AWARD NUMBER: W81XWH-18-1-0200

TITLE: Mutational Landscape of the Y Chromosome and Prostate Cancer

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REPORT DATE: July 2019

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release;
Distribution Unlimited

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REPORT DOCUMENTATION PAGE

*Form Approved*
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**1. REPORT DATE**
July 2019

**2. REPORT TYPE**
Annual

**3. DATES COVERED**
15 June 2018–14 June 2019

**4. TITLE AND SUBTITLE**
Mutational Landscape of the Y Chromosome and Prostate Cancer

**5a. CONTRACT NUMBER**

**5b. GRANT NUMBER:**
W81XWH-18-1-0200

**5c. PROGRAM ELEMENT NUMBER**

**6. AUTHOR(S)**

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**5d. PROJECT NUMBER**

**5e. TASK NUMBER**

**5f. WORK UNIT NUMBER**

**7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)**

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**8. PERFORMING ORGANIZATION REPORT NUMBER**

**9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)**

U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

**10. SPONSOR/MONITOR'S ACRONYM(S)**

**11. SPONSOR/MONITOR'S REPORT NUMBER(S)**

**12. DISTRIBUTION / AVAILABILITY STATEMENT**

Approved for Public Release; Distribution Unlimited

**13. SUPPLEMENTARY NOTES**

**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.

**15. SUBJECT TERMS**
Metastatic castration-resistant prostate cancer, Y chromosome, antiandrogen therapy, epigenetics, biomarkers, tumor suppressor, mutations, CRISPR/Cas9 library screening

| **16. SECURITY CLASSIFICATION OF:** | | | **17. LIMITATION OF ABSTRACT** | **18. NUMBER OF PAGES** | **19a. NAME OF RESPONSIBLE PERSON** |
|---|---|---|---|---|---|
| **a. REPORT** | **b. ABSTRACT** | **c. THIS PAGE** | | | USAMRMC |
| U<br>Unclassified | U<br>Unclassified | U<br>Unclassified | UU<br>Unclassified | 95 | **19b. TELEPHONE NUMBER** *(include area code)* |

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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 regiments. 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 phospo-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.

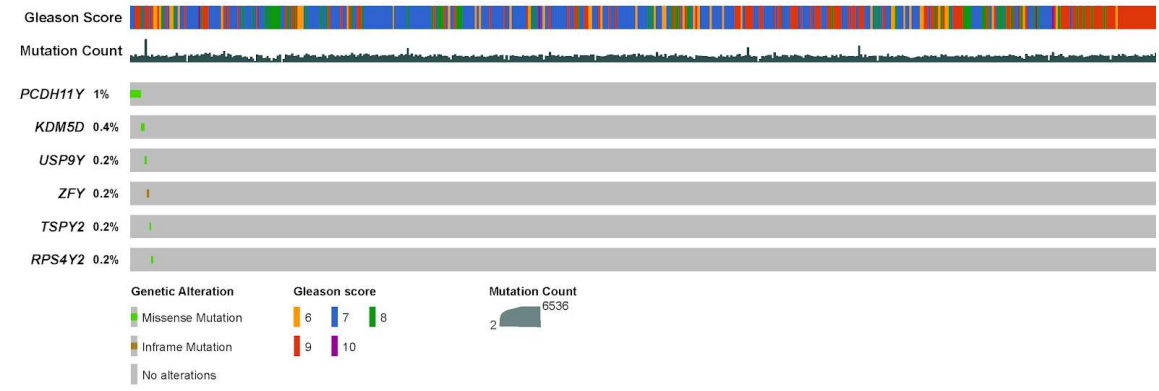


**Figure 1.** Oncoprint showing the top Y chromosome mutated genes in The Cancer Genome Atlas cohort.

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**).

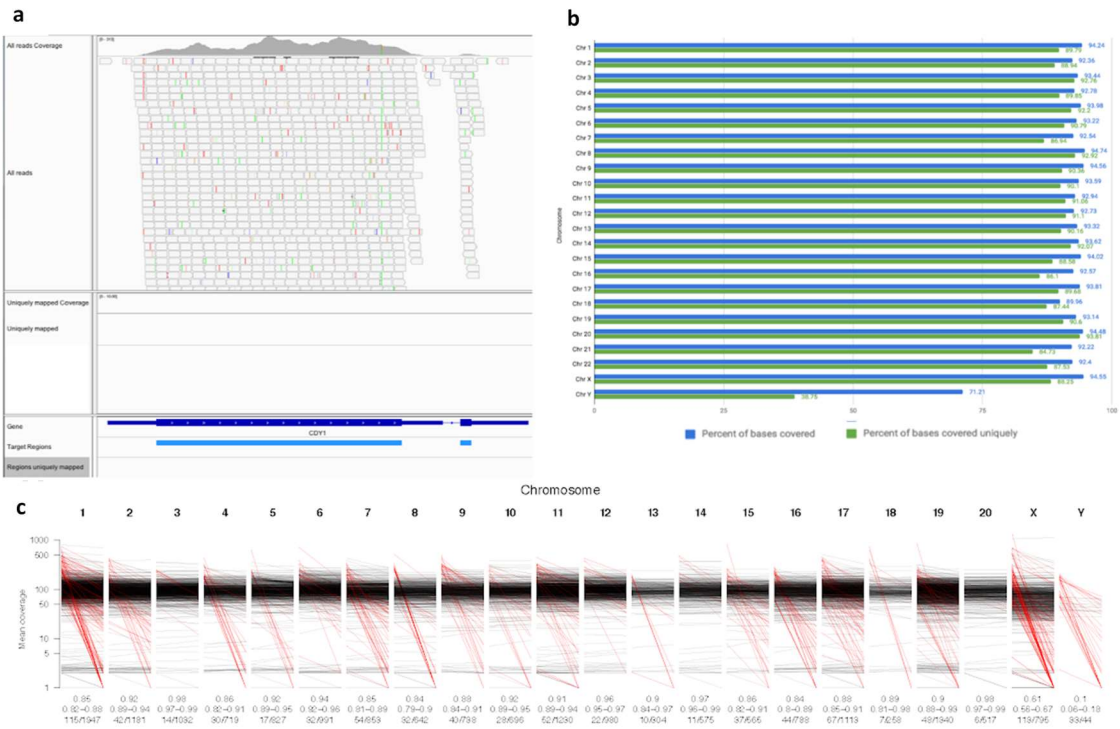


**Figure 2a–c.** Somatic variant calling of most Y chromosome genes is challenging. **a.** An example of reads that do not uniquely map to CDY1 due to the presence of multiple paralogs distributed along the Y chromosome (white filled reads indicates reads with low mapping quality). **b**. Percent of bases covered before removing low-quality reads (in blue) and in percent of bases covered uniquely (in green) from one representative sample from the The Cancer Genome Atlas (TCGA). **c.** Ladder-plot showing the mean coverage of every gene before and after removing reads that do not uniquely map from one representative sample from the TCGA cohort. Each ladder-plot represents a chromosome. Each line represents a gene. Lines are color-coded according to whether the corresponding gene can (black) or cannot (red) be accurately assessed for variant calling. Geometric mean changes, 95% confidence interval, and the proportion of genes that cannot be accurately assessed for variant calling due to a major drop in coverage are shown below each ladder-plot.

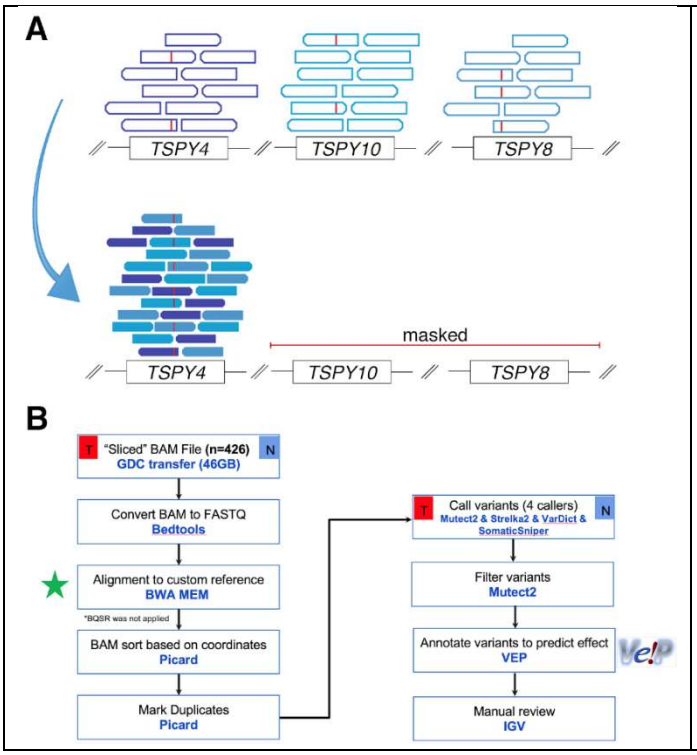


**Figure 3a and b.** Strategy employed to call mutations present in paralogs. **a.** Schematic representation of the crucial step of the strategy employed to call mutations in Y chromosome paralogs (eg. TSPY4). TSPY4 has many paralogs within the Y chromosome. Standard aligners will randomly align reads across these paralogs and assign a low mapping quality and will be discarded for subsequent variant calling (represented by white filled reads). Red lines indicate an individual's mutation that exists in one of these paralogs but reads containing this mutation also get scattered and assigned a low mapping quality. The crucial step of our method is to realign all the reads to one custom reference representative of the paralog families. **b.** Flowchart representing the workflow used for paralogs tumor/normal variant calling. Each bioinformatics tool used is colored blue. The crucial step is denoted with the green star.

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**).

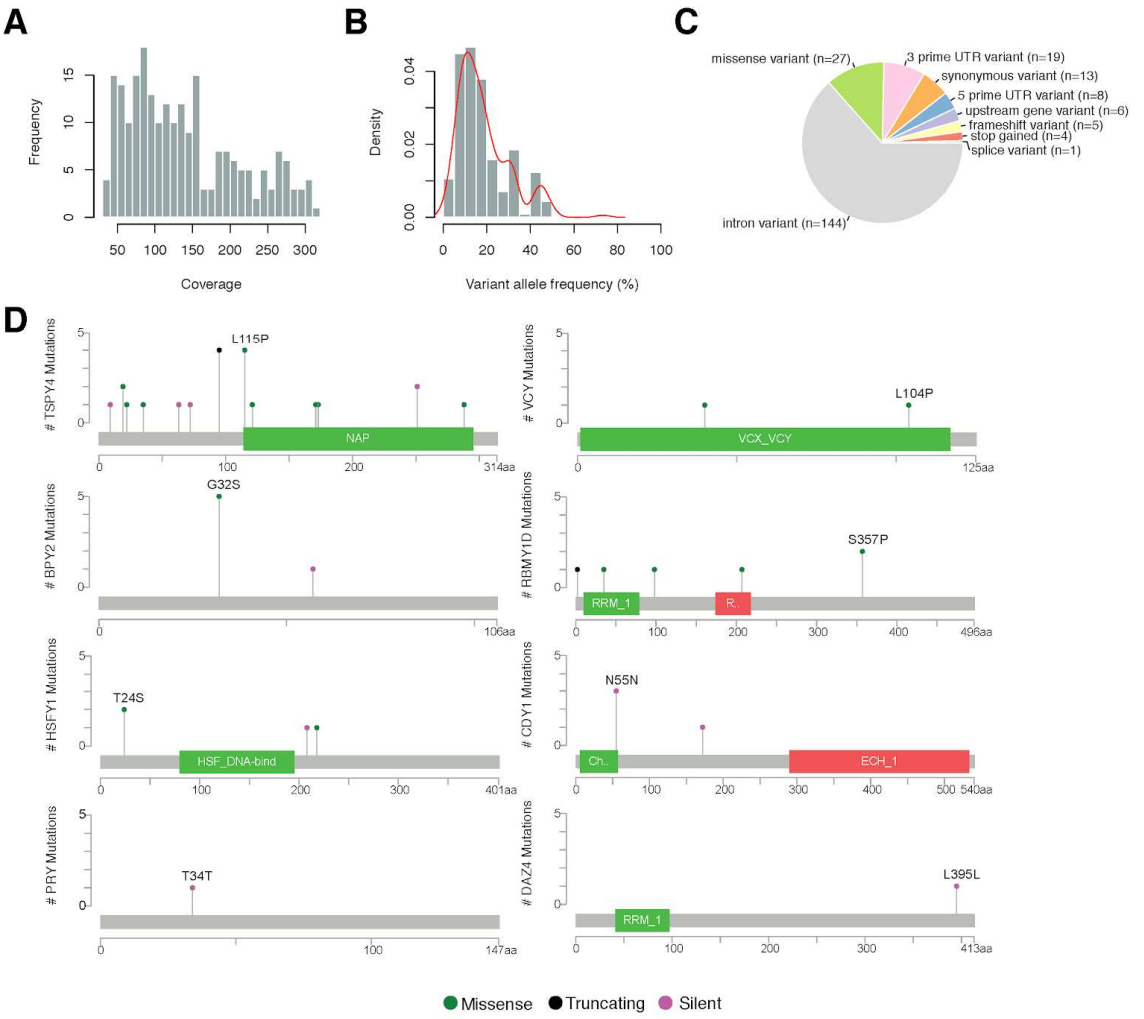


**Figure 4a–d.** Paralog variants called from the 426 The Cancer Genome Atlas prostate cancer patients. **a.** Histogram showing the coverage distribution form the 227 paralog variants called. **b.** Distribution of the variant allele frequency of the 227 paralog variants called. **c.** Pie chart representing the frequency of variant according to protein consequence. **d.** Lollipop chart showing the variant identified in the 8 representative genes from the 8 paralog families present in the Y chromosome.

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.

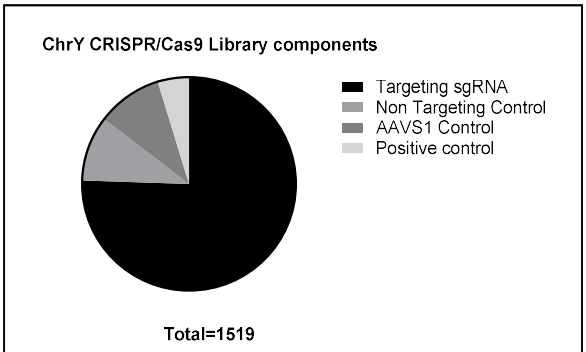


**Figure 5.** Breakdown of Chromosome Y CRISPR/Cas9 library.

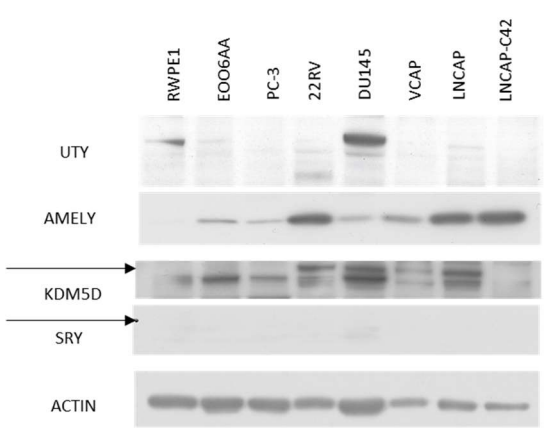


**Figure 6.** Immunoblot analysis of selected chromosome Y genes in panel of prostate cancer cell line models.

***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.

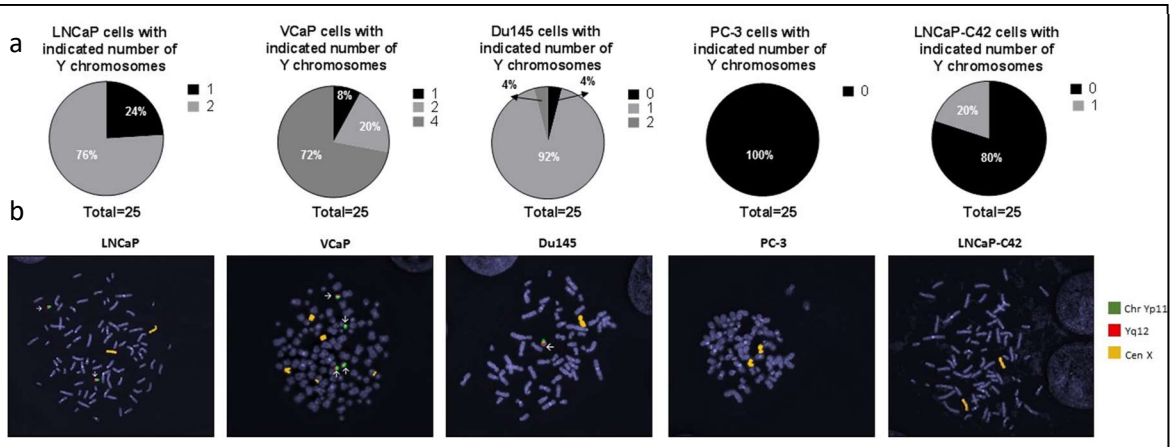


**Figure 7a and b.** XY paint conducted on indicated cell lines revealed heterogeneity in cell line models in terms of chromosome Y number. Indicated cell lines were labelled with probes specific to ChrYp11-q11 (green), Yp12 (red) and Cen X or chromosome X (orange). 25 metaphases were analyzed per cell line. **a.** Quantification of each sub population in indicated cell line based on Y chromosome number. Percentage of each population is indicated. **b.** Representative picture of XY paint analysis. White arrows annotate Y chromosome labelling.

**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 (SPORE) 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. Komura K, Jeong SH, Hinohara K, Qu F, Wang X, Hiraki M, Azuma H, Lee GS, Kantoff PW, Sweeney CJ. Resistance to docetaxel in prostate cancer is associated with

androgen receptor activation and loss of KDM5D expression. Proc Natl Acad Sci U S A 2016;113:6259-64. PMCID: PMC4896695

5. Komura K, Yoshikawa Y, Shimamura T, Chakraborty G, Gerke TA, Hinohara K, Chadalavada K, Jeong SH, Armenia J, Du SY, Mazzu YZ, Taniguchi K, Ibuki N, Meyer CA, Nanjangud GJ, Inamoto T, Lee GM, Mucci LA, Azuma H, Sweeney CJ, Kantoff PW. ATR inhibition controls aggressive prostate tumors deficient in Y-linked histone demethylase KDM5D. J Clin Invest 2018;128:2979-95. PMCID: PMC6025984

## 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 |

| | |
|---|---|
| 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 Dates12/1/2014–11/30/2018
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 resorce 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 nivoiumab 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 projec**t
   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 | CAGGCATCAGTGCTTGCTGG | Brunello | Coding |
| AMELY | AMELY_2 | CGTAACCATAGGAAGAGTAC | Brunello | Coding |
| AMELY | AMELY_3 | GATGTGGTGATGAGACTGCA | Brunello | Coding |
| AMELY | AMELY_4 | GCACCACCAAATCATCCCCG | Brunello | Coding |
| BPY2 | BPY2_1 | ATATGTCAGCAAGCCCACTA | Brunello | Coding |
| BPY2 | BPY2_2 | CAATAGTACCTGTGAAAATC | Brunello | Coding |
| BPY2 | BPY2_3 | GCCCTCTGTAAGCAGCACCT | Brunello | Coding |
| BPY2 | BPY2_4 | TGACGCTTGTCCCCAGAGCC | Brunello | Coding |
| BPY2B | BPY2B_1 | ATGAGATTATGCTGTATCAC | Brunello | Coding |
| BPY2B | BPY2B_2 | CATAATCTCATTTGTATGCT | Brunello | Coding |
| BPY2B | BPY2B_3 | GCACAATTACTTCTGTGATC | Brunello | Coding |
| BPY2B | BPY2B_4 | GTGAAGTGACTCTTCTGACT | Brunello | Coding |
| BPY2C | BPY2C_1 | AAGCTTGATCATCATACCTT | Brunello | Coding |
| BPY2C | BPY2C_2 | AATAGTACCTGTGAAAATCT | Brunello | Coding |
| BPY2C | BPY2C_3 | AGCCAGGACACGTGCAGGAC | Brunello | Coding |
| BPY2C | BPY2C_4 | GTGATGTTAATATTCTGCAT | Brunello | Coding |
| CDY1 | CDY1_1 | TACAATGTCTCTGTATGTGC | Brunello | Coding |
| CDY1 | CDY1_2 | TCTGCACCAGGACGTGACAA | Brunello | Coding |
| CDY1 | CDY1_3 | TGCTGGCAGCAAATAACTTG | Brunello | Coding |

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|---|---|---|---|---|
| CDY1 | CDY1_4 | TTTGACCACAAAACTGTGAG | Brunello | Coding |
| CDY1B | CDY1B_1 | ACAGGTTCAGCTACCCGAAA | Brunello | Coding |
| CDY1B | CDY1B_2 | AGAAGATGCACTTCACCATA | Brunello | Coding |
| CDY1B | CDY1B_3 | CAGGACGTGACAAAGGGTCC | Brunello | Coding |
| CDY1B | CDY1B_4 | TTGCTGCCAGCAAGAACGTT | Brunello | Coding |
| CDY2A | CDY2A_1 | AATATTACTGATGACAGCAG | Brunello | Coding |
| CDY2A | CDY2A_2 | CAGTGACTGATAAACACCAC | Brunello | Coding |
| CDY2A | CDY2A_3 | GACCACAAGAAAACTGTGAG | Brunello | Coding |
| CDY2A | CDY2A_4 | TCTGCACCAGGATGTGACAA | Brunello | Coding |
| CDY2B | CDY2B_1 | ATAGACCCATTAGCAGCCAA | Brunello | Coding |
| CDY2B | CDY2B_2 | ATGACAAACAGGATGACACT | Brunello | Coding |
| CDY2B | CDY2B_3 | CTGCACCAGGATGTGACAAA | Brunello | Coding |
| CDY2B | CDY2B_4 | TACAATGTCTCTGTATGTGA | Brunello | Coding |
| DAZ1 | DAZ1_1 | ACGTGCTGAGTTACAGGATT | Brunello | Coding |
| DAZ1 | DAZ1_2 | CACAGTTTCAGAACGTCTGG | Brunello | Coding |
| DAZ1 | DAZ1_3 | CGCCAGACGTTCTGAAACTG | Brunello | Coding |
| DAZ1 | DAZ1_4 | TCATCAGCTGCAGCTAGCCA | Brunello | Coding |
| DAZ2 | DAZ2_1 | GGATTAACTACCAAAGGACG | Brunello | Coding |
| DAZ2 | DAZ2_2 | TCAGCATTTCAGGTCACCAC | Brunello | Coding |
| DAZ2 | DAZ2_3 | TCTGCTTATCCACATTCACC | Brunello | Coding |
| DAZ2 | DAZ2_4 | TGTTTCGTTTGTTAATGACG | Brunello | Coding |
| DAZ3 | DAZ3_1 | ATGACCTGACCTGGTGAATG | Brunello | Coding |
| DAZ3 | DAZ3_2 | GTGACCTGAAATGCTGAATC | Brunello | Coding |

