogene
RBMV2MP	RBMV2MP_2	GATGGCTACAATGACGCC CG	BROAD	Pseudogene
RBMV2MP	RBMV2MP_3	ATACCTCAAAAAATTAAT GG	BROAD	Pseudogene
RBMV2MP	RBMV2MP_4	ATTAAAGGTCCCATATCA CA	BROAD	Pseudogene
RBMV2QP	RBMV2QP_1	GGAGCAGGTACACCCTAT CG	BROAD	Pseudogene
RBMV2QP	RBMV2QP_2	GCTGTGGCAAGAAGCAA CAG	BROAD	Pseudogene
RBMV2QP	RBMV2QP_3	TTACCGTGATGGCTACTG TG	BROAD	Pseudogene
RBMV2QP	RBMV2QP_4	AAAGCAGTATTTGTGAAA CA	BROAD	Pseudogene
RBMV3AP	RBMV3AP_1	AGAAGCAATAGTCGGAT GGG	BROAD	Pseudogene
RBMV3AP	RBMV3AP_2	TCGACGAAGTGATTGGAT TG	BROAD	Pseudogene
RBMV3AP	RBMV3AP_3	GTGTATTGTTATAATAAT GG	BROAD	Pseudogene
RBMV3AP	RBMV3AP_4	GATGAATCTGCTAGCAAC AC	BROAD	Pseudogene
RREP1Y	RREP1Y_1	GTAATCGTAGGACTTAAT GG	BROAD	Pseudogene
RREP1Y	RREP1Y_2	AGATGGTGAAAGCTCCA AGT	BROAD	Pseudogene
RREP1Y	RREP1Y_3	GGTGTGCTCAGAAATAG CG	BROAD	Pseudogene
RREP1Y	RREP1Y_4	GACACCAGATTAAATACT GG	BROAD	Pseudogene
RREP2Y	RREP2Y_1	GTCATCAGGAACCTACAC TC	BROAD	Pseudogene
RREP2Y	RREP2Y_2	AGGCTAGGGCTGCCATTC GT	BROAD	Pseudogene

REREP2Y	REREP2Y_3	TTAAAGCACAGGAACCC ATG	BROAD	Pseudogene
REREP2Y	REREP2Y_4	CAGTGGAGTCAAGCTAA GGA	BROAD	Pseudogene
RN7SL702P	RN7SL702P_1	GTGCAGACATCCGATCAA CA	BROAD	Pseudogene
RN7SL702P	RN7SL702P_2	TGAACCACCCTAAGTCAC AA	BROAD	Pseudogene
RN7SL702P	RN7SL702P_3	AGCAAGAAGTAGCATGC CTG	BROAD	Pseudogene
RN7SL702P	RN7SL702P_4	AAAACCTCCCGTGCTGATC AG	BROAD	Pseudogene
RNASEH2CP 1	RNASEH2CP1_1	GCGCGTGAATCGTTGCCG CG	BROAD	Pseudogene
RNASEH2CP 1	RNASEH2CP1_2	CTACACTTAAGAGTCCCT CG	BROAD	Pseudogene
RNASEH2CP 1	RNASEH2CP1_3	ACACTACACCTGATACCC TG	BROAD	Pseudogene
RNASEH2CP 1	RNASEH2CP1_4	ACGTATCCCACGAGGCCG GA	BROAD	Pseudogene
RNF19BPY	RNF19BPY_1	ACTTCTCTGTCCCAGCCG AG	BROAD	Pseudogene
RNF19BPY	RNF19BPY_2	AATCTGCAATATGATAGT GA	BROAD	Pseudogene
RNF19BPY	RNF19BPY_3	ATGTGTGTATATTATGTA CG	BROAD	Pseudogene
RNF19BPY	RNF19BPY_4	CATCACTCTCCAAACCAC TG	BROAD	Pseudogene
RNU2-57P	RNU2-57P_1	TCTGATGTATCCTCTGTC CG	BROAD	Pseudogene
RNU2-57P	RNU2-57P_2	GAGGGGAACACCGTTCTT GG	BROAD	Pseudogene
RNU2-57P	RNU2-57P_3	ACATCAGATATTAAACTG AT	BROAD	Pseudogene
RNU2-57P	RNU2-57P_4	TGCAATACCAGGTCAATG TG	BROAD	Pseudogene
RPL26P37	RPL26P37_1	TTTCAGCTCATTGGAAAG AG	BROAD	Pseudogene
RPL26P37	RPL26P37_2	ACCGCAAAAATATCCGTG AA	BROAD	Pseudogene
RPL26P37	RPL26P37_3	ATACATTGAACGGGTGCA GT	BROAD	Pseudogene
RPL26P37	RPL26P37_4	CCTTCAGTTGGAAGTCAC AA	BROAD	Pseudogene
SEPT14P22	SEPT14P22_1	TAAAGTGTGAACTCCTAG CA	BROAD	Pseudogene

SEPT14P22	SEPT14P22_2	TTAATTCTGACACAATAG CA	BROAD	Pseudogene
SEPT14P22	SEPT14P22_3	ATAGCTAATGTACTATCA CT	BROAD	Pseudogene
SEPT14P22	SEPT14P22_4	CTCATAGCAGTCTGTCAC CC	BROAD	Pseudogene
SEPT14P23	SEPT14P23_1	AAAAGAAAGGGTGAAC TGA	BROAD	Pseudogene
SEPT14P23	SEPT14P23_2	CTGCTATGAGTCACCACA TC	BROAD	Pseudogene
SEPT14P23	SEPT14P23_3	CATAGCTAATGTACTATC AC	BROAD	Pseudogene
SEPT14P23	SEPT14P23_4	CATGAAATTATGGTAGTA TA	BROAD	Pseudogene
SERBP1P2	SERBP1P2_1	TAGAGAAAATAAGCCAA CGG	BROAD	Pseudogene
SERBP1P2	SERBP1P2_2	TGAATGCCATAAAACAAC CA	BROAD	Pseudogene
SERBP1P2	SERBP1P2_3	CAAATGATAAAATGTCTC AG	BROAD	Pseudogene
SERBP1P2	SERBP1P2_4	CAGCCAGCTGCAATCCAT TG	BROAD	Pseudogene
SFPQP1	SFPQP1_1	AACAAAAACATGGTACC ACG	BROAD	Pseudogene
SFPQP1	SFPQP1_2	TGAAATAGGAGATGCACT CA	BROAD	Pseudogene
SFPQP1	SFPQP1_3	ATGGAGCCCAGAATTCCA CA	BROAD	Pseudogene
SFPQP1	SFPQP1_4	ATTCCATTAGAAACCACG AG	BROAD	Pseudogene
SHROOM2P1	SHROOM2P1_1	GGCCACAACACATTCACA AG	BROAD	Pseudogene
SHROOM2P1	SHROOM2P1_2	GCCCAAAATTGAACATCC CA	BROAD	Pseudogene
SHROOM2P1	SHROOM2P1_3	GGATGCCACTGATCGCTG GA	BROAD	Pseudogene
SHROOM2P1	SHROOM2P1_4	ACCACCATTTGATGCCCA GG	BROAD	Pseudogene
SLC25A15P1	SLC25A15P1_1	ATCAAAGGGACAGGGCC TAG	BROAD	Pseudogene
SLC25A15P1	SLC25A15P1_2	CTGGATATACCGCAAGCC AG	BROAD	Pseudogene
SLC25A15P1	SLC25A15P1_3	GAAGTTGATGATGAGCCA GT	BROAD	Pseudogene
SLC25A15P1	SLC25A15P1_4	CAACTTCCTGGTATATTC GT	BROAD	Pseudogene

SLC9B1P1	SLC9B1P1_1	AAACATGTGATTTCTGTA CA	BROAD	Pseudogene
SLC9B1P1	SLC9B1P1_2	CCACTTGGAAACATATGC GA	BROAD	Pseudogene
SLC9B1P1	SLC9B1P1_3	TTCAGAGCCTAAGATTGC TA	BROAD	Pseudogene
SLC9B1P1	SLC9B1P1_4	TGAATCCAGTGATAGCCA GA	BROAD	Pseudogene
SNX18P1Y	SNX18P1Y_1	GCAATAACAAGTCCATGG CT	BROAD	Pseudogene
SNX18P1Y	SNX18P1Y_2	AGCTGAATATAGAACTGT GT	BROAD	Pseudogene
SNX18P1Y	SNX18P1Y_3	GCTGATGGCATCATCATC AC	BROAD	Pseudogene
SNX18P1Y	SNX18P1Y_4	ACAGGCAACAGGTGGCA GAA	BROAD	Pseudogene
SRIP3	SRIP3_1	TCCCTCCATACCCGCCTG GG	BROAD	Pseudogene
SRIP3	SRIP3_2	ACTGCACCATGTAGTACC TG	BROAD	Pseudogene
SRIP3	SRIP3_3	GCAGCAAAGTAATCATAT AG	BROAD	Pseudogene
SRIP3	SRIP3_4	TGCATTTCCCAGAAAAAC TC	BROAD	Pseudogene
STSP1	STSP1_1	TACCTGATCAGACAGGCT AC	BROAD	Pseudogene
STSP1	STSP1_2	GAGGAAATGGACTGTAG TGT	BROAD	Pseudogene
STSP1	STSP1_3	CCACCAATGAGATTACCT GA	BROAD	Pseudogene
STSP1	STSP1_4	CCTCTGAGTGAGATTGCC AT	BROAD	Pseudogene
SURF6P1	SURF6P1_1	TGAAACGCCTCTGGTCAT TG	BROAD	Pseudogene
SURF6P1	SURF6P1_2	CCCTTCACAGGGAGTGAC CG	BROAD	Pseudogene
SURF6P1	SURF6P1_3	GCAGCAGGCAATCATCGT GG	BROAD	Pseudogene
SURF6P1	SURF6P1_4	TTGTTGAAGATCAGTCCT GG	BROAD	Pseudogene
TAB3P1	TAB3P1_1	TCTTAACAGACGGTACCA AG	BROAD	Pseudogene
TAB3P1	TAB3P1_2	GAGAGAACGCCAATTAC ATG	BROAD	Pseudogene
TAB3P1	TAB3P1_3	ACAACATCTAGCTTGCAC AG	BROAD	Pseudogene

TAB3P1	TAB3P1_4	GAAGAACATTGAGACCT AGG	BROAD	Pseudogene
TEKT4P1	TEKT4P1_1	CTTCGCCGACTGCAACCA GT	BROAD	Pseudogene
TEKT4P1	TEKT4P1_2	GGCAAAGACCCCAGTCA CAG	BROAD	Pseudogene
TEKT4P1	TEKT4P1_3	ACTGTGTCACCCAAGCAA CT	BROAD	Pseudogene
TEKT4P1	TEKT4P1_4	AGATCAGGAACACAACA TGG	BROAD	Pseudogene
TMEM167AP 1	TMEM167AP1_1	ACTTGCCTGAATAGTATA CA	BROAD	Pseudogene
TMEM167AP 1	TMEM167AP1_2	ACATGACATGAGTTACTA CG	BROAD	Pseudogene
TMEM167AP 1	TMEM167AP1_3	AGGCCTAGAAACGTAGA CAG	BROAD	Pseudogene
TMEM167AP 1	TMEM167AP1_4	ACAGGGCATTAAACAGGA CAC	BROAD	Pseudogene
TPTE2P4	TPTE2P4_1	GATATATAGATACTTCAT CA	BROAD	Pseudogene
TPTE2P4	TPTE2P4_2	TATTCTGAATAAAAGATG TG	BROAD	Pseudogene
TPTE2P4	TPTE2P4_3	TGCAGTTAAAAATATGTC AG	BROAD	Pseudogene
TPTE2P4	TPTE2P4_4	ACTGGAATCTCTCTCCAA GA	BROAD	Pseudogene
TSPY11P	TSPY11P_1	AGAGCTTATGTACGGAAC TG	BROAD	Pseudogene
TSPY11P	TSPY11P_2	CAGGACGTCAGTACTCAA CA	BROAD	Pseudogene
TSPY11P	TSPY11P_3	GATGTTGAGCCCTATCGC TG	BROAD	Pseudogene
TSPY11P	TSPY11P_4	ACTCTGGGGTTATGGGCC CA	BROAD	Pseudogene
TSPY12P	TSPY12P_1	GTTCAATAAAGGTAGCTG CA	BROAD	Pseudogene
TSPY12P	TSPY12P_2	GGCCACAGACACTACAA CAG	BROAD	Pseudogene
TSPY12P	TSPY12P_3	CAGGATTTCAGTACTCAG CA	BROAD	Pseudogene
TSPY12P	TSPY12P_4	CTCCTCCTACCACTCCAC GT	BROAD	Pseudogene
TSPY13P	TSPY13P_1	AACTGAGAAGGATACA ACA	BROAD	Pseudogene
TSPY13P	TSPY13P_2	CAGCCTCTATGGCACCCG GT	BROAD	Pseudogene

