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(71) Applicant (for all designated States except US): **ON-COMETHYLOME SCIENCES SA** [BE/BE]; CHU, Tour 5 GIGA, Niveau 3, Avenue de l'Hopital 11, B-4000 Sart-Tilman (BE).

(71) Applicant (for AG only): **BALDOCK, Sharon, Claire** [GB/GB]; BOULT WADE TENNANT, Verulam Gardens, 70 Gray's Inn Road, London WC1X 8BT (GB).

(72) Inventor; and

(75) Inventor/Applicant (for US only): **ESTELLER, Manuel** [ES/ES]; Cancer Epigenetics Laboratory, Spanish National Cancer Centre (CNIO), Madrid (ES).

(74) Agents: **SPENCER, Matthew, Peter** et al.; Boulton Wade Tennant, Verulam Gardens, 70 Gray's Inn Road, London WC1X 8BT (GB).

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(54) Title: NOVEL TUMOUR SUPPRESSOR

(57) Abstract: A method of diagnosing cancer includes the steps of, in a sample obtained from a subject, determining the level or activity of HDAC2. A reduced level or activity of HDAC2 is indicative of cancer. HDAC2 protein expression is preferably determined. Indirect determination of HDAC2 expression is also possible, preferably by looking at the expression of genes selected from NCOA4, CTSB, TBCD, PPP2R4 and CORO1C. Methods for predicting the probability of successful treatment of cancer using a hydroxamic acid based HDAC inhibitor and for selecting suitable cancer treatment regimens can also be based upon determining the level or activity of HDAC2. Methods of treatment of cancer may be based upon use of carboxylic acid based HDAC inhibitors or by reconstituting HDAC2 activity.



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Novel Tumour Suppressor

TECHNICAL FIELD

5 The present invention relates to methods and products useful for diagnosing and treating cancer and is based around the unexpected finding of HDAC2 mutations which are associated with cancer.

10 INTRODUCTION

Widespread changes in DNA methylation (1,2) and post-translational modifications of histones occur in cancer cells (3,4) and both marks have a crucial role in chromatin
15 packaging and gene expression (1,2,5,6). We are largely ignorant of the mechanisms underlying the disruption of the epigenetic landscape in transformed cells.

Histone Deacetylases (HDACs) are well known targets for
20 treating cancer. The rationale behind attempting to inhibit HDAC activity is that in many cancers expression of tumour suppressor genes may be down regulated due to the action of HDACs, such as HDAC2. HDACs cause deacetylation of histones located in the promoter regions of these genes. A range of
25 HDAC inhibitors (HDACis) are in clinical trials (13) for treatment of various cancers. Thus, for example, in colorectal cancer, HDACis are capable of inhibiting tumour growth in cell lines (13, 14) and in APC (min) mice (15). HDACis include hydroxamic acids, such as trichostatin A and
30 also carboxylic acids such as butyrate and valproate.

DESCRIPTION OF THE INVENTION

The present invention is based around the surprising discovery that HDAC2 itself actually appears to fulfil a tumour suppressor role. A mutation in HDAC2 which leads to truncation of the protein and loss of HDAC2 function has been found to be associated with cancers, in particular those cancers displaying microsatellite instability. Recovery of HDAC2 function has also been shown to induce tumour-suppressor like features in these cells. Thus, in complete contrast to previous perceptions, loss of HDAC2 function may actually be indicative of a transformed cell. Furthermore, functional abrogation of HDAC2 in cancer cells also provides the cells with an altered sensitivity to certain cancer treatments. These discoveries have a number of applications which are expounded below in further detail.

Diagnostic methods of the invention

The loss of HDAC2 function is an indicator of cancer. Accordingly, in a first aspect, the invention provides a method of diagnosing cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 is indicative of cancer. Preferably, a substantially total loss of protein expression or activity is determined. This is particularly relevant in the case of colon cancers. Partial loss of activity has also been shown to be relevant to cancer. In particular heterozygous mutations in the HDAC2 gene have been shown for the first time herein to be linked to the incidence of cancer. In a particular embodiment, the cancer linked to a heterozygous HDAC2 mutation comprises endometrial cancer.

Note that the name "HDAC2" is the standard nomenclature approved by the human genome organisation for this HDAC and its encoding gene, to ensure that each symbol is unique. The listed accession number for this gene is U31814 and the
5 chromosomal location is 6q21. Further details can be found at www.gene.ucl.ac.uk/nomenclature.

In one preferred embodiment, the cancer which is being diagnosed is one which displays microsatellite instability
10 (MSI). According to the present invention, as detailed in the experimental section below, a frameshift mutation in HDAC2 in cancer cell lines with MSI leads to a loss of HDAC2 expression. Thus, the loss of HDAC2 may be used as an indicator of this particular cancer type.

15 The method of this aspect of the invention may be utilised to diagnose cancer in general. In one particular embodiment, the method is utilised to diagnose any of colorectal, gastric and/or endometrial cancer. In one
20 preferred embodiment, the method is used to diagnose hereditary nonpolyposis colon cancer and/or sporadic colorectal cancer. All of these cancer types may be MSI associated.

25 "Diagnosis" is defined herein to include monitoring the state and progression of the disease, checking for recurrence of disease following treatment and monitoring the success of a particular treatment. The tests may also have prognostic value, and this is included within the definition
30 of the term "diagnosis". The prognostic value of the tests may be used as a marker of potential susceptibility to cancer. Thus patients at risk may be identified before the

disease has a chance to manifest itself in terms of symptoms identifiable in the patient.

The nature of the mutation which causes a decrease in the level or activity of HDAC2 is not limiting with respect to the invention. The most important aspect is that a loss of HDAC2 function has been shown for the first time herein to be linked to the incidence of cancer and also to the effectiveness of certain anti-cancer agents for treating these cancers. Thus, any type of mutation leading to functional abrogation of HDAC2 is included within the scope of the invention. In one preferred embodiment, the mutation occurs in a microsatellite repeat. In particular, the mutation may occur in the (A)₉ microsatellite. In a further embodiment, the mutation occurs in a coding exon. In another embodiment, the mutation is a frameshift mutation, particularly a truncating mutation. Single nucleotide polymorphisms which lead to a reduction in the level or activity of HDAC2 may also be included within the scope of the invention. Mutations which cause deletion, substitution or addition of one or more amino acids to HDAC2 as compared to the wild type sequence are also included within the scope of the invention, as are point mutations, inversions and translocations, with the proviso that the mutation must be one which functionally abrogates HDAC2, thus contributing to, or representing an indicator of, cancer.

The method according to the first aspect of the invention is most preferably an *ex vivo* or *in vitro* method carried out on an isolated sample. In one embodiment the method may also include the step of obtaining the sample.

The test sample is most preferably a tissue sample, taken from the subject, which is suspected of being tumorigenic. In a preferred embodiment, the sample comprises a colon, rectal, endometrial or stomach sample. However, any other
5 suitable test sample in which activity or levels of HDAC2 can be measured to indicate the presence of cancer are included within the scope of the invention. Test samples for diagnostic, prognostic, or personalized medicine uses can be obtained from surgical samples, such as biopsies or
10 fine needle aspirates, from paraffin embedded tissues, or from a body fluid.

The decreased level of expression or activity of HDAC2 may, as necessary, be measured in order to determine if it is
15 statistically significant in the sample. This helps to provide a reliable test for diagnosing cancer, in particular MSI cancers. Any method for determining whether the expression level or activity of HDAC2 is significantly reduced may be utilised. Such methods are well known in the
20 art and routinely employed. For example, statistical analyses may be performed using an analysis of variance test. Typical P values for use in such a method would be P values of < 0.05 or 0.01 or 0.001 when determining whether the relative expression or activity is statistically
25 significant. A change in expression or activity may be deemed significant if there is at least a 10% decrease for example. The test may be made more selective by making the change at least 15%, 20%, 25%, 30%, 35%, 40% or 50%, for
example, in order to be considered statistically
30 significant.

In a preferred embodiment, the decreased level of expression or activity of HDAC2 is determined with reference to a control sample. This control sample is preferably taken from normal (i.e. non tumorigenic) tissue in the subject, where HDAC2 expression and activity is present.

Additionally or alternatively control samples may also be utilised in which there is known to be a lack of HDAC2 activity and expression.

Suitable additional controls may also be included to ensure that the test is working properly, such as measuring levels of expression or activity of a suitable reference gene in both test and control samples.

In a most preferred embodiment, the subject is a human subject. Generally, the subject will be a patient wherein cancer is suspected or a potential cancer has been identified and the method may be used to determine if indeed there is a cancer present. The methods of the invention may be used in conjunction with known methods for detecting cancer.

By "level" is meant the level of expression of HDAC2. Such measurements may preferably be carried out at the protein level, but may also be carried out at the RNA level. Changes in the level of expression may be measured directly or indirectly. Indirect measurement may involve determining expression of genes whose expression is modified or at least partially determined by HDAC2 activity.

30

In one preferred embodiment, the diagnostic method of the invention is carried out by determining HDAC2 protein

expression. In a most preferred embodiment, total loss of wild type HDAC2 protein expression is observed in the sample in order to conclude a diagnosis of cancer. However, partial loss of HDAC2 expression may also be relevant.

5

Levels of protein expression may be determined by a number of techniques, as are well known to one of skill in the art. Examples include western blots, immunohistochemical staining and immunolocalization, immunofluorescence, enzyme-linked
10 immunosorbent assay (ELISA), immunoprecipitation assays, agglutination reactions, radioimmunoassay, flow cytometry and equilibrium dialysis. These methods generally depend upon a reagent specific for identification of HDAC2. The reagent is preferably an antibody and may comprise
15 monoclonal or polyclonal antibodies. Fragments and derivatized antibodies may also be utilised, to include without limitation Fab fragments, ScFv, single domain antibodies, nanoantibodies, heavy chain antibodies etc which retain HDAC2 binding function. Any detection method may be
20 employed in accordance with the invention. The nature of the reagent is not limited except that it must be capable of specifically identifying HDAC2.

Of course, in the case of a positive diagnostic of cancer,
25 there will be reduced HDAC2 levels, and perhaps no HDAC2 at all. In one embodiment this will present a negative result, if the HDAC2 specific reagent is one which binds to the wild type or full length protein. In this case, use of suitable controls ensures that false diagnoses will not be made, for
30 example caused by degraded or non-specific reagents. Thus, the same reagent can be tested on samples in which it is known that HDAC2 is expressed. A positive result in this

control sample, combined with a negative result in the test sample would provide a confident diagnosis of cancer and removes any doubt over the quality of the reagent.

- 5 In one alternative embodiment, a reagent specific for the altered HDAC2 which is associated with cancer may be employed. Thus, for example, the truncated version of HDAC2 described herein is not recognised by reagents specific for full length and wild type HDAC2. Accordingly, this
- 10 truncated version associated with cancer cells may fold differently and thus present different epitopes. As a result of this, reagents specific for truncated HDAC2 may be produced by known methods. A preferred reagent would comprise an antibody, or a truncated HDAC2 binding
- 15 derivative thereof. Both monoclonal and polyclonal antibodies can be produced according to known methods and readily derivatized by one skilled in the art.

Use of such a reagent would allow a positive result to be

20 used to diagnose cancer, since the reagent binds in the presence of the mutant HDAC2 which is indicative of a loss of wild type HDAC2 function and expression.

HDAC2 gene expression may also be monitored at the RNA level

25 in one embodiment. Thus a decreased or abolished level of HDAC2 gene expression results in lower levels of functional HDAC2 protein and this is indicative of cancer.

Suitable methods for determining HDAC2 expression at the RNA

30 level are well known in the art. Methods employing nucleic acid probe hybridization to the HDAC2 transcript may be employed for measuring the presence and/or level of HDAC2

mRNA. Such methods include use of nucleic acid probe arrays (microarray technology) and Northern blots. Advances in genomic technologies now permit the simultaneous analysis of thousands of genes, although many are based on the same
5 concept of specific probe-target hybridization.

Sequencing-based methods are an alternative. These methods started with the use of expressed sequence tags (ESTs), and now include methods based on short tags, such as serial
10 analysis of gene expression (SAGE) and massively parallel signature sequencing (MPSS). Differential display techniques provide yet another means of analyzing gene expression; this family of techniques is based on random amplification of cDNA fragments generated by restriction
15 digestion, and bands that differ between two tissues identify cDNAs of interest.

In one embodiment, the levels of HDAC2 gene expression are determined using reverse transcriptase polymerase chain
20 reaction (RT-PCR). RT-PCR is a well known technique in the art which relies upon the enzyme reverse transcriptase to reverse transcribe mRNA to form cDNA, which can then be amplified in a standard PCR reaction. Protocols and kits for carrying out RT-PCR are extremely well known to those of
25 skill in the art and are commercially available.

In a preferred embodiment, the RT-PCR is carried out in real time and in a quantitative manner. Real time quantitative RT-PCR has been thoroughly described in the literature (see
30 Gibson et al for an early example of the technique) and a variety of techniques are possible. Examples include use of Taqman, Molecular Beacons, LightCycler (Roche), Scorpion and

Amplifluour systems. All of these systems are commercially available and well characterised, and may allow multiplexing (that is, the determination of expression of multiple genes in a single sample).

5

These techniques produce a fluorescent read-out that can be continuously monitored. Real-time techniques are advantageous because they keep the reaction in a "single tube". This means there is no need for downstream analysis in order to obtain results, leading to more rapidly obtained results. Furthermore, keeping the reaction in a "single tube" environment reduces the risk of cross contamination and allows a quantitative output from the methods of the invention. This may be particularly important in the clinical setting of the present invention.