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|---|---|---|---|---|
| DAZ3 | DAZ3_3 | GTGACCTGAAATGGTGATCT | Brunello | Coding |
| DAZ3 | DAZ3_4 | TTACCTGATAATTGTATACA | Brunello | Coding |
| DAZ4 | DAZ4_1 | ACAGGATTCGGCGTGATTTG | Brunello | Coding |
| DAZ4 | DAZ4_2 | CAGACGTTCTGAAACTGTGG | Brunello | Coding |
| DAZ4 | DAZ4_3 | CATCCAGTGATGACCTGACC | Brunello | Coding |
| DAZ4 | DAZ4_4 | CATGGTAAAAAGCTGAAGCT | Brunello | Coding |
| DDX3Y | DDX3Y_1 | AGGACGAACTCTAGATCGGT | Brunello | Coding |
| DDX3Y | DDX3Y_2 | CGTGGACGGAGTGACTATGA | Brunello | Coding |
| DDX3Y | DDX3Y_3 | CTTACATTCTCAATATGTGG | Brunello | Coding |
| DDX3Y | DDX3Y_4 | TCAACTATACGACGTATCTG | Brunello | Coding |
| EIF1AY | EIF1AY_1 | AAGAGGTTATGCCATATCAG | Brunello | Coding |
| EIF1AY | EIF1AY_2 | GATTACCTGAGCATACTCTG | Brunello | Coding |
| EIF1AY | EIF1AY_3 | GGAGGTAAAAACAGGCGCAG | Brunello | Coding |
| EIF1AY | EIF1AY_4 | TGAATCTGAAAAAAGAGAGT | Brunello | Coding |
| HSFY1 | HSFY1_1 | ACAGAAGATTCCCTTGTTAG | Brunello | Coding |
| HSFY1 | HSFY1_2 | AGAATCGTCTGTCTTAAGCA | Brunello | Coding |
| HSFY1 | HSFY1_3 | GTAAGAGTGAAGAGAAGAAT | Brunello | Coding |
| HSFY1 | HSFY1_4 | TTCACACAATGGAGACCTAG | Brunello | Coding |
| HSFY2 | HSFY2_1 | ACACAATGGAGACCTAGTGG | Brunello | Coding |
| HSFY2 | HSFY2_2 | GTAACTTGGACTTTCTAACA | Brunello | Coding |
| HSFY2 | HSFY2_3 | TATAATCCAAATTTCAAGCG | Brunello | Coding |
| HSFY2 | HSFY2_4 | TTTAAATATGCCTCTAACAA | Brunello | Coding |
| KDM5D | KDM5D_1 | AGTGCATTGAACACTACCGC | Brunello | Coding |

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|---|---|---|---|---|
| KDM5D | KDM5D_2 | CAAACAAAACTTATCTCCTG | Brunello | Coding |
| KDM5D | KDM5D_3 | GGTGGAGGCCTATCAAGCTG | Brunello | Coding |
| KDM5D | KDM5D_4 | TTGCCAAGTATGCTCCCGTG | Brunello | Coding |
| NLGN4Y | NLGN4Y_1 | ACTGGACCCAAGATCTCACT | Brunello | Coding |
| NLGN4Y | NLGN4Y_2 | AGTGACTATCTTTGGCTCGG | Brunello | Coding |
| NLGN4Y | NLGN4Y_3 | CAGACATTCTACCATGTCCG | Brunello | Coding |
| NLGN4Y | NLGN4Y_4 | TGTTATGGTCTATATCCATG | Brunello | Coding |
| PCDH11Y | PCDH11Y_1 | GAACTGCATAGTAGTTGTCA | Brunello | Coding |
| PCDH11Y | PCDH11Y_2 | GATATGCTGCATTCTCCAGG | Brunello | Coding |
| PCDH11Y | PCDH11Y_3 | GTGCAACGGATGCAGACAGT | Brunello | Coding |
| PCDH11Y | PCDH11Y_4 | TCATAAGAATAGTTGTAAGG | Brunello | Coding |
| PRORY | PRORY_1 | AGAAGGCTTTCTGGATCCCG | Brunello | Coding |
| PRORY | PRORY_2 | AGGAGAAGTCCGATATGGAG | Brunello | Coding |
| PRORY | PRORY_3 | GGCCTCCGGAGAGAGCAATG | Brunello | Coding |
| PRORY | PRORY_4 | TGCTGCTGTGGACGATATCG | Brunello | Coding |
| PRY | PRY_1 | CAGGCGGTCATCTCACGAAG | Brunello | Coding |
| PRY | PRY_2 | TCTCCATTCTAGATATGGGA | Brunello | Coding |
| PRY | PRY_3 | TGGAAAATCTCTGAAATTTG | Brunello | Coding |
| PRY | PRY_4 | TTTCCAAGGCTACCACCAGA | Brunello | Coding |
| PRY2 | PRY2_1 | AAAATCTCTGAAATTTGGGG | Brunello | Coding |
| PRY2 | PRY2_2 | CATTCTAGATATGGGAAGGT | Brunello | Coding |
| PRY2 | PRY2_3 | GGCCTCAAGACCTCTGTTCA | Brunello | Coding |
| PRY2 | PRY2_4 | TTATACTTCTCTGAGACTAC | Brunello | Coding |

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|---|---|---|---|---|
| RBMY1A1 | RBMY1A1_1 | AATGCTGCCAAAGATATGAA | Brunello | Coding |
| RBMY1A1 | RBMY1A1_2 | AGATCTGCAAGAGGAAGCCG | Brunello | Coding |
| RBMY1A1 | RBMY1A1_3 | ATCCAAGTTGCCAAGAAACG | Brunello | Coding |
| RBMY1A1 | RBMY1A1_4 | GACGAGAATGACCATAATCA | Brunello | Coding |
| RBMY1B | RBMY1B_1 | CGCATGTCAACAAGACATGA | Brunello | Coding |
| RBMY1B | RBMY1B_2 | GATCGAACCAGCAAATCCAG | Brunello | Coding |
| RBMY1B | RBMY1B_3 | GGTGGCTTCCCTCACAAGAA | Brunello | Coding |
| RBMY1B | RBMY1B_4 | TGATTATGGTCATTCTCGTC | Brunello | Coding |
| RBMY1D | RBMY1D_1 | GAAGCCGTGGAGGAACAAGA | Brunello | Coding |
| RBMY1D | RBMY1D_2 | GATGGTTATGCAACTAACGA | Brunello | Coding |
| RBMY1D | RBMY1D_3 | TATCCATGGCCTCTAGATGG | Brunello | Coding |
| RBMY1D | RBMY1D_4 | TGCCAAAGATATGAATGGAA | Brunello | Coding |
| RBMY1E | RBMY1E_1 | GAGTATGCTCCACCATCTAG | Brunello | Coding |
| RBMY1E | RBMY1E_2 | GCCACCCTCTTGTTCCTCCA | Brunello | Coding |
| RBMY1E | RBMY1E_3 | TATGCATAGCCTCTAGATGG | Brunello | Coding |
| RBMY1E | RBMY1E_4 | TGACATGCGATCATTTCTCC | Brunello | Coding |
| RBMY1F | RBMY1F_1 | ATGGTTATGCAACTAACGAT | Brunello | Coding |
| RBMY1F | RBMY1F_2 | GAAGATATTGTCGCTCTGCG | Brunello | Coding |
| RBMY1F | RBMY1F_3 | GAAGCAGTGGAGGAACAAGA | Brunello | Coding |
| RBMY1F | RBMY1F_4 | TGCGAAAGATATGAATGGAA | Brunello | Coding |
| RBMY1J | RBMY1J_1 | AATGCTGCGAAAGATATGAA | Brunello | Coding |
| RBMY1J | RBMY1J_2 | CGGGATGAAAGTTATTCTAG | Brunello | Coding |
| RBMY1J | RBMY1J_3 | GATATTGTCGCTCTGCGTGG | Brunello | Coding |

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|---|---|---|---|---|
| RBMY1J | RBMY1J_4 | TCTGCAAGAGGAAGCAGTGG | Brunello | Coding |
| RPS4Y1 | RPS4Y1_1 | AGTGAAGGGAATCCCTCACC | Brunello | Coding |
| RPS4Y1 | RPS4Y1_2 | CCTTGGTGTCATAGACCAGG | Brunello | Coding |
| RPS4Y1 | RPS4Y1_3 | TGCTGTTCACCGCATCACAG | Brunello | Coding |
| RPS4Y1 | RPS4Y1_4 | TTGGATGCTTGACAAACTAA | Brunello | Coding |
| RPS4Y2 | RPS4Y2_1 | CCGCCTGGTCTATAATACCA | Brunello | Coding |
| RPS4Y2 | RPS4Y2_2 | GACAAAGGGAATTCCACACC | Brunello | Coding |
| RPS4Y2 | RPS4Y2_3 | TCACCTTGATGAGAGGATCT | Brunello | Coding |
| RPS4Y2 | RPS4Y2_4 | TTCCTGAGGAAGACTATCAG | Brunello | Coding |
| SRY | SRY_1 | AAGAGAATATTCCCGCTCTC | Brunello | Coding |
| SRY | SRY_2 | CCATGAACGCATTCATCGTG | Brunello | Coding |
| SRY | SRY_3 | GCAAGCAGCTGGGATACCAG | Brunello | Coding |
| SRY | SRY_4 | TAAGTATCGACCTCGTCGGA | Brunello | Coding |
| TBL1Y | TBL1Y_1 | AAATCCTCCAAAGAACCGAG | Brunello | Coding |
| TBL1Y | TBL1Y_2 | AGGCTAGCAAATCACTGACA | Brunello | Coding |
| TBL1Y | TBL1Y_3 | GACATTGTATACGAGAAGGG | Brunello | Coding |
| TBL1Y | TBL1Y_4 | GGGACAGGGACTCTATAGGG | Brunello | Coding |
| TGIF2LY | TGIF2LY_1 | AGACCAATTTGTCTTTGTTG | Brunello | Coding |
| TGIF2LY | TGIF2LY_2 | GCGACTGGATGTATAAGCAT | Brunello | Coding |
| TGIF2LY | TGIF2LY_3 | GCGGAGGATCTTAACGGACT | Brunello | Coding |
| TGIF2LY | TGIF2LY_4 | GTTATTTCTCGACATGATTG | Brunello | Coding |
| TMSB4Y | TMSB4Y_1 | CATGTCTGACAAACCTGGTA | Brunello | Coding |
| TMSB4Y | TMSB4Y_2 | GCAGCCATGTCTGACAAACC | Brunello | Coding |

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|---|---|---|---|---|
| TMSB4Y | TMSB4Y_3 | TCGCAGCTATCGAACAGGAG | Brunello | Coding |
| TMSB4Y | TMSB4Y_4 | TTCTCGATCTCAGCCATACC | Brunello | Coding |
| TSPY1 | TSPY1_1 | CTTGGTGTGTGCGAGTGCCA | Brunello | Coding |
| TSPY1 | TSPY1_2 | GACCCCAGAGTCTGCACCGG | Brunello | Coding |
| TSPY1 | TSPY1_3 | GGAGGGCCTCGTGGAGCGGC | Brunello | Coding |
| TSPY1 | TSPY1_4 | GGCGCCTCTGCGGTCTAGGT | Brunello | Coding |
| TSPY10 | TSPY10_1 | AAGCCCCACCTAGACCGCAG | Brunello | Coding |
| TSPY10 | TSPY10_2 | AGGCTGCGGCAGGGTTTCTG | Brunello | Coding |
| TSPY10 | TSPY10_3 | CTCCTCCAGTGCAGACTCTG | Brunello | Coding |
| TSPY10 | TSPY10_4 | CTGTACAGCCTCCATCCTGA | Brunello | Coding |
| TSPY2 | TSPY2_1 | AGGCTGCGGCAGGGTTCCTG | Brunello | Coding |
| TSPY2 | TSPY2_2 | CTGCACAGCCTCCATCCTGA | Brunello | Coding |
| TSPY2 | TSPY2_3 | GCTGTTGGATGACATAATGG | Brunello | Coding |
| TSPY2 | TSPY2_4 | TCTGGATGACGGCGCCTCTG | Brunello | Coding |
| TSPY3 | TSPY3_1 | GACCCCAGAGTCTGCACTGG | Brunello | Coding |
| TSPY3 | TSPY3_2 | GCGCCTCTGCGGTCTAGGTG | Brunello | Coding |
| TSPY3 | TSPY3_3 | GGCGGAGGAGGAGGGCCTCG | Brunello | Coding |
| TSPY3 | TSPY3_4 | GTGTGTGCGAGTGCCAAGGA | Brunello | Coding |
| TSPY4 | TSPY4_1 | AGCGGGAAAAGATGGAGCGG | Brunello | Coding |
| TSPY4 | TSPY4_2 | CAGGATGGAGGCTGTACAGG | Brunello | Coding |
| TSPY4 | TSPY4_3 | CGGCAGGGTTTCTGTGGCGT | Brunello | Coding |
| TSPY4 | TSPY4_4 | GTTGGATGACATAATGGCGG | Brunello | Coding |
| TSPY8 | TSPY8_1 | AGGAGGAGGGCCTCGTGGAG | Brunello | Coding |

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| TSPY8 | TSPY8_2 | CGGCGCCTCTGCGGTCTAGG | Brunello | Coding |
| TSPY8 | TSPY8_3 | GCTCCTCCAGTGCAGACTCT | Brunello | Coding |
| TSPY8 | TSPY8_4 | GGTGTGTGCGAGTGCCAAGG | Brunello | Coding |
| USP9Y | USP9Y_1 | GTAACGGGTGAACTACAGAC | Brunello | Coding |
| USP9Y | USP9Y_2 | TAACAATACTCATCGCCTAG | Brunello | Coding |
| USP9Y | USP9Y_3 | TGATGGTCCCAATCTAGAGG | Brunello | Coding |
| USP9Y | USP9Y_4 | TGGTACAGACCCCATAACAC | Brunello | Coding |
| UTY | UTY_1 | AGGATTCATAGAGAGTACCT | Brunello | Coding |
| UTY | UTY_2 | AGTAGAAGTAGACCAAACCA | Brunello | Coding |
| UTY | UTY_3 | TCAGAACTTCTGTTGAACTG | Brunello | Coding |
| UTY | UTY_4 | TGACTGTCAGCATCCCCCTG | Brunello | Coding |
| VCY | VCY_1 | AGTCCAAAGCCGAGAGCCTC | Brunello | Coding |
| VCY | VCY_2 | CCCCAGTGGCCCGAAGAAGA | Brunello | Coding |
| VCY | VCY_3 | CCGGCCAAGGCCAAGGAGAC | Brunello | Coding |
| VCY | VCY_4 | GAGAAGGGAGAAGCAGTTCG | Brunello | Coding |
| VCY1B | VCY1B_1 | AAGGGAGAAGCAGTTCGTGG | Brunello | Coding |
| VCY1B | VCY1B_2 | AGGCCAAGGAGACAGGAAAG | Brunello | Coding |
| VCY1B | VCY1B_3 | CCTTCTTCTTCGGGCCACTG | Brunello | Coding |
| VCY1B | VCY1B_4 | TTCTCCCTTCTCGGCCACCT | Brunello | Coding |
| ZFY | ZFY_1 | CAGTCAAAGGATGACCATCA | Brunello | Coding |
| ZFY | ZFY_2 | GAAACTATGTCACTCGTCAG | Brunello | Coding |
| ZFY | ZFY_3 | GATAAGTTTACATAACCACC | Brunello | Coding |
| ZFY | ZFY_4 | GCATGAGCAGCAAATTGATG | Brunello | Coding |

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|---|---|---|---|---|
| FAM197Y2 | FAM197Y2_1 | CAGCGGTTCTGGGATCACGA | BROAD | Non Coding |
| FAM197Y2 | FAM197Y2_2 | TGCATGTTCTCCTCATGTGG | BROAD | Non Coding |
| FAM197Y2 | FAM197Y2_3 | CTGCATGTTCTCCTCATGTG | BROAD | Non Coding |
| FAM197Y2 | FAM197Y2_4 | AAAGCAGCATCAGCAGGCAG | BROAD | Non Coding |
| FAM197Y3 | FAM197Y3_1 | GGGGGAAAAACAGCATCAGC | BROAD | Non Coding |
| FAM197Y3 | FAM197Y3_2 | AAAACAGCATCAGCAGGCAG | BROAD | Non Coding |
| FAM197Y3 | FAM197Y3_3 | TTATAAAAAATTCTGTGCCT | BROAD | Non Coding |
| FAM197Y3 | FAM197Y3_4 | TCAGCCATCCCGGTTACCGG | BROAD | Non Coding |
| FAM197Y4 | FAM197Y4_1 | GGGGGAAAAGCAGCATCAGC | BROAD | Non Coding |
| FAM197Y4 | FAM197Y4_2 | TCAGCAATCCTGCCAAAACC | BROAD | Non Coding |
| FAM197Y4 | FAM197Y4_3 | ACAGCTGAATGAGCTCAGGT | BROAD | Non Coding |
| FAM197Y4 | FAM197Y4_4 | CCTTCATGATGATTTCACTG | BROAD | Non Coding |
| FAM197Y5 | FAM197Y5_1 | GTGGAGGAACTCAGCCATCC | BROAD | Non Coding |
| FAM197Y5 | FAM197Y5_2 | AAAAAATTCTGTGCCTGGGT | BROAD | Non Coding |
| FAM197Y5 | FAM197Y5_3 | TTGGCAGGATTGCTGAGGTG | BROAD | Non Coding |
| FAM197Y5 | FAM197Y5_4 | CCACAGTGAAATCATCATGA | BROAD | Non Coding |
| FAM197Y6 | FAM197Y6_1 | AAAGGAAATCATCCTGCCAC | BROAD | Non Coding |
| FAM197Y6 | FAM197Y6_2 | CCAAACAGCTGAATGAGCTC | BROAD | Non Coding |
| FAM197Y6 | FAM197Y6_3 | GCAGAGGAATCCTTTGAAGC | BROAD | Non Coding |
| FAM197Y6 | FAM197Y6_4 | GAGGAATCCTTTGAAGCTGG | BROAD | Non Coding |
| FAM197Y7 | FAM197Y7_1 | GCTGAATGAGCTCAGGTAGG | BROAD | Non Coding |
| FAM197Y7 | FAM197Y7_2 | GTCTGCATGTTCTCCTCATG | BROAD | Non Coding |
| FAM197Y7 | FAM197Y7_3 | CCAGAACCGCTGGACTGCAG | BROAD | Non Coding |

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|---|---|---|---|---|
| FAM197Y7 | FAM197Y7_4 | CTCATTCCACTGCAGTCCAG | BROAD | Non Coding |
| FAM197Y8 | FAM197Y8_1 | ATCATGAAGGAGCACTGTGT | BROAD | Non Coding |
| FAM197Y8 | FAM197Y8_2 | CCTGCCACCGGTAACCGGGA | BROAD | Non Coding |
| FAM197Y8 | FAM197Y8_3 | CAGCAATCCTGCCAAAACCC | BROAD | Non Coding |
| FAM197Y8 | FAM197Y8_4 | CTGTGTTGGCATCCTCGGTA | BROAD | Non Coding |
| FAM197Y9 | FAM197Y9_1 | TGCAGGTTCTCCTCATGTGG | BROAD | Non Coding |
| FAM197Y9 | FAM197Y9_2 | CTGCAGGTTCTCCTCATGTG | BROAD | Non Coding |
| FAM197Y9 | FAM197Y9_3 | TCTGCAGGTTCTCCTCATGT | BROAD | Non Coding |
| FAM197Y9 | FAM197Y9_4 | GTCTGCAGGTTCTCCTCATG | BROAD | Non Coding |
| FAM224A | FAM224A_1 | TTCATTCTGAATAAGAACTG | BROAD | Non Coding |
| FAM224A | FAM224A_2 | AGTCTCATGATAGATAGACA | BROAD | Non Coding |
| FAM224A | FAM224A_3 | GATGACATCTTATGGACCCA | BROAD | Non Coding |
| FAM224A | FAM224A_4 | GGAACTTTATCACACCAAGC | BROAD | Non Coding |
| FAM224B | FAM224B_1 | GGTGTGATAAAGTTCCAACT | BROAD | Non Coding |
| FAM224B | FAM224B_2 | CTGGGTCCATAAGATGTCAT | BROAD | Non Coding |
| FAM224B | FAM224B_3 | GTCTCCTTCTGTCGCCAAGG | BROAD | Non Coding |
| FAM224B | FAM224B_4 | CCTTAACAATCCCAAGTTGA | BROAD | Non Coding |
| FAM41AY1 | FAM41AY1_1 | TATGAACCAGCATTGAAGGG | BROAD | Non Coding |
| FAM41AY1 | FAM41AY1_2 | AATAATTGAACCGGGTCACA | BROAD | Non Coding |
| FAM41AY1 | FAM41AY1_3 | AGGAGGCAGAACGAGTCTCA | BROAD | Non Coding |
| FAM41AY1 | FAM41AY1_4 | AGCTAAAGAGTTGACACGCA | BROAD | Non Coding |
| FAM41AY2 | FAM41AY2_1 | CTGACCACGTTCCTACCCTG | BROAD | Non Coding |
| FAM41AY2 | FAM41AY2_2 | GAGCCTGAAATAATTGAACC | BROAD | Non Coding |