TSPY13P	TSPY13P_3	ACATAGTTACTATAGTAT GC	BROAD	Pseudogene
TSPY13P	TSPY13P_4	TTGTGGTGTCCCCAGCGA TA	BROAD	Pseudogene
TSPY15P	TSPY15P_1	GGTTTCCAGGAGACCCCT AA	BROAD	Pseudogene
TSPY15P	TSPY15P_2	CAGGATGTCAGTATTCAG CA	BROAD	Pseudogene
TSPY15P	TSPY15P_3	GGTGGCAGATGACATAAT GG	BROAD	Pseudogene
TSPY15P	TSPY15P_4	CATCATACTCAACTCAAC AT	BROAD	Pseudogene
TSPY16P	TSPY16P_1	TTTGAGTGCAGTCCGTTA GG	BROAD	Pseudogene
TSPY16P	TSPY16P_2	GCTACAGAAAGGGCAGC GCA	BROAD	Pseudogene
TSPY16P	TSPY16P_3	AAGACGGTGCACCCTGA AGA	BROAD	Pseudogene
TSPY16P	TSPY16P_4	TCTGGATGATGGCCCCTC TG	BROAD	Pseudogene
TSPY17P	TSPY17P_1	AGCCAGGTGCATGCGCCC TG	BROAD	Pseudogene
TSPY17P	TSPY17P_2	ACCTAACGGACTGCACTC AA	BROAD	Pseudogene
TSPY17P	TSPY17P_3	TGCAGCCCGACCCATAGC AC	BROAD	Pseudogene
TSPY17P	TSPY17P_4	CACCGTCTTCACTCTGCC CG	BROAD	Pseudogene
TSPY5P	TSPY5P_1	TCAGGGCTGATATCAAGA GG	BROAD	Pseudogene
TSPY5P	TSPY5P_2	CCTAACGAACTGCACGCA AA	BROAD	Pseudogene
TSPY5P	TSPY5P_3	GGTCTGTGAGAGTCCCAA AG	BROAD	Pseudogene
TSPY5P	TSPY5P_4	AAAAAACGCAGACAGGA AGA	BROAD	Pseudogene
TSPY6P	TSPY6P_1	AAGCCCCAGCTAGACCGC AG	BROAD	Pseudogene
TSPY6P	TSPY6P_2	GCGCCTCTGCGGTCTAGC TG	BROAD	Pseudogene
TSPY6P	TSPY6P_3	GGCGCCTCTGCGGTCTAG CT	BROAD	Pseudogene
TSPY6P	TSPY6P_4	CGGCGCCTCTGCGGTCTA GC	BROAD	Pseudogene
TSPY7P	TSPY7P_1	TGTGCAGGAGGGGGCGG CCG	BROAD	Pseudogene

TSPY7P	TSPY7P_2	AGGATGGAGGCTGTGCA GGA	BROAD	Pseudogene
TSPY7P	TSPY7P_3	CTTCAGGATGGAGGCTGT GC	BROAD	Pseudogene
TSPY7P	TSPY7P_4	CTGTGCAGGAGGGGGCG GCC	BROAD	Pseudogene
TSPY9P	TSPY9P_1	GGATGGAGGCTGTACAG GAG	BROAD	Pseudogene
TSPY9P	TSPY9P_2	AGGATGGAGGCTGTACA GGA	BROAD	Pseudogene
TSPY9P	TSPY9P_3	TGACCTACCGGGTGCCAG AG	BROAD	Pseudogene
TSPY9P	TSPY9P_4	AGGATCTAACAAGATTGC TG	BROAD	Pseudogene
TUSC2P1	TUSC2P1_1	GGGAACTATTCAACCACCC TG	BROAD	Pseudogene
TUSC2P1	TUSC2P1_2	AAGTGCTGTAGCTTCTAG CA	BROAD	Pseudogene
TUSC2P1	TUSC2P1_3	CAACAACTAGTTGTAGTA GG	BROAD	Pseudogene
TUSC2P1	TUSC2P1_4	GGGAAAGTACTGGAGCC GCT	BROAD	Pseudogene
TXLNGY	TXLNGY_1	TAATCTTAATCAATGCCT AG	BROAD	Pseudogene
TXLNGY	TXLNGY_2	GAAGTCACCTCGTGGCGT AG	BROAD	Pseudogene
TXLNGY	TXLNGY_3	TAGTGACTATGATAATCA AG	BROAD	Pseudogene
TXLNGY	TXLNGY_4	ATAGATCACTCACATGCA TA	BROAD	Pseudogene
UBE2V1P3	UBE2V1P3_1	TGGAAAGAGAATAGTCA CTG	BROAD	Pseudogene
UBE2V1P3	UBE2V1P3_2	TCACCAAAAGCTAATCTC AG	BROAD	Pseudogene
UBE2V1P3	UBE2V1P3_3	CAGCCTGTGAGACTACTG CT	BROAD	Pseudogene
UBE2V1P3	UBE2V1P3_4	AGAACATGTAATCAGCA GCA	BROAD	Pseudogene
VDAC1P6	VDAC1P6_1	AGGGCTAAAAACACAA CAC	BROAD	Pseudogene
VDAC1P6	VDAC1P6_2	TAGAACACGGATAATAC ACT	BROAD	Pseudogene
VDAC1P6	VDAC1P6_3	AAAAGAGGTAACGATGA ACT	BROAD	Pseudogene
VDAC1P6	VDAC1P6_4	AGACACCTGGCATCTCAA AG	BROAD	Pseudogene

XGY2	XGY2_1	TTGAACTGATGCTTACGG AG	BROAD	Pseudogene
XGY2	XGY2_2	AGGTGAGTGTCTCTTCAG CT	BROAD	Pseudogene
XGY2	XGY2_3	GACGAAGTGGTGCTTCAC TG	BROAD	Pseudogene
XGY2	XGY2_4	CAGATATTGAAAGCAAA ATG	BROAD	Pseudogene
ZNF736P11Y	ZNF736P11Y_1	GCAAAGTGTGAATTACTA CA	BROAD	Pseudogene
ZNF736P11Y	ZNF736P11Y_2	AAGAATATGGCAGAAAC TGT	BROAD	Pseudogene
ZNF736P11Y	ZNF736P11Y_3	CACTGAAGATTGGGTACA CC	BROAD	Pseudogene
ZNF736P11Y	ZNF736P11Y_4	ATATTACTGCAGACATAT GG	BROAD	Pseudogene
ZNF736P12Y	ZNF736P12Y_1	TATTACTGCAGACATATG GT	BROAD	Pseudogene
ZNF736P12Y	ZNF736P12Y_2	TCTTCTGTTCACTGAAGA TT	BROAD	Pseudogene
ZNF736P12Y	ZNF736P12Y_3	TACTACAAATGCAAAGA ATA	BROAD	Pseudogene
ZNF736P12Y	ZNF736P12Y_4	TACACATTCTTTGCAATT GT	BROAD	Pseudogene
ZNF736P6Y	ZNF736P6Y_1	ATAAGAGAGTTCATACTG TG	BROAD	Pseudogene
ZNF736P6Y	ZNF736P6Y_2	AAACACAAGAGAATTAA TAC	BROAD	Pseudogene
ZNF736P6Y	ZNF736P6Y_3	CAATGTTTGTCAACAACC CA	BROAD	Pseudogene
ZNF736P6Y	ZNF736P6Y_4	CATATGGTGTTCACATC AG	BROAD	Pseudogene
ZNF736P7Y	ZNF736P7Y_1	TCATGCCAAATATTTAC GT	BROAD	Pseudogene
ZNF736P7Y	ZNF736P7Y_2	ATTTAATTTAACATATTG GA	BROAD	Pseudogene
ZNF736P7Y	ZNF736P7Y_3	CAACATGAAGACTTGTTA GT	BROAD	Pseudogene
ZNF736P7Y	ZNF736P7Y_4	GCCACATCTACACAGATG TA	BROAD	Pseudogene
ZNF736P8Y	ZNF736P8Y_1	CTGTTGCTGAACACAATG TG	BROAD	Pseudogene
ZNF736P8Y	ZNF736P8Y_2	AAAGTGTGGGTAATTGCA AA	BROAD	Pseudogene
ZNF736P8Y	ZNF736P8Y_3	ATAAGAAAATTCAAACGT TA	BROAD	Pseudogene

ZNF736P8Y	ZNF736P8Y_4	TTGTGTTTAAATAAGGGT TG	BROAD	Pseudogene
ZNF736P9Y	ZNF736P9Y_1	AAAGTGTGGATAATTGCA AG	BROAD	Pseudogene
ZNF736P9Y	ZNF736P9Y_2	TGCTACAGACATCAACAA TG	BROAD	Pseudogene
ZNF736P9Y	ZNF736P9Y_3	TGTACACTTGTGTTTACT AA	BROAD	Pseudogene
ZNF736P9Y	ZNF736P9Y_4	CTAAACATGATAATTCAT AG	BROAD	Pseudogene
ZNF839P1	ZNF839P1_1	AAGACAGAGACAGCCGC ACA	BROAD	Pseudogene
ZNF839P1	ZNF839P1_2	AAATACAAAGCTAAAAA CAG	BROAD	Pseudogene
ZNF839P1	ZNF839P1_3	TCACTTAGGAACCACGAA TG	BROAD	Pseudogene
ZNF839P1	ZNF839P1_4	TGGGTTGGAGGACAAAA AAG	BROAD	Pseudogene
AGPAT5P1	AGPAT5P1_1	AGGAGCATGACGTCCGA AGC	GuideScan	Pseudogene
AGPAT5P1	AGPAT5P1_2	GCTGGCGGACGGGATGA CGG	GuideScan	Pseudogene
AGPAT5P1	AGPAT5P1_3	CGTCAATTTGCTGCTCAA CA	GuideScan	Pseudogene
AGPAT5P1	AGPAT5P1_4	TCACATGTACTCGCCTGC TT	GuideScan	Pseudogene
ANKRD57P1	ANKRD57P1_1	CTTCTCTGCGGTGTCCTC GG	GuideScan	Pseudogene
ANKRD57P1	ANKRD57P1_2	GCCTCAGACCAGCGATGA CC	GuideScan	Pseudogene
ANKRD57P1	ANKRD57P1_3	GACTAATGGACTTAAAAA AC	GuideScan	Pseudogene
ANKRD57P1	ANKRD57P1_4	TCCAGGTCATCGCTGGTC TG	GuideScan	Pseudogene
ARSEP1	ARSEP1_1	TCCTAGGCCCGTAAGAAA GT	GuideScan	Pseudogene
ARSEP1	ARSEP1_2	CTGCGTTGTGATTGACAG CC	GuideScan	Pseudogene
ARSEP1	ARSEP1_3	GAGGATCACTTCGCCTCG TC	GuideScan	Pseudogene
ARSEP1	ARSEP1_4	TTGTTCGTACAAAGGCCG TG	GuideScan	Pseudogene
ARSFP1	ARSFP1_1	CAATGTGCGGGATGCGGT AC	GuideScan	Pseudogene
ARSFP1	ARSFP1_2	GCAATGTGCGGGATGCG GTA	GuideScan	Pseudogene