It should be noted that whilst PCR is a preferred amplification method, to include variants on the basic technique such as nested PCR, equivalents may also be included within the scope of the invention. Examples include isothermal amplification techniques such as NASBA, 3SR, TMA and triamplification, all of which are well known in the art and commercially available. Other suitable amplification methods include the ligase chain reaction (LCR) (Barringer et al, 1990), selective amplification of target polynucleotide sequences (US Patent No. 6,410,276), consensus sequence primed polymerase chain reaction (US Patent No 4,437,975), arbitrarily primed polymerase chain reaction (WO90/06995) and nick displacement amplification (WO2004/067726).

30

The above referenced methods are also useful in embodiments of the methods of the invention in which the level or activity of HDAC2 is measured indirectly.

- 5 Thus, in one embodiment, the method of diagnosing cancer comprises determining the levels of gene expression of a panel of genes, comprising at least one gene, but preferably more than one gene selected from
- 10 (a) CARD6 (A_23_P41854), TOP1MT (A_23_P216241), SWAP70 (A_23_P116533), KIAA1212 (A_23_P17269), IRF5 (A_23_P500271), CGI-90 (A_23_P83492), UTS2 (A_23_P63343), DJ462O23.2 (A_23_P46604), HHLA3 (A_23_P200303), NFATC4 (A_23_P140394), DKFZp686H1423 (A_23_P392235), MGC17839 (A_23_P329890), TSTA3
- 15 (A_23_P94301), ZNF175 (A_23_P332374), (A_23_P119023), KIAA1212 (A_23_P28664), LANCL1 (A_23_P50887), FLJ38819 (A_23_P385768), TAS2R9 (A_23_P336506), ZNF22 (A_23_P202458), SYT12 (A_23_P424645), KIAA1826 (A_23_P116166), ZHX1 (A_23_P43150), BAIAP1 (A_23_P96099), (A_23_P150316), ZNF22
- 20 (A_23_P384512), HMP19 (A_23_P125375), M160 (A_23_P61466), TFPI (A_23_P17095), FJX1 (A_23_P150693), (A_23_P165598), EMP3 (A_23_P119362), AP1S2 (A_23_P217384), CCRL2 (A_23_P69310), ZNF44 (A_23_P119279), VAPB (A_23_P91293), (A_23_P28797), FLJ10458 (A_23_P141315), FLJ10826
- 25 (A_23_P3775), ZNF582 (A_23_P395464), RBM9 (A_23_P103091), C14orf168 (A_23_P25913), KPNA4 (A_23_P218835), FUNDC2 (A_23_P171310), MGC29784 (A_23_P255916), DEDD2 (A_23_P141908), PHC1 (A_23_P323094), CSTF1 (A_23_P79882), SLIT2 (A_23_P144348), EFHD2 (A_23_P23443), MGC17986
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25 SCUBE1 (A_23_P211619), CDYL2 (A_23_P371871), GDFD1
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PPM1K (A_23_P167138), NUDT12 (A_23_P259090), DIAPH1
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(b) ACP6 (A_23_P160237), C3orf17 (A_23_P336670), SLC10A5 (A_23_P157428), (A_23_P60758), ALG6 (A_23_P35168), MAP4K3 (A_23_P154130), ITLN2 (A_23_P201419), PPIL4 (A_23_P42507),
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 GNRH1 (A_23_P254594), KRTAP3-3 (A_23_P89649),
 (A_23_P130496), RIP (A_23_P66758),
 25 wherein an increase in the level of expression of at least
 one gene selected from group (a) and/or (b) and/or (c)
 and/or (d) and/or wherein a decrease in the level of
 expression of at least one gene selected from group (e)
 and/or (f) and/or (g) and/or (h) indicates a reduced level
 30 or activity of HDAC2 and is therefore indicative of cancer.

Note that for all genes listed, the corresponding probe identifier as produced by Agilent is also listed in parentheses. This provides a representation of the actual
5 probe utilised in each case. As discussed below (see the experimental section and figure 8), all of these genes show significantly altered expression between normal cells and cancer cells in which HDAC2 is truncated ($p < 0.05$).

10 In one preferred embodiment, the genes assessed are taken from those genes listed in groups (a) and/or (b) and/or (e) and/or (f) above. For these groups of genes the changes in expression are calculated to be highly significant ($p < 0.01$).

15 Preferably the panel comprises at least one, two, three, four, etc of the genes listed above, up to all genes. All permutations and combinations of the genes listed above are contemplated for gene panels within the scope of the present invention.

20

For larger panels, use of microarrays may be preferable.

Thus, the invention provides, in a second aspect, a microarray for use in the methods of the invention which involve determining levels of HDAC2 indirectly by looking at
25 expression of other genes, comprising probes immobilised on a solid support hybridizing with transcripts or parts thereof of at least one gene selected from those listed (in groups (a) to (h)) above. Preferably, the genes are selected from those genes listed in groups (a) and/or (b)
30 and/or (e) and/or (f) above. For these groups of genes the changes in expression are calculated to be highly significant ($p < 0.01$).

Preferably there are probes immobilised on a solid support hybridizing with transcripts or parts thereof of at least one, two, three, four, etc of the genes listed above, up to
5 all of the genes. All permutations and combinations of the genes listed above are contemplated within the scope of the present invention, for the purposes of providing a microarray.

10 Microarrays and their means of manufacture are well known and can be manufactured to order by commercial entities such as Agilent and Affymetrix, for example.

The probes are the sequences which are immobilized onto the
15 array, by known methods, and which represent selected sequences from the genes of interest, in this case HDAC2 and/or genes whose expression is affected by a loss or reduced activity or level of HDAC2 in a cell. Probe selection and array design lie at the heart of the
20 reliability, sensitivity, specificity, and versatility of the microarrays of the invention. The methods for selecting suitable probes would be readily apparent for one of skill in the art and may involve optimization using data collected from multiple databases, bioinformatics tools, and
25 experiment-trained computer models.

The key elements of probe selection and design are common to the production of all arrays, regardless of their intended application and as such would be well known to one of skill
30 in the art. Strategies to optimize probe hybridization, for example, may be included in the process of probe selection. Hybridization under particular pH, salt, and temperature

conditions can be optimized by taking into account melting temperatures and using empirical rules that correlate with desired hybridization behaviours.

5 The GeneChip arrays produced by Affymetrix involve a Perfect Match/Mismatch probe strategy. For each probe designed to be perfectly complementary to a target sequence, a partner probe is generated that is identical except for a single base mismatch in its centre. These probe pairs, called the
10 "Perfect Match probe (PM)" and the "Mismatch probe (MM)", allow the quantitation and subtraction of signals caused by non-specific cross-hybridization. The difference in hybridization signals between the partners, as well as their intensity ratios, serve as indicators of specific target
15 abundance. Such an array design may be applicable to, and incorporated into, the arrays of the present invention.

In order to ensure specificity of the probes in terms of accurately representing the genes whose expression is
20 investigated, the microarray preferably comprises at least 10 probes representing each gene on the array. However, other numbers of probes may be utilised provided that the expression of each gene which is selected to form part of the array can be accurately and specifically measured.

25

In a preferred embodiment, the array includes probes which represent each and every one of the genes listed. However, this may not be necessary in order to be able to accurately diagnose cancer. Probes representing only one or 2, 3, 4,
30 5, 6, 7, 8, 9, 10, etc all the way up to all of the genes may be utilised in the array. Accordingly, in one preferred embodiment, the microarray comprises probes representing

transcripts of at least the NCOA4 and/or CTSB and/or TBCD and/or PPP2R4 and/or CORO1C gene.

Each probe is preferably at least about 20 nucleotides in length such that a probe of sufficient length to ensure sensitivity and specificity of hybridization is provided. However, any length of probe may be utilised within the scope of the invention, provided that accurate results are achieved in terms of detecting expression of the genes which are representative of HDAC2 levels and thus are useful in the diagnosis of cancer. Possible lengths for the probes include at least 10 nucleotides and up to 250 nucleotides and preferably between about 20 and about 50 nucleotides.

In cases where HDAC2 mRNA is present, reduction or loss of function of the protein encoded by this mRNA may be identified, in one embodiment, by transcribing and cloning its complementary DNA (cDNA). Reverse transcription is used to obtain cDNA from the mRNA, which is inserted into a vector and cloned into host cells in order to express the HDAC2 protein. Functionality of the expressed protein can then be tested using any suitable technique known in the art, including, but not limited to, the techniques described herein.

In an alternative embodiment, the level or activity of HDAC2 may be determined indirectly by assessing the recruitment of HDAC2 to one or more gene promoters. By recruitment is meant the binding of HDAC2 to the promoter region, which may be direct or indirect binding. Thus, if HDAC2 is not recruited to the relevant promoters, this is indicative of a reduced level or activity of HDAC2 and leads to a diagnosis

of cancer. In one embodiment, a loss of recruitment of HDAC2 at one or more gene promoters indicates a reduced level or activity of HDAC2 and is therefore indicative of cancer.

5

In a preferred embodiment, recruitment at any one of the HDAC2, TBCD, PPP2R4 or CORO1C promoters is monitored. Monitoring of any one, two, three or all four of these promoters together is included within the scope of the invention.

10

Recruitment of HDAC2 to a particular gene promoter may be measured by any technique known in the art. In one embodiment, chromatin immunoprecipitation is utilised in order to determine whether HDAC2 is present and active and therefore is binding to a particular gene promoter.

15

Chromatin immunoprecipitation is a well known technique in the art which relies upon cross-linking of the binding protein to the DNA, followed by isolation, shearing of the DNA, antibody detection and isolation by precipitation. The isolated DNA is then released from the binding protein by reversing the cross-linking and is amplified by PCR to determine where the binding protein was bound. (Metivier, R. et al., Estrogen receptor-alpha directs ordered, cyclical, and combinatorial recruitment of cofactors on a natural target promoter, Cell 2003, 115(6) P751-63).

20

25

As an alternative or supplementary technique, hyperacetylated chromatin is also associated with a reduction or loss of functionality of HDAC2. This can be quantified by any suitable technique. For example, standard chromatin immunoprecipitation assays may be utilised.

30

Thus, in one embodiment, analysis of histone acetylation is carried out in order to determine the level or activity of HDAC2. Preferably, an increase in the acetylation levels of one or more histones indicates a reduced level or activity of HDAC2 and is therefore indicative of cancer. In a specific embodiment, the acetylation levels of histone H3 and/or histone H4 are determined. An increase in acetylation of histones H3 and H4 has been shown to be associated with cancer cells in which HDAC2 expression is lost (see fig. 1g and supplementary figure 2d).

By "activity" is meant the enzymatic activity of HDAC2, namely its ability to deacetylate a substrate histone. Any suitable assay may be employed in order to determine the activity of HDAC2 in the sample under test.

To determine HDAC2 enzymatic activity in the sample, it may first be necessary or preferable to isolate HDAC2. Thus, for example, an immunoprecipitation step may be employed, as are well known in the art, using a suitable HDAC2 specific reagent, such as an antibody (see reference 4 of the methods section for example).

A scintillation assay may be employed for example in order to determine HDAC2 activity. This requires a suitably labelled substrate, such as [3H]labelled histones. Alternative labels and substrates may be utilised as appropriate. The sample, or immunoprecipitate may be incubated with the substrate at a suitable temperature, such as 37°C, for a suitable time period, such as 30 minutes, 1 hour, 2 hours etc. If room temperature incubations are

carried out, longer reaction times may be required. If HDAC2 is present in the sample or immunoprecipitate, [3H] acetate will be released from the histones and this release may be measured accordingly. The released [3H] acetate may
5 need to be suitably extracted by known means, such as by using ethyl acetate and centrifugation to produce a [3H] acetate containing supernatant, prior to scintillation counting.

10 For all techniques employed to determine the level or activity of HDAC2, there is preferably included a suitable control sample for comparison. Preferably, both negative and positive controls are included (as discussed in greater detail above).

15

If desired, it may be possible to identify the HDAC2 mutation at the level of the gene. Various techniques are well known in the art. For example, restriction enzyme digestion and electrophoresis techniques can be employed in
20 combination. Thus, PCR is employed to amplify the HDAC2 gene which may carry the mutation. Genomic DNA can be isolated from a tissue sample from the subject by extraction techniques well known in the art, such as phenol-chloroform extraction, for example. Suitable primers specific for the
25 HDAC2 gene are chosen. The PCR product is then treated with one or more restriction enzymes chosen so that the size of one or more fragments resulting from cleavage of the DNA amplified from mutant HDAC2 differs from the fragment size of DNA amplified from wild-type HDAC2. Fragment sizes may
30 be determined by electrophoresis.

If the mutation does not lead to restriction fragments that can easily be distinguished by size, Southern blotting may be carried out using appropriate labelled DNA probes for example. Alternatively, the gene may be sequenced by
5 techniques known in the art and the sequence compared with that of wild-type HDAC2 in order to identify whether HDAC2 is functionally affected.

Pharmacogenetic methods of the invention

10 As expounded in the experimental section below, it has been shown that cancer cell lines lacking HDAC2 have altered resistance to the usual antiproliferative and proapoptotic effects of HDAC inhibitors. Specifically, in cancer cells where HDAC2 is deficient, the cells have an increased
15 resistance to the effects of hydroxamic acid based HDAC inhibitors. Thus, the invention provides for the use of HDAC2 mutational status as a pharmacogenetic indicator.

Accordingly, the invention provides a method for predicting
20 the probability of successful treatment of cancer with a hydroxamic acid based HDAC inhibitor comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 is indicative of a low probability of successful treatment.

25

In particular, a reduced level or activity of HDAC2 is indicative of a low probability of successful treatment using trichostatin A. Additional hydroxamic acids which are contra-indicated according to the invention may include
30 suberoyl hydroxamic acid (SBHA), 6-(3-chlorophenylureido)caproic hydroxamic acid (3-Cl-UCHA), *m*-carboxycinnamic acid bishydroxylamide (CBHA),

suberoylanilide hydroxamic acid (SAHA), azelaic bishydroxamic acid (ABHA), pyroxamide, aromatic sulfonamides bearing a hydroxamic acid group and cyclic-hydroxamic-acid containing peptides.