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|---|---|---|---|---|
| FAM41AY2 | FAM41AY2_3 | CATGAACGTATGGATGCCCT | BROAD | Non Coding |
| FAM41AY2 | FAM41AY2_4 | CAGCTAAAGAGTTGACACGC | BROAD | Non Coding |
| LINC00278 | LINC00278_1 | CTGCTGTTGAGAGCGCCACT | BROAD | Non Coding |
| LINC00278 | LINC00278_2 | CAGGACAACTTCAACCCGAG | BROAD | Non Coding |
| LINC00278 | LINC00278_3 | ACAGCACAACAGAACCTAAG | BROAD | Non Coding |
| LINC00278 | LINC00278_4 | TGTGCTACAGGACCTCGGTA | BROAD | Non Coding |
| LINC00279 | LINC00279_1 | TAGTTCCATGATCTTAGTAG | BROAD | Non Coding |
| LINC00279 | LINC00279_2 | GCAAGTCTTCTCATTAGGAG | BROAD | Non Coding |
| LINC00279 | LINC00279_3 | CTGATGAGCATTCATGAAGC | BROAD | Non Coding |
| LINC00279 | LINC00279_4 | GGAGGTGTTTCAAGACAGTG | BROAD | Non Coding |
| LINC00280 | LINC00280_1 | ATGGTGATAAGTGGTGAGTT | BROAD | Non Coding |
| LINC00280 | LINC00280_2 | TCTTCTTAATGCCTGAACGC | BROAD | Non Coding |
| LINC00280 | LINC00280_3 | CTGCTACAGGAAGAAAGTGG | BROAD | Non Coding |
| LINC00280 | LINC00280_4 | TCACCTTAATTCAGCACTCA | BROAD | Non Coding |
| NLGN4Y-AS1 | NLGN4Y-AS1_1 | GAAAAAAAATATATAGCCGG | BROAD | Non Coding |
| NLGN4Y-AS1 | NLGN4Y-AS1_2 | GAGTGAGAAAATTGTTAGCA | BROAD | Non Coding |
| NLGN4Y-AS1 | NLGN4Y-AS1_3 | ATAATACACTTGATCACCTA | BROAD | Non Coding |
| NLGN4Y-AS1 | NLGN4Y-AS1_4 | AACTTTCAATCAAGGCAGAA | BROAD | Non Coding |
| TTTY1 | TTTY1_1 | CCACTGTGGGACCATAAGTG | BROAD | Non Coding |
| TTTY1 | TTTY1_2 | CCTCCGTGGAGAAGTGTCAG | BROAD | Non Coding |
| TTTY1 | TTTY1_3 | TCACCTGTGAATATAACCTG | BROAD | Non Coding |
| TTTY1 | TTTY1_4 | GGTGGGGATACAATCTTGTG | BROAD | Non Coding |
| TTTY10 | TTTY10_1 | TTACTAGATGACAGATCGTG | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY10 | TTTY10_2 | TGGTAACAGGTAGCAATCAG | BROAD | Non Coding |
| TTTY10 | TTTY10_3 | TTCTGTACTTCTGCATACGT | BROAD | Non Coding |
| TTTY10 | TTTY10_4 | ACTACTGACCACCAAGACAG | BROAD | Non Coding |
| TTTY11 | TTTY11_1 | CATTCTGCAACAACCAGCCG | BROAD | Non Coding |
| TTTY11 | TTTY11_2 | AAAGTATGGCTGCTGCAATG | BROAD | Non Coding |
| TTTY11 | TTTY11_3 | TTGTAACAGGAATAGTCAGG | BROAD | Non Coding |
| TTTY11 | TTTY11_4 | TCTTGTGGTCATGAGAACAT | BROAD | Non Coding |
| TTTY12 | TTTY12_1 | GAAGCACTGTGACATAAGGG | BROAD | Non Coding |
| TTTY12 | TTTY12_2 | TAATAGTGGTTAGCAAACAG | BROAD | Non Coding |
| TTTY12 | TTTY12_3 | CATCATAGTGATATATCACT | BROAD | Non Coding |
| TTTY12 | TTTY12_4 | GTAGATGTCAAAAACCCCTA | BROAD | Non Coding |
| TTTY13 | TTTY13_1 | TCTAATGGTAGCTACGATGG | BROAD | Non Coding |
| TTTY13 | TTTY13_2 | AGTTGGTTCACATCATAAGG | BROAD | Non Coding |
| TTTY13 | TTTY13_3 | GCAACAATAAGGTCAGACAG | BROAD | Non Coding |
| TTTY13 | TTTY13_4 | AGCAGCAATAAGGTCACATG | BROAD | Non Coding |
| TTTY14 | TTTY14_1 | TGGACCGAGATCTTCAGTTG | BROAD | Non Coding |
| TTTY14 | TTTY14_2 | CAGGGACTGAGCAAGTTATG | BROAD | Non Coding |
| TTTY14 | TTTY14_3 | ATGGACTAAGAAAACACCAG | BROAD | Non Coding |
| TTTY14 | TTTY14_4 | TGAAACCTACCCCAATGTGT | BROAD | Non Coding |
| TTTY15 | TTTY15_1 | AATGGTACTAGTAATAAGTG | BROAD | Non Coding |
| TTTY15 | TTTY15_2 | AAACTTAGAATGATGACACA | BROAD | Non Coding |
| TTTY15 | TTTY15_3 | AAAATCCCCCATAACACCCA | BROAD | Non Coding |
| TTTY15 | TTTY15_4 | ACTCACCCTTGAATCACCAA | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY16 | TTTY16_1 | CCCAGCCGTTGGGAAACATG | BROAD | Non Coding |
| TTTY16 | TTTY16_2 | GGCACAACAAAGGTGCTCCC | BROAD | Non Coding |
| TTTY16 | TTTY16_3 | GAAACATGAGGACATGGCCA | BROAD | Non Coding |
| TTTY16 | TTTY16_4 | TCTATAGCAAAAAGACACTT | BROAD | Non Coding |
| TTTY17A | TTTY17A_1 | TGGTTCACCTTGACTCACAT | BROAD | Non Coding |
| TTTY17A | TTTY17A_2 | ACACAACTTACCCCATAATG | BROAD | Non Coding |
| TTTY17A | TTTY17A_3 | ATGTGCTTCAAAGCTCAACA | BROAD | Non Coding |
| TTTY17A | TTTY17A_4 | CATTGGAAAATACTTGAACT | BROAD | Non Coding |
| TTTY17B | TTTY17B_1 | TGAAATCCTTCCTCATTATG | BROAD | Non Coding |
| TTTY17B | TTTY17B_2 | TGAACCAAAATTTCAGGCTC | BROAD | Non Coding |
| TTTY17B | TTTY17B_3 | CAGGTGTGTTCAGGCTGCTG | BROAD | Non Coding |
| TTTY17B | TTTY17B_4 | TTCCTGTTACAGGTGTGTTC | BROAD | Non Coding |
| TTTY17C | TTTY17C_1 | AACTTACCCCATAATGAGGA | BROAD | Non Coding |
| TTTY17C | TTTY17C_2 | CCAGTGAAAATCTTGAGAAT | BROAD | Non Coding |
| TTTY17C | TTTY17C_3 | CCACACTGAACCAAAATTTC | BROAD | Non Coding |
| TTTY17C | TTTY17C_4 | ACATTGGAAAATACTTGAAC | BROAD | Non Coding |
| TTTY18 | TTTY18_1 | TGTTGCCATACATCAAACTG | BROAD | Non Coding |
| TTTY18 | TTTY18_2 | CGGAGGCCCAAAATGAAGAG | BROAD | Non Coding |
| TTTY18 | TTTY18_3 | CGACAAAGGCATGTCCAAAG | BROAD | Non Coding |
| TTTY18 | TTTY18_4 | GCAAGTTCTTGAGACAGACT | BROAD | Non Coding |
| TTTY19 | TTTY19_1 | AGCAGGTGATGCATCTTGTG | BROAD | Non Coding |
| TTTY19 | TTTY19_2 | GGTGAAGATACAGTCTGTTG | BROAD | Non Coding |
| TTTY19 | TTTY19_3 | AATTTGGTTCCCAACTGAGC | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY19 | TTTY19_4 | ATGAAATAGTCTAGATTCCC | BROAD | Non Coding |
| TTTY1B | TTTY1B_1 | ACACGTGCTTCACATCATGA | BROAD | Non Coding |
| TTTY1B | TTTY1B_2 | TAGGATCATGAGACTATCTG | BROAD | Non Coding |
| TTTY1B | TTTY1B_3 | CTGCCTGTGAAATCCCACTG | BROAD | Non Coding |
| TTTY1B | TTTY1B_4 | ACACCGCTGACACTTCTCCA | BROAD | Non Coding |
| TTTY2 | TTTY2_1 | CAGCTGACATGCCTACAGCG | BROAD | Non Coding |
| TTTY2 | TTTY2_2 | TGTGGATAAGAACTCCGTGG | BROAD | Non Coding |
| TTTY2 | TTTY2_3 | ATGATGGTCTTCTGTGAACA | BROAD | Non Coding |
| TTTY2 | TTTY2_4 | TTACCTGAGAACCCAGAAGT | BROAD | Non Coding |
| TTTY20 | TTTY20_1 | TAGTCTTAGTAAATGAAGAG | BROAD | Non Coding |
| TTTY20 | TTTY20_2 | GGACGATTGAAGGTTACTTA | BROAD | Non Coding |
| TTTY20 | TTTY20_3 | ATTTACATCCAACTCTTCAC | BROAD | Non Coding |
| TTTY20 | TTTY20_4 | AAAAAAAACTGGACGATTGA | BROAD | Non Coding |
| TTTY21 | TTTY21_1 | CACCTCAAAGACTCACCAGA | BROAD | Non Coding |
| TTTY21 | TTTY21_2 | AACCCACTGCCTTACCCAAA | BROAD | Non Coding |
| TTTY21 | TTTY21_3 | AATCATTCATGAGTCTGCAG | BROAD | Non Coding |
| TTTY21 | TTTY21_4 | GTAAGGCAGTGGGTTATCTC | BROAD | Non Coding |
| TTTY21B | TTTY21B_1 | TGGTCAGGTCCAACTGAAAG | BROAD | Non Coding |
| TTTY21B | TTTY21B_2 | GAGTCTGCTCTCTTGGGGAT | BROAD | Non Coding |
| TTTY21B | TTTY21B_3 | GCTCTAGAGTCTAGACCTTT | BROAD | Non Coding |
| TTTY21B | TTTY21B_4 | GACCATGGAGACTGCCCAAA | BROAD | Non Coding |
| TTTY22 | TTTY22_1 | AGAACCATTTCATGACTGTG | BROAD | Non Coding |
| TTTY22 | TTTY22_2 | AGTGGGTGCTTCATGTTGTG | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY22 | TTTY22_3 | GACTCCTATGACCATCACCA | BROAD | Non Coding |
| TTTY22 | TTTY22_4 | AGGATCATGGGACTATACTG | BROAD | Non Coding |
| TTTY23 | TTTY23_1 | CAGCAATCCTACCAAAACCC | BROAD | Non Coding |
| TTTY23 | TTTY23_2 | TCTACACAGATATCCACCTG | BROAD | Non Coding |
| TTTY23 | TTTY23_3 | CAGTTGTTCTGGGATCATGA | BROAD | Non Coding |
| TTTY23 | TTTY23_4 | CCTCCCTGGACACATACTGA | BROAD | Non Coding |
| TTTY23B | TTTY23B_1 | ATAAGACAGTCCACTTCACA | BROAD | Non Coding |
| TTTY23B | TTTY23B_2 | AAACAGAACATGACAGACCT | BROAD | Non Coding |
| TTTY23B | TTTY23B_3 | GAATGAGATACCCTGTACCC | BROAD | Non Coding |
| TTTY23B | TTTY23B_4 | TCAGCAATCCTACCAAAACC | BROAD | Non Coding |
| TTTY2B | TTTY2B_1 | TTCTTATCCACAAAGTCACA | BROAD | Non Coding |
| TTTY2B | TTTY2B_2 | AGTCTCATGATCCTACAAGA | BROAD | Non Coding |
| TTTY2B | TTTY2B_3 | GAACAGGGAAGAGTTTAGTG | BROAD | Non Coding |
| TTTY2B | TTTY2B_4 | CCTTGTGTCTAAGAGTATGC | BROAD | Non Coding |
| TTTY3 | TTTY3_1 | CATGATGTAGTCCCTTGAAG | BROAD | Non Coding |
| TTTY3 | TTTY3_2 | TCTTCTGCAGGATGATTGGG | BROAD | Non Coding |
| TTTY3 | TTTY3_3 | TGCAGAAGATTCTTCAAATG | BROAD | Non Coding |
| TTTY3 | TTTY3_4 | GCTACAAGCAGATCAAAACC | BROAD | Non Coding |
| TTTY3B | TTTY3B_1 | ATTGGGAGGTCATTAGAAAC | BROAD | Non Coding |
| TTTY3B | TTTY3B_2 | CTTTAAGGTTGCCACTTCAA | BROAD | Non Coding |
| TTTY3B | TTTY3B_3 | CCATTTGAAGAATCTTCTGC | BROAD | Non Coding |
| TTTY3B | TTTY3B_4 | GTTGTCTCATTACTGTACTG | BROAD | Non Coding |
| TTTY4 | TTTY4_1 | GAATGAATTGTGACATACGA | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY4 | TTTY4_2 | ACACCCTCTATTCAACACAA | BROAD | Non Coding |
| TTTY4 | TTTY4_3 | AAAGGAGGTTCAGACAAATG | BROAD | Non Coding |
| TTTY4 | TTTY4_4 | GTGTGAGAACCACCCTCATG | BROAD | Non Coding |
| TTTY4B | TTTY4B_1 | TGATTCAAGACTGAGAACAC | BROAD | Non Coding |
| TTTY4B | TTTY4B_2 | TACGACGGAGTACAAAACCT | BROAD | Non Coding |
| TTTY4B | TTTY4B_3 | CTATCGCATAATGCCTCTTG | BROAD | Non Coding |
| TTTY4B | TTTY4B_4 | TGCTATTGTGACATACACCT | BROAD | Non Coding |
| TTTY4C | TTTY4C_1 | TCACAGACTGCCTCACACAA | BROAD | Non Coding |
| TTTY4C | TTTY4C_2 | CCACACTCTTCACTGAAAGG | BROAD | Non Coding |
| TTTY4C | TTTY4C_3 | GGTGTATGTCACAATAGCAC | BROAD | Non Coding |
| TTTY4C | TTTY4C_4 | GCCTGGACATTGTCCACAAG | BROAD | Non Coding |
| TTTY5 | TTTY5_1 | CACTTACCACTAAGCCACGT | BROAD | Non Coding |
| TTTY5 | TTTY5_2 | TGACACACTCCTTAACCCGG | BROAD | Non Coding |
| TTTY5 | TTTY5_3 | GACCTGAAATGACATCCGGA | BROAD | Non Coding |
| TTTY5 | TTTY5_4 | GGATTCACTTCACCACACCT | BROAD | Non Coding |
| TTTY6 | TTTY6_1 | ATGAATGCCACAATTCCCTG | BROAD | Non Coding |
| TTTY6 | TTTY6_2 | TGCAAGAATTGAGTCCCAGG | BROAD | Non Coding |
| TTTY6 | TTTY6_3 | ACAATGAAGGAGTGACGTGA | BROAD | Non Coding |
| TTTY6 | TTTY6_4 | ATAAAGGTGAGGATACAAGC | BROAD | Non Coding |
| TTTY6B | TTTY6B_1 | GTGCAAGAATTGAGTCCCAG | BROAD | Non Coding |
| TTTY6B | TTTY6B_2 | GAGATGTCTAGACTGTGATG | BROAD | Non Coding |
| TTTY6B | TTTY6B_3 | GTGTATCCCACAAAGAAGAC | BROAD | Non Coding |
| TTTY6B | TTTY6B_4 | ATTCTCCAGTGTACATCCCA | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY7 | TTTY7_1 | CTGCCTGCAATAATGCACTG | BROAD | Non Coding |
| TTTY7 | TTTY7_2 | CAGGCAAGAGTCCACCACCA | BROAD | Non Coding |
| TTTY7 | TTTY7_3 | AAATGCACATGCACGCCTCA | BROAD | Non Coding |
| TTTY7 | TTTY7_4 | ATTCAAGGGACCCTGCGGAC | BROAD | Non Coding |
| TTTY7B | TTTY7B_1 | CACTAGCAGTCCGGTCCACA | BROAD | Non Coding |
| TTTY7B | TTTY7B_2 | GTATACAATCTGGTGAAAGG | BROAD | Non Coding |
| TTTY7B | TTTY7B_3 | CAGGACCTCCACACCGTGAG | BROAD | Non Coding |
| TTTY7B | TTTY7B_4 | ATGAATGTCACAATTCCGTG | BROAD | Non Coding |
| TTTY8 | TTTY8_1 | GCCAGCCCGAAGGAACATCA | BROAD | Non Coding |
| TTTY8 | TTTY8_2 | CAGTGTTTCACGCTAACCCA | BROAD | Non Coding |
| TTTY8 | TTTY8_3 | ACACACCCCTAAGCACACAA | BROAD | Non Coding |
| TTTY8 | TTTY8_4 | AACCAAACTCAGGAGCTACC | BROAD | Non Coding |
| TTTY8B | TTTY8B_1 | AATGAACCGTGAAATCCCTA | BROAD | Non Coding |
| TTTY8B | TTTY8B_2 | GTTGACTTTAAGCACCTGCT | BROAD | Non Coding |
| TTTY8B | TTTY8B_3 | TTCTTCAGGAAGACCCACCT | BROAD | Non Coding |
| TTTY8B | TTTY8B_4 | GTAGATGTGAGCCAGCCCGA | BROAD | Non Coding |
| TTTY9A | TTTY9A_1 | CAAAATCTAGGACACTCTAG | BROAD | Non Coding |
| TTTY9A | TTTY9A_2 | AAATAGTACAATATTGCCTG | BROAD | Non Coding |
| TTTY9A | TTTY9A_3 | AATACAGTGTCCTCTAATGG | BROAD | Non Coding |
| TTTY9A | TTTY9A_4 | TGTGATAGAATTAAAAAGTG | BROAD | Non Coding |
| TTTY9B | TTTY9B_1 | TGTGTGATAGAATTAAAAAG | BROAD | Non Coding |
| TTTY9B | TTTY9B_2 | GTAGAAAACAGAAATATGCT | BROAD | Non Coding |
| TTTY9B | TTTY9B_3 | TCTGGAGTGTGATTAGAGCT | BROAD | Non Coding |

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|---|---|---|---|---|
| TTTY9B | TTTY9B_4 | AATGAGATCAATTGTAAAGG | BROAD | Non Coding |
| ZFY-AS1 | ZFY-AS1_1 | CATCTTGGAAACCCTAAGTG | BROAD | Non Coding |
| ZFY-AS1 | ZFY-AS1_2 | CTGTGATAACATTACCTGCA | BROAD | Non Coding |
| ZFY-AS1 | ZFY-AS1_3 | AGAAATGGGTTCCAAAAACA | BROAD | Non Coding |
| ZFY-AS1 | ZFY-AS1_4 | GCTGGACTCTTCTACTGTGA | BROAD | Non Coding |
| ACTR3BP1 | ACTR3BP1_1 | AATCTATGTATGCCACAAAG | BROAD | Pseudogene |
| ACTR3BP1 | ACTR3BP1_2 | GGGAGTGAAAGAATGAGGAG | BROAD | Pseudogene |
| ACTR3BP1 | ACTR3BP1_3 | GTCTCCAGTGACGTTCAAGA | BROAD | Pseudogene |
| ACTR3BP1 | ACTR3BP1_4 | TGATGTGGATCCCTGGAAGT | BROAD | Pseudogene |
| AGKP1 | AGKP1_1 | TTGTAAGAAGAGACAGACAC | BROAD | Pseudogene |
| AGKP1 | AGKP1_2 | TGTGATGGATAGTTCAATGG | BROAD | Pseudogene |
| AGKP1 | AGKP1_3 | TCAGTCCAGAAATGTATATG | BROAD | Pseudogene |
| AGKP1 | AGKP1_4 | AGGTTATGAGGGATAAGTCA | BROAD | Pseudogene |
| ANKRD20A6P | ANKRD20A6P_1 | TCCATAGAACATGTCTACAT | BROAD | Pseudogene |
| ANKRD20A6P | ANKRD20A6P_2 | GCTCAAGAGCCAGAGGTTGG | BROAD | Pseudogene |
| ANKRD20A6P | ANKRD20A6P_3 | ATTCGGCTTCGGGAGCTGCA | BROAD | Pseudogene |
| ANKRD20A6P | ANKRD20A6P_4 | AGACATGTTCTATGGAGCCG | BROAD | Pseudogene |
| ANKRD36P1 | ANKRD36P1_1 | TACCATTTCTGGTTGGACAG | BROAD | Pseudogene |
| ANKRD36P1 | ANKRD36P1_2 | CATCATGATACGTCGACAGA | BROAD | Pseudogene |
| ANKRD36P1 | ANKRD36P1_3 | ACAGGCTGTACAACTAGGGC | BROAD | Pseudogene |
| ANKRD36P1 | ANKRD36P1_4 | TGAAAAATTGACCCTTACAT | BROAD | Pseudogene |
| ANOS2P | ANOS2P_1 | CTGACATAAGACCCAACTGA | BROAD | Pseudogene |
| ANOS2P | ANOS2P_2 | ACATAGCCGATTGTATACAG | BROAD | Pseudogene |

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|---|---|---|---|---|
| ANOS2P | ANOS2P_3 | CTTCCAAGTAAAGTGACTGG | BROAD | Pseudogene |
| ANOS2P | ANOS2P_4 | GTTCCTCAAATACACCCTGT | BROAD | Pseudogene |
| ARSDP1 | ARSDP1_1 | AAGTCATCATGACTTATACG | BROAD | Pseudogene |
| ARSDP1 | ARSDP1_2 | ATAGCTGAGAGAGATCACCT | BROAD | Pseudogene |
| ARSDP1 | ARSDP1_3 | TGTGAATTGTGCATTCCGCG | BROAD | Pseudogene |
| ARSDP1 | ARSDP1_4 | AAAACACAAGAAGCCCATGC | BROAD | Pseudogene |
| ASS1P6 | ASS1P6_1 | CAAATGGGCACCTACGTGAG | BROAD | Pseudogene |
| ASS1P6 | ASS1P6_2 | CTATGCTCATTTACACATCG | BROAD | Pseudogene |
| ASS1P6 | ASS1P6_3 | CAGCCACACAAGCATGCAGG | BROAD | Pseudogene |
| ASS1P6 | ASS1P6_4 | CCTCATGTGTATCAGCTATG | BROAD | Pseudogene |
| ATP5PFP1 | ATP5PFP1_1 | GGATCTTCAAATTTGAAGTG | BROAD | Pseudogene |
| ATP5PFP1 | ATP5PFP1_2 | TCCATAAAGAGTTTCTGTAG | BROAD | Pseudogene |
| ATP5PFP1 | ATP5PFP1_3 | CTTATTAAATGCCACTGCAG | BROAD | Pseudogene |
| ATP5PFP1 | ATP5PFP1_4 | TGAAGTCATTGAAAAACCCC | BROAD | Pseudogene |
| BCORP1 | BCORP1_1 | GGGAATCCTCCTACTCTACG | BROAD | Pseudogene |
| BCORP1 | BCORP1_2 | GATTACTTAAATGACCTACA | BROAD | Pseudogene |
| BCORP1 | BCORP1_3 | TTAACGAAGCATGTTTACAC | BROAD | Pseudogene |
| BCORP1 | BCORP1_4 | AAGTACAACTACTTCTGTGG | BROAD | Pseudogene |
| BPY2DP | BPY2DP_1 | TGCATACTGGGTCTAGTCAG | BROAD | Pseudogene |
| BPY2DP | BPY2DP_2 | GTATAATTGACACAACACTT | BROAD | Pseudogene |
| BPY2DP | BPY2DP_3 | GTCATTGCCTCACAAGAACA | BROAD | Pseudogene |
| BPY2DP | BPY2DP_4 | AATGTCACATCCGATCACCT | BROAD | Pseudogene |
| C2orf27AP1 | C2orf27AP1_1 | GAGGCCGGTGGCTGTACATG | BROAD | Pseudogene |

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|---|---|---|---|---|
| C2orf27AP1 | C2orf27AP1_2 | ATGGAGATTTGCCCTCACCT | BROAD | Pseudogene |
| C2orf27AP1 | C2orf27AP1_3 | AGTGTGGCAGGAGCTAGAGG | BROAD | Pseudogene |
| C2orf27AP1 | C2orf27AP1_4 | TCTTCTTGACAGGCAGACAG | BROAD | Pseudogene |
| CD24P4 | CD24P4_1 | GCTGCCGAAACAATACGTTG | BROAD | Pseudogene |
| CD24P4 | CD24P4_2 | TCTGCCCATGTCCCCTACGT | BROAD | Pseudogene |
| CD24P4 | CD24P4_3 | GAGTACTTCCAACACTGGGT | BROAD | Pseudogene |
| CD24P4 | CD24P4_4 | TGGCGTCTGGAAGTCCAATG | BROAD | Pseudogene |
| CDC27P2 | CDC27P2_1 | GCGACCTGTTCTTACTACCC | BROAD | Pseudogene |
| CDC27P2 | CDC27P2_2 | GATGACACATCAATTACAGA | BROAD | Pseudogene |
| CDC27P2 | CDC27P2_3 | GTACGCAACCAGAATTGTAG | BROAD | Pseudogene |
| CDC27P2 | CDC27P2_4 | CTGAATCTCAGGTGTGATTG | BROAD | Pseudogene |
| CDY3P | CDY3P_1 | CAGAACAACTGGATTACATG | BROAD | Pseudogene |
| CDY3P | CDY3P_2 | TAAAGAAAGAGACCGATTTG | BROAD | Pseudogene |
| CDY3P | CDY3P_3 | GCACTACACCAGAGTAGGAG | BROAD | Pseudogene |
| CDY3P | CDY3P_4 | TAACATATATTGTATCCCAT | BROAD | Pseudogene |
| CSPG4P1Y | CSPG4P1Y_1 | TTGCTGAAGGCCATGTTGTG | BROAD | Pseudogene |
| CSPG4P1Y | CSPG4P1Y_2 | GTGCACACAGACAGTGCACA | BROAD | Pseudogene |
| CSPG4P1Y | CSPG4P1Y_3 | CGGCCATATTGATGGTACCC | BROAD | Pseudogene |
| CSPG4P1Y | CSPG4P1Y_4 | CCATGATACTGCCAGACAGG | BROAD | Pseudogene |
| CTBP2P1 | CTBP2P1_1 | GCAATTCATCCAGTCATCGT | BROAD | Pseudogene |
| CTBP2P1 | CTBP2P1_2 | TGGAGTAAACTATTTGCCTG | BROAD | Pseudogene |
| CTBP2P1 | CTBP2P1_3 | AAATAGTAGTGAATGCCGGA | BROAD | Pseudogene |
| CTBP2P1 | CTBP2P1_4 | GGGACTCAAGTGACAAGATG | BROAD | Pseudogene |