ARSFP1	ARSFP1_3	TCTGCGGGGCTCGTATAC AT	GuideScan	Pseudogene
ARSFP1	ARSFP1_4	ATGTGCGGGATGCGGTAC GG	GuideScan	Pseudogene
CASKP1	CASKP1_1	TGAGAGGTACCGGTTACC AG	GuideScan	Pseudogene
CASKP1	CASKP1_2	CGATTAACTTATGCTTA CC	GuideScan	Pseudogene
CASKP1	CASKP1_3	TAAGCCCCCTAAAGTATG AG	GuideScan	Pseudogene
CASKP1	CASKP1_4	GTACCTTGACGTAGCTAC CT	GuideScan	Pseudogene
CCNQP2	CCNQP2_1	GACCAGCCATCGTGGTGA CA	GuideScan	Pseudogene
CCNQP2	CCNQP2_2	TTGCCACCATGTCACCAC GA	GuideScan	Pseudogene
CCNQP2	CCNQP2_3	ATTCTTCTGCGAGACCTG AC	GuideScan	Pseudogene
CCNQP2	CCNQP2_4	CCAAGCGGCGAGGTTTCAT CA	GuideScan	Pseudogene
CDY10P	CDY10P_1	ATGAGGCAAGCTCCTTAA TA	GuideScan	Pseudogene
CDY10P	CDY10P_2	TACATTTACCGCAGTTCA CG	GuideScan	Pseudogene
CDY10P	CDY10P_3	ATGGCTGGCTAGGTAGCG TC	GuideScan	Pseudogene
CDY10P	CDY10P_4	TCTGCACTACATCCGTGA GA	GuideScan	Pseudogene
CDY11P	CDY11P_1	CAATGGGCCCCGCGATTGG AC	GuideScan	Pseudogene
CDY11P	CDY11P_2	TCAGTCAATGGGCCCCGCG AT	GuideScan	Pseudogene
CDY11P	CDY11P_3	AATGGGCCCCGCGATTGGA CT	GuideScan	Pseudogene
CDY11P	CDY11P_4	CTTAGCACCTGGTGAAGC AC	GuideScan	Pseudogene
CDY4P	CDY4P_1	GGCGTGGCTTCCAATACC TT	GuideScan	Pseudogene
CDY4P	CDY4P_2	ATCGATCCATTAATAGCC CA	GuideScan	Pseudogene
CDY4P	CDY4P_3	TTTAGACTCGGCATTCTA GG	GuideScan	Pseudogene
CDY4P	CDY4P_4	TATGGATGTGACGAGTCC AA	GuideScan	Pseudogene
CDY7P	CDY7P_1	GCAACTATACTATGTCTGA TT	GuideScan	Pseudogene

CDY7P	CDY7P_2	CGAATTCATTAACAGCCA AT	GuideScan	Pseudogene
CDY7P	CDY7P_3	TGGCTCGATTAACACTTC CA	GuideScan	Pseudogene
CDY7P	CDY7P_4	GCAGCTGAATCCACGGG AGG	GuideScan	Pseudogene
CHEK2P1	CHEK2P1_1	ATCATCAGGAATACGAAT AC	GuideScan	Pseudogene
CHEK2P1	CHEK2P1_2	GTAGCATAACCAACTTCC TC	GuideScan	Pseudogene
CHEK2P1	CHEK2P1_3	TATCAGAAAACCTGCCCA AT	GuideScan	Pseudogene
CHEK2P1	CHEK2P1_4	GACCTGAGCTCTGGGATA TT	GuideScan	Pseudogene
CICP2	CICP2_1	TCAGCAAGCGGCACCAG GCC	GuideScan	Pseudogene
CICP2	CICP2_2	AAGCGGCACCAGGCCTG GCA	GuideScan	Pseudogene
CICP2	CICP2_3	AGGCCTGGCAGGGCACA CCA	GuideScan	Pseudogene
CICP2	CICP2_4	CAAGCGGCACCAGGCCT GGC	GuideScan	Pseudogene
CYCSP46	CYCSP46_1	GTAAACAGTGATAGCGTT TA	GuideScan	Pseudogene
CYCSP46	CYCSP46_2	TGGTACACATCAAAAAA GTT	GuideScan	Pseudogene
CYCSP46	CYCSP46_3	TTCAACCCTTGCCTTTAA GA	GuideScan	Pseudogene
CYCSP46	CYCSP46_4	GTGGCTGTGTAAGAATAT GC	GuideScan	Pseudogene
CYCSP48	CYCSP48_1	ATTTTACCTTGGTGTGGC AT	GuideScan	Pseudogene
CYCSP48	CYCSP48_2	TGCCACACCAAGGTAAA ATG	GuideScan	Pseudogene
CYCSP48	CYCSP48_3	TTTTACCTTGGTGTGGCA TT	GuideScan	Pseudogene
CYCSP48	CYCSP48_4	TGCCTCATTTTACCTTGGT G	GuideScan	Pseudogene
DLGAP5P1	DLGAP5P1_1	TCATAGTCCATCCATTTA GC	GuideScan	Pseudogene
DLGAP5P1	DLGAP5P1_2	TTCTACACAGAGAGGCTT AA	GuideScan	Pseudogene
DLGAP5P1	DLGAP5P1_3	TGGATGGACTATGACAGT TT	GuideScan	Pseudogene
DLGAP5P1	DLGAP5P1_4	TTGATGTCTCTCCAGCTA AA	GuideScan	Pseudogene

DUX4L31	DUX4L31_1	CACGTGGGAACATGAATC CG	GuideScan	Pseudogene
DUX4L31	DUX4L31_2	CCGTACTGGGTCTGCGGC CA	GuideScan	Pseudogene
DUX4L31	DUX4L31_3	TCCGTACTGGGTCTGCGG CC	GuideScan	Pseudogene
DUX4L31	DUX4L31_4	CCCAACTTGCCGCGGCAC AT	GuideScan	Pseudogene
ELOCP4	ELOCP4_1	GAAACCCATTTGAGTGAC CC	GuideScan	Pseudogene
ELOCP4	ELOCP4_2	CTATTTGATATCATGGGA TT	GuideScan	Pseudogene
ELOCP4	ELOCP4_3	AGGACTTTCACAACCATT GT	GuideScan	Pseudogene
ELOCP4	ELOCP4_4	AATGGGTTTCATTGTTGT TG	GuideScan	Pseudogene
ELOCP5	ELOCP5_1	GAAACCCGTTTGAGTGAT CC	GuideScan	Pseudogene
ELOCP5	ELOCP5_2	AACGGGTTTCATTGTTGC TG	GuideScan	Pseudogene
ELOCP5	ELOCP5_3	TGTTTGATATCATGGCAT TA	GuideScan	Pseudogene
ELOCP5	ELOCP5_4	GATATATCTGTTTGATAT CA	GuideScan	Pseudogene
FAM199YP	FAM199YP_1	TGTCCAGTTCATCTGTCC CT	GuideScan	Pseudogene
FAM199YP	FAM199YP_2	GTGTATTACAATGTGTAG TG	GuideScan	Pseudogene
FAM199YP	FAM199YP_3	AATCCAAGGGACAGATG AAC	GuideScan	Pseudogene
FAM199YP	FAM199YP_4	GAAACTGAATTAAAGGA AGG	GuideScan	Pseudogene
FAM8A10P	FAM8A10P_1	AAACTACTGCCTGTATTG AT	GuideScan	Pseudogene
FAM8A10P	FAM8A10P_2	GCCCGTGCCCAGACAAAT CT	GuideScan	Pseudogene
FAM8A10P	FAM8A10P_3	TTCCTGGTCCGCAATACC AC	GuideScan	Pseudogene
FAM8A10P	FAM8A10P_4	CAAGCACGTGATGTGAA GAG	GuideScan	Pseudogene
FAM8A7P	FAM8A7P_1	CACATATTGTGGTTGTAA CG	GuideScan	Pseudogene
FAM8A7P	FAM8A7P_2	CACGTTACAACCACAATA TG	GuideScan	Pseudogene
FAM8A7P	FAM8A7P_3	TTCAGACTAGTATCCATA TA	GuideScan	Pseudogene

FAM8A7P	FAM8A7P_4	TGGATTTGACTGACCCTA TA	GuideScan	Pseudogene
FAM8A9P	FAM8A9P_1	GAGGGTAGTATGTATGTT AA	GuideScan	Pseudogene
FAM8A9P	FAM8A9P_2	GACTCTAACTTATAACCC CA	GuideScan	Pseudogene
FAM8A9P	FAM8A9P_3	ACATACATACTACCCTCA AA	GuideScan	Pseudogene
FAM8A9P	FAM8A9P_4	GTGGTTGCAGATTATACT AA	GuideScan	Pseudogene
GAPDHP17	GAPDHP17_1	GTCAACCTTATTGTTTAC AT	GuideScan	Pseudogene
GAPDHP17	GAPDHP17_2	ACCATTCATGGTATTCTG GG	GuideScan	Pseudogene
GAPDHP17	GAPDHP17_3	ATTAGACACCGATTATGT TG	GuideScan	Pseudogene
GAPDHP17	GAPDHP17_4	CGATTATGTTGTGGAGTC AA	GuideScan	Pseudogene
GAPDHP19	GAPDHP19_1	AGGTTAGGTCCATGACCA AC	GuideScan	Pseudogene
GAPDHP19	GAPDHP19_2	GTCAATGATTAGGCCATA TT	GuideScan	Pseudogene
GAPDHP19	GAPDHP19_3	GGTAGGTTTTTCACATATG GC	GuideScan	Pseudogene
GAPDHP19	GAPDHP19_4	TGTAGGTCACAAGGTCTA TC	GuideScan	Pseudogene
GOT2P5	GOT2P5_1	GCTAGTCTTCAACCTGAA TA	GuideScan	Pseudogene
GOT2P5	GOT2P5_2	CGTTCCACTGTTCTGCAT AA	GuideScan	Pseudogene
GOT2P5	GOT2P5_3	CTCTACTATTCTGAACAC CC	GuideScan	Pseudogene
GOT2P5	GOT2P5_4	CTGTTCTGCATAAGGGTT CC	GuideScan	Pseudogene
GPR143P	GPR143P_1	GAAACATACGCATGCACT AT	GuideScan	Pseudogene
GPR143P	GPR143P_2	AAATTAGAGAGCACACG TCC	GuideScan	Pseudogene
GPR143P	GPR143P_3	ATCTTATGTAGGGTCATG AT	GuideScan	Pseudogene
GPR143P	GPR143P_4	GAGGGTGCTCAATCAACA TG	GuideScan	Pseudogene
HSFY4P	HSFY4P_1	ACGCGCTGCTTTGGATGT CG	GuideScan	Pseudogene
HSFY4P	HSFY4P_2	GGTGCCAGAACTATACGG CC	GuideScan	Pseudogene

HSFY4P	HSFY4P_3	AACTATACGGCCTGGTAA TT	GuideScan	Pseudogene
HSFY4P	HSFY4P_4	ACGGGATCGGGCCAAAA TGT	GuideScan	Pseudogene
KDM5DP1	KDM5DP1_1	GCAAGAGATTTCTCGGCA TC	GuideScan	Pseudogene
KDM5DP1	KDM5DP1_2	GGAGAATCCCGAACATTA AA	GuideScan	Pseudogene
KDM5DP1	KDM5DP1_3	TGGAGAATCCCGAACATT AA	GuideScan	Pseudogene
KDM5DP1	KDM5DP1_4	TGCCGAGCCCTTTAATGT TC	GuideScan	Pseudogene
LINC00265- 3P	LINC00265-3P_1	CTCTTTTGGCTCAGCTCT GC	GuideScan	Pseudogene
LINC00268- 2P	LINC00268-2P_1	CAAAACCATGGAAGCCTC TG	GuideScan	Pseudogene
LINC00268- 2P	LINC00268-2P_2	TAGAATTGTGATAGAAGC CT	GuideScan	Pseudogene
MED13P1	MED13P1_1	ATTCAGTACCATGCATC TC	GuideScan	Pseudogene
MED13P1	MED13P1_2	TGAGATGCATGGTACTGA AA	GuideScan	Pseudogene
MED14P1	MED14P1_1	AGACGGTTAACGATCTGT TT	GuideScan	Pseudogene
MED14P1	MED14P1_2	GTGCTCCGTTCTTCCGCC CG	GuideScan	Pseudogene
MED14P1	MED14P1_3	GGTTAACGATCTGTTTGG GT	GuideScan	Pseudogene
MED14P1	MED14P1_4	TTAGGCTGTCGTCCATCC CT	GuideScan	Pseudogene
MRPL57P10	MRPL57P10_1	ACTGGCAGTTGAGGACG ATG	GuideScan	Pseudogene
MRPL57P10	MRPL57P10_2	GTTCTTCTATAATAAATC TG	GuideScan	Pseudogene
MRPL57P10	MRPL57P10_3	TTCTTCTATAATAAATCT GT	GuideScan	Pseudogene
MRPL57P10	MRPL57P10_4	AATAAATCTGTGGGAGAT GC	GuideScan	Pseudogene
MTCO1P37	MTCO1P37_1	TATCGGGGCGCCAATTAT CA	GuideScan	Pseudogene
MTCO1P37	MTCO1P37_2	ATATCGGGGCGCCAATTA TC	GuideScan	Pseudogene
MTCO1P37	MTCO1P37_3	ACGCCATAACACACTATT CT	GuideScan	Pseudogene
MTCO1P37	MTCO1P37_4	ATCGGGGCGCCAATTATC AG	GuideScan	Pseudogene