5

Similarly, the invention also provides a method of selecting a suitable treatment regimen for cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 indicates that treatment using a hydroxamic acid based HDAC inhibitor is unsuitable.

In particular, a reduced level or activity of HDAC2 indicates that treatment using trichostatin A is unsuitable. Additional hydroxamic acids which are contra-indicated according to the invention may include suberoyl hydroxamic acid (SBHA), 6-(3-chlorophenylureido)caproic hydroxamic acid (3-Cl-UCHA), *m*-carboxycinnamic acid bishydroxylamide (CBHA), suberoylanilide hydroxamic acid (SAHA), azelaic bishydroxamic acid (ABHA), pyroxamide, aromatic sulfonamides bearing a hydroxamic acid group and cyclic-hydroxamic-acid containing peptides.

In stark contrast to the situation in respect of hydroxamic acid HDAC inhibitors, it has been found that HDAC2 deficient cancers remain susceptible to the action of other HDAC inhibitors, in particular carboxylic acid based HDAC inhibitors.

Accordingly, in one embodiment according to the method described above, a reduced level or activity of HDAC2 leads to treatment using a carboxylic acid based HDAC inhibitor

being selected (in preference to use of a hydroxamic acid based HDAC inhibitor).

Thus, in a further aspect of the invention there is provided
5 a method of selecting a suitable treatment regimen for cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 indicates that treatment using a carboxylic acid based HDAC inhibitor should be
10 selected.

In particular, a reduced level or activity of HDAC2 indicates that treatment using valproate and/or butyrate should be selected.

15

The pharmacogenetic methods of the invention may incorporate any and all of the preferred aspects described in respect of the diagnostic methods described above. In particular, preferably a total loss of, or a significant reduction in,
20 HDAC2 expression and/or activity is investigated. Thus, the absence of HDAC2 expression and/or activity is indicative of cancer and is also indicative that treatment using a carboxylic acid based HDAC inhibitor is positively indicated, whereas treatment using a hydroxamic acid based
25 HDAC inhibitor is contra-indicated. Preferably, the diagnostic methods of the invention are carried out as a prelude to, or as an integral part of, the pharmacogenetic methods of the invention.

30 Thus, for example, the description of suitable methods for determining levels or activity of HDAC2, suitable test samples, preferred subjects and specific types of cancer

which may be monitored all apply *mutatis mutandis* to these aspects of the invention and are not repeated here simply for reasons of conciseness. Accordingly, according to these aspects of the invention, in a preferred embodiment, the

5 cancer which is to be treated is one which displays microsatellite instability (MSI). The methods of these aspects of the invention may be utilised to select suitable treatment regimens for, or determine the likelihood of successful treatment of, any of colorectal, gastric and/or
10 endometrial cancer. In one preferred embodiment, the methods may be used to select suitable treatment regimens for, or determine the likelihood of successful treatment of, hereditary nonpolyposis colon cancer and/or sporadic colorectal cancer.

15

Methods of treatment and medical uses of the invention

As aforementioned, it has been shown herein for the first time that cancer cell lines lacking HDAC2 have altered resistance to the usual antiproliferative and proapoptotic
20 effects of HDAC inhibitors. Specifically, in cancer cells where HDAC2 is deficient, the cells have an increased resistance to the effects of hydroxamic acid HDAC inhibitors. This resistance is not seen for carboxylic acid based HDAC inhibitors.

25

In light of these surprising discoveries, the invention provides a method for treating cancer in a subject using carboxylic acid based HDAC inhibitors, the method comprising selecting a subject for treatment according to the
30 diagnostic and/or pharmacogenetic methods of the invention.

In a related aspect, the invention provides for the use of carboxylic acid based HDAC inhibitors in the manufacture of a medicament for treating cancer in a subject, wherein the subject has been selected for treatment according to the
5 diagnostic and/or pharmacogenetic methods of the invention.

Thus, the invention allows, through use of the diagnostic and pharmacogenetic methods of the invention described above, a new patient population which is resistant to
10 treatment with hydroxamic acid based HDAC inhibitors to be selected. This patient population is thus given an alternative treatment, based upon use of carboxylic acid based HDAC inhibitors, which is much more likely to provide successful treatment of their cancer.

15 Preferably, the carboxylic acid based HDAC inhibitors comprise valproate and/or butyrate. It should be noted that there are a number of suitable HDAC inhibitors in clinical trials and accordingly, the skilled person is aware of
20 suitable formulations etc which may be utilised.

In similar fashion, the invention also provides a method for treating cancer in a subject using hydroxamic acid based
HDAC inhibitors, the method comprising selecting a subject
25 for treatment according to the diagnostic and/or pharmacogenetic methods of the invention. Thus, if HDAC2 activity is present, treatment using a hydroxamic acid based HDAC inhibitor is possible.

30 In a related aspect, the invention provides for the use of hydroxamic acid based HDAC inhibitors in the manufacture of a medicament for treating cancer in a subject, wherein the

subject has been selected for treatment according to the diagnostic and/or pharmacogenetic methods of the invention.

Thus, the invention allows, through use of the diagnostic
5 and pharmacogenetic methods of the invention described
above, a new patient population which remains susceptible to
treatment with hydroxamic acid based HDAC inhibitors to be
selected. This patient population may thus be recommended a
treatment regiment based upon use of hydroxamic acid based
10 HDAC inhibitors, which has the potential to provide
successful treatment of their cancer.

In one embodiment, the presence of HDAC2 indicates that
treatment using trichostatin A remains possible. Additional
15 hydroxamic acids include suberoyl hydroxamic acid (SBHA), 6-
(3-chlorophenylureido)caproic hydroxamic acid (3-Cl-UCHA),
m-carboxycinnamic acid bishydroxylamide (CBHA),
suberoylanilide hydroxamic acid (SAHA), azelaic
bishydroxamic acid (ABHA), pyroxamide, aromatic sulfonamides
20 bearing a hydroxamic acid group and cyclic-hydroxamic-acid
containing peptides.

It should be noted that, for the purposes of the present
invention, the designation of a particular HDAC inhibitor is
25 considered to encompass all pharmaceutically acceptable
forms of the active compound which are useful as HDAC
inhibitors. Thus, stereoisomers, enantiomers, salts, esters
etc are all encompassed within the scope of the invention as
appropriate.

30

Thus, in a pharmaceutical composition incorporating a
suitable HDAC inhibitor, preferred compositions include

pharmaceutically acceptable carriers including, for example, non-toxic salts, sterile water or the like. A suitable buffer may also be present allowing the compositions to be lyophilized and stored in sterile conditions prior to reconstitution by the addition of sterile water for subsequent administration. The carrier may also contain other pharmaceutically acceptable excipients for modifying other conditions such as pH, osmolarity, viscosity, sterility, lipophilicity, somobility or the like.

Pharmaceutical compositions which permit sustained or delayed release following administration may also be used.

Suitable pharmaceutical compositions for use in the treatment methods or medical uses of the invention may be used together with other standard chemotherapeutic treatments which target tumour cells directly. Non limiting examples include paclitaxel, cyclaphosphomide and 5-tumor-uracil (5-FU) and pharmaceutically acceptable derivatives thereof including salts, etc.

In one embodiment, the pharmaceutical composition, preferably comprising a carboxylic acid based HDAC inhibitor, for use in the treatment methods or medical uses of the invention is in a form suitable for metronomic dosing.

The therapeutic agent may, for example, be encapsulated and/or combined with suitable carriers in solid dosage forms for oral administration which would be well known to those of skill in the art or alternatively with suitable carriers for administration in an aerosol spray. Examples of oral dosage forms include tablets, capsules and liquids.

Alternatively, the therapeutic agent may be administered parenterally. Specific examples include intradermal injection, subcutaneous injection (which may advantageously
5 give slower absorption of the therapeutic agent), intramuscular injection (which can provide more rapid absorption), intravenous delivery (meaning the drug does not need to be absorbed into the blood stream from elsewhere), sublingual delivery (for example by dissolving of a tablet
10 under the tongue or by a sublingual spray), rectal delivery, vaginal delivery, topical delivery, transdermal delivery and inhalation.

Furthermore, as would be appreciated by the skilled
15 practitioner, the specific dosage regime may be calculated according to the body surface area of the patient or the volume of body space to be occupied, dependent on the particular route of administration to be used. The amount of the composition actually administered will, however, be
20 determined by a medical practitioner based on the circumstances pertaining to the disorder to be treated, such as the severity of the symptoms, the age, weight and response of the individual.

25 The methods of treatment and medical uses according to the invention described supra may incorporate any and all of the preferred aspects described in respect of the diagnostic and pharmacogenetic methods described above. Preferably, the diagnostic methods and/or the pharmacogenetic methods of
30 the invention are carried out as a prelude to, or as an integral part of, the methods of treating cancer according to the invention.

Thus, for example, the description of suitable methods for determining levels or activity of HDAC2, suitable test samples, preferred subjects and specific types of cancer which may be monitored all apply *mutatis mutandis* to these aspects of the invention and are not repeated here simply for reasons of conciseness.

According to the treatment method aspects of the invention, in a preferred embodiment, the cancer which is treated in the patient subpopulation identified according to the diagnostic and/or pharmacogenetic methods of the invention is one which displays microsatellite instability (MSI). These methods of the invention may be utilised to treat any of colorectal, gastric and/or endometrial cancer. In one preferred embodiment, the methods may be used to treat hereditary nonpolyposis colon cancer and/or sporadic colorectal cancer.

Gene Therapy Methods

With the realisation of HDAC2's role as a tumour suppressor gene, whose functional abrogation is linked to specific cancers, there is the possibility of restoring HDAC2 functionality in order to treat cancer. As shown in the experimental section below, transfection of HDAC2 deficient cells, including HDAC2 deficient cancer cells, with a suitable HDAC2 containing vector induces tumour suppressor-like features.

Accordingly, in a still further aspect, the invention provides a method for treating cancer in a subject, said

subject displaying a reduced level or activity of HDAC2, comprising reconstitution of HDAC2 activity in the subject.

5 In a preferred embodiment, the cancer has been diagnosed or assessed according to the diagnostic and pharmacogenetic methods of the invention. This method may, in a further embodiment, be used in conjunction with the other treatment methods and medical uses described herein.

10 Thus, also provided is the use of a vector carrying the HDAC2 gene in the manufacture of a medicament for treating cancer in a subject, wherein the subject has been selected for treatment according to the diagnostic and/or pharmacogenetic methods of the invention.

15 Preferably, the reconstitution of HDAC2 activity comprises introducing wild type copies of the HDAC2 gene into the subject.

20 Any suitable vector for delivery of functional copies of the HDAC2 gene may be utilised according to the method of the invention. One principal requirement is that tissue specificity of delivery and expression is achieved. The two major sources of vectors which may be utilised comprise
25 viral vectors and non-viral vectors.

Within the group of viral vectors, preferred types include adenoviruses, retroviruses, in particular Moloney murine leukaemia virus (Mo-MLV), adeno-related viruses and herpes
30 simplex virus type I. Typically, the gene of interest, in this case encoding HDAC2, will be included in the viral genome, preferably in the "non-essential" region of the

viral genome. In addition, it is important to remove virally encoded protooncogenes from the viral vector genome. The virus may be made replication incompetent to prevent unwanted replication once the virus has been targeted.

5

In terms of targeting the viral vector to the desired site, a number of possibilities exist. For example, the env gene (which encodes the viral vector's envelope) may be engineered or replaced with the env gene from a different virus to alter the range of cells the viral vector will "infect". Furthermore, alteration of the viral tropism may be achieved by using suitable antibodies raised against antigenic determinants on the cell surface of the desired target cells. The antibodies, which include all derivatives thereof, such as scFV, nanobodies, VH domains, Fab fragments etc., may be genetically incorporated into the viral vectors to provide targeted gene delivery of the HDAC2 gene. Most preferred is use of scFV (Hedley et al., Gene Therapy (2006) 13, 88-94). The viral vectors may have many genes removed, such as packaging genes, in order to reduce immunogenicity and/or infectivity. These functions may thus be supplied by a helper virus.

Due to their high efficiency of integration, low pathogenicity and high efficacy, adenoviruses are a preferred vector according to the methods of the invention.

Alternatives to viral vectors include direct gene delivery, use of other delivery agents and use of molecular conjugates. Tissue specific promoters may be employed as appropriate. Direct gene delivery may be achieved for example by microinjection of a suitable vector, such as a

plasmid carrying the HDAC2 gene, directly into the tissue of interest. Alternatives include use of ballistic transformation, for example using vector coated onto suitable particles (e.g. gold particles). Additional
5 delivery agents include liposomes and derivatives thereof. As discussed above, targeting proteins such as antibodies and derivatives thereof may be utilised in order to ensure delivery to the cells of interest. Molecular conjugates may include suitable proteins conjugated to the DNA of interest
10 using a suitable DNA binding agent.

The methods of treatment and medical uses according to The gene therapy aspects of the invention may incorporate any and all of the preferred aspects described in respect of
15 the diagnostic and pharmacogenetic methods and also methods of treating cancer as described above. Preferably, the diagnostic methods and/or the pharmacogenetic methods of the invention are carried out as a prelude to, or as an integral part of the methods of treating cancer according to the gene
20 therapy aspects of the invention.

Thus, for example, the description of suitable methods for determining levels or activity of HDAC2, suitable test samples, preferred subjects and specific types of cancer
25 which may be treated all apply *mutatis mutandis* to these aspects of the invention and are not repeated here simply for reasons of conciseness.