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|---|---|---|---|---|
| CYCSP49 | CYCSP49_1 | TGGTACATAGAGTGGGACAT | BROAD | Pseudogene |
| CYCSP49 | CYCSP49_2 | AAGACTGGGCCTAAACTCCA | BROAD | Pseudogene |
| CYCSP49 | CYCSP49_3 | TTATTTGCCACTTAAAGGCA | BROAD | Pseudogene |
| CYCSP49 | CYCSP49_4 | ACAGGGAATTCTAATTACAA | BROAD | Pseudogene |
| DPPA2P1 | DPPA2P1_1 | TGTTGACAGCAATCCCACAA | BROAD | Pseudogene |
| DPPA2P1 | DPPA2P1_2 | GCAACGTTCGAGGAAACGCA | BROAD | Pseudogene |
| DPPA2P1 | DPPA2P1_3 | GAAGTGGTAACTTAAGCGCA | BROAD | Pseudogene |
| DPPA2P1 | DPPA2P1_4 | AGAAAACAGAAGTTAGTCTG | BROAD | Pseudogene |
| DUX4L16 | DUX4L16_1 | GTGGTTCCCACGCCGCATCG | BROAD | Pseudogene |
| DUX4L16 | DUX4L16_2 | TTGGACCCGGAGCCAAAGTG | BROAD | Pseudogene |
| DUX4L16 | DUX4L16_3 | CTGCGTCACCGGATCCCAGA | BROAD | Pseudogene |
| DUX4L16 | DUX4L16_4 | CGGTATACTTCCTCGCTGAG | BROAD | Pseudogene |
| DUX4L17 | DUX4L17_1 | ACAACCAGGCATAAGCCAGG | BROAD | Pseudogene |
| DUX4L17 | DUX4L17_2 | ATGGAGGAATTTAGGTCGCG | BROAD | Pseudogene |
| DUX4L17 | DUX4L17_3 | TCCTAGAAATGGAGGCCCCG | BROAD | Pseudogene |
| DUX4L17 | DUX4L17_4 | TCATCCAGTATCAGGCCGGA | BROAD | Pseudogene |
| DUX4L18 | DUX4L18_1 | TGGGAAAGCGTTCCTTACGG | BROAD | Pseudogene |
| DUX4L18 | DUX4L18_2 | CAGGCTGTCCCACTGCACAA | BROAD | Pseudogene |
| DUX4L18 | DUX4L18_3 | GTTTCGGGGTCTTGTGACGG | BROAD | Pseudogene |
| DUX4L18 | DUX4L18_4 | TGTTCCAAACACGCTAGTGT | BROAD | Pseudogene |
| DUX4L19 | DUX4L19_1 | AGGCAGGCGAAAGCGGACCG | BROAD | Pseudogene |
| DUX4L19 | DUX4L19_2 | CCACGTGCCCTGCACGACTG | BROAD | Pseudogene |
| DUX4L19 | DUX4L19_3 | AGTTGTCGGGAAGGCCATCG | BROAD | Pseudogene |

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|---|---|---|---|---|
| DUX4L19 | DUX4L19_4 | AGAATACCGGACTCTGCTGG | BROAD | Pseudogene |
| EEF1A1P41 | EEF1A1P41_1 | GAATAAGTCCACATTCACAG | BROAD | Pseudogene |
| EEF1A1P41 | EEF1A1P41_2 | ACTTATTCTAACTATCCTCT | BROAD | Pseudogene |
| EEF1A1P41 | EEF1A1P41_3 | CTGATTAAAACTGGGGTAGC | BROAD | Pseudogene |
| EEF1A1P41 | EEF1A1P41_4 | GTGTATTATGGGTCACTGGT | BROAD | Pseudogene |
| EIF4A1P2 | EIF4A1P2_1 | GGAGCAAGACGTGATCATGA | BROAD | Pseudogene |
| EIF4A1P2 | EIF4A1P2_2 | GGGCACCAATATGCGTGCTG | BROAD | Pseudogene |
| EIF4A1P2 | EIF4A1P2_3 | TCAACGTGGAACAAGAGGAG | BROAD | Pseudogene |
| EIF4A1P2 | EIF4A1P2_4 | AAAATGACAAGTCTATCCCT | BROAD | Pseudogene |
| FAM8A4P | FAM8A4P_1 | GTGCCACCATCCCTGCACAT | BROAD | Pseudogene |
| FAM8A4P | FAM8A4P_2 | TGGACTGATGGCTACACATG | BROAD | Pseudogene |
| FAM8A4P | FAM8A4P_3 | TGCTCTCCCAGTCATGACAA | BROAD | Pseudogene |
| FAM8A4P | FAM8A4P_4 | AGATATCATTTATCCCACTG | BROAD | Pseudogene |
| GOLGA2P2Y | GOLGA2P2Y_1 | CCAGTACCGAGAACTAGCAG | BROAD | Pseudogene |
| GOLGA2P2Y | GOLGA2P2Y_2 | CTCATCCCAGAAAAAGCCAG | BROAD | Pseudogene |
| GOLGA2P2Y | GOLGA2P2Y_3 | GCCCATGCTGAACATTCCAG | BROAD | Pseudogene |
| GOLGA2P2Y | GOLGA2P2Y_4 | AGCTCCTCAAAGCTGCTGTG | BROAD | Pseudogene |
| GOLGA2P3Y | GOLGA2P3Y_1 | ACAATGAGGAGGAGGCACCT | BROAD | Pseudogene |
| GOLGA2P3Y | GOLGA2P3Y_2 | AGAGTGCACTGCAGTTGGAG | BROAD | Pseudogene |
| GOLGA2P3Y | GOLGA2P3Y_3 | TATTGCGGAGCTTGAGTGCA | BROAD | Pseudogene |
| GOLGA2P3Y | GOLGA2P3Y_4 | AGTGCCAAAGACGCAGCACT | BROAD | Pseudogene |
| GOLGA6L16P | GOLGA6L16P_1 | CAGAGGGCGGAGTCACACAG | BROAD | Pseudogene |
| GOLGA6L16P | GOLGA6L16P_2 | GCACGTTCGCACATCGAAGG | BROAD | Pseudogene |

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| GOLGA6L16P | GOLGA6L16P_3 | AGCAGCAGGTATCTACAGGG | BROAD | Pseudogene |
| GOLGA6L16P | GOLGA6L16P_4 | GGGAGCAGGATGAGAGACTG | BROAD | Pseudogene |
| GYG2P1 | GYG2P1_1 | GTCACGAACCCGCAGAACAG | BROAD | Pseudogene |
| GYG2P1 | GYG2P1_2 | TACTCACCCGACATGGTCCG | BROAD | Pseudogene |
| GYG2P1 | GYG2P1_3 | AAGATCACTTGGGCCAGTGA | BROAD | Pseudogene |
| GYG2P1 | GYG2P1_4 | CTGGCAGTAGATGTCATCTG | BROAD | Pseudogene |
| HSFY3P | HSFY3P_1 | GCCGATGTATCAAATGTCAT | BROAD | Pseudogene |
| HSFY3P | HSFY3P_2 | GAGACACAAACTGTGTAACG | 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 | AAAAGAAGGTGTGTGCATAG | BROAD | Pseudogene |
| LINC00266-2P | LINC00266-2P_4 | GCATCTTAAAATGATTCAGC | BROAD | Pseudogene |
| LINC00266-4P | LINC00266-4P_1 | TGGAGCAGCCCACAAGGCTG | BROAD | Pseudogene |
| LINC00266-4P | LINC00266-4P_2 | CACACAAACCTTGGAAAAGA | BROAD | Pseudogene |
| LINC00266-4P | LINC00266-4P_3 | GCCGCTGGGAGCTGCTGCAT | BROAD | Pseudogene |
| LINC00266-4P | LINC00266-4P_4 | CAGTTGGGGGGTGGTCCAGT | BROAD | Pseudogene |
| MXRA5Y | MXRA5Y_1 | GATAGTAGGAGTCTAACACG | BROAD | Pseudogene |

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|---|---|---|---|---|
| MXRA5Y | MXRA5Y_2 | GGGGCAGACCATATCACGGT | BROAD | Pseudogene |
| MXRA5Y | MXRA5Y_3 | CTCAACTTGAATCCCACCGG | BROAD | Pseudogene |
| MXRA5Y | MXRA5Y_4 | GTTGCACACTCCATGGACCA | BROAD | Pseudogene |
| NAP1L1P2 | NAP1L1P2_1 | TCAAATCACGTATCAAATAG | BROAD | Pseudogene |
| NAP1L1P2 | NAP1L1P2_2 | GGGTTCTACAGGGTGCCAGA | BROAD | Pseudogene |
| NAP1L1P2 | NAP1L1P2_3 | ACTTAAATGTGCACAGACAG | BROAD | Pseudogene |
| NAP1L1P2 | NAP1L1P2_4 | GCATTCTCAGAACTTCAGGC | BROAD | Pseudogene |
| PARP4P1 | PARP4P1_1 | CAATCATTGTGAAACAACGA | BROAD | Pseudogene |
| PARP4P1 | PARP4P1_2 | GAAGCCCAGTCAGAGTACCG | BROAD | Pseudogene |
| PARP4P1 | PARP4P1_3 | TGTCTTCTGGACGAATCAGT | BROAD | Pseudogene |
| PARP4P1 | PARP4P1_4 | TTCACATCAACTTTGGAACG | BROAD | Pseudogene |
| PCMTD1P1 | PCMTD1P1_1 | TGATTACCCACAAATACGTG | BROAD | Pseudogene |
| PCMTD1P1 | PCMTD1P1_2 | CAGTGAAGCGATGAAGCCAG | BROAD | Pseudogene |
| PCMTD1P1 | PCMTD1P1_3 | AGGCCAAGGGTATTCCTCAA | BROAD | Pseudogene |
| PCMTD1P1 | PCMTD1P1_4 | GGAAGAAGATAGTAAAGAAG | BROAD | Pseudogene |
| PRKY | PRKY_1 | ATGATCTATAGGATGTGAGT | BROAD | Pseudogene |
| PRKY | PRKY_2 | TTATTACATAAATTAGACAG | BROAD | Pseudogene |
| PRKY | PRKY_3 | TGGGGGAATAAGATATCCGG | BROAD | Pseudogene |
| PRKY | PRKY_4 | TACCTGGAAACTGCCCATGG | BROAD | Pseudogene |
| PRRC2CP1 | PRRC2CP1_1 | CCATTTAAAAAAATGGCGGG | BROAD | Pseudogene |
| PRRC2CP1 | PRRC2CP1_2 | CAACTCAACACAGTAAACTG | BROAD | Pseudogene |
| PRRC2CP1 | PRRC2CP1_3 | GTTCAGATGACCGCAGAACC | BROAD | Pseudogene |
| PRRC2CP1 | PRRC2CP1_4 | TTAGCTTCTGAATCATCATG | BROAD | Pseudogene |

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|---|---|---|---|---|
| PSIP1P2 | PSIP1P2_1 | CATTGTATGGTTGACCCACT | BROAD | Pseudogene |
| PSIP1P2 | PSIP1P2_2 | AGTCTGTACATTGATGTGTA | BROAD | Pseudogene |
| PSIP1P2 | PSIP1P2_3 | ATAACAGAATGGGTATATAC | BROAD | Pseudogene |
| PSIP1P2 | PSIP1P2_4 | TTTAACAGCATAGAAACTTG | BROAD | Pseudogene |
| PSMA6P1 | PSMA6P1_1 | ATATTTCTCAGGTCTACACA | BROAD | Pseudogene |
| PSMA6P1 | PSMA6P1_2 | ACAACAAACAAATATCATGG | BROAD | Pseudogene |
| PSMA6P1 | PSMA6P1_3 | GGGTGTAAAGCCACTGCAGT | BROAD | Pseudogene |
| PSMA6P1 | PSMA6P1_4 | GATCACACTTACATACCTGA | BROAD | Pseudogene |
| RBMY1A3P | RBMY1A3P_1 | GAAGCAGTGGAGGAACAGGA | BROAD | Pseudogene |
| RBMY1A3P | RBMY1A3P_2 | CATTTACAGCACAATGGTAG | BROAD | Pseudogene |
| RBMY1A3P | RBMY1A3P_3 | CCCTCACATGAAGGACACCT | BROAD | Pseudogene |
| RBMY1A3P | RBMY1A3P_4 | AAATATGGTCCCATATCAGA | BROAD | Pseudogene |
| RBMY2EP | RBMY2EP_1 | GGTGGCTACGACGAAACCCG | BROAD | Pseudogene |
| RBMY2EP | RBMY2EP_2 | GATCATTCTGATCGTACAAG | BROAD | Pseudogene |
| RBMY2EP | RBMY2EP_3 | GTGTATTGTTATAATCAGGG | BROAD | Pseudogene |
| RBMY2EP | RBMY2EP_4 | TGCCAAAGATATGAATGGAG | BROAD | Pseudogene |
| RBMY2FP | RBMY2FP_1 | ACACACATTCTCAGACATGG | BROAD | Pseudogene |
| RBMY2FP | RBMY2FP_2 | TAATCCCAACTACTCAGCTG | BROAD | Pseudogene |
| RBMY2FP | RBMY2FP_3 | GATAATACAAGTTAACCGAT | BROAD | Pseudogene |
| RBMY2FP | RBMY2FP_4 | AAATGTAAAGATGGAACCAT | BROAD | Pseudogene |
| RBMY2HP | RBMY2HP_1 | CGATATGCATAGTCTCAAGG | BROAD | Pseudogene |
| RBMY2HP | RBMY2HP_2 | GTGTATTATTATAATCATGG | BROAD | Pseudogene |
| RBMY2HP | RBMY2HP_3 | GGTCACCACAAGGCCAACTG | BROAD | Pseudogene |

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|---|---|---|---|---|
| RBMY2HP | RBMY2HP_4 | GGCATCTATAGGAGATGATG | BROAD | Pseudogene |
| RBMY2KP | RBMY2KP_1 | AGAGATCATTCTGAACACCA | BROAD | Pseudogene |
| RBMY2KP | RBMY2KP_2 | AGAAGCAATAGTTGTATGGG | BROAD | Pseudogene |
| RBMY2KP | RBMY2KP_3 | ATATGGTAGCTCAAGATATG | BROAD | Pseudogene |
| RBMY2KP | RBMY2KP_4 | GAAGTCGTGAGAGTTACTCA | BROAD | Pseudogene |
| RBMY2MP | RBMY2MP_1 | CTTCCACCGTAAGACAACTG | BROAD | Pseudogene |
| RBMY2MP | RBMY2MP_2 | GATGGCTACAATGACGCCCG | BROAD | Pseudogene |
| RBMY2MP | RBMY2MP_3 | ATACCTCAAAAAATTAATGG | BROAD | Pseudogene |
| RBMY2MP | RBMY2MP_4 | ATTAAAGGTCCCATATCACA | BROAD | Pseudogene |
| RBMY2QP | RBMY2QP_1 | GGAGCAGGTACACCCTATCG | BROAD | Pseudogene |
| RBMY2QP | RBMY2QP_2 | GCTGTGGCAAGAAGCAACAG | BROAD | Pseudogene |
| RBMY2QP | RBMY2QP_3 | TTACCGTGATGGCTACTGTG | BROAD | Pseudogene |
| RBMY2QP | RBMY2QP_4 | AAAGCAGTATTTGTGAAACA | BROAD | Pseudogene |
| RBMY3AP | RBMY3AP_1 | AGAAGCAATAGTCGGATGGG | BROAD | Pseudogene |
| RBMY3AP | RBMY3AP_2 | TCGACGAAGTGATTGGATTG | BROAD | Pseudogene |
| RBMY3AP | RBMY3AP_3 | GTGTATTGTTATAATAATGG | BROAD | Pseudogene |
| RBMY3AP | RBMY3AP_4 | GATGAATCTGCTAGCAACAC | BROAD | Pseudogene |
| REREP1Y | REREP1Y_1 | GTAATCGTAGGACTTAATGG | BROAD | Pseudogene |
| REREP1Y | REREP1Y_2 | AGATGGTGAAAGCTCCAAGT | BROAD | Pseudogene |
| REREP1Y | REREP1Y_3 | GGTGTTGCTCAGAAATAGCG | BROAD | Pseudogene |
| REREP1Y | REREP1Y_4 | GACACCAGATTAAATACTGG | BROAD | Pseudogene |
| REREP2Y | REREP2Y_1 | GTCATCAGGAACCTACACTC | BROAD | Pseudogene |
| REREP2Y | REREP2Y_2 | AGGCTAGGGCTGCCATTCGT | BROAD | Pseudogene |

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|---|---|---|---|---|
| REREP2Y | REREP2Y_3 | TTAAAGCACAGGAACCCATG | BROAD | Pseudogene |
| REREP2Y | REREP2Y_4 | CAGTGGAGTCAAGCTAAGGA | BROAD | Pseudogene |
| RN7SL702P | RN7SL702P_1 | GTGCAGACATCCGATCAACA | BROAD | Pseudogene |
| RN7SL702P | RN7SL702P_2 | TGAACCACCCTAAGTCACAA | BROAD | Pseudogene |
| RN7SL702P | RN7SL702P_3 | AGCAAGAAGTAGCATGCCTG | BROAD | Pseudogene |
| RN7SL702P | RN7SL702P_4 | AAAACTCCCGTGCTGATCAG | BROAD | Pseudogene |
| RNASEH2CP1 | RNASEH2CP1_1 | GCGCGTGAATCGTTGCCGCG | BROAD | Pseudogene |
| RNASEH2CP1 | RNASEH2CP1_2 | CTACACTTAAGAGTCCCTCG | BROAD | Pseudogene |
| RNASEH2CP1 | RNASEH2CP1_3 | ACACTACACCTGATACCCTG | BROAD | Pseudogene |
| RNASEH2CP1 | RNASEH2CP1_4 | ACGTATCCCACGAGGCCGGA | BROAD | Pseudogene |
| RNF19BPY | RNF19BPY_1 | ACTTCTCTGTCCCAGCCGAG | BROAD | Pseudogene |
| RNF19BPY | RNF19BPY_2 | AATCTGCAATATGATAGTGA | BROAD | Pseudogene |
| RNF19BPY | RNF19BPY_3 | ATGTGTGTATATTATGTACG | BROAD | Pseudogene |
| RNF19BPY | RNF19BPY_4 | CATCACTCTCCAAACCACTG | BROAD | Pseudogene |
| RNU2-57P | RNU2-57P_1 | TCTGATGTATCCTCTGTCCG | BROAD | Pseudogene |
| RNU2-57P | RNU2-57P_2 | GAGGGGAACACCGTTCTTGG | BROAD | Pseudogene |
| RNU2-57P | RNU2-57P_3 | ACATCAGATATTAAACTGAT | BROAD | Pseudogene |
| RNU2-57P | RNU2-57P_4 | TGCAATACCAGGTCAATGTG | BROAD | Pseudogene |
| RPL26P37 | RPL26P37_1 | TTTCAGCTCATTGGAAAGAG | BROAD | Pseudogene |
| RPL26P37 | RPL26P37_2 | ACCGCAAAAATATCCGTGAA | BROAD | Pseudogene |
| RPL26P37 | RPL26P37_3 | ATACATTGAACGGGTGCAGT | BROAD | Pseudogene |
| RPL26P37 | RPL26P37_4 | CCTTCAGTTGGAAGTCACAA | BROAD | Pseudogene |
| SEPT14P22 | SEPT14P22_1 | TAAAGTGTGAACTCCTAGCA | BROAD | Pseudogene |

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|---|---|---|---|---|
| SEPT14P22 | SEPT14P22_2 | TTAATTCTGACACAATAGCA | BROAD | Pseudogene |
| SEPT14P22 | SEPT14P22_3 | ATAGCTAATGTACTATCACT | BROAD | Pseudogene |
| SEPT14P22 | SEPT14P22_4 | CTCATAGCAGTCTGTCACCC | BROAD | Pseudogene |
| SEPT14P23 | SEPT14P23_1 | AAAAGAAAGGGTGAACTTGA | BROAD | Pseudogene |
| SEPT14P23 | SEPT14P23_2 | CTGCTATGAGTCACCACATC | BROAD | Pseudogene |
| SEPT14P23 | SEPT14P23_3 | CATAGCTAATGTACTATCAC | BROAD | Pseudogene |
| SEPT14P23 | SEPT14P23_4 | CATGAAATTATGGTAGTATA | BROAD | Pseudogene |
| SERBP1P2 | SERBP1P2_1 | TAGAGAAAATAAGCCAACGG | BROAD | Pseudogene |
| SERBP1P2 | SERBP1P2_2 | TGAATGCCATAAAACAACCA | BROAD | Pseudogene |
| SERBP1P2 | SERBP1P2_3 | CAAATGATAAAATGTCTCAG | BROAD | Pseudogene |
| SERBP1P2 | SERBP1P2_4 | CAGCCAGCTGCAATCCATTG | BROAD | Pseudogene |
| SFPQP1 | SFPQP1_1 | AACAAAAACATGGTACCACG | BROAD | Pseudogene |
| SFPQP1 | SFPQP1_2 | TGAAATAGGAGATGCACTCA | BROAD | Pseudogene |
| SFPQP1 | SFPQP1_3 | ATGGAGCCCAGAATTCCACA | BROAD | Pseudogene |
| SFPQP1 | SFPQP1_4 | ATTCCATTAGAAACCACGAG | BROAD | Pseudogene |
| SHROOM2P1 | SHROOM2P1_1 | GGCCACAACACATTCACAAG | BROAD | Pseudogene |
| SHROOM2P1 | SHROOM2P1_2 | GCCCAAAATTGAACATCCCA | BROAD | Pseudogene |
| SHROOM2P1 | SHROOM2P1_3 | GGATGCCACTGATCGCTGGA | BROAD | Pseudogene |
| SHROOM2P1 | SHROOM2P1_4 | ACCACCATTTGATGCCCAGG | BROAD | Pseudogene |
| SLC25A15P1 | SLC25A15P1_1 | ATCAAAGGGACAGGGCCTAG | BROAD | Pseudogene |
| SLC25A15P1 | SLC25A15P1_2 | CTGGATATACCGCAAGCCAG | BROAD | Pseudogene |
| SLC25A15P1 | SLC25A15P1_3 | GAAGTTGATGATGAGCCAGT | BROAD | Pseudogene |
| SLC25A15P1 | SLC25A15P1_4 | CAACTTCCTGGTATATTCGT | BROAD | Pseudogene |

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| SLC9B1P1 | SLC9B1P1_1 | AAACATGTGATTTCTGTACA | BROAD | Pseudogene |
| SLC9B1P1 | SLC9B1P1_2 | CCACTTGGAAACATATGCGA | BROAD | Pseudogene |
| SLC9B1P1 | SLC9B1P1_3 | TTCAGAGCCTAAGATTGCTA | BROAD | Pseudogene |
| SLC9B1P1 | SLC9B1P1_4 | TGAATCCAGTGATAGCCAGA | BROAD | Pseudogene |
| SNX18P1Y | SNX18P1Y_1 | GCAATAACAAGTCCATGGCT | BROAD | Pseudogene |
| SNX18P1Y | SNX18P1Y_2 | AGCTGAATATAGAACTGTGT | BROAD | Pseudogene |
| SNX18P1Y | SNX18P1Y_3 | GCTGATGGCATCATCATCAC | BROAD | Pseudogene |
| SNX18P1Y | SNX18P1Y_4 | ACAGGCAACAGGTGGCAGAA | BROAD | Pseudogene |
| SRIP3 | SRIP3_1 | TCCCTCCATACCCGCCTGGG | BROAD | Pseudogene |
| SRIP3 | SRIP3_2 | ACTGCACCATGTAGTACCTG | BROAD | Pseudogene |
| SRIP3 | SRIP3_3 | GCAGCAAAGTAATCATATAG | BROAD | Pseudogene |
| SRIP3 | SRIP3_4 | TGCATTTCCCAGAAAAACTC | BROAD | Pseudogene |
| STSP1 | STSP1_1 | TACCTGATCAGACAGGCTAC | BROAD | Pseudogene |
| STSP1 | STSP1_2 | GAGGAAATGGACTGTAGTGT | BROAD | Pseudogene |
| STSP1 | STSP1_3 | CCACCAATGAGATTACCTGA | BROAD | Pseudogene |
| STSP1 | STSP1_4 | CCTCTGAGTGAGATTGCCAT | BROAD | Pseudogene |
| SURF6P1 | SURF6P1_1 | TGAAACGCCTCTGGTCATTG | BROAD | Pseudogene |
| SURF6P1 | SURF6P1_2 | CCCTTCACAGGGAGTGACCG | BROAD | Pseudogene |
| SURF6P1 | SURF6P1_3 | GCAGCAGGCAATCATCGTGG | BROAD | Pseudogene |
| SURF6P1 | SURF6P1_4 | TTGTTGAAGATCAGTCCTGG | BROAD | Pseudogene |
| TAB3P1 | TAB3P1_1 | TCTTAACAGACGGTACCAAG | BROAD | Pseudogene |
| TAB3P1 | TAB3P1_2 | GAGAGAACGCCAATTACATG | BROAD | Pseudogene |
| TAB3P1 | TAB3P1_3 | ACAACATCTAGCTTGCACAG | BROAD | Pseudogene |