MTCYBP1	MTCYBP1_1	TGAATCGTTGCTAGAGCT GT	GuideScan	Pseudogene
MTCYBP1	MTCYBP1_2	CTACCTATCCCTAACAAC CT	GuideScan	Pseudogene
MTCYBP1	MTCYBP1_3	ACAATATATTGGAAGTGA CC	GuideScan	Pseudogene
MTCYBP1	MTCYBP1_4	TAACAACCTAGGAAGTGT AC	GuideScan	Pseudogene
MTCYBP2	MTCYBP2_1	GATATTCCAACCATTAAG TC	GuideScan	Pseudogene
MTCYBP2	MTCYBP2_2	GATGGGTCATAAGATTGT GT	GuideScan	Pseudogene
MTCYBP2	MTCYBP2_3	TGTTTAGATGTGTGACGC AT	GuideScan	Pseudogene
MTCYBP2	MTCYBP2_4	ATATTCCAACCATTAAGT CA	GuideScan	Pseudogene
MTND1P1	MTND1P1_1	ACTTAACACTGTAGGTCC TA	GuideScan	Pseudogene
MTND1P1	MTND1P1_2	TAGTGTATTCCATCAGTG AA	GuideScan	Pseudogene
MTND1P1	MTND1P1_3	GGGGTGTAATGCTCAAAA TT	GuideScan	Pseudogene
MTND1P1	MTND1P1_4	GAATGGTTGAATCAGTCC GT	GuideScan	Pseudogene
MTND2P3	MTND2P3_1	TATTCTGAGTCGTATTAC TA	GuideScan	Pseudogene
MTND2P3	MTND2P3_2	CTATTCTGAGTCGTATTA CT	GuideScan	Pseudogene
MTND2P3	MTND2P3_3	TAATAGTATTCATTGCCT GG	GuideScan	Pseudogene
MTND2P3	MTND2P3_4	CAGGCTAGTTTACTCATG TG	GuideScan	Pseudogene
MTND6P1	MTND6P1_1	ACCTACAAACCTTACAGC CA	GuideScan	Pseudogene
MTND6P1	MTND6P1_2	GTGGTCGTGTGAGGATTC TG	GuideScan	Pseudogene
MTND6P1	MTND6P1_3	ATTATTAAGAGAGTTGGC AT	GuideScan	Pseudogene
MTND6P1	MTND6P1_4	TGGTCGTGTGAGGATTCT GT	GuideScan	Pseudogene
NEFLP1	NEFLP1_1	CATGGCTACTGTAGTAGG AC	GuideScan	Pseudogene
NEFLP1	NEFLP1_2	CACCTACATCAGTAGTGT GC	GuideScan	Pseudogene
NEFLP1	NEFLP1_3	CTACAGTAGCCATGTGCA AG	GuideScan	Pseudogene

NEFLP1	NEFLP1_4	GTATTGAGGCTGCAGCTC AG	GuideScan	Pseudogene
OFD1P13Y	OFD1P13Y_1	TAAATAAAAAATATTTTA GA	GuideScan	Pseudogene
OFD1P14Y	OFD1P14Y_1	TAAGTCACAGACTCAGTG GC	GuideScan	Pseudogene
OFD1P16Y	OFD1P16Y_1	CAACATCGAGTACCCATC CT	GuideScan	Pseudogene
OFD1P16Y	OFD1P16Y_2	CAACTGTGGTTGGGCTAG CC	GuideScan	Pseudogene
OFD1P16Y	OFD1P16Y_3	CTACGTCAGAGCTGCAAC TG	GuideScan	Pseudogene
OFD1P16Y	OFD1P16Y_4	TACAGCTTCTACCGTCTG CA	GuideScan	Pseudogene
OFD1P3Y	OFD1P3Y_1	TGCTAAGACGCTAGTTCA TG	GuideScan	Pseudogene
OFD1P3Y	OFD1P3Y_2	TATCCTAGCGTTTACATT TC	GuideScan	Pseudogene
OFD1P3Y	OFD1P3Y_3	GGCCAATACTATTATTGG TC	GuideScan	Pseudogene
OFD1P3Y	OFD1P3Y_4	GCTGTAACAAGCTTCCCT TC	GuideScan	Pseudogene
OFD1P5Y	OFD1P5Y_1	GTAGATCCTTTTCCAGAG GA	GuideScan	Pseudogene
OFD1P5Y	OFD1P5Y_2	TGCTGTAGATCCTTTTCC AG	GuideScan	Pseudogene
OFD1P5Y	OFD1P5Y_3	TGTAGATCCTTTTCCAGA GG	GuideScan	Pseudogene
OFD1P5Y	OFD1P5Y_4	CTATACTCAACCTCCTCC CC	GuideScan	Pseudogene
OFD1P6Y	OFD1P6Y_1	GGCACTCAACTTGGGACA CA	GuideScan	Pseudogene
OFD1P6Y	OFD1P6Y_2	TAGGTAACGTGTGGTCAA TG	GuideScan	Pseudogene
OFD1P6Y	OFD1P6Y_3	GAACCATATCGCATTCTT TA	GuideScan	Pseudogene
OFD1P6Y	OFD1P6Y_4	TCATTGGTTATACGTGAT GA	GuideScan	Pseudogene
OFD1P8Y	OFD1P8Y_1	CCCCTTTCCAACACTCC GC	GuideScan	Pseudogene
OFD1P8Y	OFD1P8Y_2	CCACTTTCCAACACTCCG CA	GuideScan	Pseudogene
OFD1P8Y	OFD1P8Y_3	GGTTTTTTTTTAACTCAG AA	GuideScan	Pseudogene
OFD1P8Y	OFD1P8Y_4	CCTGCGGAGTGTTGGAAA GT	GuideScan	Pseudogene

OFD1P9Y	OFD1P9Y_1	AGAGAAACTTTACTATAT GG	GuideScan	Pseudogene
OFD1P9Y	OFD1P9Y_2	CAAAGAGAACTTTACTA TA	GuideScan	Pseudogene
OFD1P9Y	OFD1P9Y_3	AAAGAGAACTTTACTAT AT	GuideScan	Pseudogene
PABPC1P5	PABPC1P5_1	CTGGAAAACTTTGTCCA CT	GuideScan	Pseudogene
PABPC1P5	PABPC1P5_2	TTGAAAAGATCAAGTAAT AT	GuideScan	Pseudogene
PABPC1P5	PABPC1P5_3	GAAAAGCAATGAACAGA AAC	GuideScan	Pseudogene
PNPLA4P1	PNPLA4P1_1	GTCATTCGGGGCAGTAAC AC	GuideScan	Pseudogene
PNPLA4P1	PNPLA4P1_2	TCATTCGGGGCAGTAACA CT	GuideScan	Pseudogene
PNPLA4P1	PNPLA4P1_3	ATGACTTCATGGCCCAGC TA	GuideScan	Pseudogene
PNPLA4P1	PNPLA4P1_4	GTACTGTGTATACCTTAG CT	GuideScan	Pseudogene
PPP1R12BP1	PPP1R12BP1_1	TTAGCATAGACACGCCGT TA	GuideScan	Pseudogene
PPP1R12BP1	PPP1R12BP1_2	GAACTCCCGCAAATTAGG CC	GuideScan	Pseudogene
PPP1R12BP1	PPP1R12BP1_3	AGAACTCCCGCAAATTAG GC	GuideScan	Pseudogene
PPP1R12BP1	PPP1R12BP1_4	GCGCTTTTAGTAGCACGT GT	GuideScan	Pseudogene
PRYP2	PRYP2_1	AGGCGGCTTGCAGTGAGC CA	GuideScan	Pseudogene
PUDPP1	PUDPP1_1	CACAAGCATACTATGACC TG	GuideScan	Pseudogene
PUDPP1	PUDPP1_2	CAGGCCTATGATGTCCTT AG	GuideScan	Pseudogene
PUDPP1	PUDPP1_3	CATTCCTACATGGCTTC AT	GuideScan	Pseudogene
PUDPP1	PUDPP1_4	CTCAAATGATTTCCCAC TA	GuideScan	Pseudogene
RAB9AP4	RAB9AP4_1	ACGGCAAGATGAGCTAG TCC	GuideScan	Pseudogene
RAB9AP4	RAB9AP4_2	GTATACACAAAATCACCA CG	GuideScan	Pseudogene
RAB9AP4	RAB9AP4_3	TCTTCAAACCGCCTCCTC AA	GuideScan	Pseudogene
RAB9AP4	RAB9AP4_4	GTCCTTCTATATTAGCTG GT	GuideScan	Pseudogene

RBMY1GP	RBMY1GP_1	TCTACGCACAGCAGTTCC AT	GuideScan	Pseudogene
RBMY1GP	RBMY1GP_2	CGCCGAGCTCCTGAGAAT GG	GuideScan	Pseudogene
RBMY1GP	RBMY1GP_3	AACGCAACTATCCCGGGT AC	GuideScan	Pseudogene
RBMY1GP	RBMY1GP_4	GCAACTATCCCGGGTACC GG	GuideScan	Pseudogene
RBMY1HP	RBMY1HP_1	TCAAACGTAGTTCAATT CG	GuideScan	Pseudogene
RBMY1KP	RBMY1KP_1	CACCGCGATTGGGCAATA CA	GuideScan	Pseudogene
RBMY1KP	RBMY1KP_2	ACCGCGATTGGGCAATAC AT	GuideScan	Pseudogene
RBMY1KP	RBMY1KP_3	CATGTATTGCCCAATCGC GG	GuideScan	Pseudogene
RBMY1KP	RBMY1KP_4	ACCCATGTATTGCCCAAT CG	GuideScan	Pseudogene
RBMY2AP	RBMY2AP_1	TAATATCCTGACAAAGAC AG	GuideScan	Pseudogene
RBMY2AP	RBMY2AP_2	GAGTATGGGGTGGGTGG ACC	GuideScan	Pseudogene
RBMY2AP	RBMY2AP_3	TACTTTCCTCTGTCTTTGT C	GuideScan	Pseudogene
RBMY2GP	RBMY2GP_1	CTAAAAGAACTTGTTTT TG	GuideScan	Pseudogene
RBMY2JP	RBMY2JP_1	GACTGCGGTTGCATGCCA AG	GuideScan	Pseudogene
RBMY2JP	RBMY2JP_2	CATGCGCATAAGTATCAT TC	GuideScan	Pseudogene
RBMY2JP	RBMY2JP_3	GGACCGTATTTCCCAAAT AC	GuideScan	Pseudogene
RBMY2JP	RBMY2JP_4	TGGTGAGTCCGTTACATT AA	GuideScan	Pseudogene
RBMY2OP	RBMY2OP_1	CGTGTGTTGGTCCCTTCAT GT	GuideScan	Pseudogene
RBMY2OP	RBMY2OP_2	ACACACGTTGTCTTCCAA TA	GuideScan	Pseudogene
RBMY2OP	RBMY2OP_3	ACAGTTCGTAACCAATAA TG	GuideScan	Pseudogene
RBMY2OP	RBMY2OP_4	ATAGCGGACATTAAAGCC TT	GuideScan	Pseudogene
RBMY2SP	RBMY2SP_1	GACCGTGATGGCTACCAA GG	GuideScan	Pseudogene
RBMY2SP	RBMY2SP_2	GAGCTATCGTATCCTTCA TG	GuideScan	Pseudogene