According to the gene therapy treatment method aspects of
30 the invention, in a preferred embodiment, the cancer which is treated, preferably in the patient subpopulation identified according to the diagnostic and/or

pharmacogenetic methods of the invention, is one which displays microsatellite instability (MSI). These methods of the invention may be utilised to treat any of colorectal, gastric and/or endometrial cancer. In one preferred
5 embodiment, the methods may be used to treat hereditary nonpolyposis colon cancer and/or sporadic colorectal cancer.

Kits

The invention also provides kits which may be used in order
10 to carry out the methods of the invention. The kits may incorporate any of the preferred features mentioned in connection with the methods of the invention above.

Kits for use in diagnostic methods

15 Kits for use in the diagnostic methods of the invention may incorporate suitable means for obtaining a sample. They may also incorporate suitable means for safely handling this sample.

20 Kits for determining the level or activity of HDAC2 will typically include one or more reagents specific for HDAC2. Preferably, the reagent includes an antibody or an HDAC2 binding derivative thereof. Suitable derivatives are widely known in the art and include Fab fragment, scFv fragments,
25 VH domains, nanobodies, heavy chain antibodies etc. Polyclonal and monoclonal antibodies may be included in the kits of the invention. Other reagents may include any molecule which binds specifically to HDAC2. For example the reagent could be based around a labelled version of an HDAC
30 inhibitor such as trichostatin A for example.

Kits may include the necessary components for immunoprecipitation of HDAC2 followed by the components necessary to monitor HDAC2 activity. Such components are well known in the art. Kits for use in western blotting, immunofluorescence, agglutination assays, radioimmunoassay, flow cytometry and equilibrium analysis are also contemplated within the scope of the invention.

In one embodiment, an ELISA kit contains a suitable chromogenic or chemiluminescent substrate, together with an HDAC2 specific reagent, preferably an antibody (monoclonal or polyclonal or target binding derivative thereof) in order to detect if HDAC2 is present in the sample.

Suitable control enzymes or other markers may also be analysed in the methods of the invention, to confirm the method is working in a satisfactory manner. Thus, the kits may also incorporate suitable reagents specific for the identification of these control enzymes or other markers.

Where the methods of the invention incorporate tests on suitable control samples (both positive and negative controls) the kits will contain sufficient reagents to test all of the controls and the test samples. The reagents may be separately packaged and aliquoted to allow for individual tests to be carried out on both test and control samples using the same kit.

If determining HDAC2 expression, or if indirect gene expression is being utilised in order to determine HDAC2 activity, at the mRNA level, kits may incorporate gene specific primers and/or probes. The kits may further

comprise RNA isolation reagents, polymerase enzymes for amplification, buffers etc. The kits may also incorporate suitable RNase inhibitors to prevent degradation of any isolated RNA molecules.

5

Kits for use in RT-PCR applications may additionally include a reverse transcriptase enzyme together with suitable buffers. Appropriate mixtures of nucleotides, as would be well known to one of skill in the art, may also be included
10 in the kits to facilitate amplification of the template molecules (both RNA to cDNA and amplification of the cDNA).

In a northern blotting embodiment, the kits may include suitable probes which cross react with the appropriate gene.
15 Such probes may be labelled as appropriate, for example with a radiolabel or mass label or fluorescent label.

As mentioned above, the methods of the invention may incorporate nucleic acid amplification techniques. As
20 aforementioned preferred amplification techniques include PCR, nested PCR, Rolling circle replication, NASBA, 3SR, ligase chain reaction (LCR), selective amplification of target polynucleotide sequences, consensus sequence primed polymerase chain reaction, arbitrarily primed polymerase
25 chain reaction, nick displacement amplification and TMA techniques. In the case of nucleic acid amplification techniques, well known in the art, sequence specific primers are required to allow specific amplification of the product with minimal production of false positive results. To this
30 end, the kits of the invention may preferably include sequence specific primers.

The kit may also include reagents necessary for a nucleic acid amplification step. Reagents may include, by way of

example and not limitation, amplification enzymes, probes, positive control amplification templates, reaction buffers etc. For example, in the PCR method of amplification, possible reagents include a suitable polymerase such as Taq polymerase and appropriate PCR buffers, and in the TMA method the appropriate reagents include RNA polymerase and reverse transcriptase enzymes. All of these reagents are commercially available and well known in the art.

- 10 The kit may further include components required for real time detection of amplification products, such as fluorescent probes for example. As aforementioned the relevant real-time technologies, and the reagents required for such methods, are well known in the art and are
- 15 commercially available. Thus, for example using the TAQMAN[®] technique, the probes may need to be of sequence such that they can bind between PCR primer sites on the nucleic acid molecule of interest that is subsequently detected in real-time. Similarly, MOLECULAR BEACONS probes may be designed
- 20 that bind to a relevant portion of the relevant nucleic acid sequence. If using the SCORPION probe technique for real time detection the probe will need to be designed such that it hybridizes to its target only when the target site has been incorporated into the same molecule by extension of the
- 25 tailed primer. In the AMPLIFLUOUR method, the primers will be suitably labelled with an appropriate probe. Suitable probes are accordingly included in a further aspect of the kits of the invention.
- 30 Kits for use in methods where recruitment to a promoter, or levels of histone acetylation are measured, may include suitable components necessary for carrying out a chromatin immunoprecipitation.

Pharmacogenetic kits

These kits may include all the components listed above, since determining the level or activity of HDAC2 is also critical to this aspect of the invention.

5

Once the level or activity of HDAC2 has been determined, it is then possible to conclude which type of treatment is suitable or not. Accordingly, a suitable information sheet may be incorporated in the kit which allows the user of the
10 kit to interpret the results to thus decide on an appropriate course of treatment. The sheet may take the form of written instructions, or a flow chart or decision tree for example.

15 Gene therapy kits

Kits for use in the gene therapy aspects of the invention may include a suitable HDAC2 containing construct which allows expression levels of HDAC2 to be restored to normal levels.

20

The construct is preferably an expression vector which drives expression of HDAC2 in the targeted tissue, which may be a tumour. The types of cancer which are relevant are discussed in detail supra.

25

The expression vector preferably contains a wild type copy of the HDAC2 gene. However, altered version may be utilised provided they retain substantially wild type, or improved, HDAC activity.

30

Any suitable vector for delivery of functional copies of the HDAC2 gene may be included in the kits of the invention.

One principal requirement is that tissue specificity of delivery and expression is achieved. The two major sources of vectors which may be utilised comprise viral vectors and non-viral vectors.

5

Within the group of viral vectors, preferred types include adenoviruses, retroviruses, in particular Moloney murine leukaemia virus (Mo-MLV), adeno-related viruses and herpes simplex virus type I. Typically, the gene encoding HDAC2, will be included in the viral genome, preferably in the "non-essential" region of the viral genome. The virus may be made replication incompetent to prevent unwanted replication once the virus has been targeted.

15 In terms of targeting the viral vector to the desired site, a number of possibilities exist. For example, the env gene (which encodes the viral vector's envelope) may be engineered or replaced with the env gene from a different virus to alter the range of cells the viral vector will "infect". Furthermore, alteration of the viral tropism may be achieved by using suitable antibodies raised against antigenic determinants on the cell surface of the desired target cells. The antibodies, which include all derivatives thereof, such as scFV, nanobodies, heavy chain antibodies, VH domains, Fab fragments etc., may be genetically incorporated into the viral vectors to provide targeted gene delivery of the HDAC2 gene. Most preferred is use of scFV (Hedley et al., Gene Therapy (2006) 13, 88-94). The viral vectors may have many genes removed, such as packaging genes, in order to reduce immunogenicity and/or infectivity. These functions may thus be supplied by a helper virus, and

kits further including a suitable helper virus are contemplated within the scope of the invention.

Adenoviruses are a preferred vector for inclusion in the
5 kits of the invention.

Alternatives to viral vectors include direct gene delivery, use of other delivery agents and use of molecular conjugates. Tissue specific promoters may be employed as
10 appropriate. Direct gene delivery may be achieved for example by microinjection of a suitable vector, such as a plasmid carrying the HDAC2 gene, directly into the tissue of interest. Kits for direct delivery are included in the scope of the invention. Alternatives include use of
15 ballistic transformation, for example using vector coated onto suitable particles (e.g. gold particles). Additional delivery agents include liposomes and derivatives thereof. As discussed above, targeting proteins such as antibodies and derivatives thereof may be utilised in order to ensure
20 delivery to the cells of interest. Molecular conjugates may include suitable proteins conjugated to the DNA of interest using a suitable DNA binding agent. Kits for use in all of these techniques are envisaged.

25 Thus, the kit may also include reagents to facilitate transfection, as appropriate.

Since, in a preferred embodiment, the cancer has been diagnosed or assessed according to the diagnostic and
30 pharmacogenetic methods of the invention, the gene therapy kits may also incorporate components from these kits (as described supra).

The invention will now be described with respect to the following non-limiting examples in which:

5 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Biochemical and biological effects of HDAC2 mutations in human cancer.

- 10 (a) Schematic representation of the HDAC2 gene, with the location of the (A)₉ repeat, and the amino acid sequence of wild type and mutant HDAC2 proteins. Black and grey arrows represent the transcription and translation start site respectively.
- 15 (b) Electropherograms of HDAC2 wild-type (normal colon and SW48) and mutant (RKO and CO115) cells.
- (c) HDAC2 protein expression analyzed by western-blot (*left*) and immunofluorescence (*right*) is lost in the mutant RKO and
20 CO115 cells, but not in the other colon cancer cell lines with a wild-type sequence. HDAC1 protein and HDAC2 mRNA levels cells are not significantly different.
- 25 (d) HDAC2 enzymatic activity analyzed in the HDAC2-immunoprecipitated extracts is deeply depleted in RKO cells.
- (e) Quantification of histone H3 and H4 acetylation levels using western-blot (*left*) and high performance capillary
30 electrophoresis (*right*) after treatment with HDAC inhibitors. The hydroxamic acid TSA does not induce histone hyperacetylation in the HDAC2-deficient RKO and CO115 cells,

whilst in HDAC2-proficient cells (HCT-116, SW48 and LoVo) hyperacetylation is achieved. The carboxylic acids valproate (Val) and butyrate (But) induce hyperacetylation in all cells.

5

(f) TSA induces cell growth inhibition, apoptosis and G2/M cell cycle arrest in HDAC2-proficient cells, but HDAC2-mutant cells (RKO) show a marked resistance to the these three typical effects of the administration of a HDAC inhibitor.

10

(g) Butyrate induced tumor shrinkage in all cancer cells xenografted in nude mice independently of their HDAC2 status, whereas TSA was only able to accomplish these effects in the HDAC2-proficient cell line (HCT-116), whilst RKO and CO115 remained resistant (*upper right*).

15

Left, unsupervised clustering expression analysis discriminates between HDAC2-mutant (RKO and CO115) and HDAC2-wild-type (HCT-15, LoVo, HCT-116 and SW48) cell lines. *Lower right*, chromatin immunoprecipitation demonstrates that the loss of HDAC2 occupancy at a particular promoter (NCOA4) in HDAC2-mutant cells (CO115 and RKO) is associated with overexpression of the corresponding gene.

20

(h) HDAC2 mutations in human cancer. Immunohistochemistry of HDAC2 in sporadic MSI+ colon tumours: *Upper*, strong HDAC2 expression in two tumours with wild-type sequences; *Lower*, loss of HDAC2 staining in two tumours harbouring the HDAC2 mutation.

25

30

(i) FISH analysis of HDAC2. Metaphases spreads from HCT-116, RKO and CO115 cell lines show two copies of chromosome 6 with green signals (labelled as B in the figure) that correspond to the clone covering the HDAC2 gene and red signals (labelled as A in the figure) that correspond to the control BAC clone mapping to the 6p21 region.

Figure 2. HDAC2 haploinsufficiency in two endometrial cancer cell lines with HDAC2 heterozygous mutations.

a, Metaphases spreads from AN3CA and SKUT1 cell lines show two copies of chromosome 6 with green signals (labelled as B in the figure) that correspond to the clone covering the HDAC2 gene and red signals (labelled as A in the figure) that correspond to the control BAC clone mapping to the 6p21 region.

b, Western blot showing the levels of HDAC2 expression in SKUT1, AN3CA, RKO and HCT116.

c, Bisulfite genomic sequencing of the HDAC2 promoter gene demonstrates an unmethylated CpG island. A schematic representation of the CpG sites included in the PCR fragment is shown. CpG sites are represented as squares: black (methylated) and white (unmethylated).

d, Quantification of histone H3 and H4 acetylation levels using western blot (left) and high performance capillary electrophoresis (right) after treatment of SKUT1 cells with TSA and sodium valproate.

e, Effects of TSA on cell viability (MTT assay) of SKUT1 cells.

Figure 3. Response of colon cancer cell lines to TSA.

a, HDAC2 activity in immunoprecipitated extracts of HCT116 and CO115 colon cancer cell lines.

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b, Effects of the HDAC inhibitor TSA on cell viability (MTT assay) of the same cell lines. Cells were treated with 250 nM TSA for 48h

c, Dose response curves of the effects of the HDAC inhibitor TSA on cell viability (MTT assay) of colon cancer cell lines. Cells were treated for 48 h with different concentrations of TSA (0-1000 nM). Experiments were performed in triplicate. The HDAC2-deficient cell lines RKO and CO115 show an enhanced resistance to cell growth inhibition by TSA.