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|---|---|---|---|---|
| TAB3P1 | TAB3P1_4 | GAAGAACATTGAGACCTAGG | BROAD | Pseudogene |
| TEKT4P1 | TEKT4P1_1 | CTTCGCCGACTGCAACCAGT | BROAD | Pseudogene |
| TEKT4P1 | TEKT4P1_2 | GGCAAAGACCCCAGTCACAG | BROAD | Pseudogene |
| TEKT4P1 | TEKT4P1_3 | ACTGTGTCACCCAAGCAACT | BROAD | Pseudogene |
| TEKT4P1 | TEKT4P1_4 | AGATCAGGAACACAACATGG | BROAD | Pseudogene |
| TMEM167AP1 | TMEM167AP1_1 | ACTTGCCTGAATAGTATACA | BROAD | Pseudogene |
| TMEM167AP1 | TMEM167AP1_2 | ACATGACATGAGTTACTACG | BROAD | Pseudogene |
| TMEM167AP1 | TMEM167AP1_3 | AGGCCTAGAAACGTAGACAG | BROAD | Pseudogene |
| TMEM167AP1 | TMEM167AP1_4 | ACAGGGCATTAACAGGACAC | BROAD | Pseudogene |
| TPTE2P4 | TPTE2P4_1 | GATATATAGATACTTCATCA | BROAD | Pseudogene |
| TPTE2P4 | TPTE2P4_2 | TATTCTGAATAAAAGATGTG | BROAD | Pseudogene |
| TPTE2P4 | TPTE2P4_3 | TGCAGTTAAAAATATGTCAG | BROAD | Pseudogene |
| TPTE2P4 | TPTE2P4_4 | ACTGGAATCTCTCTCCAAGA | BROAD | Pseudogene |
| TSPY11P | TSPY11P_1 | AGAGCTTATGTACGGAACTG | BROAD | Pseudogene |
| TSPY11P | TSPY11P_2 | CAGGACGTCAGTACTCAACA | BROAD | Pseudogene |
| TSPY11P | TSPY11P_3 | GATGTTGAGCCCTATCGCTG | BROAD | Pseudogene |
| TSPY11P | TSPY11P_4 | ACTCTGGGGTTATGGGCCCA | BROAD | Pseudogene |
| TSPY12P | TSPY12P_1 | GTTCAATAAAGGTAGCTGCA | BROAD | Pseudogene |
| TSPY12P | TSPY12P_2 | GGCCACAGACACTACAACAG | BROAD | Pseudogene |
| TSPY12P | TSPY12P_3 | CAGGATTTCAGTACTCAGCA | BROAD | Pseudogene |
| TSPY12P | TSPY12P_4 | CTCCTCCTACCACTCCACGT | BROAD | Pseudogene |
| TSPY13P | TSPY13P_1 | ACACTGAGAAGGATACAACA | BROAD | Pseudogene |
| TSPY13P | TSPY13P_2 | CAGCCTCTATGGCACCCGGT | BROAD | Pseudogene |

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| TSPY13P | TSPY13P_3 | ACATAGTTACTATAGTATGC | BROAD | Pseudogene |
| TSPY13P | TSPY13P_4 | TTGTGGTGTCCCCAGCGATA | BROAD | Pseudogene |
| TSPY15P | TSPY15P_1 | GGTTTCCAGGAGACCCCTAA | BROAD | Pseudogene |
| TSPY15P | TSPY15P_2 | CAGGATGTCAGTATTCAGCA | BROAD | Pseudogene |
| TSPY15P | TSPY15P_3 | GGTGGCAGATGACATAATGG | BROAD | Pseudogene |
| TSPY15P | TSPY15P_4 | CATCATACTCAACTCAACAT | BROAD | Pseudogene |
| TSPY16P | TSPY16P_1 | TTTGAGTGCAGTCCGTTAGG | BROAD | Pseudogene |
| TSPY16P | TSPY16P_2 | GCTACAGAAAGGGCAGCGCA | BROAD | Pseudogene |
| TSPY16P | TSPY16P_3 | AAGACGGTGCACCCTGAAGA | BROAD | Pseudogene |
| TSPY16P | TSPY16P_4 | TCTGGATGATGGCCCCTCTG | BROAD | Pseudogene |
| TSPY17P | TSPY17P_1 | AGCCAGGTGCATGCGCCCTG | BROAD | Pseudogene |
| TSPY17P | TSPY17P_2 | ACCTAACGGACTGCACTCAA | BROAD | Pseudogene |
| TSPY17P | TSPY17P_3 | TGCAGCCCGACCCATAGCAC | BROAD | Pseudogene |
| TSPY17P | TSPY17P_4 | CACCGTCTTCACTCTGCCCG | BROAD | Pseudogene |
| TSPY5P | TSPY5P_1 | TCAGGGCTGATATCAAGAGG | BROAD | Pseudogene |
| TSPY5P | TSPY5P_2 | CCTAACGAACTGCACGCAAA | BROAD | Pseudogene |
| TSPY5P | TSPY5P_3 | GGTCTGTGAGAGTCCCAAAG | BROAD | Pseudogene |
| TSPY5P | TSPY5P_4 | AAAAAACGCAGACAGGAAGA | BROAD | Pseudogene |
| TSPY6P | TSPY6P_1 | AAGCCCCAGCTAGACCGCAG | BROAD | Pseudogene |
| TSPY6P | TSPY6P_2 | GCGCCTCTGCGGTCTAGCTG | BROAD | Pseudogene |
| TSPY6P | TSPY6P_3 | GGCGCCTCTGCGGTCTAGCT | BROAD | Pseudogene |
| TSPY6P | TSPY6P_4 | CGGCGCCTCTGCGGTCTAGC | BROAD | Pseudogene |
| TSPY7P | TSPY7P_1 | TGTGCAGGAGGGGGCGGCCG | BROAD | Pseudogene |

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|---|---|---|---|---|
| TSPY7P | TSPY7P_2 | AGGATGGAGGCTGTGCAGGA | BROAD | Pseudogene |
| TSPY7P | TSPY7P_3 | CTTCAGGATGGAGGCTGTGC | BROAD | Pseudogene |
| TSPY7P | TSPY7P_4 | CTGTGCAGGAGGGGGCGGCC | BROAD | Pseudogene |
| TSPY9P | TSPY9P_1 | GGATGGAGGCTGTACAGGAG | BROAD | Pseudogene |
| TSPY9P | TSPY9P_2 | AGGATGGAGGCTGTACAGGA | BROAD | Pseudogene |
| TSPY9P | TSPY9P_3 | TGACCTACCGGGTGCCAGAG | BROAD | Pseudogene |
| TSPY9P | TSPY9P_4 | AGGATCTAACAAGATTGCTG | BROAD | Pseudogene |
| TUSC2P1 | TUSC2P1_1 | GGGAACTATTCACCACCCTG | BROAD | Pseudogene |
| TUSC2P1 | TUSC2P1_2 | AAGTGCTGTAGCTTCTAGCA | BROAD | Pseudogene |
| TUSC2P1 | TUSC2P1_3 | CAACAACTAGTTGTAGTAGG | BROAD | Pseudogene |
| TUSC2P1 | TUSC2P1_4 | GGGAAAGTACTGGAGCCGCT | BROAD | Pseudogene |
| TXLNGY | TXLNGY_1 | TAATCTTAATCAATGCCTAG | BROAD | Pseudogene |
| TXLNGY | TXLNGY_2 | GAAGTCACCTCGTGGCGTAG | BROAD | Pseudogene |
| TXLNGY | TXLNGY_3 | TAGTGACTATGATAATCAAG | BROAD | Pseudogene |
| TXLNGY | TXLNGY_4 | ATAGATCACTCACATGCATA | BROAD | Pseudogene |
| UBE2V1P3 | UBE2V1P3_1 | TGGAAAGAGAATAGTCACTG | BROAD | Pseudogene |
| UBE2V1P3 | UBE2V1P3_2 | TCACCAAAAGCTAATCTCAG | BROAD | Pseudogene |
| UBE2V1P3 | UBE2V1P3_3 | CAGCCTGTGAGACTACTGCT | BROAD | Pseudogene |
| UBE2V1P3 | UBE2V1P3_4 | AGAACATGTAATCAGCAGCA | BROAD | Pseudogene |
| VDAC1P6 | VDAC1P6_1 | AGGGCTAAAAAACACAACAC | BROAD | Pseudogene |
| VDAC1P6 | VDAC1P6_2 | TAGAACACGGATAATACACT | BROAD | Pseudogene |
| VDAC1P6 | VDAC1P6_3 | AAAAGAGGTAACGATGAACT | BROAD | Pseudogene |
| VDAC1P6 | VDAC1P6_4 | AGACACCTGGCATCTCAAAG | BROAD | Pseudogene |

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|---|---|---|---|---|
| XGY2 | XGY2_1 | TTGAACTGATGCTTACGGAG | BROAD | Pseudogene |
| XGY2 | XGY2_2 | AGGTGAGTGTCTCTTCAGCT | BROAD | Pseudogene |
| XGY2 | XGY2_3 | GACGAAGTGGTGCTTCACTG | BROAD | Pseudogene |
| XGY2 | XGY2_4 | CAGATATTGAAAGCAAAATG | BROAD | Pseudogene |
| ZNF736P11Y | ZNF736P11Y_1 | GCAAAGTGTGAATTACTACA | BROAD | Pseudogene |
| ZNF736P11Y | ZNF736P11Y_2 | AAGAATATGGCAGAAACTGT | BROAD | Pseudogene |
| ZNF736P11Y | ZNF736P11Y_3 | CACTGAAGATTGGGTACACC | BROAD | Pseudogene |
| ZNF736P11Y | ZNF736P11Y_4 | ATATTACTGCAGACATATGG | BROAD | Pseudogene |
| ZNF736P12Y | ZNF736P12Y_1 | TATTACTGCAGACATATGGT | BROAD | Pseudogene |
| ZNF736P12Y | ZNF736P12Y_2 | TCTTCTGTTCACTGAAGATT | BROAD | Pseudogene |
| ZNF736P12Y | ZNF736P12Y_3 | TACTACAAATGCAAAGAATA | BROAD | Pseudogene |
| ZNF736P12Y | ZNF736P12Y_4 | TACACATTCTTTGCAATTGT | BROAD | Pseudogene |
| ZNF736P6Y | ZNF736P6Y_1 | ATAAGAGAGTTCATACTGTG | BROAD | Pseudogene |
| ZNF736P6Y | ZNF736P6Y_2 | AAACACAAGAGAATTAATAC | BROAD | Pseudogene |
| ZNF736P6Y | ZNF736P6Y_3 | CAATGTTTGTCAACAACCCA | BROAD | Pseudogene |
| ZNF736P6Y | ZNF736P6Y_4 | CATATGGTGTTCAACATCAG | BROAD | Pseudogene |
| ZNF736P7Y | ZNF736P7Y_1 | TCATGCCAAATATTTCACGT | BROAD | Pseudogene |
| ZNF736P7Y | ZNF736P7Y_2 | ATTTAATTTAACATATTGGA | BROAD | Pseudogene |
| ZNF736P7Y | ZNF736P7Y_3 | CAACATGAAGACTTGTTAGT | BROAD | Pseudogene |
| ZNF736P7Y | ZNF736P7Y_4 | GCCACATCTACACAGATGTA | BROAD | Pseudogene |
| ZNF736P8Y | ZNF736P8Y_1 | CTGTTGCTGAACACAATGTG | BROAD | Pseudogene |
| ZNF736P8Y | ZNF736P8Y_2 | AAAGTGTGGGTAATTGCAAA | BROAD | Pseudogene |
| ZNF736P8Y | ZNF736P8Y_3 | ATAAGAAAATTCAAACTGTA | BROAD | Pseudogene |

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| ZNF736P8Y | ZNF736P8Y_4 | TTGTGTTTAAATAAGGGTTG | BROAD | Pseudogene |
| ZNF736P9Y | ZNF736P9Y_1 | AAAGTGTGGATAATTGCAAG | BROAD | Pseudogene |
| ZNF736P9Y | ZNF736P9Y_2 | TGCTACAGACATCAACAATG | BROAD | Pseudogene |
| ZNF736P9Y | ZNF736P9Y_3 | TGTACACTTGTGTTTACTAA | BROAD | Pseudogene |
| ZNF736P9Y | ZNF736P9Y_4 | CTAAACATGATAATTCATAG | BROAD | Pseudogene |
| ZNF839P1 | ZNF839P1_1 | AAGACAGAGACAGCCGCACA | BROAD | Pseudogene |
| ZNF839P1 | ZNF839P1_2 | AAATACAAAGCTAAAAACAG | BROAD | Pseudogene |
| ZNF839P1 | ZNF839P1_3 | TCACTTAGGAACCACGAATG | BROAD | Pseudogene |
| ZNF839P1 | ZNF839P1_4 | TGGGTTGGAGGACAAAAAAG | BROAD | Pseudogene |
| AGPAT5P1 | AGPAT5P1_1 | AGGAGCATGACGTCCGAAGC | GuideScan | Pseudogene |
| AGPAT5P1 | AGPAT5P1_2 | GCTGGCGGACGGGATGACGG | GuideScan | Pseudogene |
| AGPAT5P1 | AGPAT5P1_3 | CGTCAATTTGCTGCTCAACA | GuideScan | Pseudogene |
| AGPAT5P1 | AGPAT5P1_4 | TCACATGTACTCGCCTGCTT | GuideScan | Pseudogene |
| ANKRD57P1 | ANKRD57P1_1 | CTTCTCTGCGGTGTCCTCGG | GuideScan | Pseudogene |
| ANKRD57P1 | ANKRD57P1_2 | GCCTCAGACCAGCGATGACC | GuideScan | Pseudogene |
| ANKRD57P1 | ANKRD57P1_3 | GACTAATGGACTTAAAAAAC | GuideScan | Pseudogene |
| ANKRD57P1 | ANKRD57P1_4 | TCCAGGTCATCGCTGGTCTG | GuideScan | Pseudogene |
| ARSEP1 | ARSEP1_1 | TCCTAGGCCCGTAAGAAAGT | GuideScan | Pseudogene |
| ARSEP1 | ARSEP1_2 | CTGCGTTGTGATTGACAGCC | GuideScan | Pseudogene |
| ARSEP1 | ARSEP1_3 | GAGGATCACTTCGCCTCGTC | GuideScan | Pseudogene |
| ARSEP1 | ARSEP1_4 | TTGTTCGTACAAAGGCCGTG | GuideScan | Pseudogene |
| ARSFP1 | ARSFP1_1 | CAATGTGCGGGATGCGGTAC | GuideScan | Pseudogene |
| ARSFP1 | ARSFP1_2 | GCAATGTGCGGGATGCGGTA | GuideScan | Pseudogene |

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| ARSFP1 | ARSFP1_3 | TCTGCGGGGCTCGTATACAT | GuideScan | Pseudogene |
| ARSFP1 | ARSFP1_4 | ATGTGCGGGATGCGGTACGG | GuideScan | Pseudogene |
| CASKP1 | CASKP1_1 | TGAGAGGTACCGGTTACCAG | GuideScan | Pseudogene |
| CASKP1 | CASKP1_2 | CGATTAAACTTATGCTTACC | GuideScan | Pseudogene |
| CASKP1 | CASKP1_3 | TAAGCCCCCTAAAGTATGAG | GuideScan | Pseudogene |
| CASKP1 | CASKP1_4 | GTACCTTGACGTAGCTACCT | GuideScan | Pseudogene |
| CCNQP2 | CCNQP2_1 | GACCAGCCATCGTGGTGACA | GuideScan | Pseudogene |
| CCNQP2 | CCNQP2_2 | TTGCCACCATGTCACCACGA | GuideScan | Pseudogene |
| CCNQP2 | CCNQP2_3 | ATTCTTCTGCGAGACCTGAC | GuideScan | Pseudogene |
| CCNQP2 | CCNQP2_4 | CCAAGCGGCGAGGTTCATCA | GuideScan | Pseudogene |
| CDY10P | CDY10P_1 | ATGAGGCAAGCTCCTTAATA | GuideScan | Pseudogene |
| CDY10P | CDY10P_2 | TACATTTACCGCAGTTCACG | GuideScan | Pseudogene |
| CDY10P | CDY10P_3 | ATGGCTGGCTAGGTAGCGTC | GuideScan | Pseudogene |
| CDY10P | CDY10P_4 | TCTGCACTACATCCGTGAGA | GuideScan | Pseudogene |
| CDY11P | CDY11P_1 | CAATGGGCCCGCGATTGGAC | GuideScan | Pseudogene |
| CDY11P | CDY11P_2 | TCAGTCAATGGGCCCGCGAT | GuideScan | Pseudogene |
| CDY11P | CDY11P_3 | AATGGGCCCGCGATTGGACT | GuideScan | Pseudogene |
| CDY11P | CDY11P_4 | CTTAGCACCTGGTGAAGCAC | GuideScan | Pseudogene |
| CDY4P | CDY4P_1 | GGCGTGGCTTCCAATACCTT | GuideScan | Pseudogene |
| CDY4P | CDY4P_2 | ATCGATCCATTAATAGCCCA | GuideScan | Pseudogene |
| CDY4P | CDY4P_3 | TTTAGACTCGGCATTCTAGG | GuideScan | Pseudogene |
| CDY4P | CDY4P_4 | TATGGATGTGACGAGTCCAA | GuideScan | Pseudogene |
| CDY7P | CDY7P_1 | GCAACTATACTATGTCGATT | GuideScan | Pseudogene |

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|---|---|---|---|---|
| CDY7P | CDY7P_2 | CGAATTCATTAACAGCCAAT | GuideScan | Pseudogene |
| CDY7P | CDY7P_3 | TGGCTCGATTAACACTTCCA | GuideScan | Pseudogene |
| CDY7P | CDY7P_4 | GCAGCTGAATCCACGGGAGG | GuideScan | Pseudogene |
| CHEK2P1 | CHEK2P1_1 | ATCATCAGGAATACGAATAC | GuideScan | Pseudogene |
| CHEK2P1 | CHEK2P1_2 | GTAGCATAACCAACTTCCTC | GuideScan | Pseudogene |
| CHEK2P1 | CHEK2P1_3 | TATCAGAAAACCTGCCCAAT | GuideScan | Pseudogene |
| CHEK2P1 | CHEK2P1_4 | GACCTGAGCTCTGGGATATT | GuideScan | Pseudogene |
| CICP2 | CICP2_1 | TCAGCAAGCGGCACCAGGCC | GuideScan | Pseudogene |
| CICP2 | CICP2_2 | AAGCGGCACCAGGCCTGGCA | GuideScan | Pseudogene |
| CICP2 | CICP2_3 | AGGCCTGGCAGGGCACACCA | GuideScan | Pseudogene |
| CICP2 | CICP2_4 | CAAGCGGCACCAGGCCTGGC | GuideScan | Pseudogene |
| CYCSP46 | CYCSP46_1 | GTAAACAGTGATAGCGTTTA | GuideScan | Pseudogene |
| CYCSP46 | CYCSP46_2 | TGGTACACATCAAAAAAGTT | GuideScan | Pseudogene |
| CYCSP46 | CYCSP46_3 | TTCAACCCTTGCCTTTAAGA | GuideScan | Pseudogene |
| CYCSP46 | CYCSP46_4 | GTGGCTGTGTAAGAATATGC | GuideScan | Pseudogene |
| CYCSP48 | CYCSP48_1 | ATTTTACCTTGGTGTGGCAT | GuideScan | Pseudogene |
| CYCSP48 | CYCSP48_2 | TGCCACACCAAGGTAAAATG | GuideScan | Pseudogene |
| CYCSP48 | CYCSP48_3 | TTTTACCTTGGTGTGGCATT | GuideScan | Pseudogene |
| CYCSP48 | CYCSP48_4 | TGCCTCATTTTACCTTGGTG | GuideScan | Pseudogene |
| DLGAP5P1 | DLGAP5P1_1 | TCATAGTCCATCCATTTAGC | GuideScan | Pseudogene |
| DLGAP5P1 | DLGAP5P1_2 | TTCTACACAGAGAGGCTTAA | GuideScan | Pseudogene |
| DLGAP5P1 | DLGAP5P1_3 | TGGATGGACTATGACAGTTT | GuideScan | Pseudogene |
| DLGAP5P1 | DLGAP5P1_4 | TTGATGTCTCTCCAGCTAAA | GuideScan | Pseudogene |

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|---|---|---|---|---|
| DUX4L31 | DUX4L31_1 | CACGTGGGAACATGAATCCG | GuideScan | Pseudogene |
| DUX4L31 | DUX4L31_2 | CCGTACTGGGTCTGCGGCCA | GuideScan | Pseudogene |
| DUX4L31 | DUX4L31_3 | TCCGTACTGGGTCTGCGGCC | GuideScan | Pseudogene |
| DUX4L31 | DUX4L31_4 | CCCAACTTGCCGCGGCACAT | GuideScan | Pseudogene |
| ELOCP4 | ELOCP4_1 | GAAACCCATTTGAGTGACCC | GuideScan | Pseudogene |
| ELOCP4 | ELOCP4_2 | CTATTTGATATCATGGGATT | GuideScan | Pseudogene |
| ELOCP4 | ELOCP4_3 | AGGACTTTCACAACCATTGT | GuideScan | Pseudogene |
| ELOCP4 | ELOCP4_4 | AATGGGTTTCATTGTTGTTG | GuideScan | Pseudogene |
| ELOCP5 | ELOCP5_1 | GAAACCCGTTTGAGTGATCC | GuideScan | Pseudogene |
| ELOCP5 | ELOCP5_2 | AACGGGTTTCATTGTTGCTG | GuideScan | Pseudogene |
| ELOCP5 | ELOCP5_3 | TGTTTGATATCATGGCATTA | GuideScan | Pseudogene |
| ELOCP5 | ELOCP5_4 | GATATATCTGTTTGATATCA | GuideScan | Pseudogene |
| FAM199YP | FAM199YP_1 | TGTCCAGTTCATCTGTCCCT | GuideScan | Pseudogene |
| FAM199YP | FAM199YP_2 | GTGTATTACAATGTGTAGTG | GuideScan | Pseudogene |
| FAM199YP | FAM199YP_3 | AATCCAAGGGACAGATGAAC | GuideScan | Pseudogene |
| FAM199YP | FAM199YP_4 | GAAACTGAATTAAAGGAAGG | GuideScan | Pseudogene |
| FAM8A10P | FAM8A10P_1 | AAACTACTGCCTGTATTGAT | GuideScan | Pseudogene |
| FAM8A10P | FAM8A10P_2 | GCCCGTGCCCAGACAAATCT | GuideScan | Pseudogene |
| FAM8A10P | FAM8A10P_3 | TTCCTGGTCCGCAATACCAC | GuideScan | Pseudogene |
| FAM8A10P | FAM8A10P_4 | CAAGCACGTGATGTGAAGAG | GuideScan | Pseudogene |
| FAM8A7P | FAM8A7P_1 | CACATATTGTGGTTGTAACG | GuideScan | Pseudogene |
| FAM8A7P | FAM8A7P_2 | CACGTTACAACCACAATATG | GuideScan | Pseudogene |
| FAM8A7P | FAM8A7P_3 | TTCAGACTAGTATCCATATA | GuideScan | Pseudogene |