RBMY2SP	RBMY2SP_3	CACTGGAGGACCACTACC CA	GuideScan	Pseudogene
RBMY2SP	RBMY2SP_4	AATGACCGTGATGGCTAC CA	GuideScan	Pseudogene
RBMY2TP	RBMY2TP_1	GGGGAATCCTCTAGCAAC AC	GuideScan	Pseudogene
RBMY2TP	RBMY2TP_2	AGGGACTCGACTTCTTGA AG	GuideScan	Pseudogene
RBMY2TP	RBMY2TP_3	GGTAAGGTATTTTCCTGA AG	GuideScan	Pseudogene
RBMY2TP	RBMY2TP_4	CTAGGTACATTTTCAGGTT TA	GuideScan	Pseudogene
RCC2P1	RCC2P1_1	TTCATGTCTTGGACCGCA GT	GuideScan	Pseudogene
RCC2P1	RCC2P1_2	TGACACGGGGTGGCTATT GC	GuideScan	Pseudogene
RCC2P1	RCC2P1_3	GCCTTGTATACCTTCTGC GC	GuideScan	Pseudogene
RCC2P1	RCC2P1_4	CTTCATGTCTTGGACCGC AG	GuideScan	Pseudogene
RCC2P2	RCC2P2_1	AGCCCTGAGTATGATTTG CT	GuideScan	Pseudogene
RCC2P2	RCC2P2_2	TGAAGCCTGTAAATTCGT GG	GuideScan	Pseudogene
RCC2P2	RCC2P2_3	ACAACTTGAAGGGTCTA CG	GuideScan	Pseudogene
RCC2P2	RCC2P2_4	GACACCCTCCACGAATTT AC	GuideScan	Pseudogene
RFTN1P1	RFTN1P1_1	CGTCTACATACCTTACTC GC	GuideScan	Pseudogene
RFTN1P1	RFTN1P1_2	GCCCCATTCGAGAGCCG GT	GuideScan	Pseudogene
RFTN1P1	RFTN1P1_3	CCTAGTATTAACTACGC TC	GuideScan	Pseudogene
RFTN1P1	RFTN1P1_4	CCCGACACTGCAGCATTA AA	GuideScan	Pseudogene
RN7SKP282	RN7SKP282_1	TCTGCCTGCCATTGATCA CC	GuideScan	Pseudogene
RN7SKP282	RN7SKP282_2	ATCACATATATTAGCATC TA	GuideScan	Pseudogene
RN7SKP282	RN7SKP282_3	TTGACCGAACACGCAGCT TT	GuideScan	Pseudogene
RN7SKP282	RN7SKP282_4	CTGCCTGCCATTGATCAC CA	GuideScan	Pseudogene
RNA18SP2	RNA18SP2_1	GCTTTGCAACCATACTCG CC	GuideScan	Pseudogene

RNA18SP2	RNA18SP2_2	TCCATAGTTGAACCTGTC GA	GuideScan	Pseudogene
RNA18SP2	RNA18SP2_3	TCCCTCGACAGGTTCAAC TA	GuideScan	Pseudogene
RNA18SP2	RNA18SP2_4	ACTAGATAACCTCAGGCC AA	GuideScan	Pseudogene
RNA5SP518	RNA5SP518_1	GTCAAGATCCCATGTGTT CA	GuideScan	Pseudogene
RNA5SP518	RNA5SP518_2	GCCATACCACCCTGAACA CA	GuideScan	Pseudogene
RNA5SP518	RNA5SP518_3	AGTCAAGATCCCATGTGT TC	GuideScan	Pseudogene
RNA5SP518	RNA5SP518_4	TACAGCACTCAGTATTCA CA	GuideScan	Pseudogene
RNA5SP519	RNA5SP519_1	GAGGCAAGCGGGTGCGT TCA	GuideScan	Pseudogene
RNA5SP519	RNA5SP519_2	AGAGGCAAGCGGGTGCG TTC	GuideScan	Pseudogene
RNA5SP519	RNA5SP519_3	CCAAGGTACCTGCTATTA CC	GuideScan	Pseudogene
RNA5SP519	RNA5SP519_4	CCTGGTAATAGCAGGTAC CT	GuideScan	Pseudogene
RNU6-1334P	RNU6-1334P_1	TTTGAATACCCTCCTGGC CC	GuideScan	Pseudogene
RNU6-1334P	RNU6-1334P_2	TTCACATTTGAATACCCT CC	GuideScan	Pseudogene
RNU6-1334P	RNU6-1334P_3	AGAAGAATAACACTGTCC CT	GuideScan	Pseudogene
RNU6-1334P	RNU6-1334P_4	AATAAACTGTCCCTGGG CC	GuideScan	Pseudogene
RNU6-255P	RNU6-255P_1	TGCATTTTATTCTTGTGCA G	GuideScan	Pseudogene
RNU6-255P	RNU6-255P_2	TTTGCATTTTATTCTTGTG C	GuideScan	Pseudogene
RNU6-255P	RNU6-255P_3	TTGCATTTTATTCTTGTGC A	GuideScan	Pseudogene
RNU6-521P	RNU6-521P_1	TGATGACAGGTAAATTCG TG	GuideScan	Pseudogene
RNU6-521P	RNU6-521P_2	AAGGCCCATGCAATGATG AC	GuideScan	Pseudogene
RNU6-521P	RNU6-521P_3	ATTTACCTGTCATCATTG CA	GuideScan	Pseudogene
RNU6-521P	RNU6-521P_4	TTTACCTGTCATCATTGC AT	GuideScan	Pseudogene
RPS24P1	RPS24P1_1	TACCTAGGCCAAACCAAG CC	GuideScan	Pseudogene

RPS24P1	RPS24P1_2	CACATAACGGGCCCCCAC GG	GuideScan	Pseudogene
RPS24P1	RPS24P1_3	AACCGACTGAATGAATCT TC	GuideScan	Pseudogene
RPS24P1	RPS24P1_4	ATTCAGTCGGTTGTGCAA AA	GuideScan	Pseudogene
SNX3P1Y	SNX3P1Y_1	TATGAGCAACGGGCAGA CTG	GuideScan	Pseudogene
TBL1YP1	TBL1YP1_1	AATCGCGTGCACTGCTAA TC	GuideScan	Pseudogene
TBL1YP1	TBL1YP1_2	ATCGCGTGCACTGCTAAT CT	GuideScan	Pseudogene
TBL1YP1	TBL1YP1_3	GGGAACACTCCTATAACG CA	GuideScan	Pseudogene
TBL1YP1	TBL1YP1_4	ACGGTTTCTGCCGACTGC AC	GuideScan	Pseudogene
TOMM22P1	TOMM22P1_1	AGCAAGAACGAGTAACA TAA	GuideScan	Pseudogene
TOMM22P1	TOMM22P1_2	CTGTGCAACTGAACCATC TC	GuideScan	Pseudogene
TOMM22P1	TOMM22P1_3	AAGAACGAGTAACATAA AGG	GuideScan	Pseudogene
TOMM22P1	TOMM22P1_4	AAGACCTAGATGAGACC CTG	GuideScan	Pseudogene
TOMM22P2	TOMM22P2_1	TCCAGCATTATAGTGCTG TA	GuideScan	Pseudogene
TOMM22P2	TOMM22P2_2	TCCTTACAGCACTATAAT GC	GuideScan	Pseudogene
TOMM22P2	TOMM22P2_3	AGCATTATAGTGCTGTAA GG	GuideScan	Pseudogene
TOMM22P2	TOMM22P2_4	CCATAGCAGCCTTGTCAA TT	GuideScan	Pseudogene
TRAPPC2P7	TRAPPC2P7_1	GTACGTACTGATATCAAC AC	GuideScan	Pseudogene
TRAPPC2P7	TRAPPC2P7_2	ACATCTATTACAAGTCTG TC	GuideScan	Pseudogene
TRAPPC2P7	TRAPPC2P7_3	GACCAAATAGTCACTAAA GA	GuideScan	Pseudogene
TRAPPC2P7	TRAPPC2P7_4	TTCCATATCAGAGGTATC TC	GuideScan	Pseudogene
TRIM60P1Y	TRIM60P1Y_1	CTGGGTTTATTATGGGCA AT	GuideScan	Pseudogene
TRIM60P1Y	TRIM60P1Y_2	ACTACTTGCAGAAGGTGG GT	GuideScan	Pseudogene
TRIM60P1Y	TRIM60P1Y_3	TGGGTTGGCATAGAACAT GA	GuideScan	Pseudogene

TRIM60P1Y	TRIM60P1Y_4	GGCTGACAGACATTACTA GA	GuideScan	Pseudogene
TRIM60P2Y	TRIM60P2Y_1	GAGGGCAGATGGTAAGC CTA	GuideScan	Pseudogene
TRIM60P2Y	TRIM60P2Y_2	CAGATGGTAAGCCTATGG AA	GuideScan	Pseudogene
TRIM60P2Y	TRIM60P2Y_3	ACATGTGTCAGCCATTCC AT	GuideScan	Pseudogene
TRIM60P2Y	TRIM60P2Y_4	CATTACTAAGGAGGGCA GA	GuideScan	Pseudogene
TRIM60P3Y	TRIM60P3Y_1	GGGGTGCATACTATTTAC AT	GuideScan	Pseudogene
TRIM60P3Y	TRIM60P3Y_2	GACCAGGTCCTAAGAAA ACC	GuideScan	Pseudogene
TRIM60P3Y	TRIM60P3Y_3	TGGTCGATCTCCTGATCT CC	GuideScan	Pseudogene
TRIM60P3Y	TRIM60P3Y_4	TTAGCCACTCCATGTTTG AC	GuideScan	Pseudogene
TSPY14P	TSPY14P_1	GGCCCTTACGTAGGATCT AT	GuideScan	Pseudogene
TSPY14P	TSPY14P_2	TTGGCATCGATGCGACTA TT	GuideScan	Pseudogene
TSPY14P	TSPY14P_3	TGGCATCGATGCGACTAT TT	GuideScan	Pseudogene
TSPY14P	TSPY14P_4	CCTCCGATAGATCCTACG TA	GuideScan	Pseudogene
TSPY18P	TSPY18P_1	AACGTCTGATGCTCAGCA TC	GuideScan	Pseudogene
TSPY20P	TSPY20P_1	TAAGTGCACGAGCGTGTC CT	GuideScan	Pseudogene
TSPY20P	TSPY20P_2	AGGTCCGTAGGCGTCTCC CG	GuideScan	Pseudogene
TSPY20P	TSPY20P_3	CGCCCCGGCTGGCAAAG GAC	GuideScan	Pseudogene
TSPY20P	TSPY20P_4	ACACGCTCGTGCAGTTAG AA	GuideScan	Pseudogene
TSPY22P	TSPY22P_1	TATCCCTACCTCGTGCCC GC	GuideScan	Pseudogene
TSPY22P	TSPY22P_2	ATCCCTACCTCGTGCCCC CA	GuideScan	Pseudogene
TSPY22P	TSPY22P_3	TCCCCTGCGGGCACGAGG TA	GuideScan	Pseudogene
TSPY22P	TSPY22P_4	TCCAGCGAGTCCGTTGCC GG	GuideScan	Pseudogene
TSPY24P	TSPY24P_1	TATCGCCTAGATCTTTGA CC	GuideScan	Pseudogene

TSPY24P	TSPY24P_2	ACACCGGGAGCGTGGTTC CA	GuideScan	Pseudogene
TSPY24P	TSPY24P_3	AAGACTTGGGTTCACGGT GC	GuideScan	Pseudogene
TSPY24P	TSPY24P_4	CGTTGCGTGCTGGGGCAT AA	GuideScan	Pseudogene
TSPY25P	TSPY25P_1	ACAAATCCGTCAAGTAGC TT	GuideScan	Pseudogene
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TSPY25P	TSPY25P_3	CGTCTTTGGGTGCAGTGC CG	GuideScan	Pseudogene
TSPY25P	TSPY25P_4	GGGTGGGCTTGTACACAC GA	GuideScan	Pseudogene
TTY24P	TTY24P_1	TATCCTGGAGACGATGTA CG	GuideScan	Pseudogene
TTY24P	TTY24P_2	GTTACAGTTATCATTTAG CC	GuideScan	Pseudogene
TTY24P	TTY24P_3	GTATCCTGGAGACGATGT AC	GuideScan	Pseudogene
TTY24P	TTY24P_4	GCACTGGAATGGGGTATC AT	GuideScan	Pseudogene
TTY25P	TTY25P_1	GTGTTCAAGTCGGTACATT CA	GuideScan	Pseudogene
TTY25P	TTY25P_2	TGTGTTCAAGTCGGTACAT TC	GuideScan	Pseudogene
TTY25P	TTY25P_3	CAGTTCCAGTACTGCATG TG	GuideScan	Pseudogene
TTY25P	TTY25P_4	AATGTACCGACTGAACAC AC	GuideScan	Pseudogene
TTY30P	TTY30P_1	CAATGGAGCCTGCGTTAC TT	GuideScan	Pseudogene
TTY30P	TTY30P_2	AATGGAGCCTGCGTTACT TT	GuideScan	Pseudogene
TTY30P	TTY30P_3	AGCGAATCCCAAAGTAA CGC	GuideScan	Pseudogene
TTY30P	TTY30P_4	TACAGACCTGCGCTGTCT TG	GuideScan	Pseudogene
TTY31P	TTY31P_1	TTACCGACCCGCACCCTC CT	GuideScan	Pseudogene
TTY31P	TTY31P_2	CTTACCGACCCGCACCCT CC	GuideScan	Pseudogene
TTY31P	TTY31P_3	TACCAGGTGTACTCTCCT TC	GuideScan	Pseudogene
TTY31P	TTY31P_4	TACCGACCCGCACCCTCC TG	GuideScan	Pseudogene