Figure 4. Tumor xenografts from colon cancer cell lines with HDAC2-mutations (RKO and CO115) are resistant to TSA actions.

a, PBS, BUT and TSA treated female athymic nude mice 17 days after injection of RKO (left flank) and HCT116 (right flank) cells.

b, Tumors were excised and weighed. Tumor detail in cm and weight in mg for PBS-, BUT- and TSA-HCT116, RKO and CO115 cells.

c, Effect of the HDAC inhibitors TSA and sodium butyrate (But) on the *in vivo* growth of HCT116, RKO and CO115. Tumor size was monitored over time and size in mm³. Dark square: PBS treatment, Dark circle: TSA treatment, Dark triangle: BUT treatment.

Figure 5. Effects of the HDAC inhibitor suberoylanilide hydroxamic acid (SAHA) on cell viability (MTT assay) and apoptosis (propidium iodide) of colon cancer cell lines.

Cells were treated for 24h with 5 mM SAHA. Experiments were performed in triplicate. The HDAC2-deficient cell line RKO

shows an enhanced resistance to cell growth inhibition and apoptosis by SAHA.

Figure 6: Reconstitution and interference of HDAC2

5 functions.

a, HDAC2 activity of immunoprecipitated extracts of RKO transfected with empty vector or HDAC2.

HDAC2 and HDAC1 expression levels are shown in the western blot below.

10 *b*, Quantification of H4 acetylation by HPCE. RKO-HDAC2-transfected cells show resistance to histone acetylation mediated by TSA.

c, Reduction in colony formation in RKO cells transfected with HDAC2.

15 *d*, Reduction in tumor growth in xenografted nude mice in RKO cells transfected with HDAC2.

e, *Left*, Western blot of HDAC2-knocked down HCT116 cells by siRNA. *Right*, Quantification of histone H4 acetylation by HPCE. HDAC2-knocked down HCT116 cells are resistant to

20 histone acetylation mediated by TSA.

f, Effect of HDAC silencing by siRNA on the in vivo growth of HCT116 cells. Large tumor on the right flank corresponding to HDAC2-Knocked down HCT116 cells and small tumor on the left flank corresponding to HCT116 cells. Tumor
25 size was monitored over time and size in mm³

Figure 7: HDAC2 mutant cells have a characteristic expression signature.

a, Chromatin immunoprecipitation (ChIP) analysis of the
30 occupancy by HDAC2 of several promoters obtained from the microarray expression studies. HDAC2 is present in the HCT-116 HDAC2-wild-type cells, but absent in CO115 and RKO. The

bound fraction of the 'no antibody' (NAB) control is shown as negative control.

b, RT-PCR expression analysis of the HDAC2-target genes demonstrates gene overexpression in HDAC2 mutant cells.

5 c, Dendrogram representing the cluster analysis of 12 colon tumours with microsatellite instability and normal controls generated by the SOTA software

(<http://bioinfo.cnio.es/cgi-bin/tools/cluster-ing/sotarray>).

The HDAC2-mutant tumors show a distinct pattern of gene
10 expression compared to HDAC2-wild type tumors

Figure 8. The data produced from the gene expression analysis is reproduced in full in the table shown in figure 3. Note that all probes were supplied by Agilent and the
15 probe numbers are designated accordingly.

EXPERIMENTAL SECTION

1. Introduction

Widespread changes in DNA methylation^{1,2} and post-
5 translational modifications of histones occur in cancer
cells^{3,4}, and both marks have a crucial role in chromatin
packaging and gene expression^{1,2,5,6}. We are largely ignorant
of the mechanisms underlying the disruption of the
10 epigenetic landscape in transformed cells. One interesting
possibility is that the enzymes that epigenetically modify
DNA and histones, and the transcription factors that "read"
these marks, may themselves be targets of genetic
disruption, such as it occurs with the p300 histone
acetyltransferase^{7,8}.

15

To explore the presence of inactivating mutations in the
described "epigenetic modifier genes" it is useful to
consider tumors displaying microsatellite instability (MSI),
both in the context of hereditary nonpolyposis colon cancer
20 (HNPCC) associated with germline mutations in the mismatch
repair genes⁹, and in sporadic cancers associated with
hMLH1 inactivation by promoter CpG-island methylation^{9,10}.
Tumors with MSI progress along a genetic pathway that
exhibits a high rate of insertion/deletion mutations in
25 mononucleotide repeats, which often result in the generation
of premature stop codons. Illustrative target genes include
the growth-control gene TGFBR1¹¹ and the proapoptotic gene
BAX¹².

2. Results

30

We first screened six colorectal (RKO, SW48, LoVo, HCT-15,
Col15 and HCT-116) and four endometrial (AN3CA, SKUT-1,

SKUT-1B and HEC1B) cancer cell lines with MSI for the presence of mutations in all the exonic mononucleotide repeats present in the coding sequences of histone deacetylases (HDAC1 and HDAC2), histone acetyltransferases (pCAF), histone methyltransferases (G9a), DNA methyltransferases (DNMT1 and DNMT3b), and methyl-CpG binding proteins (MBD1, MBD2 and MeCP2). The location of the corresponding repeats and the PCR primers used are shown in Supplementary Methods. Only the wild-type sequences were detected for all the genes described, with the single important exception of HDAC2 (Fig. 1a,b).

We found a frameshift mutation in the HDAC2 gene in the (A)₉ coding microsatellite repeat of exon 1, consisting of the deletion of an A, in two colorectal cell lines (RKO and Col15) and two endometrial cell lines (AN3CA and SKUT-1). We analyzed the RKO and Col15 cell lines and found no evidence of the HDAC2 protein in nuclear extracts (Fig. 1c) and in the immunofluorescence staining (Fig. 1c).

Most importantly, we demonstrated HDAC2 functional abrogation in RKO cells by showing the lack of histone deacetylase enzymatic activity in HDAC2-immunoprecipitated cell extracts of RKO cells compared with HCT-116, SW48 and LoVo cells, these last three having the wild-type HDAC2 coding repeat (Fig. 1d). Since the two alleles of HDAC2 in RKO and Col15 cells are retained by FISH analysis (Fig 1i) and only mutant alleles were obtained by the sequencing of multiple clones, these observations imply the biallelic inactivation of HDAC2 by the described mutation. In contrast, the two endometrial cancer cell lines were heterozygous for the HDAC2 mutation and haploinsufficiency

for HDAC2 function was observed (Fig. 2a). For all cell lines, no significant differences in the levels of HDAC2 mRNA were observed (Fig. 1c, left) and no evidence of HDAC2 mutations were found in colorectal (SW480, SW620, CaCo2 and COLO250) and endometrial (KLE) cancer cell lines that were not MSI.

Once the presence of an inactivating mutation of HDAC2 in cancer cells had been confirmed, it became very important to establish whether the abolition of HDAC2 function altered the biochemical and cellular effects mediated by the histone deacetylase inhibitors (HDACis). This could be a potentially relevant clinical issue, since HDACis are drugs that have significant anticancer activities at doses that are well tolerated by patients in clinical trials¹³. In the case of colorectal cancer, HDACis induce tumor growth inhibition in cell lines^{13,14} and in Apc (min) mice¹⁵. Could the detection of a HDAC2 inactivation mutation in a given tumor predict the response to HDACis? An equivalent pharmacogenetic scenario has been recently presented itself in the presence of somatic mutations in the Epidermal Growth Factor (EGFR) gene in lung neoplasms that render these tumors more sensitive to the killing effect of small-molecule kinase inhibitors of EGFR¹⁶.

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To address these issues we assessed the effects of three classical HDACis, the hydroxamic acid trichostatin A and the carboxylic acids butyrate and valproate, on five colorectal cancer cell lines: the HDAC2-mutant cell lines RKO and Col15, and the HDAC2-wild type cell lines HCT-116, SW48 and LoVo. We analyzed the acetylation levels at histones H3 and H4 using western blotting with antibodies raised against

30

tetraacetylated peptides of histones H3 and H4, and high-performance capillary electrophoresis (HPCE)³. We found that whilst butyrate and valproate were able to induce hyperacetylation of histones H3 and H4 in all colorectal cell lines irrespective of their HDAC2 status, trichostatin A was unable to induce the hyperacetylation of either histone in the HDAC2-deficient RKO and Col15 cell lines, but was effective in the HDAC2-wild type cells (Fig. 1e). The HDAC2-deficient cells were resistant to trichostatin A action from a biochemical and also a cellular point of view. We found that valproate and butyrate were able to induce blockage of the cell cycle at G2/M, significantly inhibited proliferation, and induced apoptosis in all cancer cell lines independently of their HDAC2 status, while trichostatin A was only able to accomplish these effects in the HDAC2-proficient cell lines; RKO remained highly resistant (Fig. 1f and Fig 3c).

We reproduced these results in xenografted nude mice models: butyrate induced tumor shrinkage in all cancer cell lines independently of their HDAC2 status, whereas trichostatin A was only able to accomplish these effects in the HDAC2-proficient cell line (HCT-116), whilst RKO and Col15 remained highly resistant (Fig. 1f). Interestingly, suberoylanilide hydroxamic acid (SAHA), another HDAC is from the same chemical family as trichostatin A, was also unable to efficiently inhibit cell growth and induce apoptosis in HDAC2-deficient RKO cells (Fig. 5).

To further establish a link between HDAC2 mutations and the phenotypes observed, we reconstituted HDAC2 function in

HDAC2-deficient cancer cells (RKO) or knocked-down HDAC2 in HDAC2-proficient cells (HCT-116). Transfection of wild-type HDAC2 in RKO cells restored HDAC2 activity (Fig. 6a) and rendered these cells more sensitive to the actions of trichostatin A (Fig. 6b). Most interestingly, the ectopic expression of HDAC2 in these HDAC2-deficient cells induced tumor suppressor-like features, such as growth inhibition in xenografted nude mice and reduced colony formation (Fig. 6c and 6d). In sharp contrast, the downregulation of HDAC2 by RNA interference in HDAC2 wild-type cells (HCT-116) was associated with a resistance to the effects of trichostatin A and an enhanced tumor growth in the xenograft nude model (Fig. 6e and 6f).

The involvement of HDAC2 in human cancer was reinforced in an additional experiment. Since HDAC2 seems to be a central player in the epigenetics network at the level of regulation of gene transcription, we wondered whether HDAC2 truncating mutations conferred a particular expression signature to the cancer cells harboring this alteration. Using expression microarray analysis, we found that in unsupervised clustering analysis, the MSI+ HDAC2-mutant cell lines (RKO and Col115) grouped together in a separate branch to the MSI+ HDAC2-wild-type cell lines (HCT-116, SW48, HCT-15, LoVo) (Fig. 1g). HDAC2-mutant cells are characterized by the overexpression of many tumor-promoting and oncogenic genes, in association with the loss of HDAC2 recruitment to those particular promoters, as determined by chromatin immunoprecipitation (Fig. 1g, 7a and 7b).

30

Finally, once we had demonstrated the functional molecular and cellular consequences of harboring an inactivating

mutation of HDAC2 in cancer cells, we sought to measure the frequency of the described HDAC2 disruption in human primary tumors. We assessed the HDAC2 mutational status of 228 human primary malignancies with microsatellite instability, including colorectal tumors from HNPCC patients (n=47) and sporadic colorectal (n=127), gastric (n=38) and endometrial (n=16) neoplasms (Table 1). We found that the frameshift mutation in the HDAC2 gene in the (A)₉ coding microsatellite repeat of exon 1 was present in 21% (48 of 228) of the primary tumors analyzed. No significant differences in HDAC2 mutation frequency were found between inherited and sporadic tumors or between tumor types (Table 1).

Table 1. Frequency of HDAC2 mutations in cancer cell lines, primary tumors and normal tissues.

Frequency of HDAC2 mutation in human samples		
Sample type	Cell lines	Tissue samples
Colon Tumors from HPNCC	-	8/47 (17%)
Sporadic Colon Tumors MSI+	2/6	26/127 (20.4%) ^b
Sporadic Gastric Tumors MSI+	-	11/38 (28.9%)
Sporadic Endometrial Tumors	2/4 (50%) ^c	3/16 (18.7%)
Sporadic Colon Tumors MSI-	0/4	0/40
Normal Colon	-	0/50
Normal Lymphocytes	-	0/50

^aHomozygous mutations.
^bFor six cases analyzed, five homozygous and one heterozygous mutations were observed.
^cHeterozygous mutations

For 17 cases of sporadic colon tumors with microsatellite instability, we conducted a double-blind immunohistochemical analysis of HDAC2 mutational status (Fig. 2). In all cases with the wild-type HDAC2 gene (n=11), HDAC2 protein was

strongly expressed. In contrast, of the six HDAC2 mutant tumors, five (83%) completely lacked HDAC2 expression, whilst a heterogeneous pattern of loss of expression was observed in the remaining case. Laser microdissection analysis of the HDAC2-stained sections confirmed that the presence of the HDAC2 mutation was always associated with the loss of HDAC2 signal. The described HDAC2 mutation was not present in primary colorectal tumors without microsatellite instability (0/40), normal colorectal mucosa (0/50) or in normal lymphocytes from healthy donors (0/50) (Table 1, supra).

Furthermore, similar to what we observed in the cancer cell lines, an expression microarray analysis of twelve MSI+ primary colorectal tumors, eight wild-type and four HDAC2 mutant, clustered in a separate branch to the HDCA2-mutant samples, underscoring the particular tumor phenotype associated with the mutation (Fig. 7c and the data produced from the gene expression analysis is reproduced in full for those genes whose expression was significantly altered between tumors and wild type cells in the table in Figure 8).