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|---|---|---|---|---|
| FAM8A7P | FAM8A7P_4 | TGGATTTGACTGACCCTATA | GuideScan | Pseudogene |
| FAM8A9P | FAM8A9P_1 | GAGGGTAGTATGTATGTTAA | GuideScan | Pseudogene |
| FAM8A9P | FAM8A9P_2 | GACTCTAACTTATAACCCCA | GuideScan | Pseudogene |
| FAM8A9P | FAM8A9P_3 | ACATACATACTACCCTCAAA | GuideScan | Pseudogene |
| FAM8A9P | FAM8A9P_4 | GTGGTTGCAGATTATACTAA | GuideScan | Pseudogene |
| GAPDHP17 | GAPDHP17_1 | GTCAACCTTATTGTTCACAT | GuideScan | Pseudogene |
| GAPDHP17 | GAPDHP17_2 | ACCATTCATGGTATTCTGGG | GuideScan | Pseudogene |
| GAPDHP17 | GAPDHP17_3 | ATTAGACACCGATTATGTTG | GuideScan | Pseudogene |
| GAPDHP17 | GAPDHP17_4 | CGATTATGTTGTGGAGTCAA | GuideScan | Pseudogene |
| GAPDHP19 | GAPDHP19_1 | AGGTTAGGTCCATGACCAAC | GuideScan | Pseudogene |
| GAPDHP19 | GAPDHP19_2 | GTCAATGATTAGGCCATATT | GuideScan | Pseudogene |
| GAPDHP19 | GAPDHP19_3 | GGTAGGTTTTCACATATGGC | GuideScan | Pseudogene |
| GAPDHP19 | GAPDHP19_4 | TGTAGGTCACAAGGTCTATC | GuideScan | Pseudogene |
| GOT2P5 | GOT2P5_1 | GCTAGTCTTCAACCTGAATA | GuideScan | Pseudogene |
| GOT2P5 | GOT2P5_2 | CGTTCCACTGTTCTGCATAA | GuideScan | Pseudogene |
| GOT2P5 | GOT2P5_3 | CTCTACTATTCTGAACACCC | GuideScan | Pseudogene |
| GOT2P5 | GOT2P5_4 | CTGTTCTGCATAAGGGTTCC | GuideScan | Pseudogene |
| GPR143P | GPR143P_1 | GAAACATACGCATGCACTAT | GuideScan | Pseudogene |
| GPR143P | GPR143P_2 | AAATTAGAGAGCACACGTCC | GuideScan | Pseudogene |
| GPR143P | GPR143P_3 | ATCTTATGTAGGGTCATGAT | GuideScan | Pseudogene |
| GPR143P | GPR143P_4 | GAGGGTGCTCAATCAACATG | GuideScan | Pseudogene |
| HSFY4P | HSFY4P_1 | ACGCGCTGCTTTGGATGTCG | GuideScan | Pseudogene |
| HSFY4P | HSFY4P_2 | GGTGCCAGAACTATACGGCC | GuideScan | Pseudogene |

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|---|---|---|---|---|
| HSFY4P | HSFY4P_3 | AACTATACGGCCTGGTAATT | GuideScan | Pseudogene |
| HSFY4P | HSFY4P_4 | ACGGGATCGGGCCAAAATGT | GuideScan | Pseudogene |
| KDM5DP1 | KDM5DP1_1 | GCAAGAGATTTCTCGGCATC | GuideScan | Pseudogene |
| KDM5DP1 | KDM5DP1_2 | GGAGAATCCCGAACATTAAA | GuideScan | Pseudogene |
| KDM5DP1 | KDM5DP1_3 | TGGAGAATCCCGAACATTAA | GuideScan | Pseudogene |
| KDM5DP1 | KDM5DP1_4 | TGCCGAGCCCTTTAATGTTC | GuideScan | Pseudogene |
| LINC00265-3P | LINC00265-3P_1 | CTCTTTTGGCTCAGCTCTGC | GuideScan | Pseudogene |
| LINC00268-2P | LINC00268-2P_1 | CAAAACCATGGAAGCCTCTG | GuideScan | Pseudogene |
| LINC00268-2P | LINC00268-2P_2 | TAGAATTGTGATAGAAGCCT | GuideScan | Pseudogene |
| MED13P1 | MED13P1_1 | ATTTCAGTACCATGCATCTC | GuideScan | Pseudogene |
| MED13P1 | MED13P1_2 | TGAGATGCATGGTACTGAAA | GuideScan | Pseudogene |
| MED14P1 | MED14P1_1 | AGACGGTTAACGATCTGTTT | GuideScan | Pseudogene |
| MED14P1 | MED14P1_2 | GTGCTCCGTTCTTCCGCCCG | GuideScan | Pseudogene |
| MED14P1 | MED14P1_3 | GGTTAACGATCTGTTTGGGT | GuideScan | Pseudogene |
| MED14P1 | MED14P1_4 | TTAGGCTGTCGTCCATCCCT | GuideScan | Pseudogene |
| MRPL57P10 | MRPL57P10_1 | ACTGGCAGTTGAGGACGATG | GuideScan | Pseudogene |
| MRPL57P10 | MRPL57P10_2 | GTTCTTCTATAATAAATCTG | GuideScan | Pseudogene |
| MRPL57P10 | MRPL57P10_3 | TTCTTCTATAATAAATCTGT | GuideScan | Pseudogene |
| MRPL57P10 | MRPL57P10_4 | AATAAATCTGTGGGAGATGC | GuideScan | Pseudogene |
| MTCO1P37 | MTCO1P37_1 | TATCGGGGCGCCAATTATCA | GuideScan | Pseudogene |
| MTCO1P37 | MTCO1P37_2 | ATATCGGGGCGCCAATTATC | GuideScan | Pseudogene |
| MTCO1P37 | MTCO1P37_3 | ACGCCATAACACACTATTCT | GuideScan | Pseudogene |
| MTCO1P37 | MTCO1P37_4 | ATCGGGGCGCCAATTATCAG | GuideScan | Pseudogene |

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|---|---|---|---|---|
| MTCYBP1 | MTCYBP1_1 | TGAATCGTTGCTAGAGCTGT | GuideScan | Pseudogene |
| MTCYBP1 | MTCYBP1_2 | CTACCTATCCCTAACAACCT | GuideScan | Pseudogene |
| MTCYBP1 | MTCYBP1_3 | ACAATATATTGGAACTGACC | GuideScan | Pseudogene |
| MTCYBP1 | MTCYBP1_4 | TAACAACCTAGGAAGTGTAC | GuideScan | Pseudogene |
| MTCYBP2 | MTCYBP2_1 | GATATTCCAACCATTAAGTC | GuideScan | Pseudogene |
| MTCYBP2 | MTCYBP2_2 | GATGGGTCATAAGATTGTGT | GuideScan | Pseudogene |
| MTCYBP2 | MTCYBP2_3 | TGTTTAGATGTGTGACGCAT | GuideScan | Pseudogene |
| MTCYBP2 | MTCYBP2_4 | ATATTCCAACCATTAAGTCA | GuideScan | Pseudogene |
| MTND1P1 | MTND1P1_1 | ACTTAACACTGTAGGTCCTA | GuideScan | Pseudogene |
| MTND1P1 | MTND1P1_2 | TAGTGTATTCCATCAGTGAA | GuideScan | Pseudogene |
| MTND1P1 | MTND1P1_3 | GGGGTGTAATGCTCAAAATT | GuideScan | Pseudogene |
| MTND1P1 | MTND1P1_4 | GAATGGTTGAATCAGTCCGT | GuideScan | Pseudogene |
| MTND2P3 | MTND2P3_1 | TATTCTGAGTCGTATTACTA | GuideScan | Pseudogene |
| MTND2P3 | MTND2P3_2 | CTATTCTGAGTCGTATTACT | GuideScan | Pseudogene |
| MTND2P3 | MTND2P3_3 | TAATAGTATTCATTGCCTGG | GuideScan | Pseudogene |
| MTND2P3 | MTND2P3_4 | CAGGCTAGTTTACTCATGTG | GuideScan | Pseudogene |
| MTND6P1 | MTND6P1_1 | ACCTACAAACCTTACAGCCA | GuideScan | Pseudogene |
| MTND6P1 | MTND6P1_2 | GTGGTCGTGTGAGGATTCTG | GuideScan | Pseudogene |
| MTND6P1 | MTND6P1_3 | ATTATTAAGAGAGTTGGCAT | GuideScan | Pseudogene |
| MTND6P1 | MTND6P1_4 | TGGTCGTGTGAGGATTCTGT | GuideScan | Pseudogene |
| NEFLP1 | NEFLP1_1 | CATGGCTACTGTAGTAGGAC | GuideScan | Pseudogene |
| NEFLP1 | NEFLP1_2 | CACCTACATCAGTAGTGTGC | GuideScan | Pseudogene |
| NEFLP1 | NEFLP1_3 | CTACAGTAGCCATGTGCAAG | GuideScan | Pseudogene |

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|---|---|---|---|---|
| NEFLP1 | NEFLP1_4 | GTATTGAGGCTGCAGCTCAG | GuideScan | Pseudogene |
| OFD1P13Y | OFD1P13Y_1 | TAAATAAAAAATATTTTAGA | GuideScan | Pseudogene |
| OFD1P14Y | OFD1P14Y_1 | TAAGTCACAGACTCAGTGGC | GuideScan | Pseudogene |
| OFD1P16Y | OFD1P16Y_1 | CAACATCGAGTACCCATCCT | GuideScan | Pseudogene |
| OFD1P16Y | OFD1P16Y_2 | CAACTGTGGTTGGGCTAGCC | GuideScan | Pseudogene |
| OFD1P16Y | OFD1P16Y_3 | CTACGTCAGAGCTGCAACTG | GuideScan | Pseudogene |
| OFD1P16Y | OFD1P16Y_4 | TACAGCTTCTACCGTCTGCA | GuideScan | Pseudogene |
| OFD1P3Y | OFD1P3Y_1 | TGCTAAGACGCTAGTTCATG | GuideScan | Pseudogene |
| OFD1P3Y | OFD1P3Y_2 | TATCCTAGCGTTTACATTTC | GuideScan | Pseudogene |
| OFD1P3Y | OFD1P3Y_3 | GGCCAATACTATTATTGGTC | GuideScan | Pseudogene |
| OFD1P3Y | OFD1P3Y_4 | GCTGTAACAAGCTTCCCTTC | GuideScan | Pseudogene |
| OFD1P5Y | OFD1P5Y_1 | GTAGATCCTTTTCCAGAGGA | GuideScan | Pseudogene |
| OFD1P5Y | OFD1P5Y_2 | TGCTGTAGATCCTTTTCCAG | GuideScan | Pseudogene |
| OFD1P5Y | OFD1P5Y_3 | TGTAGATCCTTTTCCAGAGG | GuideScan | Pseudogene |
| OFD1P5Y | OFD1P5Y_4 | CTATACTCAACCTCCTCCCC | GuideScan | Pseudogene |
| OFD1P6Y | OFD1P6Y_1 | GGCACTCAACTTGGGACACA | GuideScan | Pseudogene |
| OFD1P6Y | OFD1P6Y_2 | TAGGTAACGTGTGGTCAATG | GuideScan | Pseudogene |
| OFD1P6Y | OFD1P6Y_3 | GAACCATATCGCATTCTTTA | GuideScan | Pseudogene |
| OFD1P6Y | OFD1P6Y_4 | TCATTGGTTATACGTGATGA | GuideScan | Pseudogene |
| OFD1P8Y | OFD1P8Y_1 | CCCACTTTCCAACACTCCGC | GuideScan | Pseudogene |
| OFD1P8Y | OFD1P8Y_2 | CCACTTTCCAACACTCCGCA | GuideScan | Pseudogene |
| OFD1P8Y | OFD1P8Y_3 | GGTTTTTTTTTAACTCAGAA | GuideScan | Pseudogene |
| OFD1P8Y | OFD1P8Y_4 | CCTGCGGAGTGTTGGAAAGT | GuideScan | Pseudogene |

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|---|---|---|---|---|
| OFD1P9Y | OFD1P9Y_1 | AGAGAAACTTTACTATATGG | GuideScan | Pseudogene |
| OFD1P9Y | OFD1P9Y_2 | CAAAGAGAAACTTTACTATA | GuideScan | Pseudogene |
| OFD1P9Y | OFD1P9Y_3 | AAAGAGAAACTTTACTATAT | GuideScan | Pseudogene |
| PABPC1P5 | PABPC1P5_1 | CTGGAAAAACTTTGTCCACT | GuideScan | Pseudogene |
| PABPC1P5 | PABPC1P5_2 | TTGAAAAGATCAAGTAATAT | GuideScan | Pseudogene |
| PABPC1P5 | PABPC1P5_3 | GAAAAGCAATGAACAGAAAC | GuideScan | Pseudogene |
| PNPLA4P1 | PNPLA4P1_1 | GTCATTCGGGGCAGTAACAC | GuideScan | Pseudogene |
| PNPLA4P1 | PNPLA4P1_2 | TCATTCGGGGCAGTAACACT | GuideScan | Pseudogene |
| PNPLA4P1 | PNPLA4P1_3 | ATGACTTCATGGCCCAGCTA | GuideScan | Pseudogene |
| PNPLA4P1 | PNPLA4P1_4 | GTACTGTGTATACCTTAGCT | GuideScan | Pseudogene |
| PPP1R12BP1 | PPP1R12BP1_1 | TTAGCATAGACACGCCGTTA | GuideScan | Pseudogene |
| PPP1R12BP1 | PPP1R12BP1_2 | GAACTCCCGCAAATTAGGCC | GuideScan | Pseudogene |
| PPP1R12BP1 | PPP1R12BP1_3 | AGAACTCCCGCAAATTAGGC | GuideScan | Pseudogene |
| PPP1R12BP1 | PPP1R12BP1_4 | GCGCTTTTAGTAGCACGTGT | GuideScan | Pseudogene |
| PRYP2 | PRYP2_1 | AGGCGGCTTGCAGTGAGCCA | GuideScan | Pseudogene |
| PUDPP1 | PUDPP1_1 | CACAAGCATACTATGACCTG | GuideScan | Pseudogene |
| PUDPP1 | PUDPP1_2 | CAGGCCTATGATGTCCTTAG | GuideScan | Pseudogene |
| PUDPP1 | PUDPP1_3 | CATTTCCTACATGGCTTCAT | GuideScan | Pseudogene |
| PUDPP1 | PUDPP1_4 | CTCAAAATGATTTCCCACTA | GuideScan | Pseudogene |
| RAB9AP4 | RAB9AP4_1 | ACGGCAAGATGAGCTAGTCC | GuideScan | Pseudogene |
| RAB9AP4 | RAB9AP4_2 | GTATACACAAAATCACCACG | GuideScan | Pseudogene |
| RAB9AP4 | RAB9AP4_3 | TCTTCAAACCGCCTCCTCAA | GuideScan | Pseudogene |
| RAB9AP4 | RAB9AP4_4 | GTCCTTCTATATTAGCTGGT | GuideScan | Pseudogene |

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|---|---|---|---|---|
| RBMY1GP | RBMY1GP_1 | TCTACGCACAGCAGTTCCAT | GuideScan | Pseudogene |
| RBMY1GP | RBMY1GP_2 | CGCCGAGCTCCTGAGAATGG | GuideScan | Pseudogene |
| RBMY1GP | RBMY1GP_3 | AACGCAACTATCCCGGGTAC | GuideScan | Pseudogene |
| RBMY1GP | RBMY1GP_4 | GCAACTATCCCGGGTACCGG | GuideScan | Pseudogene |
| RBMY1HP | RBMY1HP_1 | TCAAACTGTAGTTCAATTCG | GuideScan | Pseudogene |
| RBMY1KP | RBMY1KP_1 | CACCGCGATTGGGCAATACA | GuideScan | Pseudogene |
| RBMY1KP | RBMY1KP_2 | ACCGCGATTGGGCAATACAT | GuideScan | Pseudogene |
| RBMY1KP | RBMY1KP_3 | CATGTATTGCCCAATCGCGG | GuideScan | Pseudogene |
| RBMY1KP | RBMY1KP_4 | ACCCATGTATTGCCCAATCG | GuideScan | Pseudogene |
| RBMY2AP | RBMY2AP_1 | TAATATCCTGACAAAGACAG | GuideScan | Pseudogene |
| RBMY2AP | RBMY2AP_2 | GAGTATGGGGTGGGTGGACC | GuideScan | Pseudogene |
| RBMY2AP | RBMY2AP_3 | TACTTTCCTCTGTCTTTGTC | GuideScan | Pseudogene |
| RBMY2GP | RBMY2GP_1 | CTAAAAGAAACTTGTTTTTG | GuideScan | Pseudogene |
| RBMY2JP | RBMY2JP_1 | GACTGCGGTTGCATGCCAAG | GuideScan | Pseudogene |
| RBMY2JP | RBMY2JP_2 | CATGCGCATAAGTATCATTC | GuideScan | Pseudogene |
| RBMY2JP | RBMY2JP_3 | GGACCGTATTTCCCAAATAC | GuideScan | Pseudogene |
| RBMY2JP | RBMY2JP_4 | TGGTGAGTCCGTTACATTAA | GuideScan | Pseudogene |
| RBMY2OP | RBMY2OP_1 | CGTGTTTGGTCCCTTCATGT | GuideScan | Pseudogene |
| RBMY2OP | RBMY2OP_2 | ACACACGTTGTCTTCCAATA | GuideScan | Pseudogene |
| RBMY2OP | RBMY2OP_3 | ACAGTTCGTAACCAATAATG | GuideScan | Pseudogene |
| RBMY2OP | RBMY2OP_4 | ATAGCGGACATTAAAGCCTT | GuideScan | Pseudogene |
| RBMY2SP | RBMY2SP_1 | GACCGTGATGGCTACCAAGG | GuideScan | Pseudogene |
| RBMY2SP | RBMY2SP_2 | GAGCTATCGTATCCTTCATG | GuideScan | Pseudogene |

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|---|---|---|---|---|
| RBMY2SP | RBMY2SP_3 | CACTGGAGGACCACTACCCA | GuideScan | Pseudogene |
| RBMY2SP | RBMY2SP_4 | AATGACCGTGATGGCTACCA | GuideScan | Pseudogene |
| RBMY2TP | RBMY2TP_1 | GGGGAATCCTCTAGCAACAC | GuideScan | Pseudogene |
| RBMY2TP | RBMY2TP_2 | AGGGACTCGACTTCTTGAAG | GuideScan | Pseudogene |
| RBMY2TP | RBMY2TP_3 | GGTAAGGTATTTTCCTGAAG | GuideScan | Pseudogene |
| RBMY2TP | RBMY2TP_4 | CTAGGTACATTTCAGGTTTA | GuideScan | Pseudogene |
| RCC2P1 | RCC2P1_1 | TTCATGTCTTGGACCGCAGT | GuideScan | Pseudogene |
| RCC2P1 | RCC2P1_2 | TGACACGGGGTGGCTATTGC | GuideScan | Pseudogene |
| RCC2P1 | RCC2P1_3 | GCCTTGTATACCTTCTGCGC | GuideScan | Pseudogene |
| RCC2P1 | RCC2P1_4 | CTTCATGTCTTGGACCGCAG | GuideScan | Pseudogene |
| RCC2P2 | RCC2P2_1 | AGCCCTGAGTATGATTTGCT | GuideScan | Pseudogene |
| RCC2P2 | RCC2P2_2 | TGAAGCCTGTAAATTCGTGG | GuideScan | Pseudogene |
| RCC2P2 | RCC2P2_3 | ACAAACTTGAAGGGTCTACG | GuideScan | Pseudogene |
| RCC2P2 | RCC2P2_4 | GACACCCTCCACGAATTTAC | GuideScan | Pseudogene |
| RFTN1P1 | RFTN1P1_1 | CGTCTACATACCTTACTCGC | GuideScan | Pseudogene |
| RFTN1P1 | RFTN1P1_2 | GCCCCCATTCGAGAGCCGGT | GuideScan | Pseudogene |
| RFTN1P1 | RFTN1P1_3 | CCTAGTATTAAACTACGCTC | GuideScan | Pseudogene |
| RFTN1P1 | RFTN1P1_4 | CCCGACACTGCAGCATTAAA | GuideScan | Pseudogene |
| RN7SKP282 | RN7SKP282_1 | TCTGCCTGCCATTGATCACC | GuideScan | Pseudogene |
| RN7SKP282 | RN7SKP282_2 | ATCACATATATTAGCATCTA | GuideScan | Pseudogene |
| RN7SKP282 | RN7SKP282_3 | TTGACCGAACACGCAGCTTT | GuideScan | Pseudogene |
| RN7SKP282 | RN7SKP282_4 | CTGCCTGCCATTGATCACCA | GuideScan | Pseudogene |
| RNA18SP2 | RNA18SP2_1 | GCTTTGCAACCATACTCGCC | GuideScan | Pseudogene |

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|---|---|---|---|---|
| RNA18SP2 | RNA18SP2_2 | TCCATAGTTGAACCTGTCGA | GuideScan | Pseudogene |
| RNA18SP2 | RNA18SP2_3 | TCCCTCGACAGGTTCAACTA | GuideScan | Pseudogene |
| RNA18SP2 | RNA18SP2_4 | ACTAGATAACCTCAGGCCAA | GuideScan | Pseudogene |
| RNA5SP518 | RNA5SP518_1 | GTCAAGATCCCATGTGTTCA | GuideScan | Pseudogene |
| RNA5SP518 | RNA5SP518_2 | GCCATACCACCCTGAACACA | GuideScan | Pseudogene |
| RNA5SP518 | RNA5SP518_3 | AGTCAAGATCCCATGTGTTC | GuideScan | Pseudogene |
| RNA5SP518 | RNA5SP518_4 | TACAGCACTCAGTATTCACA | GuideScan | Pseudogene |
| RNA5SP519 | RNA5SP519_1 | GAGGCAAGCGGGTGCGTTCA | GuideScan | Pseudogene |
| RNA5SP519 | RNA5SP519_2 | AGAGGCAAGCGGGTGCGTTC | GuideScan | Pseudogene |
| RNA5SP519 | RNA5SP519_3 | CCAAGGTACCTGCTATTACC | GuideScan | Pseudogene |
| RNA5SP519 | RNA5SP519_4 | CCTGGTAATAGCAGGTACCT | GuideScan | Pseudogene |
| RNU6-1334P | RNU6-1334P_1 | TTTGAATACCCTCCTGGCCC | GuideScan | Pseudogene |
| RNU6-1334P | RNU6-1334P_2 | TTCACATTTGAATACCCTCC | GuideScan | Pseudogene |
| RNU6-1334P | RNU6-1334P_3 | AGAAGAATAACACTGTCCCT | GuideScan | Pseudogene |
| RNU6-1334P | RNU6-1334P_4 | AATAACACTGTCCCTGGGCC | GuideScan | Pseudogene |
| RNU6-255P | RNU6-255P_1 | TGCATTTTATTCTTGTGCAG | GuideScan | Pseudogene |
| RNU6-255P | RNU6-255P_2 | TTTGCATTTTATTCTTGTGC | GuideScan | Pseudogene |
| RNU6-255P | RNU6-255P_3 | TTGCATTTTATTCTTGTGCA | GuideScan | Pseudogene |
| RNU6-521P | RNU6-521P_1 | TGATGACAGGTAAATTCGTG | GuideScan | Pseudogene |
| RNU6-521P | RNU6-521P_2 | AAGGCCCATGCAATGATGAC | GuideScan | Pseudogene |
| RNU6-521P | RNU6-521P_3 | ATTTACCTGTCATCATTGCA | GuideScan | Pseudogene |
| RNU6-521P | RNU6-521P_4 | TTTACCTGTCATCATTGCAT | GuideScan | Pseudogene |
| RPS24P1 | RPS24P1_1 | TACCTAGGCCAAACCAAGCC | GuideScan | Pseudogene |