USP12PY	USP12PY_1	GTCATCGCCGCCGGTCCC TC	GuideScan	Pseudogene
USP12PY	USP12PY_2	TGAGGGACCGGCGGCGA TGA	GuideScan	Pseudogene
USP12PY	USP12PY_3	CTAGGCCCGGGAGTACCT GA	GuideScan	Pseudogene
USP12PY	USP12PY_4	GCCGGTCCCTCAGGTACT CC	GuideScan	Pseudogene
USP9YP20	USP9YP20_1	ATGGTGCTTTGTAGCCCA CC	GuideScan	Pseudogene
USP9YP20	USP9YP20_2	TGGTGCTTTGTAGCCCAC CT	GuideScan	Pseudogene
USP9YP22	USP9YP22_1	TCACCAAACACCATCAAT TC	GuideScan	Pseudogene
USP9YP28	USP9YP28_1	TGGGCAGGGGAAGCCC CAA	GuideScan	Pseudogene
USP9YP29	USP9YP29_1	TATGGTGCTTTGTAGCCA CC	GuideScan	Pseudogene
USP9YP29	USP9YP29_2	ATGGTGCTTTGTAGCCAC CT	GuideScan	Pseudogene
USP9YP3	USP9YP3_1	AGAGCAGGTGGTTCTAGC GT	GuideScan	Pseudogene
USP9YP3	USP9YP3_2	GGAGACGGTTACGGGTC ATA	GuideScan	Pseudogene
USP9YP3	USP9YP3_3	ATAATCACGTATGTATGA CA	GuideScan	Pseudogene
USP9YP3	USP9YP3_4	TAGTGGTGGACTGCATAT GT	GuideScan	Pseudogene
USP9YP4	USP9YP4_1	TTTAGACAGCCAATAACT CG	GuideScan	Pseudogene
USP9YP4	USP9YP4_2	TCACACGCTACGATCAAT GC	GuideScan	Pseudogene
USP9YP4	USP9YP4_3	CACTAATGTCTTCCGGTC TC	GuideScan	Pseudogene
USP9YP4	USP9YP4_4	CCCGTACCTTTGTGCTTG TT	GuideScan	Pseudogene
USP9YP8	USP9YP8_1	GGGGATCAGGTATAGCTG CT	GuideScan	Pseudogene
USP9YP8	USP9YP8_2	ACGCCACCAAAAAGATT TG	GuideScan	Pseudogene
USP9YP8	USP9YP8_3	GTGGGAATATCAGCTCCT GC	GuideScan	Pseudogene
USP9YP8	USP9YP8_4	TTTGGTGGGCGTGGTCCA GC	GuideScan	Pseudogene
XGY1	XGY1_1	ACACGGTCAACTACTACC GC	GuideScan	Pseudogene

XGY1	XGY1_2	TGATTTGTCCATCCGTTG GC	GuideScan	Pseudogene
XGY1	XGY1_3	GAAGCTCCAAATGCAGC ATA	GuideScan	Pseudogene
XGY1	XGY1_4	GTGCTCAGGCGGCCATAT GC	GuideScan	Pseudogene
XKRYP3	XKRYP3_1	AAAATATATGATTAATAG TA	GuideScan	Pseudogene
ZNF736P10Y	ZNF736P10Y_1	GTCAGTAAAGTTTGTGGA GC	GuideScan	Pseudogene
ZNF736P10Y	ZNF736P10Y_2	CACTGAGGATTGAGCACA CC	GuideScan	Pseudogene
ZNF736P10Y	ZNF736P10Y_3	GTCTGTGCATTCTCTTAC AA	GuideScan	Pseudogene
ZNF736P10Y	ZNF736P10Y_4	AAAGTTTGTGGAGCAGGT AA	GuideScan	Pseudogene
ZNF884P	ZNF884P_1	TCGACCCTTACACAGCAT TT	GuideScan	Pseudogene
ZNF884P	ZNF884P_2	TTCGACCCTTACACAGCA TT	GuideScan	Pseudogene
ZNF884P	ZNF884P_3	TGCAGGATATCTCTCCAA AA	GuideScan	Pseudogene
ZNF884P	ZNF884P_4	CGCTACATATATAAGAAA TG	GuideScan	Pseudogene
ZNF885P	ZNF885P_1	TGCTGCAAATTTACAGAA CG	GuideScan	Pseudogene
ZNF885P	ZNF885P_2	GGTGTACTATGCATTCTC TG	GuideScan	Pseudogene
ZNF885P	ZNF885P_3	ATCATGTAAGGTGAGCAT AC	GuideScan	Pseudogene
ZNF885P	ZNF885P_4	AGATTCTCTGACATCATG TA	GuideScan	Pseudogene
ZNF886P	ZNF886P_1	AGTAATATATAAGCCCCT GT	GuideScan	Pseudogene
ZNF886P	ZNF886P_2	GTGTGGCAAAGTCTCCAA CA	GuideScan	Pseudogene
ZNF886P	ZNF886P_3	CAACATCAAATACTCTCT CC	GuideScan	Pseudogene
ZNF886P	ZNF886P_4	AATTTAACAACACTCTCA AC	GuideScan	Pseudogene
ZNF92P1Y	ZNF92P1Y_1	GCCATATTTATTAGGTTG GC	GuideScan	Pseudogene
ZNF92P1Y	ZNF92P1Y_2	TAGGTTGGCAGGTTTTGC TG	GuideScan	Pseudogene
ZNF92P1Y	ZNF92P1Y_3	AAGTTCTGAGAACTATCG AT	GuideScan	Pseudogene

ZNF92P1Y	ZNF92P1Y_4	GGCTTTTTTATGTTTCAGT GA	GuideScan	Pseudogene
COPB1	COPB1_1	GTGATAGTGTGATCCTGA AG	Provided	positive_controls
COPB1	COPB1_2	GTAACCAGAAACCATGA CGG	Provided	positive_controls
COPB1	COPB1_3	GGAAGGAATCCTCTCAAG GG	Provided	positive_controls
COPB1	COPB1_4	GTCTAGACCCACCAAGAA AG	Provided	positive_controls
EEF2	EEF2_1	GCAGGGTGAAGGCCAC CCG	Provided	positive_controls
EEF2	EEF2_2	GCTGCAGCTCCAGCAGGG CG	Provided	positive_controls
EEF2	EEF2_3	GGAGGACATCGATAAAG GCG	Provided	positive_controls
EEF2	EEF2_4	GGCGAGGACAAGGACAA AGA	Provided	positive_controls
EIF5B	EIF5B_1	GGAAAGACAGAAGAGAG AAG	Provided	positive_controls
EIF5B	EIF5B_2	GTTCTTTATAAGCCACAA GG	Provided	positive_controls
EIF5B	EIF5B_3	GGAAGCCAAGCGTAAAG AAG	Provided	positive_controls
EIF5B	EIF5B_4	GAGACTCTTTGCCAAAGA AG	Provided	positive_controls
HEATR1	HEATR1_1	GATGGTGGCAAATACCC AA	Provided	positive_controls
HEATR1	HEATR1_2	GGATGGCTCACCAATGGC GA	Provided	positive_controls
HEATR1	HEATR1_3	GCACAGTTCAGCAAAAA AGA	Provided	positive_controls
HEATR1	HEATR1_4	GCAGCGTAAGAAAAAGG AAG	Provided	positive_controls
LSM3	LSM3_1	GCACATAAATTCGCTCAT CT	Provided	positive_controls
LSM3	LSM3_2	GGAAATGACCGAGAGCT TCG	Provided	positive_controls
LSM3	LSM3_3	GATGGCGGACGACGTAG ACC	Provided	positive_controls
LSM3	LSM3_4	GTCTCTTCTAGTCAACGA AA	Provided	positive_controls
PRPF19	PRPF19_1	GTAGTAACCATTCTCAGA GA	Provided	positive_controls
PRPF19	PRPF19_2	GTAATCATGTTTATGAGC GG	Provided	positive_controls

PRPF19	PRPF19_3	GCTCAGCAAATACCGGCA GG	Provided	positive_controls
PRPF19	PRPF19_4	GAGACGGGCAATGACAC GGC	Provided	positive_controls
PSMB2	PSMB2_1	GTGATTCGAACACTGAAG GT	Provided	positive_controls
PSMB2	PSMB2_2	GTACCTGGCAGCCTTGGC CA	Provided	positive_controls
PSMB2	PSMB2_3	GGTGAAGTTAGCTGCTGC CG	Provided	positive_controls
PSMB2	PSMB2_4	GATCTGGACAATATTGCT GG	Provided	positive_controls
PSMB3	PSMB3_1	GCCGTACATTTGTTCGGC GC	Provided	positive_controls
PSMB3	PSMB3_2	GTTCAGCATGGCTTGGGA GA	Provided	positive_controls
PSMB3	PSMB3_3	GAAGCGCCTGTCTGCAGC GA	Provided	positive_controls
PSMB3	PSMB3_4	GTCACCGTTTCTCATACA AG	Provided	positive_controls
PSMD1	PSMD1_1	GTACAGATGACAAAAAC TGC	Provided	positive_controls
PSMD1	PSMD1_2	GGTACCAAAAGAAAAAG AAA	Provided	positive_controls
PSMD1	PSMD1_3	GCCAGAGCCACAATAAG CCA	Provided	positive_controls
PSMD1	PSMD1_4	GCAAGGACGCCAACCAC AGA	Provided	positive_controls
RBM17	RBM17_1	GGCAGCTCTCACTCAGGC AA	Provided	positive_controls
RBM17	RBM17_2	GAAGACAGACATGAAGC AAG	Provided	positive_controls
RBM17	RBM17_3	GCAGTCATTGACCTGAAG CG	Provided	positive_controls
RBM17	RBM17_4	GTCTCCTGCCAGGGGCAC GG	Provided	positive_controls
RPL10	RPL10_1	GGCCCTTTCAC TTCAGAA AC	Provided	positive_controls
RPL10	RPL10_2	GGTTTGCTGCCTCATGAG CA	Provided	positive_controls
RPL10	RPL10_3	GATGACCCAAAGGTTCCC AG	Provided	positive_controls
RPL10	RPL10_4	GTGTATCTACATTCTTGA CG	Provided	positive_controls
RPL10A	RPL10A_1	GGCCGTGGATATCCCCCA CA	Provided	positive_controls

RPL10A	RPL10A_2	GCCCACTCACCTTCTTCA TT	Provided	positive_controls
RPL10A	RPL10A_3	GTCCTCCCAGGTGTTATG TC	Provided	positive_controls
RPL10A	RPL10A_4	GCGCGACACCCTGTACGA GG	Provided	positive_controls
RPL11	RPL11_1	GGGCCCTCGAACTGTGC AG	Provided	positive_controls
RPL11	RPL11_2	GTGAAAAGGAGAACCCC ATG	Provided	positive_controls
RPL11	RPL11_3	GTCACCTTTGGAAAACAC AG	Provided	positive_controls
RPL11	RPL11_4	GTCAAATATGACCCAAGC AT	Provided	positive_controls
RPL37	RPL37_1	GGGCCTTAGAGCCACAGC GG	Provided	positive_controls
RPL37	RPL37_2	GCGAAGGGAACGTCATC GTT	Provided	positive_controls
RPL37	RPL37_3	GTGACATTCTTAAGATGA AC	Provided	positive_controls
RPL37	RPL37_4	GGCAGGCATGGATTCCGT GA	Provided	positive_controls
RPL4	RPL4_1	GTTGCAGCACAAGCTCCG GG	Provided	positive_controls
RPL4	RPL4_2	GAAGAGCCCTTCGAGCAC CA	Provided	positive_controls
RPL4	RPL4_3	GCTTTATCTTCAACTACC AA	Provided	positive_controls
RPL4	RPL4_4	GAAATCAGATGAGAAGG CGG	Provided	positive_controls
RRM1	RRM1_1	GATTGAAAGATCTTACCG AG	Provided	positive_controls
RRM1	RRM1_2	GTTCCCCAGGATCTGAGC AG	Provided	positive_controls
RRM1	RRM1_3	GGAGTACACCAGCAAAG ATG	Provided	positive_controls
RRM1	RRM1_4	GTTCTCCAAAGAGCACAC CA	Provided	positive_controls
RUVBL2	RUVBL2_1	GATCACCATCGACAAGGC GA	Provided	positive_controls
RUVBL2	RUVBL2_2	GCTCCAGAAACGCAAGG AGG	Provided	positive_controls
RUVBL2	RUVBL2_3	GGCTGACGCAGGCCTTCC GG	Provided	positive_controls
RUVBL2	RUVBL2_4	GTGATCATGGCCACCAAC CG	Provided	positive_controls