References

1. Jones, P.A. & Baylin, S.B. Nat. Rev. Genet. 3, 415-428 (2002).
- 5 2. Feinberg, A.P. & Tycko, B. Nat. Rev. Cancer 4, 143-153 (2004).
3. Fraga MF, et al. Nat. Genet. 37, 391-400 (2005).
4. Seligson DB, et al. Nature 435, 1262-1266 (2005).
5. Jenuwein, T. & Allis, C.D. Science 293, 1074-1080 (2001).
- 10 6. Bannister, A.J. & Kouzarides, T. 376, 269-288 (2004).
7. Gayther, S.A., et al. Nat. Genet. 24, 300-303 (2000).
8. Ionov, Y., Matsui, S. & Cowell, J.K. Proc. Natl. Acad. Sci. USA 101, 1273-1278 (2004).
9. Lynch, H.T. & de la Chapelle, A. N. Engl. J. Med. 348, 919-932 (2003).
- 15 10. Herman, J.G., et al. Proc Natl Acad Sci USA 95, 6870-6875 (1998).
11. Markowitz, S., et al. Science 268, 1336-1338 (1995).
12. Rampino, N., et al. Science 275, 967-969 (1997).
- 20 13. Marks, P.A. & Jiang, X. Cell Cycle 4, 549-551 (2005).
14. Archer, S.Y., Meng, S., Shei, A. & Hodin, R.A. Proc. Natl. Acad. Sci. USA 95, 6791-6796 (1998).
15. Myzak, M.C., et al., FASEB J. Jan 11, (2006).
16. Pao, W. & Miller, V.A. J. Clin. Oncol. 23, 2556-2568 25 (2005).

3. Methods

Cell lines and primary tumor samples.

5 Human colorectal and endometrial cancer cell lines were obtained from the American Type Culture Collection. HDAC inhibition treatment was developed adding 0.25 μ M trichostatin A, 10 mM sodium valproate or 10 mM sodium butyrate to the culture medium for 24 hours. We obtained DNA
10 samples from 228 human primary malignancies corresponding to colon tumors of HPNCC patients (n=47) and sporadic MSI+ colon (n=127), MSI- colon (n=40), gastric (n=38) and endometrial carcinomas (n=16), as well as normal colon tissue (n=6), at the time of clinically indicated surgical
15 procedures. Normal lymphocytes from healthy donors (n=50) was also used. DNA was extracted using standard protocols.

Mutation analysis.

Genomic DNA from cell lines and primary tumors and cDNA from
20 the cell lines were amplified by PCR. Direct sequencing of PCR products and recombinant plasmids from ten clones of every sample were sequence in a automatized sequencer ABI Prism 3700. The genes studied, their locations and the primers used are described in the following table:

25

Table 2. Primers used for amplification of various genes.

Gene	Location	Repeat	Repeat location	Primers
HDAC2	6q21	(A) ₉	Exon1	F: 5'-ACCTCCGATTCCGAGCTTT-3' R: 5'-ACCTCCGATTCCGAGCTTT-3'
DNMT3B	20q11.2	(G) ₆	Exon 7	F: 5'-CAGAGCAGCAGTACCCCCTA-3' R: 5'-CCTCTCGGCCATACCTGATA-3'
DNMT1	19p13.2	(A) ₇	Exon 24	F: 5'TGACGATGAGGAAGTCGATG-3' R: 5'-CTTCTCCGACCCAAGAGATG-3'

DNMT1	19p13.2	(G) ₆	Exon 32	F: 5'-CGAGCGAGCCAGAGATAGAG-3' R: 5'-GGGCTCACCAGGTATTCAGA-3'
HDAC1	1p34	(G) ₆	Exon 12	F: 5'-ACGAATTGCCTGTGAGGAAG-3' R: 5'-TGGGTCTTTCTCTTTTTCATCC-3'
MBD1	18q21	(A) ₆	Exon 16	F: 5'-GACCTGCTCCCTTTTCCCTA-3' R: 5'-AGCCAGTCTGCAAATATCACC-3'
MBD2	18q21	(C) ₇	Exon 1	F: 5'-AGCGGGAAGAGGATGGATT-3' R: 5'-CCCAGGGAGGTACCTGAAGT-3'
MeCP2	Xq28	(G) ₆	Exon 5	F: 5'-TGAAAAGGGTCCTGGAGAAA-3' R: 5'-CGTTTGATCACCATGACCTG-3'
MeCP2	Xq28	(C) ₆	Exon 6	F: 5'-ACCACTCAGAGTCCCCAAAG-3' R: 5'-TCTGGGCATCTTCTCCTCTT-3'
PCAF	3p24	(C) ₆	Exon 2	F: 5'-CCATTTTATAGGCCGAGGAGT-3' R: 5'-ATGGCTACAACCTCCGACAGG-3'
G9a	9q34.3	(C) ₆	Exon3	F: 5'-CCCAGAGAAGTTCGAGAAGC-3' R: 5'-GCCATGTAGCACTGGTTCTG-3'
G9a	9q34.3	(A) ₆	Exon 5	F: 5'-GCTTGCTTGCCTTTTGTGTTT-3' R: 5'-TCTCAATCACCGTCCTCTGTT-3'

FISH analysis

Fluorescence in situ hybridization (FISH) was performed by standard methods, which include denaturations steps,
 5 overnight hybridization at 37°C, and two washes, one in 0.4xSSC at 75°C and another in 2xSSC at room temperature. The BAC clone containing the HDAC2 gene (RP11 456N11) was a kind gift from Dr. Mariano Rocci, at the University of Bari (Italy). Control BAC clone from chromosome 6p21 region was
 10 from our own library.

Histone extraction.

We prepared histones in accordance with established protocols¹. We obtained histones from cell lines and tumor
 15 samples in parallel with their matching controls under identical conditions. For cell lines, we isolated nuclei with RSB buffer (10 mM Tris 10 (pH 7.5), 10 mM NaCl and 3 mM MgCl₂) containing 1% Nonidet-P40 and protease inhibitors. We extracted nuclei with 0.25 M HCl and precipitated them with

eight volumes of acetone. For tumors and their normal tissue counterparts, we homogenized samples with a Polytron homogenizer (Brinkman Instruments) in 0.25 M HCl and incubated them with gentle agitation for 4 h. We

5 precipitated the resulting supernatant with eight volumes of acetone. We then fractionated individual histones by reverse-phase HPLC on a Jupiter C18 column. We made comparisons only between samples extracted with identical methodology.

10

Western blotting, immunolocalization and immunohistochemistry assays.

For western blotting, we collected cells by centrifugation and washed cell pellets twice with phosphate-buffered saline
15 buffer. For HDAC2 expression, nuclear extracts were fractionated on a 7.5% SDS-PAGE gel, transferred the fractions to a polyvinylidene difluoride membrane with 45- m pore size (Immobilon PSQ, Millipore), blocked the membrane in 5% milk PBS-T (phosphate-buffered saline with 0.1% Tween-
20) and immunoprobed it with antibodies to HDAC2 (1:1000) and HDAC1 (1:1000; both from Abcam). The acetylated forms of histones 3 and 4 were analyzed as previously described². We extracted the histones directly from the cell pellets with 0.250 M HCl. We fractionated 10 µg of the acid-extracted
25 proteins on a 10% SDS-PAGE gel. Transferred membranes were immunoprobed with antibodies to acetylated H4 (1:2,000, Upstate) and acetylated H3 (1:50,000, Upstate). We used horseradish peroxidase-conjugated antibody to rabbit IgG (Amersham) at 1:3,000 dilution in PBS-T as the secondary
30 antibody and antibody to H4 (1:3,000; Upstate) as a loading control. For immunolocalization experiments, we grew cells on coverslips and stained them with antibodies against HDAC2

and HDAC1 (Abcam) as previously described. We obtained images with a Leica DMRD photomicroscope coupled to a Leica DC200 camera, processed them using Adobe Photoshop software and analyzed them using public National Institutes of Health
5 Image software. Immunohistochemical staining of HDAC2 was performed using a polyclonal antibody (Abcam, Cambridge, UK) at a 1:1500 dilution. After antigen retrieval with citrate buffer, immunodetection was performed by the DAKO EnVision Visualization Method (DAKO, Glostrup, Denmark), with
10 diaminobenzidine chromogen as the substrate

HPCE quantification of global histone acetylation.

We quantified global histone H4 acetylation as previously described³. We prepared individual histone fractions from
15 cell nuclei and purified them by reverse-phase HPLC on a Jupiter C18 column (Phenomenex, Inc.) with an acetonitrile gradient (20-60%) in 0.3% trifluoroacetic acid, using a HPLC gradient system (Beckman-Coulter). We resolved non-, mono, di-, tri- and tetra-acetylated histone H4 derivatives by
20 HPCE. We used an uncoated fused-silica capillary (Beckman-Coulter; 60.2 cm 75 µm, effective length = 50 cm) in a capillary electrophoresis system (P/ACE MDQ, Beckman-Coulter) with 100 mM phosphate buffer (pH 2.0) 0.02% (w/v) HPM-cellulose as running buffer and operating voltages of 12
25 kV.

HDAC2 activity

For HDAC2 activity determinations, HDAC2 was immunoprecipitated as described elsewhere⁴ from nuclear
30 extracts using the same antibody used for Western blotting and immunolocalization experiments. We then determined the HDAC2 activity by measuring released [3H]acetate in a

scintillation counter after 1 hour incubations of HDAC2 immunoprecipitates at 37°C with 3H-labeled histones4.

Apoptosis and cell cycle analysis

5 The percentage of apoptotic cells was determined by flow cytometry using Vybrant® Apoptosis Assay Kit #4-YO-PRO®-1/propidium iodide (Molecular Probes/Invitrogen). To analyze the cell cycle profiles, we stained with propidium iodide and the percentage of cells in G2/M was determined by flow
10 cytometry.

Cell viability assay

Cell viability was determined as previously described5. Aliquots of 1.5×10^4 cells were plated in 96-well
15 microdilution plates. Following overnight cell adherence, experimental media containing the drugs or control media was added to appropriate wells. After 48 hours, the media was replaced by drug-free fresh media (100 µl/well) containing MTT (50 µg). After a 3 hour incubation at 37°C in 5% CO2
20 atmosphere, the MTT was removed and MTT-formazan crystals were dissolved in DMSO (100 µl/well). Absorbance at 570 nm was determined on an automatized microtiter plate reader. It was established that optical density was directly proportional to the cell number up to the density reached by
25 the end of the assay.

Analysis of HDAC2 CpG island promoter methylation.

DNA samples were treated with sodium bisulfite and primers spanning the CpG island of HDAC2 promoter were used for
30 bisulfite genomic sequencing. Primer sequences and PCR conditions are available upon request. Eighteen clones were analyzed.

HDAC2 transfection and colony formation assay

The HDAC2 expression vector pcDNA3-HDAC2 was constructed by cloning the cDNA corresponding to the gene HDAC2 in pcDNA
5 vector (Invitrogen). Transfection of RKO cells was performed by electroporating 107 cells in 0.8 ml PBS with 40 µg of the vector at 250 V and 975 µF. After electroporation, cells were washed with PBS and seeded with 106 cells/ml in fresh medium containing 20% FBS. Clones expressing HDAC2 were
10 selected in complete medium supplemented with 1 mg/mL G418. Stable clones were maintained in complete medium with 1 mg/mL G418. For colony formation experiments, stable G418-resistant colonies were fixed, stained with 2% methylene blue in 60% methanol, and the average number of colonies
15 present in each well was determined.

HDAC2 siRNA

The HDAC2-specific siRNA was designed and synthesized by
20 Qiagen. Two siRNA duplex were used against the HDAC2 gene that recognize the sequences 5'-CTG GGT TGT TTC AAT CTA ACA-3' and 5'-ACG GTC AAT AAG ACC AGA TAA-3'. Scramble siRNA was also purchased from Qiagen and used as a control. Transfection was carried out using oligofectamine
25 (Invitrogen) according to the manufacturer's specifications. At 12h after transfections the cells were washed with fresh medium, and maintained in a 10% FBS-supplemented medium. The cells were harvested at specific times for total protein and histones extraction, and HDCA2 content was analyzed by
30 western blotting and histone acetylation was quantified by HPCE.

Mouse xenograft model.

Six-week-old female athymic nude mice nu/nu (Harlan Sprague-Dawley, Indianapolis, IN), housed under specific pathogen-free conditions (Institutional Animal Welfare Committee Agreement), were used for HCT116, RKO and CO115 tumor xenografts. For treatments, animals were randomly separated in three seven-specimens-groups, differentiated for PBS (Control), TSA (Trichostatin A) and BUT (Butyric acid) treatments. Both flanks of each animal were injected s.c. with 10⁶ (HCT116) or 2x10⁶ (RKO and CO115) cells in a total volume of 200 µL of PBS. For transfections assays both flanks of each animal were injected subcutaneously with 2x10⁶ RKO (left) or RKO-HDAC2-transfected (right) cells in a total volume of 200 µL of PBS. Tumor development at the site of injection was evaluated daily. Animals were sacrificed at 21 days. The tumors were then excised and weighed.

References

1. Turner, B.M. & Fellows, G. Eur. J. Biochem. 179, 131-139 (1989).
2. Fraga, M.F. et al. Proc Natl Acad Sci U S A. 102, 10604-10609 (2005).
3. Fraga, M.F. et al. Nat. Genet. 37, 391 - 400 (2005)
4. Espada, J. et al.. J. Biol. Chem. 279, 37175-37184 (2004).
5. Ropero, S. et al. Breast Cancer Res. Treat. 86, 125-37 (2004).

4. Summary

Disruption of histone acetylation patterns is a common feature of cancer cells, although very little is known about its genetic basis. We have identified truncating mutations
5 in one of the primary human histone deacetylases, HDAC2, in sporadic carcinomas with microsatellite instability, and in tumors arising in individuals with hereditary nonpolyposis colorectal cancer syndrome. The presence of the HDAC2 frameshift mutation causes a loss of HDAC2 protein
10 expression and enzymatic activity, and renders these cells more resistant to the usual antiproliferative and proapoptotic effects of histone deacetylase inhibitors. Since such drugs may serve as cancer-therapeutic agents, our findings support the use of HDAC2 mutational status in
15 future pharmacogenetic-oriented treatment of these patients.