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|---|---|---|---|---|
| RPS24P1 | RPS24P1_2 | CACATAACGGGCCCCCACGG | GuideScan | Pseudogene |
| RPS24P1 | RPS24P1_3 | AACCGACTGAATGAATCTTC | GuideScan | Pseudogene |
| RPS24P1 | RPS24P1_4 | ATTCAGTCGGTTGTGCAAAA | GuideScan | Pseudogene |
| SNX3P1Y | SNX3P1Y_1 | TATGAGCAACGGGCAGACTG | GuideScan | Pseudogene |
| TBL1YP1 | TBL1YP1_1 | AATCGCGTGCACTGCTAATC | GuideScan | Pseudogene |
| TBL1YP1 | TBL1YP1_2 | ATCGCGTGCACTGCTAATCT | GuideScan | Pseudogene |
| TBL1YP1 | TBL1YP1_3 | GGGAACACTCCTATAACGCA | GuideScan | Pseudogene |
| TBL1YP1 | TBL1YP1_4 | ACGGTTTCTGCCGACTGCAC | GuideScan | Pseudogene |
| TOMM22P1 | TOMM22P1_1 | AGCAAGAACGAGTAACATAA | GuideScan | Pseudogene |
| TOMM22P1 | TOMM22P1_2 | CTGTGCAACTGAACCATCTC | GuideScan | Pseudogene |
| TOMM22P1 | TOMM22P1_3 | AAGAACGAGTAACATAAAGG | GuideScan | Pseudogene |
| TOMM22P1 | TOMM22P1_4 | AAGACCTAGATGAGACCCTG | GuideScan | Pseudogene |
| TOMM22P2 | TOMM22P2_1 | TCCAGCATTATAGTGCTGTA | GuideScan | Pseudogene |
| TOMM22P2 | TOMM22P2_2 | TCCTTACAGCACTATAATGC | GuideScan | Pseudogene |
| TOMM22P2 | TOMM22P2_3 | AGCATTATAGTGCTGTAAGG | GuideScan | Pseudogene |
| TOMM22P2 | TOMM22P2_4 | CCATAGCAGCCTTGTCAATT | GuideScan | Pseudogene |
| TRAPPC2P7 | TRAPPC2P7_1 | GTACGTACTGATATCAACAC | GuideScan | Pseudogene |
| TRAPPC2P7 | TRAPPC2P7_2 | ACATCTATTACAAGTCTGTC | GuideScan | Pseudogene |
| TRAPPC2P7 | TRAPPC2P7_3 | GACCAAATAGTCACTAAAGA | GuideScan | Pseudogene |
| TRAPPC2P7 | TRAPPC2P7_4 | TTCCATATCAGAGGTATCTC | GuideScan | Pseudogene |
| TRIM60P1Y | TRIM60P1Y_1 | CTGGGTTTATTATGGGCAAT | GuideScan | Pseudogene |
| TRIM60P1Y | TRIM60P1Y_2 | ACTACTTGCAGAAGGTGGGT | GuideScan | Pseudogene |
| TRIM60P1Y | TRIM60P1Y_3 | TGGGTTGGCATAGAACATGA | GuideScan | Pseudogene |

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|---|---|---|---|---|
| TRIM60P1Y | TRIM60P1Y_4 | GGCTGACAGACATTACTAGA | GuideScan | Pseudogene |
| TRIM60P2Y | TRIM60P2Y_1 | GAGGGCAGATGGTAAGCCTA | GuideScan | Pseudogene |
| TRIM60P2Y | TRIM60P2Y_2 | CAGATGGTAAGCCTATGGAA | GuideScan | Pseudogene |
| TRIM60P2Y | TRIM60P2Y_3 | ACATGTGTCAGCCATTCCAT | GuideScan | Pseudogene |
| TRIM60P2Y | TRIM60P2Y_4 | CATTTACTAAGGAGGGCAGA | GuideScan | Pseudogene |
| TRIM60P3Y | TRIM60P3Y_1 | GGGGTGCATACTATTTACAT | GuideScan | Pseudogene |
| TRIM60P3Y | TRIM60P3Y_2 | GACCAGGTCCTAAGAAAACC | GuideScan | Pseudogene |
| TRIM60P3Y | TRIM60P3Y_3 | TGGTCGATCTCCTGATCTCC | GuideScan | Pseudogene |
| TRIM60P3Y | TRIM60P3Y_4 | TTAGCCACTCCATGTTTGAC | GuideScan | Pseudogene |
| TSPY14P | TSPY14P_1 | GGCCCTTACGTAGGATCTAT | GuideScan | Pseudogene |
| TSPY14P | TSPY14P_2 | TTGGCATCGATGCGACTATT | GuideScan | Pseudogene |
| TSPY14P | TSPY14P_3 | TGGCATCGATGCGACTATTT | GuideScan | Pseudogene |
| TSPY14P | TSPY14P_4 | CCTCCGATAGATCCTACGTA | GuideScan | Pseudogene |
| TSPY18P | TSPY18P_1 | AACGTCTGATGCTCAGCATC | GuideScan | Pseudogene |
| TSPY20P | TSPY20P_1 | TAACTGCACGAGCGTGTCCT | GuideScan | Pseudogene |
| TSPY20P | TSPY20P_2 | AGGTCCGTAGGCGTCTCCCG | GuideScan | Pseudogene |
| TSPY20P | TSPY20P_3 | CGCCCCGGCTGGCAAAGGAC | GuideScan | Pseudogene |
| TSPY20P | TSPY20P_4 | ACACGCTCGTGCAGTTAGAA | GuideScan | Pseudogene |
| TSPY22P | TSPY22P_1 | TATCCCTACCTCGTGCCCGC | GuideScan | Pseudogene |
| TSPY22P | TSPY22P_2 | ATCCCTACCTCGTGCCCGCA | GuideScan | Pseudogene |
| TSPY22P | TSPY22P_3 | TCCCCTGCGGGCACGAGGTA | GuideScan | Pseudogene |
| TSPY22P | TSPY22P_4 | TCCAGCGAGTCCGTTGCCGG | GuideScan | Pseudogene |
| TSPY24P | TSPY24P_1 | TATCGCCTAGATCTTTGACC | GuideScan | Pseudogene |

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|---|---|---|---|---|
| TSPY24P | TSPY24P_2 | ACACCGGGAGCGTGGTTCCA | GuideScan | Pseudogene |
| TSPY24P | TSPY24P_3 | AAGACTTGGGTTCACGGTGC | GuideScan | Pseudogene |
| TSPY24P | TSPY24P_4 | CGTTGCGTGCTGGGGCATAA | GuideScan | Pseudogene |
| TSPY25P | TSPY25P_1 | ACAAATCCGTCAAGTAGCTT | GuideScan | Pseudogene |
| TSPY25P | TSPY25P_2 | TTGAGGTCGCTCTGGGGCCG | GuideScan | Pseudogene |
| TSPY25P | TSPY25P_3 | CGTCTTTGGGTGCAGTGCCG | GuideScan | Pseudogene |
| TSPY25P | TSPY25P_4 | GGGTGGGCTTGTACACACGA | GuideScan | Pseudogene |
| TTTY24P | TTTY24P_1 | TATCCTGGAGACGATGTACG | GuideScan | Pseudogene |
| TTTY24P | TTTY24P_2 | GTTACAGTTATCATTTAGCC | GuideScan | Pseudogene |
| TTTY24P | TTTY24P_3 | GTATCCTGGAGACGATGTAC | GuideScan | Pseudogene |
| TTTY24P | TTTY24P_4 | GCACTGGAATGGGGTATCAT | GuideScan | Pseudogene |
| TTTY25P | TTTY25P_1 | GTGTTCAGTCGGTACATTCA | GuideScan | Pseudogene |
| TTTY25P | TTTY25P_2 | TGTGTTCAGTCGGTACATTC | GuideScan | Pseudogene |
| TTTY25P | TTTY25P_3 | CAGTTCCAGTACTGCATGTG | GuideScan | Pseudogene |
| TTTY25P | TTTY25P_4 | AATGTACCGACTGAACACAC | GuideScan | Pseudogene |
| TTTY30P | TTTY30P_1 | CAATGGAGCCTGCGTTACTT | GuideScan | Pseudogene |
| TTTY30P | TTTY30P_2 | AATGGAGCCTGCGTTACTTT | GuideScan | Pseudogene |
| TTTY30P | TTTY30P_3 | AGCGAATCCCAAAGTAACGC | GuideScan | Pseudogene |
| TTTY30P | TTTY30P_4 | TACAGACCTGCGCTGTCTTG | GuideScan | Pseudogene |
| TTTY31P | TTTY31P_1 | TTACCGACCCGCACCCTCCT | GuideScan | Pseudogene |
| TTTY31P | TTTY31P_2 | CTTACCGACCCGCACCCTCC | GuideScan | Pseudogene |
| TTTY31P | TTTY31P_3 | TACCAGGTGTACTCTCCTTC | GuideScan | Pseudogene |
| TTTY31P | TTTY31P_4 | TACCGACCCGCACCCTCCTG | GuideScan | Pseudogene |

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|---|---|---|---|---|
| USP12PY | USP12PY_1 | GTCATCGCCGCCGGTCCCTC | GuideScan | Pseudogene |
| USP12PY | USP12PY_2 | TGAGGGACCGGCGGCGATGA | GuideScan | Pseudogene |
| USP12PY | USP12PY_3 | CTAGGCCCGGGAGTACCTGA | GuideScan | Pseudogene |
| USP12PY | USP12PY_4 | GCCGGTCCCTCAGGTACTCC | GuideScan | Pseudogene |
| USP9YP20 | USP9YP20_1 | ATGGTGCTTTGTAGCCCACC | GuideScan | Pseudogene |
| USP9YP20 | USP9YP20_2 | TGGTGCTTTGTAGCCCACCT | GuideScan | Pseudogene |
| USP9YP22 | USP9YP22_1 | TCACCAAACACCATCAATTC | GuideScan | Pseudogene |
| USP9YP28 | USP9YP28_1 | TGGGCAGGGGGAAGCCCCAA | GuideScan | Pseudogene |
| USP9YP29 | USP9YP29_1 | TATGGTGCTTTGTAGCCACC | GuideScan | Pseudogene |
| USP9YP29 | USP9YP29_2 | ATGGTGCTTTGTAGCCACCT | GuideScan | Pseudogene |
| USP9YP3 | USP9YP3_1 | AGAGCAGGTGGTTCTAGCGT | GuideScan | Pseudogene |
| USP9YP3 | USP9YP3_2 | GGAGACGGTTACGGGTCATA | GuideScan | Pseudogene |
| USP9YP3 | USP9YP3_3 | ATAATCACGTATGTATGACA | GuideScan | Pseudogene |
| USP9YP3 | USP9YP3_4 | TAGTGGTGGACTGCATATGT | GuideScan | Pseudogene |
| USP9YP4 | USP9YP4_1 | TTTAGACAGCCAATAACTCG | GuideScan | Pseudogene |
| USP9YP4 | USP9YP4_2 | TCACACGCTACGATCAATGC | GuideScan | Pseudogene |
| USP9YP4 | USP9YP4_3 | CACTAATGTCTTCCGGTCTC | GuideScan | Pseudogene |
| USP9YP4 | USP9YP4_4 | CCCGTACCTTTGTGCTTGTT | GuideScan | Pseudogene |
| USP9YP8 | USP9YP8_1 | GGGGATCAGGTATAGCTGCT | GuideScan | Pseudogene |
| USP9YP8 | USP9YP8_2 | ACGCCCACCAAAAAGATTTG | GuideScan | Pseudogene |
| USP9YP8 | USP9YP8_3 | GTGGGAATATCAGCTCCTGC | GuideScan | Pseudogene |
| USP9YP8 | USP9YP8_4 | TTTGGTGGGCGTGGTCCAGC | GuideScan | Pseudogene |
| XGY1 | XGY1_1 | ACACGGTCAACTACTACCGC | GuideScan | Pseudogene |

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|---|---|---|---|---|
| XGY1 | XGY1_2 | TGATTTGTCCATCCGTTGGC | GuideScan | Pseudogene |
| XGY1 | XGY1_3 | GAAGCTCCAAATGCAGCATA | GuideScan | Pseudogene |
| XGY1 | XGY1_4 | GTGCTCAGGCGGCCATATGC | GuideScan | Pseudogene |
| XKRYP3 | XKRYP3_1 | AAAATATATGATTAATAGTA | GuideScan | Pseudogene |
| ZNF736P10Y | ZNF736P10Y_1 | GTCAGTAAAGTTTGTGGAGC | GuideScan | Pseudogene |
| ZNF736P10Y | ZNF736P10Y_2 | CACTGAGGATTGAGCACACC | GuideScan | Pseudogene |
| ZNF736P10Y | ZNF736P10Y_3 | GTCTGTGCATTCTCTTACAA | GuideScan | Pseudogene |
| ZNF736P10Y | ZNF736P10Y_4 | AAAGTTTGTGGAGCAGGTAA | GuideScan | Pseudogene |
| ZNF884P | ZNF884P_1 | TCGACCCTTACACAGCATTT | GuideScan | Pseudogene |
| ZNF884P | ZNF884P_2 | TTCGACCCTTACACAGCATT | GuideScan | Pseudogene |
| ZNF884P | ZNF884P_3 | TGCAGGATATCTCTCCAAAA | GuideScan | Pseudogene |
| ZNF884P | ZNF884P_4 | CGCTACATATATAAGAAATG | GuideScan | Pseudogene |
| ZNF885P | ZNF885P_1 | TGCTGCAAATTTACAGAACG | GuideScan | Pseudogene |
| ZNF885P | ZNF885P_2 | GGTGTACTATGCATTCTCTG | GuideScan | Pseudogene |
| ZNF885P | ZNF885P_3 | ATCATGTAAGGTGAGCATAC | GuideScan | Pseudogene |
| ZNF885P | ZNF885P_4 | AGATTCTCTGACATCATGTA | GuideScan | Pseudogene |
| ZNF886P | ZNF886P_1 | AGTAATATATAAGCCCCTGT | GuideScan | Pseudogene |
| ZNF886P | ZNF886P_2 | GTGTGGCAAAGTCTCCAACA | GuideScan | Pseudogene |
| ZNF886P | ZNF886P_3 | CAACATCAAATACTCTCTCC | GuideScan | Pseudogene |
| ZNF886P | ZNF886P_4 | AATTTAACAACACTCTCAAC | GuideScan | Pseudogene |
| ZNF92P1Y | ZNF92P1Y_1 | GCCATATTTATTAGGTTGGC | GuideScan | Pseudogene |
| ZNF92P1Y | ZNF92P1Y_2 | TAGGTTGGCAGGTTTTGCTG | GuideScan | Pseudogene |
| ZNF92P1Y | ZNF92P1Y_3 | AAGTTCTGAGAACTATCGAT | GuideScan | Pseudogene |

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|---|---|---|---|---|
| ZNF92P1Y | ZNF92P1Y_4 | GGCTTTTTTATGTTCAGTGA | GuideScan | Pseudogene |
| COPB1 | COPB1_1 | GTGATAGTGTGATCCTGAAG | Provided | positive_controls |
| COPB1 | COPB1_2 | GTAACCAGAAACCATGACGG | Provided | positive_controls |
| COPB1 | COPB1_3 | GGAAGGAATCCTCTCAAGGG | Provided | positive_controls |
| COPB1 | COPB1_4 | GTCTAGACCCACCAAGAAAG | Provided | positive_controls |
| EEF2 | EEF2_1 | GCAGGGTGAAGGCCCACCCG | Provided | positive_controls |
| EEF2 | EEF2_2 | GCTGCAGCTCCAGCAGGGCG | Provided | positive_controls |
| EEF2 | EEF2_3 | GGAGGACATCGATAAAGGCG | Provided | positive_controls |
| EEF2 | EEF2_4 | GGCGAGGACAAGGACAAAGA | Provided | positive_controls |
| EIF5B | EIF5B_1 | GGAAAGACAGAAGAGAGAAG | Provided | positive_controls |
| EIF5B | EIF5B_2 | GTTCTTTATAAGCCACAAGG | Provided | positive_controls |
| EIF5B | EIF5B_3 | GGAAGCCAAGCGTAAAGAAG | Provided | positive_controls |
| EIF5B | EIF5B_4 | GAGACTCTTTGCCAAAGAAG | Provided | positive_controls |
| HEATR1 | HEATR1_1 | GATGGTGGCAAAATACCCAA | Provided | positive_controls |
| HEATR1 | HEATR1_2 | GGATGGCTCACCAATGGCGA | Provided | positive_controls |
| HEATR1 | HEATR1_3 | GCACAGTTCAGCAAAAAAGA | Provided | positive_controls |
| HEATR1 | HEATR1_4 | GCAGCGTAAGAAAAAGGAAG | Provided | positive_controls |
| LSM3 | LSM3_1 | GCACATAAATTCGCTCATCT | Provided | positive_controls |
| LSM3 | LSM3_2 | GGAAATGACCGAGAGCTTCG | Provided | positive_controls |
| LSM3 | LSM3_3 | GATGGCGGACGACGTAGACC | Provided | positive_controls |
| LSM3 | LSM3_4 | GTCTCTTCTAGTCAACGAAA | Provided | positive_controls |
| PRPF19 | PRPF19_1 | GTAGTAACCATTCTCAGAGA | Provided | positive_controls |
| PRPF19 | PRPF19_2 | GTAATCATGTTTATGAGCGG | Provided | positive_controls |

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|---|---|---|---|---|
| PRPF19 | PRPF19_3 | GCTCAGCAAATACCGGCAGG | Provided | positive_controls |
| PRPF19 | PRPF19_4 | GAGACGGGCAATGACACGGC | Provided | positive_controls |
| PSMB2 | PSMB2_1 | GTGATTCGAACACTGAAGGT | Provided | positive_controls |
| PSMB2 | PSMB2_2 | GTACCTGGCAGCCTTGGCCA | Provided | positive_controls |
| PSMB2 | PSMB2_3 | GGTGAAGTTAGCTGCTGCCG | Provided | positive_controls |
| PSMB2 | PSMB2_4 | GATCTGGACAATATTGCTGG | Provided | positive_controls |
| PSMB3 | PSMB3_1 | GCCGTACATTTGTTCGGCGC | Provided | positive_controls |
| PSMB3 | PSMB3_2 | GTTCAGCATGGCTTGGGAGA | Provided | positive_controls |
| PSMB3 | PSMB3_3 | GAAGCGCCTGTCTGCAGCGA | Provided | positive_controls |
| PSMB3 | PSMB3_4 | GTCACCGTTTCTCATACAAG | Provided | positive_controls |
| PSMD1 | PSMD1_1 | GTACAGATGACAAAAACTGC | Provided | positive_controls |
| PSMD1 | PSMD1_2 | GGTACCAAAAGAAAAAGAAA | Provided | positive_controls |
| PSMD1 | PSMD1_3 | GCCAGAGCCACAATAAGCCA | Provided | positive_controls |
| PSMD1 | PSMD1_4 | GCAAGGACGCCAACCACAGA | Provided | positive_controls |
| RBM17 | RBM17_1 | GGCAGCTCTCACTCAGGCAA | Provided | positive_controls |
| RBM17 | RBM17_2 | GAAGACAGACATGAAGCAAG | Provided | positive_controls |
| RBM17 | RBM17_3 | GCAGTCATTGACCTGAAGCG | Provided | positive_controls |
| RBM17 | RBM17_4 | GTCTCCTGCCAGGGGCACGG | Provided | positive_controls |
| RPL10 | RPL10_1 | GGCCCTTTCACTTCAGAAAC | Provided | positive_controls |
| RPL10 | RPL10_2 | GGTTTGCTGCCTCATGAGCA | Provided | positive_controls |
| RPL10 | RPL10_3 | GATGACCCAAAGGTTCCCAG | Provided | positive_controls |
| RPL10 | RPL10_4 | GTGTATCTACATTCTTGACG | Provided | positive_controls |
| RPL10A | RPL10A_1 | GGCCGTGGATATCCCCCACA | Provided | positive_controls |

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|---|---|---|---|---|
| RPL10A | RPL10A_2 | GCCCACTCACCTTCTTCATT | Provided | positive_controls |
| RPL10A | RPL10A_3 | GTCCTCCCAGGTGTTATGTC | Provided | positive_controls |
| RPL10A | RPL10A_4 | GCGCGACACCCTGTACGAGG | Provided | positive_controls |
| RPL11 | RPL11_1 | GGGCCCCTCGAACTGTGCAG | Provided | positive_controls |
| RPL11 | RPL11_2 | GTGAAAAGGAGAACCCCATG | Provided | positive_controls |
| RPL11 | RPL11_3 | GTCACCTTTGGAAAACACAG | Provided | positive_controls |
| RPL11 | RPL11_4 | GTCAAATATGACCCAAGCAT | Provided | positive_controls |
| RPL37 | RPL37_1 | GGGCCTTAGAGCCACAGCGG | Provided | positive_controls |
| RPL37 | RPL37_2 | GCGAAGGGAACGTCATCGTT | Provided | positive_controls |
| RPL37 | RPL37_3 | GTGACATTCTTAAGATGAAC | Provided | positive_controls |
| RPL37 | RPL37_4 | GGCAGGCATGGATTCCGTGA | Provided | positive_controls |
| RPL4 | RPL4_1 | GTTGCAGCACAAGCTCCGGG | Provided | positive_controls |
| RPL4 | RPL4_2 | GAAGAGCCCTTCGAGCACCA | Provided | positive_controls |
| RPL4 | RPL4_3 | GCTTTATCTTCAACTACCAA | Provided | positive_controls |
| RPL4 | RPL4_4 | GAAATCAGATGAGAAGGCGG | Provided | positive_controls |
| RRM1 | RRM1_1 | GATTGAAAGATCTTACCGAG | Provided | positive_controls |
| RRM1 | RRM1_2 | GTTCCCCAGGATCTGAGCAG | Provided | positive_controls |
| RRM1 | RRM1_3 | GGAGTACACCAGCAAAGATG | Provided | positive_controls |
| RRM1 | RRM1_4 | GTTCTCCAAAGAGCACACCA | Provided | positive_controls |
| RUVBL2 | RUVBL2_1 | GATCACCATCGACAAGGCGA | Provided | positive_controls |
| RUVBL2 | RUVBL2_2 | GCTCCAGAAACGCAAGGAGG | Provided | positive_controls |
| RUVBL2 | RUVBL2_3 | GGCTGACGCAGGCCTTCCGG | Provided | positive_controls |
| RUVBL2 | RUVBL2_4 | GTGATCATGGCCACCAACCG | Provided | positive_controls |