WDR5	WDR5_1	GAGACAATAAGGTTGGA CTG	Provided	positive_controls
WDR5	WDR5_2	GCCAATTTCTCTGTTACT GG	Provided	positive_controls
WDR5	WDR5_3	GACTCACTTGTCAGCGT GG	Provided	positive_controls
WDR5	WDR5_4	GATCTGAGGCAGAAACA AGA	Provided	positive_controls
AAVS1_chr1 9	AAVS1_chr19_1	GGGGACTCTTTAAGGAAA GA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_2	GCCCCGTCGTTCTGGCC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_3	GGAATTGGAGCCGCTTCA AC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_4	GGCTTTCTGTCTGCAGCT TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_5	GATGATGCAGGCCTACAA GA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_6	GCATCCTAAGAAACGAG AGA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_7	GCGTGGGTTTATCAACCA CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_8	GCCCGGCGTCTCCCGGGG CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_9	GTTGAGTCCTTGCAAGC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_10	GCAGCCCCAGGTGGAGA AAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11	GTTCCGGAGCACTTCCTT CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12	GATCAACCACTTGGTGAG GC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13	GCCCGGAGGAGGCCCTC ATC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14	GCTCCAATGCGGAAGAG AGT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_15	GGCCTCTCCTGGGCTTGC CA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_16	GCTAGCCACTAAGGCAAT TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_17	GCTCAAAGTGGTCCGGAC TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_18	GGACCCAATATCAGGAG ACT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_19	GGACCACCCCACTTCCGA AT	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_20	GGGATCTCCCGGTCCCCG CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_21	GAAAAGGCAGCCTGGTA GAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_22	GTGGAGTCCATTAGCAGA AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_23	GGATCCTGTGTCCCCGAG CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_24	GCCGTGTCTGGGTCTCT CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_25	GTTAGGATGGCCTTCTCC GA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_26	GGCAGCTCCGAGGCGCCC AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_27	GAGTGACAATGGCCAGG GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_28	GCATTAGCAGAAGTGGCC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_29	GCACCGCCCCAAGGATCT CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_30	GATTCCCTTCTCAGGTTA CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_31	GTGTGAGAATGGTGCGTC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_32	GATAAGGTGGTCCCAGCT CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_33	GGCGGCACAGCAAGGGC ACT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_34	GAGAAAAACGGTGATGA TGC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_35	GAGCCGCTTCAACTGGCC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_36	GTCCTTGGCAAGCCCAGG AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_37	GGTGGGGTACCCTAAGA ACT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_38	GGGACCACCTTATATTCC CA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_39	GCCCACTGTTTCCCCTTC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_40	GTGGGAAGTCCGCAGCTC CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_41	GTCCGGACTCAGGAGAG AGA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_42	GTGCGTCCTAGGTGTTCA CC	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_43	GCCCTAGCCACTAAGGCA AT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_44	GCTAGGTGTTACCAGGT CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_45	GCTCGGGGACACAGGAT CCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_46	GGTGACACACCCCCATTT CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_47	GCGACCTGCCCAGCACAC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_48	GCCCTAGTGGCCCCACTG TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_49	GGGAACCCAGCGAGTGA AGA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_50	GATCCACCCAAAAGGCA GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_51	GCCCAGGGCCAGGAACG ACG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_52	GAGAGGTGACCCGAATC CAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_53	GCCAGCCGTAGAGGTGA CCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_54	GGACGTCACGGCGCTGCC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_55	GCACCCTCTGCTGCGCCA CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_56	GAAAGTCCAGGACCGGC TGG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_57	GCTGGCCCCCACC GCC CA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_58	GGACCTGCATTCTCTCCC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_59	GAGTTCCTGGCGGCCTGT GC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_60	GCAGACTGAGCTATGGG AGC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_61	GTGGACTCCACCAACGCC GA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_62	GGGGGAGCTGCCCAAAT GAA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_63	GAAGCCCAGGAGAGGCG CTC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_64	GCTGATACCGTCGGCGTT GG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_65	GGTCCCTAGTGGCCCCAC TG	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_66	GAGTAGAGGCGGCCACG ACC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_67	GAACCTTAGAGGTCTGG CA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_68	GGCTTGGCAAACCTCACTC TT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_69	GGAACCAGAGCCACATT AAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_70	GAGATGGCACAGGCCCC AGA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_71	GCCTTTTCCTTCTCCTTCT G	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_72	GCCAGGCCAAGTAGGTG GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_73	GAGTCTTCTTCCTCCAAC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_74	GGAGTCGCTTTAACTGGC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_75	GTGGTTGATAAACCCACG TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_76	GTTCTTAGGGTACCCAC GT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_77	GGCGCTGATACCGTCGGC GT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_78	GTCACTCTTCGGGGTATC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_79	GCAGCTCCCATAGCTCAG TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_80	GCAGAGTGGTCAGCACA GAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_81	GTTGGGAACAGCCACAG CAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_82	GGCACAGGCCGCCAGGA ACT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_83	GGCCGCCCCGCACAGGCC GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_84	GCAGAGCCAGGAACCCC TGT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_85	GAGCGGCTCCAATTCGGA AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_86	GCAGGGTGGCCACTGAG AAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_87	GTGCAGACAGAAAGCGG CAC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_88	GCTTCCTTACACTTCCCA AG	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_89	GCCTGCCTGGAGAAGGAT GC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_90	GACCTGGCCCCGGGAGA CGC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_91	GCGCGCCGCCGAGTTCCT GG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_92	GAGGGGCTCAACATCGG AAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_93	GCCCCGCCCGGCGTCTCC CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_94	GTGTCCTGAAGTGGACAT AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_95	GGGGCCCCTATGTCCACT TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_96	GGACAAAGTCCAGGACC GGC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_97	GGCGGATCCTCCCCGTGT CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_98	GAGCTGAGCTCTCGGACC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_99	GGCTCCGGAAAGAGCAT CCT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_100	GTCCCGCCTCCCCTTCTT GT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_101	GTACCAGGCTGCCTTTTG GG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_102	GCAAGGGCCACTTCTGCT AA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_103	GTCTCCTGCCCCTTCCCT AC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_104	GAAGCCCAGAGCAGGGC CTT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_105	GCAGAAAGCGGCACAGG CCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_106	GAGTTGAAGCGGCTCCAA TT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_107	GAGCATGTTTGCTGCCTC CA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_108	GCCCGGAGAGGACCCAG ACA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_109	GGCGCAAAGTGACAATG GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_110	GGTTTATCAACCACTTGG TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_111	GCCGCTCAGAGGACATCA CG	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_11 2	GGATGCAGGCCTACAAG AAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 3	GCAGGTCAGCGCCCCCG CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 4	GCCCAAATGAAAGGAGT GAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 5	GAGTTAAAGCGACTCCAA TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 6	GCTGTTTCCCCTTCCCAG GC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 7	GAGTAGAGCTCAAAGTG GTC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 8	GCAGTCTGAAGAGCAGA GCC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_11 9	GCACGACCTGGTGAACAC CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 0	GTCACCAATCCTGTCCCT AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 1	GGGGCTCAACATCGGAA GAG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 2	GCCCTCTGCTGCGCCACC TG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 3	GCCGAATCCACAGGAGA ACG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 4	GTTGGCAAACCTCACTCTT CG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 5	GCTGCCAAGCTCTCCCTC CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 6	GCCCCACAGTGGGGCCAC TA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 7	GGACTCCTGGAAGTGGCC AA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 8	GAATGCAGGTCAGAGAA AGC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_12 9	GACGCAAGGGAGACATC CGT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 0	GCTCTTCGGGGTATCCCA GG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 1	GCCTGCATCCTTCTCCAG GC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 2	GACAGAAAAGCCCCATC CTT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 3	GGCTTACGATGGAGCCAG AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 4	GCAACTGTGGGGTGACTG CT	Provided	AAVS1

AAVS1_chr1 9	AAVS1_chr19_13 5	GGCCGTCTCTCTCCTGAG TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 6	GATATAAGGTGGTCCCAG CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 7	GGTCAGAGCAGCTCAGGT TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 8	GGAGCGCGCCGCCGAGTT CC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_13 9	GAGAAGACTAGCTGAGC TCT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 0	GTCCCTCCCAGGATCCTC TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 1	GCCCTGGAAGATGCCATG AC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 2	GTTCCCTAAGGCCCTGCT CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 3	GCCCAACCCCCTAGCCAC TA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 4	GCTCCTTGCCAGAACCTC TA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 5	GCATGCCGTCTTCACTCG CT	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 6	GGAGGAGGGATTCCCTTC TC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 7	GGGTCCCAGCTCGGGGAC AC	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 8	GCCAGCGAGTGAAGACG GCA	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_14 9	GTGCACCCCAATTGCCTT AG	Provided	AAVS1
AAVS1_chr1 9	AAVS1_chr19_15 0	GGCCAGATGAGGGCCTCC TC	Provided	AAVS1
non_specific	Zhang_886	GAACGAGATCGAGAAAG GTA	Provided	non_specific
non_specific	Zhang_852	GTGGCTTATTAGCTATAA AG	Provided	non_specific
non_specific	Zhang_959	GAGAGACAATGACATGT AGA	Provided	non_specific
non_specific	Zhang_40	GCATAGTCGACGGCTCGA TT	Provided	non_specific
non_specific	Zhang_832	GCAGAGCCTTGGTTTATA TC	Provided	non_specific
non_specific	CTRL0082	GCGGATCCAGATCTCATT CG	Provided	non_specific
non_specific	Zhang_887	GTCTGCCATGGCGTCCTG GC	Provided	non_specific

non_specific	Zhang_431	GACTTTTTGGAATCCGTC TA	Provided	non_specific
non_specific	Zhang_365	GGGTCGGCCGAACATAC GGT	Provided	non_specific
non_specific	Zhang_166	GTATATTGTCGCGCAGTG GA	Provided	non_specific
non_specific	CTRL0054	GCCGCAATATATGCGGTA AG	Provided	non_specific
non_specific	Zhang_78	GCGCGGACATAGGGCTCT AA	Provided	non_specific
non_specific	Zhang_17	GAACGGGTTCTCCCGGCT AC	Provided	non_specific
non_specific	Zhang_603	GGCTGGTTGACCTTCCCG CT	Provided	non_specific
non_specific	Zhang_265	GTACGAGGCGCTTTTCTT TG	Provided	non_specific
non_specific	Zhang_856	GTGATATCTGACATGCAG CG	Provided	non_specific
non_specific	Zhang_268	GATACTGCGGATCAATCT GA	Provided	non_specific
non_specific	Zhang_85	GCTGGCTTGACACGACCG TT	Provided	non_specific
non_specific	Zhang_333	GCCCGTAGCTCATTAGTC TG	Provided	non_specific
non_specific	Zhang_501	GGTCTTGGCCAATGTCAC GG	Provided	non_specific
non_specific	CTRL0009	GATCCATGTAATGCGTTC GA	Provided	non_specific
non_specific	Zhang_577	GATGAGCGCATTGAATAA TA	Provided	non_specific
non_specific	Zhang_156	GAGAGATATCCGATCGTG GT	Provided	non_specific
non_specific	Zhang_432	GAGCGGTGCTATTTGGTC TT	Provided	non_specific
non_specific	Zhang_130	GAACGCGCATATCTGAAC AC	Provided	non_specific
non_specific	Zhang_330	GTTGGGTTTATCCGCCCC CA	Provided	non_specific
non_specific	CTRL0007	GATACACGAAGCATCACT AG	Provided	non_specific
non_specific	Zhang_374	GATTGCACGCCACAGCAT TG	Provided	non_specific
non_specific	Zhang_247	GTATGTGAGCACGCCATT AC	Provided	non_specific
non_specific	Zhang_651	GAAAAGTCTCGCTTGGTC CT	Provided	non_specific