In summary, we have demonstrated the presence of an inactivating mutation in the HDAC2 gene in human cancer cell lines and primary tumors with microsatellite instability
20 that impairs these transformed cells' biochemical and cellular responses to trichostatin A, the archetypcal hydroxamic acid with histone deacetylase inhibitory activity. This finding supports the role of epigenetics, and especially of histone modifications, in tumorigenesis and it
25 may have potential relevance for the pharmacogenetic selection of cancer patients treated with histone deacetylase inhibitors.

CLAIMS

1. A method of diagnosing cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 is indicative of cancer.

2. The method of claim 1 wherein HDAC2 protein expression is determined.

3. The method of claim 2, wherein a loss of HDAC2 protein expression is indicative of cancer.

4. The method of any preceding claim wherein analysis of gene expression of genes other than HDAC2 is utilised in order to determine the level or activity of HDAC2.

5. The method of claim 4 which comprises determining the levels of gene expression of a panel of genes, wherein the panel of genes comprises at least one gene selected from

(a) CARD6 (A_23_P41854), TOP1MT (A_23_P216241), SWAP70 (A_23_P116533), KIAA1212 (A_23_P17269), IRF5 (A_23_P500271), CGI-90 (A_23_P83492), UTS2 (A_23_P63343), DJ462O23.2 (A_23_P46604), HHLA3 (A_23_P200303), NFATC4 (A_23_P140394), DKFZp686H1423 (A_23_P392235), MGC17839 (A_23_P329890), TSTA3 (A_23_P94301), ZNF175 (A_23_P332374), (A_23_P119023), KIAA1212 (A_23_P28664), LANCL1 (A_23_P50887), FLJ38819 (A_23_P385768), TAS2R9 (A_23_P336506), ZNF22 (A_23_P202458), SYT12 (A_23_P424645), KIAA1826 (A_23_P116166), ZHX1 (A_23_P43150), BAIAP1 (A_23_P96099), (A_23_P150316), ZNF22 (A_23_P384512), HMP19 (A_23_P125375), M160 (A_23_P61466),

TFPI (A_23_P17095), FJX1 (A_23_P150693), (A_23_P165598),
EMP3 (A_23_P119362), AP1S2 (A_23_P217384), CCRL2
(A_23_P69310), ZNF44 (A_23_P119279), VAPB (A_23_P91293),
(A_23_P28797), FLJ10458 (A_23_P141315), FLJ10826
5 (A_23_P3775), ZNF582 (A_23_P395464), RBM9 (A_23_P103091),
C14orf168 (A_23_P25913), KPNA4 (A_23_P218835), FUNDC2
(A_23_P171310), MGC29784 (A_23_P255916), DEDD2
(A_23_P141908), PHC1 (A_23_P323094), CSTF1 (A_23_P79882),
SLIT2 (A_23_P144348), EFHD2 (A_23_P23443), MGC17986
10 (A_23_P368777), ODF3L1 (A_23_P357900), SGSH (A_23_P254254),
DEFB127 (A_23_P385843), UCHL5 (A_23_P148798), LTA4H
(A_23_P204593), MFN1 (A_23_P253817), IKIP (A_23_P53467),
LTA4H (A_23_P388670), EIF3S6 (A_23_P43141), GSDM1
(A_23_P152605), ZZANK1 (A_23_P72725), KPNA5 (A_23_P156443),
15 CHRAC1 (A_23_P123544), FBXW2 (A_23_P254645), PTGFRN
(A_23_P114968), DUSP19 (A_23_P90938), PLEKHB2 (A_23_P28642),
TNFAIP6 (A_23_P165624), (A_23_P57836), C20orf45
(A_23_P210658), PRPS1 (A_23_P95764), PLSCR3 (A_23_P49597),
LOC92689 (A_23_P132914), TRIM38 (A_23_P93236), BRD4
20 (A_23_P425104), KIAA0649 (A_23_P146497), FBXO28
(A_23_P137578), PPP2R4 (A_23_P60458), IRAK1 (A_23_P73780),
SSH2 (A_23_P118712), EIF5A (A_23_P100925), C9orf103
(A_23_P123732), EEF1D (A_23_P31838), PRPS2 (A_23_P96641),
ABCC9 (A_23_P368691), WDFY2 (A_23_P218108), MGC75360
25 (A_23_P163373), LTK (A_23_P14853), (A_23_P348015), ZNF571
(A_23_P108342), FLJ12517 (A_23_P115523), (A_23_P90070),
FLJ31951 (A_23_P167556), MGC29875 (A_23_P46337), KIAA0103
(A_23_P60000), LARS (A_23_P218967), PEX19 (A_23_P160188),
GPR83 (A_23_P202740), ATAD2 (A_23_P216068), OR5AK2
30 (A_23_P1863), OR6Q1 (A_23_P161891), ITR (A_23_P88021),
MGC41816 (A_23_P95027), NDUFB9 (A_23_P157669), HSF1
(A_23_P253841), FAM48A (A_23_P140050), RPL10L (A_23_P99754),

KIAA1223 (A_23_P81012), RRM2B (A_23_P20223), LOC90806
(A_23_P97697), LY6E (A_23_P169077), FLII (A_23_P4425), IL3
(A_23_P122012), FLJ21168 (A_23_P85993), BCL2L2
(A_23_P140219), PIG8 (A_23_P86822), SMARCA1 (A_23_P44244),
5 SCUBE1 (A_23_P211619), CDYL2 (A_23_P371871), GDPD1
(A_23_P96060), SERAC1 (A_23_P145419), C11orf23
(A_23_P202637), FKBP10 (A_23_P15727), WDR35 (A_23_P108463),
PPM1K (A_23_P167138), NUDT12 (A_23_P259090), DIAPH1
(A_23_P213344), SIGIRR (A_23_P84344), SCGN (A_23_P251412),
10 CTNNAL1 (A_23_P157795), DIPA (A_23_P150249), SGPP1
(A_23_P347048), LOC196549 (A_23_P311039), KREMEN2
(A_23_P77612), FMNL2 (A_23_P332744),

(b) ACP6 (A_23_P160237), C3orf17 (A_23_P336670), SLC10A5
15 (A_23_P157428), (A_23_P60758), ALG6 (A_23_P35168), MAP4K3
(A_23_P154130), ITLN2 (A_23_P201419), PPIL4 (A_23_P42507),
RAE1 (A_23_P346206), DDX20 (A_23_P63153), CMKLR1
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PTK6 (A_23_P56978), PGM2L1 (A_23_P396765), (A_23_P250528),
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CHRM3 (A_23_P401472), CHRNA10 (A_23_P411188), LGR6
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(A_23_P38978), KIF4A (A_23_P148475), CRYBB1 (A_23_P143621),
10 SELE (A_23_P97112), LOC199675 (A_23_P330561), APOC4
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OR8A1 (A_23_P75677), RNF13 (A_23_P29378), TBX21
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IPO13 (A_23_P384600), (A_23_P44054), SLC37A4 (A_23_P35970),
ATR (A_23_P136054), GNAZ (A_23_P416581), ZFPM2
20 (A_23_P168909), PAPP A (A_23_P351270), BVES (A_23_P502782),
MMP15 (A_23_P100177), SFXN2 (A_23_P161253), AQP6
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(A_23_P115805), SQSTM1 (A_23_P81401), SEC3L1 (A_23_P113972),
(A_23_P104867), OR52J3 (A_23_P53119), POLD2 (A_23_P71140),
25 KIAA0363 (A_23_P93937), INSL5 (A_23_P51479), ZNF76
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(A_23_P10091), BAPX1 (A_23_P386254), ADRB2 (A_23_P145024),
TRIM49 (A_23_P1575), ODZ1 (A_23_P257263), BT D
(A_23_P155348), UMODL1 (A_23_P315964), C9orf19
30 (A_23_P414913), FLJ23834 (A_23_P348253), TNRC5
(A_23_P19352), (A_23_P33429), DKFZP434H2010 (A_23_P23617),
LOC220929 (A_23_P161156), PIGC (A_23_P86250),

(A_23_P99498), DTNA (A_23_P208158), GPR161 (A_23_P354320),
GNRH1 (A_23_P254594), KRTAP3-3 (A_23_P89649),
(A_23_P130496), RIP (A_23_P66758),

5 wherein an increase in the level of expression of at least
one gene selected from group (a) and/or (b) and/or (c)
and/or (d) and/or wherein a decrease in the level of
expression of at least one gene selected from group (e)
and/or (f) and/or (g) and/or (h) indicates a reduced level
10 or activity of HDAC2 and is therefore indicative of cancer.

6. The method of claim 5 wherein the panel of genes
comprises at least one gene taken from those genes listed in
groups (a) and/or (b) and/or (e) and/or (f).

15

7. The method of any of claims 4 to 6 wherein an increase
in the expression of any one or more of NCOA4, CTSB, TBCD,
PPP2R4 and/or CORO1C indicates a reduced level or activity
of HDAC2 and is therefore indicative of cancer.

20

8. The method of any preceding claim wherein analysis of
HDAC2 recruitment to one or more gene promoters is utilised
in order to determine the level or activity of HDAC2.

25 9. The method of claim 8 wherein a loss of recruitment of
HDAC2 at one or more gene promoters indicates a reduced
level or activity of HDAC2 and is therefore indicative of
cancer.

30 10. The method of claim 9 wherein the one or more gene
promoters comprise the HDAC2 and/or TBCD and/or PPP2R4
and/or CORO1C promoter.

11. The method of any preceding claim wherein analysis of histone acetylation is carried out in order to determine the level or activity of HDAC2.

5

12. The method of claim 11 wherein an increase in the acetylation levels of one or more histones indicates a reduced level or activity of HDAC2 and is therefore indicative of cancer.

10

13. The method of claim 12 wherein the one or more histones comprises histone H3 and/or histone H4.

14. The method of any preceding claim wherein the level or activity of HDAC2 is compared to a control sample in which HDAC2 is known to be expressed and/or active and/or a control sample in which HDAC2 is known to be inactive and/or not expressed.

15. A method for predicting the probability of successful treatment of cancer with a hydroxamic acid based HDAC inhibitor comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 is indicative of a low probability of successful treatment with the hydroxamic acid based HDAC inhibitor.

16. A method of selecting a suitable treatment regimen for cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 indicates that treatment using a hydroxamic acid based HDAC inhibitor is unsuitable.

17. The method of claim 16, wherein a reduced level or activity of HDAC2 leads to treatment using a carboxylic acid based HDAC inhibitor being selected.

5

18. A method of selecting a suitable treatment regimen for cancer comprising, in a sample obtained from a subject, determining the level or activity of HDAC2, wherein a reduced level or activity of HDAC2 indicates that treatment using a carboxylic acid based HDAC inhibitor should be selected.

10

19. The method of any of claims 15 to 18 wherein the level or activity of HDAC2 is determined according to the methods described in any of claims 2 to 14.

15

20. A method for treating cancer in a subject using a carboxylic acid based HDAC inhibitor, the method comprising selecting a subject for treatment according to the method of any one of claims 1 to 19.

20

21. A method for treating cancer in a subject, said subject having a reduced level or activity of HDAC2, comprising reconstitution of HDAC2 activity in the subject.

25

22. The method of claim 21 wherein reconstituting HDAC2 activity comprises delivery of wild type copies of the HDAC2 gene into the subject.

23. The method of claim 22 wherein delivery comprises use of a vector.

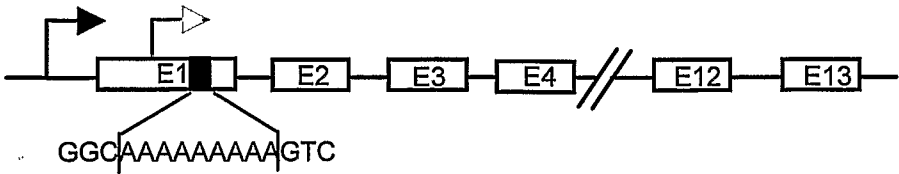
30

24. The method of claim 19 wherein the vector comprises an adenovirus.

25. The method of any preceding claim wherein the cancer is
5 associated with microsatellite instability.

26. The method of any preceding claim wherein the cancer comprises any of colorectal, gastric or endometrial cancer.

10 27. The method of claim 26 wherein the colorectal cancer comprises hereditary nonpolyposis colon cancer or sporadic colorectal cancer.