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| WDR5 | WDR5_1 | GAGACAATAAGGTTGGACTG | Provided | positive_controls |
| WDR5 | WDR5_2 | GCCAATTTCTCTGTTACTGG | Provided | positive_controls |
| WDR5 | WDR5_3 | GACTCACTTGTCCAGCGTGG | Provided | positive_controls |
| WDR5 | WDR5_4 | GATCTGAGGCAGAAACAAGA | Provided | positive_controls |
| AAVS1_chr19 | AAVS1_chr19_1 | GGGGACTCTTTAAGGAAAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_2 | GCCCCGTCGTTCCTGGCCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_3 | GGAATTGGAGCCGCTTCAAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_4 | GGCTTTCTGTCTGCAGCTTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_5 | GATGATGCAGGCCTACAAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_6 | GCATCCTAAGAAACGAGAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_7 | GCGTGGGTTTATCAACCACT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_8 | GCCCGGCGTCTCCCGGGGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_9 | GTTGAGTCCTTGGCAAGCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_10 | GCAGCCCCAGGTGGAGAAAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_11 | GTTCCGGAGCACTTCCTTCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_12 | GATCAACCACTTGGTGAGGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_13 | GCCCGGAGGAGGCCCTCATC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_14 | GCTCCAATGCGGAAGAGAGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_15 | GGCCTCTCCTGGGCTTGCCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_16 | GCTAGCCACTAAGGCAATTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_17 | GCTCAAAGTGGTCCGGACTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_18 | GGACCCAATATCAGGAGACT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_19 | GGACCACCCCACTTCCGAAT | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_20 | GGGATCTCCCGGTCCCCGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_21 | GAAAAGGCAGCCTGGTAGAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_22 | GTGGAGTCCATTAGCAGAAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_23 | GGATCCTGTGTCCCCGAGCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_24 | GCCGTGTCTGGGTCCTCTCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_25 | GTTAGGATGGCCTTCTCCGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_26 | GGCAGCTCCGAGGCGCCCAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_27 | GAGTGACAATGGCCAGGGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_28 | GCATTAGCAGAAGTGGCCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_29 | GCACCGCCCCAAGGATCTCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_30 | GATTCCCTTCTCAGGTTACG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_31 | GTGTGAGAATGGTGCGTCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_32 | GATAAGGTGGTCCCAGCTCG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_33 | GGCGGCACAGCAAGGGCACT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_34 | GAGAAAAACGGTGATGATGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_35 | GAGCCGCTTCAACTGGCCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_36 | GTCCTTGGCAAGCCCAGGAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_37 | GGTGGGGTACCCTAAGAACT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_38 | GGGACCACCTTATATTCCCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_39 | GCCCACTGTTTCCCCTTCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_40 | GTGGGAAGTCCGCAGCTCCG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_41 | GTCCGGACTCAGGAGAGAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_42 | GTGCGTCCTAGGTGTTCACC | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_43 | GCCCTAGCCACTAAGGCAAT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_44 | GCTAGGTGTTCACCAGGTCG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_45 | GCTCGGGGACACAGGATCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_46 | GGTGACACACCCCCATTTCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_47 | GCGACCTGCCCAGCACACCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_48 | GCCCTAGTGGCCCCACTGTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_49 | GGGAACCCAGCGAGTGAAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_50 | GATCCACCCAAAAGGCAGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_51 | GCCCAGGGCCAGGAACGACG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_52 | GAGAGGTGACCCGAATCCAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_53 | GCCAGCCGTAGAGGTGACCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_54 | GGACGTCACGGCGCTGCCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_55 | GCACCCTCTGCTGCGCCACC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_56 | GAAAGTCCAGGACCGGCTGG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_57 | GCTGGCCCCCCACCGCCCCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_58 | GGACCTGCATTCTCTCCCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_59 | GAGTTCCTGGCGGCCTGTGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_60 | GCAGACTGAGCTATGGGAGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_61 | GTGGACTCCACCAACGCCGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_62 | GGGGGAGCTGCCCAAATGAA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_63 | GAAGCCCAGGAGAGGCGCTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_64 | GCTGATACCGTCGGCGTTGG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_65 | GGTCCCTAGTGGCCCCACTG | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_66 | GAGTAGAGGCGGCCACGACC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_67 | GAACCTTAGAGGTTCTGGCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_68 | GGCTTGGCAAACTCACTCTT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_69 | GGAACCAGAGCCACATTAAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_70 | GAGATGGCACAGGCCCCAGA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_71 | GCCTTTTCCTTCTCCTTCTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_72 | GCCAGGCCAAGTAGGTGGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_73 | GAGTCTTCTTCCTCCAACCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_74 | GGAGTCGCTTTAACTGGCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_75 | GTGGTTGATAAACCCACGTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_76 | GTTCTTAGGGTACCCCACGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_77 | GGCGCTGATACCGTCGGCGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_78 | GTCACTCTTCGGGGTATCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_79 | GCAGCTCCCATAGCTCAGTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_80 | GCAGAGTGGTCAGCACAGAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_81 | GTTGGGAACAGCCACAGCAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_82 | GGCACAGGCCGCCAGGAACT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_83 | GGCCGCCCGCACAGGCCGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_84 | GCAGAGCCAGGAACCCCTGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_85 | GAGCGGCTCCAATTCGGAAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_86 | GCAGGGTGGCCACTGAGAAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_87 | GTGCAGACAGAAAGCGGCAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_88 | GCTTCCTTACACTTCCCAAG | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_89 | GCCTGCCTGGAGAAGGATGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_90 | GACCTGGCCCCGGGAGACGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_91 | GCGCGCCGCCGAGTTCCTGG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_92 | GAGGGGCTCAACATCGGAAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_93 | GCCCCGCCCGGCGTCTCCCG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_94 | GTGTCCTGAAGTGGACATAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_95 | GGGGCCCCTATGTCCACTTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_96 | GGACAAAGTCCAGGACCGGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_97 | GGCGGATCCTCCCCGTGTCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_98 | GAGCTGAGCTCTCGGACCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_99 | GGCTCCGGAAAGAGCATCCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_100 | GTCCCGCCTCCCCTTCTTGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_101 | GTACCAGGCTGCCTTTTGGG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_102 | GCAAGGGCCACTTCTGCTAA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_103 | GTCTCCTGCCCCTTCCCTAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_104 | GAAGCCCAGAGCAGGGCCTT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_105 | GCAGAAAGCGGCACAGGCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_106 | GAGTTGAAGCGGCTCCAATT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_107 | GAGCATGTTTGCTGCCTCCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_108 | GCCCGGAGAGGACCCAGACA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_109 | GGCGCAAAGTGACAATGGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_110 | GGTTTATCAACCACTTGGTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_111 | GCCGCTCAGAGGACATCACG | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_112 | GGATGCAGGCCTACAAGAAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_113 | GCAGGTCAGCGCCCCCCGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_114 | GCCCAAATGAAAGGAGTGAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_115 | GAGTTAAAGCGACTCCAATG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_116 | GCTGTTTCCCCTTCCCAGGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_117 | GAGTAGAGCTCAAAGTGGTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_118 | GCAGTCTGAAGAGCAGAGCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_119 | GCACGACCTGGTGAACACCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_120 | GTCACCAATCCTGTCCCTAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_121 | GGGGCTCAACATCGGAAGAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_122 | GCCCTCTGCTGCGCCACCTG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_123 | GCCGAATCCACAGGAGAACG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_124 | GTTGGCAAACTCACTCTTCG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_125 | GCTGCCAAGCTCTCCCTCCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_126 | GCCCCACAGTGGGGCCACTA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_127 | GGACTCCTGGAAGTGGCCAA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_128 | GAATGCAGGTCAGAGAAAGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_129 | GACGCAAGGGAGACATCCGT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_130 | GCTCTTCGGGGTATCCCAGG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_131 | GCCTGCATCCTTCTCCAGGC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_132 | GACAGAAAAGCCCCATCCTT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_133 | GGCTTACGATGGAGCCAGAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_134 | GCAACTGTGGGGTGACTGCT | Provided | AAVS1 |

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| AAVS1_chr19 | AAVS1_chr19_135 | GGCCGTCTCTCTCCTGAGTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_136 | GATATAAGGTGGTCCCAGCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_137 | GGTCAGAGCAGCTCAGGTTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_138 | GGAGCGCGCCGCCGAGTTCC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_139 | GAGAAGACTAGCTGAGCTCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_140 | GTCCCTCCCAGGATCCTCTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_141 | GCCCTGGAAGATGCCATGAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_142 | GTTCCCTAAGGCCCTGCTCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_143 | GCCCAACCCCCTAGCCACTA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_144 | GCTCCTTGCCAGAACCTCTA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_145 | GCATGCCGTCTTCACTCGCT | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_146 | GGAGGAGGGATTCCCTTCTC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_147 | GGGTCCCAGCTCGGGGACAC | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_148 | GCCAGCGAGTGAAGACGGCA | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_149 | GTGCACCCCAATTGCCTTAG | Provided | AAVS1 |
| AAVS1_chr19 | AAVS1_chr19_150 | GGCCAGATGAGGGCCTCCTC | Provided | AAVS1 |
| non_specific | Zhang_886 | GAACGAGATCGAGAAAGGTA | Provided | non_specific |
| non_specific | Zhang_852 | GTGGCTTATTAGCTATAAAG | Provided | non_specific |
| non_specific | Zhang_959 | GAGAGACAATGACATGTAGA | Provided | non_specific |
| non_specific | Zhang_40 | GCATAGTCGACGGCTCGATT | Provided | non_specific |
| non_specific | Zhang_832 | GCAGAGCCTTGGTTTATATC | Provided | non_specific |
| non_specific | CTRL0082 | GCGGATCCAGATCTCATTCG | Provided | non_specific |
| non_specific | Zhang_887 | GTCTGCCATGGCGTCCTGGC | Provided | non_specific |

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| non_specific | Zhang_431 | GACTTTTTGGAATCCGTCTA | Provided | non_specific |
| non_specific | Zhang_365 | GGGTCGGCCGAACATACGGT | Provided | non_specific |
| non_specific | Zhang_166 | GTATATTGTCGCGCAGTGGA | Provided | non_specific |
| non_specific | CTRL0054 | GCCGCAATATATGCGGTAAG | Provided | non_specific |
| non_specific | Zhang_78 | GCGCGGACATAGGGCTCTAA | Provided | non_specific |
| non_specific | Zhang_17 | GAACGGGTTCTCCCGGCTAC | Provided | non_specific |
| non_specific | Zhang_603 | GGCTGGTTGACCTTCCCGCT | Provided | non_specific |
| non_specific | Zhang_265 | GTACGAGGCGCTTTTCTTTG | Provided | non_specific |
| non_specific | Zhang_856 | GTGATATCTGACATGCAGCG | Provided | non_specific |
| non_specific | Zhang_268 | GATACTGCGGATCAATCTGA | Provided | non_specific |
| non_specific | Zhang_85 | GCTGGCTTGACACGACCGTT | Provided | non_specific |
| non_specific | Zhang_333 | GCCCGTAGCTCATTAGTCTG | Provided | non_specific |
| non_specific | Zhang_501 | GGTCTTGGCCAATGTCACGG | Provided | non_specific |
| non_specific | CTRL0009 | GATCCATGTAATGCGTTCGA | Provided | non_specific |
| non_specific | Zhang_577 | GATGAGCGCATTGAATAATA | Provided | non_specific |
| non_specific | Zhang_156 | GAGAGATATCCGATCGTGGT | Provided | non_specific |
| non_specific | Zhang_432 | GAGCGGTGCTATTTGGTCTT | Provided | non_specific |
| non_specific | Zhang_130 | GAACGCGCATATCTGAACAC | Provided | non_specific |
| non_specific | Zhang_330 | GTTGGGTTTATCCGCCCCCA | Provided | non_specific |
| non_specific | CTRL0007 | GATACACGAAGCATCACTAG | Provided | non_specific |
| non_specific | Zhang_374 | GATTGCACGCCACAGCATTG | Provided | non_specific |
| non_specific | Zhang_247 | GTATGTGAGCACGCCATTAC | Provided | non_specific |
| non_specific | Zhang_651 | GAAAAGTCTCGCTTGGTCCT | Provided | non_specific |

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| non_specific | Zhang_120 | GCAAACCCGAGTGACACGTC | Provided | non_specific |
| non_specific | CTRL0095 | GTACTCCAATCCGCGATGAC | Provided | non_specific |
| non_specific | Zhang_514 | GCACTGGTAAAGGCTAGACT | Provided | non_specific |
| non_specific | Zhang_905 | GGTACCCCTAGGTATGGGGA | Provided | non_specific |
| non_specific | Zhang_159 | GGATTGAATGGCTAACGCGG | Provided | non_specific |
| non_specific | Zhang_380 | GCATAGCTCTAGCGATAAAC | Provided | non_specific |
| non_specific | Zhang_634 | GGAAGTCTTTCTTAGATGGT | Provided | non_specific |
| non_specific | Zhang_77 | GTAGACGTCGTGAGCTTCAC | Provided | non_specific |
| non_specific | Zhang_705 | GATTAGCAGCCCAGCGCCCA | Provided | non_specific |
| non_specific | Zhang_404 | GCACCTCCGAACGAACACCT | Provided | non_specific |
| non_specific | CTRL0052 | GTACGGCACTCCTAGCCGCT | Provided | non_specific |
| non_specific | Zhang_24 | GTATCTCGAGTGGTAATGCG | Provided | non_specific |
| non_specific | CTRL0013 | GAAGTGACGTCGATTCGATA | Provided | non_specific |
| non_specific | Zhang_561 | GGCCACAAAAACTCGCTAAG | Provided | non_specific |
| non_specific | Zhang_556 | GGGAGTTAACCTGGAACCTT | Provided | non_specific |
| non_specific | Zhang_931 | GAAATTCAGACCACAGCTAA | Provided | non_specific |
| non_specific | Zhang_277 | GCTGTTGCCGCGCCAACTGC | Provided | non_specific |
| non_specific | Zhang_327 | GCCGTGGTATCAAGTCGGTA | Provided | non_specific |
| non_specific | Zhang_57 | GCGCTATTGAAACCGCCCAC | Provided | non_specific |
| non_specific | Zhang_480 | GCTGCTCCCGGTCGCCCCTC | Provided | non_specific |
| non_specific | Zhang_18 | GAGGAGTCGCCGATACGCGT | Provided | non_specific |
| non_specific | Zhang_565 | GCTAAGGGGTACCACCATGG | Provided | non_specific |
| non_specific | Zhang_828 | GTTATTACTCCAGTATAAGA | Provided | non_specific |

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|---|---|---|---|---|
| non_specific | Zhang_111 | GAACGCCGCTCAAGTTGATA | Provided | non_specific |
| non_specific | Zhang_335 | GACGCCCTAATGCCCATCGT | Provided | non_specific |
| non_specific | Zhang_630 | GCAATTCTCACTCACGACCA | Provided | non_specific |
| non_specific | Zhang_93 | GGCGGCGTAATGCTTGAAAG | Provided | non_specific |
| non_specific | Zhang_411 | GCGGCTACAATCTTTGGCAT | Provided | non_specific |
| non_specific | Zhang_2 | GGCTTCCGCGGCCCGTTCAA | Provided | non_specific |
| non_specific | Zhang_892 | GACCTTCATTGAAGAAAAGC | Provided | non_specific |
| non_specific | Zhang_216 | GGTTTCACTTCGAGACCGGC | Provided | non_specific |
| non_specific | Zhang_184 | GAAACATCGACCGAAAGCGT | Provided | non_specific |
| non_specific | Zhang_118 | GTCTCGGGTCGACTGCGGAT | Provided | non_specific |
| non_specific | Zhang_110 | GTTGTTGCGTATACGAGACT | Provided | non_specific |
| non_specific | Zhang_416 | GGAGCGGCCTCTAATTAATC | Provided | non_specific |
| non_specific | CTRL0051 | GTCAGCCATCGGATAGAGAT | Provided | non_specific |
| non_specific | Zhang_470 | GCCAGGGTATGGGCATCTCG | Provided | non_specific |
| non_specific | Zhang_13 | GCGTGCGTCCCGGGTTACCC | Provided | non_specific |
| non_specific | Zhang_357 | GCCAACAAGAATCGGATCCC | Provided | non_specific |
| non_specific | Zhang_336 | GGATATTGAGTAAACCCGAT | Provided | non_specific |
| non_specific | Zhang_462 | GTTGCTCTGTCGCATCAATC | Provided | non_specific |
| non_specific | Zhang_202 | GGAGCATTCGTAGCCCAGCA | Provided | non_specific |
| non_specific | Zhang_755 | GGAATCCGGAGCTCATGAGG | Provided | non_specific |
| non_specific | Zhang_233 | GATCAATCGTCCGGGTCACT | Provided | non_specific |
| non_specific | Zhang_557 | GGCGCTCTGGTTGCATCCCT | Provided | non_specific |
| non_specific | Zhang_82 | GCGTCCATACTGTCGGCTAC | Provided | non_specific |

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| non_specific | Zhang_531 | GAGCGGGCACACATGACAAG | Provided | non_specific |
| non_specific | Zhang_690 | GCCCTCCTAGTCAAGAAGAG | Provided | non_specific |
| non_specific | Zhang_937 | GCAGCGAGATAACTTGACTC | Provided | non_specific |
| non_specific | Zhang_98 | GTACGGGGCGATCATCCACA | Provided | non_specific |
| non_specific | Zhang_407 | GAACTGGCAAACAGGCGTGG | Provided | non_specific |
| non_specific | CTRL0084 | GTCATCATTATGGCGTAAGG | Provided | non_specific |
| non_specific | Zhang_951 | GGTGTGGAAAAGCTAACAGA | Provided | non_specific |
| non_specific | Zhang_299 | GATATCCCGCGAAAAAATCT | Provided | non_specific |
| non_specific | Zhang_197 | GGTTAAGACTAGCTCGGTTT | Provided | non_specific |
| non_specific | Zhang_665 | GCAGTGCCCTTTTGTCGCAA | Provided | non_specific |
| non_specific | Zhang_347 | GGCTGGTTGACGACTCCTGA | Provided | non_specific |
| non_specific | Zhang_660 | GGGCTTAAATGGCGAGATTG | Provided | non_specific |
| non_specific | Zhang_456 | GGAGCAAAGATTGTTGGATA | Provided | non_specific |
| non_specific | Zhang_942 | GCAAGGTCATGAAACCAAGC | Provided | non_specific |
| non_specific | Zhang_737 | GTTTAGTAATGCACACCCAG | Provided | non_specific |
| non_specific | CTRL0001 | GTAGCGAACGTGTCCGGCGT | Provided | non_specific |
| non_specific | CTRL0079 | GTAGCGAAGACTTGCCGACG | Provided | non_specific |
| non_specific | Zhang_793 | GTTTTCGAAAGCTTAGGCCA | Provided | non_specific |
| non_specific | Zhang_507 | GTTACGAAGTATACCAGGTC | Provided | non_specific |
| non_specific | Zhang_224 | GGTCATTAGCGTAACGATAT | Provided | non_specific |
| non_specific | Zhang_545 | GAAAAGCTTCCGCCTGATGG | Provided | non_specific |
| non_specific | Zhang_37 | GGTGGCCGGAACCGTCATAG | Provided | non_specific |
| non_specific | Zhang_524 | GTCAAGTCAGGTTATGCGGG | Provided | non_specific |

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| non_specific | Zhang_649 | GTCAGCGAGTGTGACTAAGC | Provided | non_specific |
| non_specific | Zhang_25 | GATCGACTCGAACTTCGTGT | Provided | non_specific |
| non_specific | Zhang_398 | GAGGCTGCGCTTCGCAAGCT | Provided | non_specific |
| non_specific | Zhang_67 | GACTAGCCCGAGCAGCTTCG | Provided | non_specific |
| non_specific | Zhang_80 | GTTCGCTTCGTAACGAGGAA | Provided | non_specific |
| non_specific | Zhang_293 | GTCCCATTGATCTACGATGG | Provided | non_specific |
| non_specific | CTRL0080 | GTCGGCGTTCTGTTGTGACT | Provided | non_specific |
| non_specific | CTRL0004 | GCTTGAGCACATACGCGAAT | Provided | non_specific |
| non_specific | Zhang_689 | GATCATAAATGTACAACGGG | Provided | non_specific |
| non_specific | Zhang_424 | GCTGAACGCCGACAGGACGG | Provided | non_specific |
| non_specific | Zhang_376 | GCAGCAATACCCCGGTATGG | Provided | non_specific |
| non_specific | Zhang_812 | GGATTAATTCGCTAAATGAT | Provided | non_specific |
| non_specific | Zhang_337 | GGACTCGGGCAATATCGGTT | Provided | non_specific |
| non_specific | Zhang_928 | GAAGACTTGCTCCAAAACAC | Provided | non_specific |
| non_specific | Zhang_990 | GTGTAGTCCTAGCCATGGGG | Provided | non_specific |
| non_specific | Zhang_386 | GACGGATCACCAAATCTTAG | Provided | non_specific |
| non_specific | Zhang_359 | GATATGGCTCGAGTAATCTT | Provided | non_specific |
| non_specific | Zhang_361 | GTGCTGCAGCTTTACGATCA | Provided | non_specific |
| non_specific | Zhang_840 | GTGCACTGTGGAGACGCCCG | Provided | non_specific |
| non_specific | CTRL0033 | GCCGACCAACGTCAGCGGTA | Provided | non_specific |
| non_specific | Zhang_516 | GTGGTGACCGACAATTACAC | Provided | non_specific |
| non_specific | Zhang_508 | GTAGCTGCTGTAAATCGCAT | Provided | non_specific |
| non_specific | Zhang_275 | GAGTAATTTCGAACGTATTG | Provided | non_specific |

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| non_specific | Zhang_787 | GAATAGATTTGTCAGTTAGG | Provided | non_specific |
| non_specific | Zhang_95 | GCCGTGTTGCTGGATACGCC | Provided | non_specific |
| non_specific | Zhang_903 | GCTAACCCCTGGCCAGGAAG | Provided | non_specific |
| non_specific | Zhang_137 | GGGAAATCGACTGTGCGCTT | Provided | non_specific |
| non_specific | Zhang_900 | GGTACTGGAAGTCCGAAACC | Provided | non_specific |
| non_specific | Zhang_602 | GGAGAGGGCCCGCGAACTCA | Provided | non_specific |
| non_specific | Zhang_158 | GGCAGTCGCGCTGAGCGTCA | Provided | non_specific |
| non_specific | Zhang_749 | GGGAGAAACGAGGTGTAATA | Provided | non_specific |
| non_specific | Zhang_738 | GAGTTCTAATCGTTCCTTGA | Provided | non_specific |
| non_specific | Zhang_550 | GAGTTACAGACTCAGCGGGT | Provided | non_specific |
| non_specific | Zhang_513 | GTAATTTGGGTGGGCCCTGC | Provided | non_specific |
| non_specific | Zhang_578 | GACTTTGGTTGAGCTTCAAT | Provided | non_specific |
| non_specific | Zhang_526 | GTCCGTTATGTGGCATGAGA | Provided | non_specific |
| non_specific | Zhang_511 | GACGTAAGTGACGACAGGAA | Provided | non_specific |
| non_specific | Zhang_47 | GGGGACGTCGCGAAAATGTA | Provided | non_specific |
| non_specific | Zhang_467 | GAGGAGCTGTATCTAGTGGC | Provided | non_specific |
| non_specific | Zhang_808 | GACCATAGAACCTGAAATAC | Provided | non_specific |
| non_specific | Zhang_829 | GGGGAAACCTCTATGGGTAA | Provided | non_specific |
| non_specific | Zhang_280 | GCGCTGTCTCACTAATCTCA | Provided | non_specific |
| non_specific | Zhang_885 | GTTAAGTCATGAGCAAAGAT | Provided | non_specific |
| non_specific | Zhang_394 | GCCAGGGTTCTTGGTCCCGA | Provided | non_specific |
| non_specific | Zhang_116 | GACGGCCTAACTTGCTGATA | Provided | non_specific |
| non_specific | Zhang_784 | GTTTATAAACACAGGGTCGC | Provided | non_specific |

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| non_specific | Zhang_211 | GCGCTCAGCACCCGCTATGC | Provided | non_specific |
| non_specific | Zhang_351 | GAGGTATGTCATCGCCATGA | Provided | non_specific |
| non_specific | Zhang_341 | GGGCGGCCCAAACTTAACAC | Provided | non_specific |
| non_specific | Zhang_344 | GCTTGCTATATGGGTGCGAG | Provided | non_specific |
| non_specific | Zhang_132 | GATATTTGGCTCGGCTGCGC | Provided | non_specific |