non_specific	Zhang_120	GCAAACCCGAGTGACAC GTC	Provided	non_specific
non_specific	CTRL0095	GTACTCCAATCCGCGATG AC	Provided	non_specific
non_specific	Zhang_514	GCACTGGTAAAGGCTAG ACT	Provided	non_specific
non_specific	Zhang_905	GGTACCCCTAGGTATGGG GA	Provided	non_specific
non_specific	Zhang_159	GGATTGAATGGCTAACGC GG	Provided	non_specific
non_specific	Zhang_380	GCATAGCTCTAGCGATAA AC	Provided	non_specific
non_specific	Zhang_634	GGAAGTCTTTCTTAGATG GT	Provided	non_specific
non_specific	Zhang_77	GTAGACGTCGTGAGCTTC AC	Provided	non_specific
non_specific	Zhang_705	GATTAGCAGCCCAGCGCC CA	Provided	non_specific
non_specific	Zhang_404	GCACCTCCGAACGAACAC CT	Provided	non_specific
non_specific	CTRL0052	GTACGGCACTCCTAGCCG CT	Provided	non_specific
non_specific	Zhang_24	GTATCTCGAGTGGTAATG CG	Provided	non_specific
non_specific	CTRL0013	GAAGTGACGTCGATTCGA TA	Provided	non_specific
non_specific	Zhang_561	GGCCACAAAACTCGCTA AG	Provided	non_specific
non_specific	Zhang_556	GGGAGTTAACCTGGAACC TT	Provided	non_specific
non_specific	Zhang_931	GAAATTCAGACCACAGCT AA	Provided	non_specific
non_specific	Zhang_277	GCTGTTGCCGCGCCAACT GC	Provided	non_specific
non_specific	Zhang_327	GCCGTGGTATCAAGTCGG TA	Provided	non_specific
non_specific	Zhang_57	GCGCTATTGAAACCGCCC AC	Provided	non_specific
non_specific	Zhang_480	GCTGCTCCCGGTGCGCCCC TC	Provided	non_specific
non_specific	Zhang_18	GAGGAGTCGCCGATACG CGT	Provided	non_specific
non_specific	Zhang_565	GCTAAGGGGTACCACCAT GG	Provided	non_specific
non_specific	Zhang_828	GTTATTACTCCAGTATAA GA	Provided	non_specific

non_specific	Zhang_111	GAACGCCGCTCAAGTTGA TA	Provided	non_specific
non_specific	Zhang_335	GACGCCCTAATGCCCATC GT	Provided	non_specific
non_specific	Zhang_630	GCAATTCTCACTCACGAC CA	Provided	non_specific
non_specific	Zhang_93	GGCGGCGTAATGCTTGAA AG	Provided	non_specific
non_specific	Zhang_411	GCGGCTACAATCTTTGGC AT	Provided	non_specific
non_specific	Zhang_2	GGCTTCCGCGGCCCGTTC AA	Provided	non_specific
non_specific	Zhang_892	GACCTTCATTGAAGAAAA GC	Provided	non_specific
non_specific	Zhang_216	GGTTTCACTTCGAGACCG GC	Provided	non_specific
non_specific	Zhang_184	GAAACATCGACCGAAAG CGT	Provided	non_specific
non_specific	Zhang_118	GTCTCGGGTCGACTGCGG AT	Provided	non_specific
non_specific	Zhang_110	GTTGTTGCGTATACGAGA CT	Provided	non_specific
non_specific	Zhang_416	GGAGCGGCCTCTAATTAA TC	Provided	non_specific
non_specific	CTRL0051	GTCAGCCATCGGATAGAG AT	Provided	non_specific
non_specific	Zhang_470	GCCAGGGTATGGGCATCT CG	Provided	non_specific
non_specific	Zhang_13	GCGTGCGTCCCGGGTTAC CC	Provided	non_specific
non_specific	Zhang_357	GCCAACAAGAATCGGAT CCC	Provided	non_specific
non_specific	Zhang_336	GGATATTGAGTAAACCCG AT	Provided	non_specific
non_specific	Zhang_462	GTTGCTCTGTGCATCAA TC	Provided	non_specific
non_specific	Zhang_202	GGAGCATTCGTAGCCCAG CA	Provided	non_specific
non_specific	Zhang_755	GGAATCCGGAGCTCATGA GG	Provided	non_specific
non_specific	Zhang_233	GATCAATCGTCCGGGTCA CT	Provided	non_specific
non_specific	Zhang_557	GGCGCTCTGGTTGCATCC CT	Provided	non_specific
non_specific	Zhang_82	GCGTCCATACTGTCTGGCT AC	Provided	non_specific

non_specific	Zhang_531	GAGCGGGCACACATGAC AAG	Provided	non_specific
non_specific	Zhang_690	GCCCTCCTAGTCAAGAAG AG	Provided	non_specific
non_specific	Zhang_937	GCAGCGAGATAACTTGAC TC	Provided	non_specific
non_specific	Zhang_98	GTACGGGGCGATCATCCA CA	Provided	non_specific
non_specific	Zhang_407	GAAGTGGCAAACAGGCG TGG	Provided	non_specific
non_specific	CTRL0084	GTCATCATTATGGCGTAA GG	Provided	non_specific
non_specific	Zhang_951	GGTGTGGAAAAGCTAAC AGA	Provided	non_specific
non_specific	Zhang_299	GATATCCCGCGAAAAAAT CT	Provided	non_specific
non_specific	Zhang_197	GGTTAAGACTAGCTCGGT TT	Provided	non_specific
non_specific	Zhang_665	GCAGTGCCCTTTTGTGCG AA	Provided	non_specific
non_specific	Zhang_347	GGCTGGTTGACGACTCCT GA	Provided	non_specific
non_specific	Zhang_660	GGGCTTAAATGGCGAGAT TG	Provided	non_specific
non_specific	Zhang_456	GGAGCAAAGATTGTTGG ATA	Provided	non_specific
non_specific	Zhang_942	GCAAGGTCATGAAACCA AGC	Provided	non_specific
non_specific	Zhang_737	GTTTAGTAATGCACACCC AG	Provided	non_specific
non_specific	CTRL0001	GTAGCGAACGTGTCCGGC GT	Provided	non_specific
non_specific	CTRL0079	GTAGCGAAGACTTGCCGA CG	Provided	non_specific
non_specific	Zhang_793	GTTTTCGAAAGCTTAGGC CA	Provided	non_specific
non_specific	Zhang_507	GTTACGAAGTATACCAGG TC	Provided	non_specific
non_specific	Zhang_224	GGTCATTAGCGTAACGAT AT	Provided	non_specific
non_specific	Zhang_545	GAAAAGCTTCCGCCTGAT GG	Provided	non_specific
non_specific	Zhang_37	GGTGGCCGGAACCGTCAT AG	Provided	non_specific
non_specific	Zhang_524	GTCAAGTCAGGTTATGCG GG	Provided	non_specific

non_specific	Zhang_649	GTCAGCGAGTGTGACTAA GC	Provided	non_specific
non_specific	Zhang_25	GATCGACTCGAACTTCGT GT	Provided	non_specific
non_specific	Zhang_398	GAGGCTGCGCTTCGCAAG CT	Provided	non_specific
non_specific	Zhang_67	GACTAGCCCCGAGCAGCTT CG	Provided	non_specific
non_specific	Zhang_80	GTTCGCTTCGTAACGAGG AA	Provided	non_specific
non_specific	Zhang_293	GTCCCATTTGATCTACGAT GG	Provided	non_specific
non_specific	CTRL0080	GTCGGCGTTCTGTTGTGA CT	Provided	non_specific
non_specific	CTRL0004	GCTTGAGCACATACGCGA AT	Provided	non_specific
non_specific	Zhang_689	GATCATAAATGTACAACG GG	Provided	non_specific
non_specific	Zhang_424	GCTGAACGCCGACAGGA CGG	Provided	non_specific
non_specific	Zhang_376	GCAGCAATACCCCGGTAT GG	Provided	non_specific
non_specific	Zhang_812	GGATTAATTCGCTAAATG AT	Provided	non_specific
non_specific	Zhang_337	GGACTCGGGCAATATCGG TT	Provided	non_specific
non_specific	Zhang_928	GAAGACTTGCTCCAAAAC AC	Provided	non_specific
non_specific	Zhang_990	GTGTAGTCCTAGCCATGG GG	Provided	non_specific
non_specific	Zhang_386	GACGGATCACCAAATCTT AG	Provided	non_specific
non_specific	Zhang_359	GATATGGCTCGAGTAATC TT	Provided	non_specific
non_specific	Zhang_361	GTGCTGCAGCTTTACGAT CA	Provided	non_specific
non_specific	Zhang_840	GTGCACTGTGGAGACGCC CG	Provided	non_specific
non_specific	CTRL0033	GCCGACCAACGTCAGCG GTA	Provided	non_specific
non_specific	Zhang_516	GTGGTGACCGACAATTAC AC	Provided	non_specific
non_specific	Zhang_508	GTAGCTGCTGTAAATCGC AT	Provided	non_specific
non_specific	Zhang_275	GAGTAATTTCGAACGTAT TG	Provided	non_specific

non_specific	Zhang_787	GAATAGATTTGTCAGTTA GG	Provided	non_specific
non_specific	Zhang_95	GCCGTGTTGCTGGATACG CC	Provided	non_specific
non_specific	Zhang_903	GCTAACCCCTGGCCAGGA AG	Provided	non_specific
non_specific	Zhang_137	GGGAAATCGACTGTGCGC TT	Provided	non_specific
non_specific	Zhang_900	GGTACTGGAAGTCCGAA ACC	Provided	non_specific
non_specific	Zhang_602	GGAGAGGGCCCGCGAAC TCA	Provided	non_specific
non_specific	Zhang_158	GGCAGTCGCGCTGAGCGT CA	Provided	non_specific
non_specific	Zhang_749	GGGAGAAACGAGGTGTA ATA	Provided	non_specific
non_specific	Zhang_738	GAGTTCTAATCGTTCCTT GA	Provided	non_specific
non_specific	Zhang_550	GAGTTACAGACTCAGCGG GT	Provided	non_specific
non_specific	Zhang_513	GTAATTTGGGTGGGCCCT GC	Provided	non_specific
non_specific	Zhang_578	GACTTTGGTTGAGCTTCA AT	Provided	non_specific
non_specific	Zhang_526	GTCCGTTATGTGGCATGA GA	Provided	non_specific
non_specific	Zhang_511	GACGTAAGTGACGACAG GAA	Provided	non_specific
non_specific	Zhang_47	GGGGACGTCGCGAAAAT GTA	Provided	non_specific
non_specific	Zhang_467	GAGGAGCTGTATCTAGTG GC	Provided	non_specific
non_specific	Zhang_808	GACCATAGAACCTGAAAT AC	Provided	non_specific
non_specific	Zhang_829	GGGGAAACCTCTATGGGT AA	Provided	non_specific
non_specific	Zhang_280	GCGCTGTCTCACTAATCT CA	Provided	non_specific
non_specific	Zhang_885	GTTAAGTCATGAGCAAAG AT	Provided	non_specific
non_specific	Zhang_394	GCCAGGGTTCTTGGTCCC GA	Provided	non_specific
non_specific	Zhang_116	GACGGCCTAACTTGCTGA TA	Provided	non_specific
non_specific	Zhang_784	GTTTATAAACACAGGGTC GC	Provided	non_specific

non_specific	Zhang_211	GCGCTCAGCACCCGCTAT GC	Provided	non_specific
non_specific	Zhang_351	GAGGTATGTCATCGCCAT GA	Provided	non_specific
non_specific	Zhang_341	GGGCGGCCCAAACCTAAC AC	Provided	non_specific
non_specific	Zhang_344	GCTTGCTATATGGGTGCG AG	Provided	non_specific
non_specific	Zhang_132	GATATTTGGCTCGGCTGC GC	Provided	non_specific