NORMAL- M A Y S Q G G G K K K V C Y Y Y D G D I G N Y Y Y G K G H P M Y ...
MUTATED- M A Y S Q G G G K K K S A T T T T V I L E I I I M D R V I P S T O P

FIG. 1a



FIG. 1b

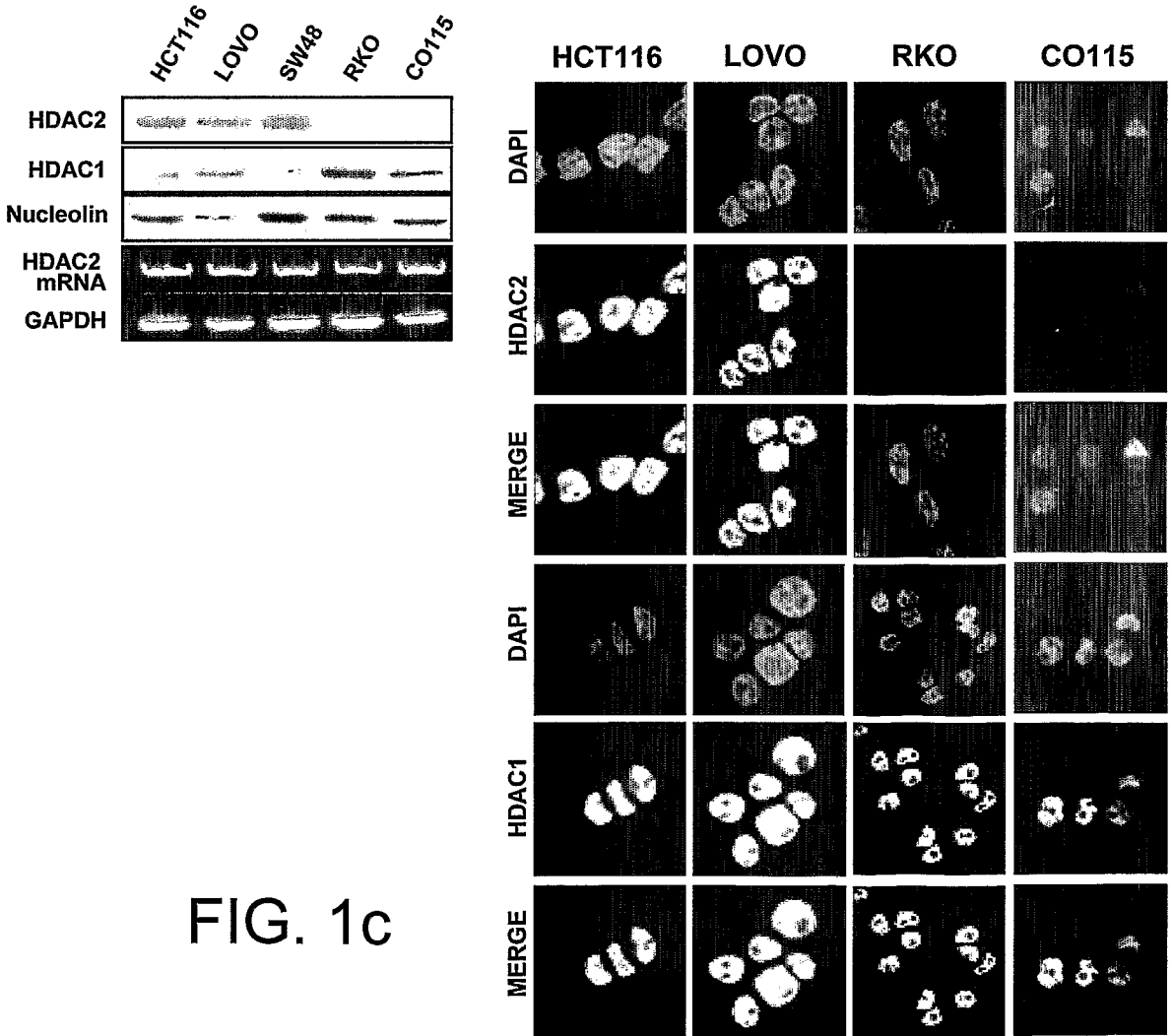


FIG. 1c

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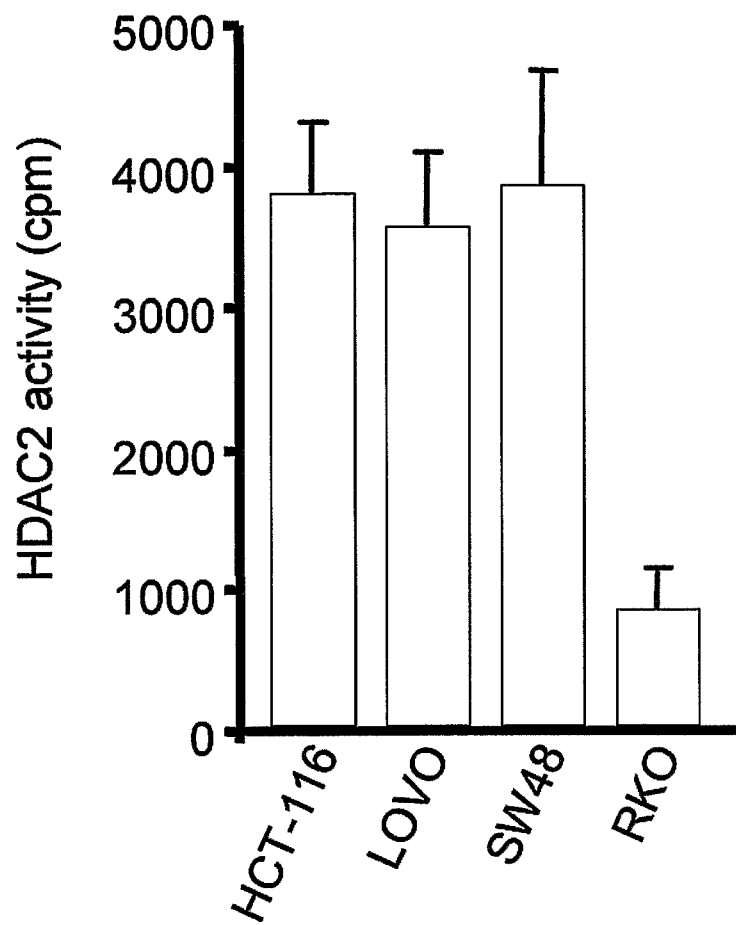


FIG. 1d

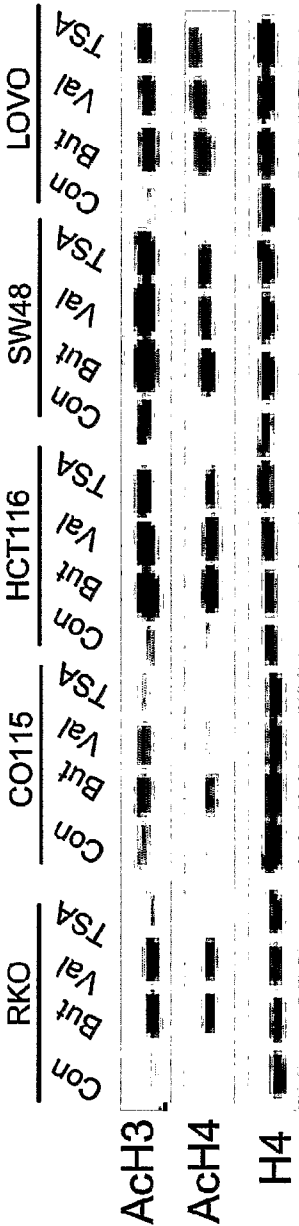
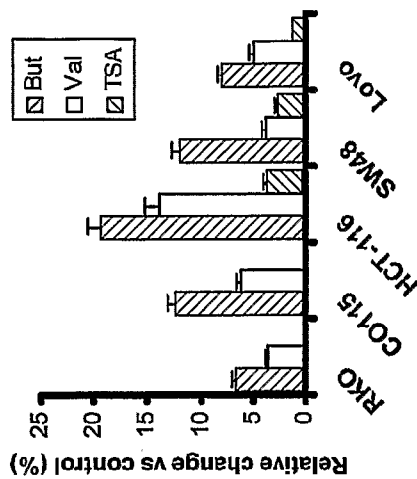


FIG. 1e

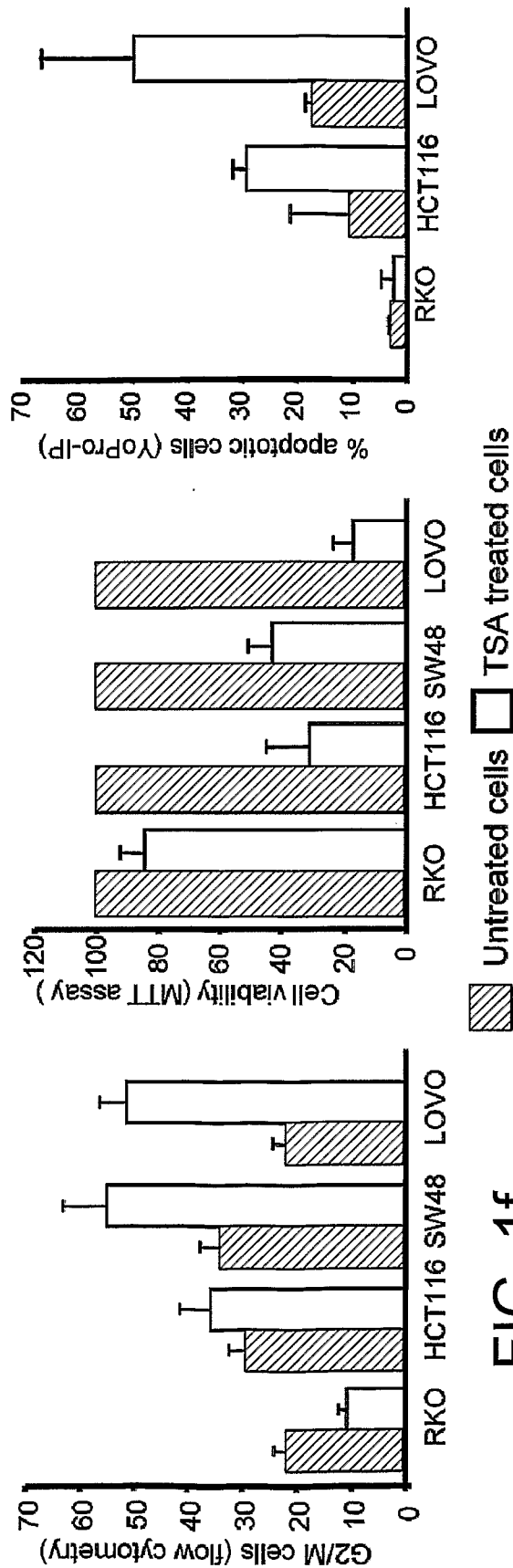


FIG. 1f

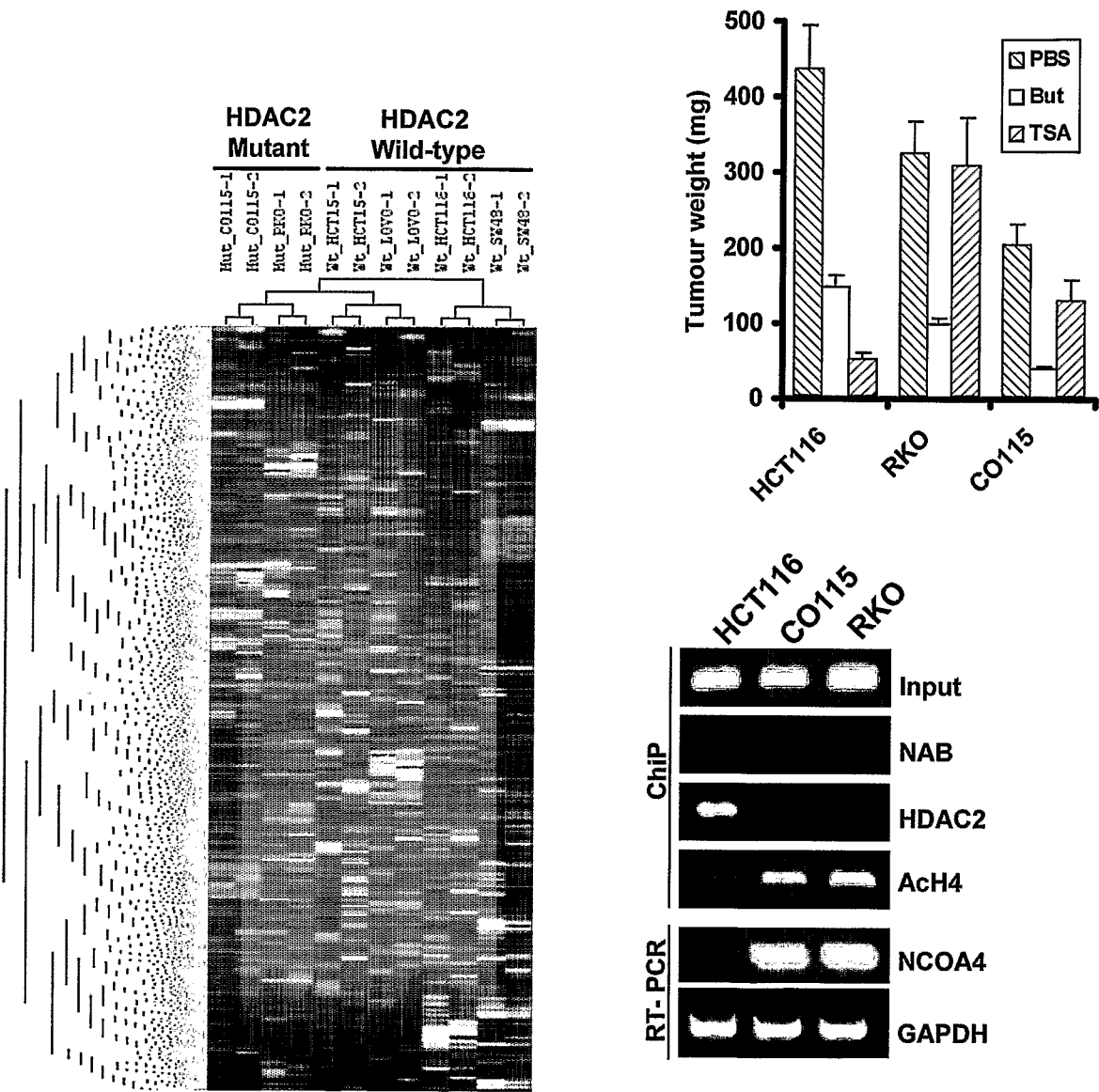
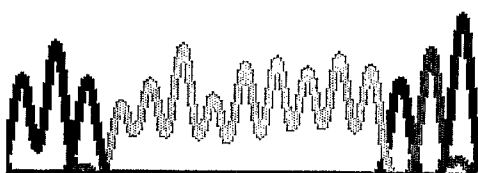


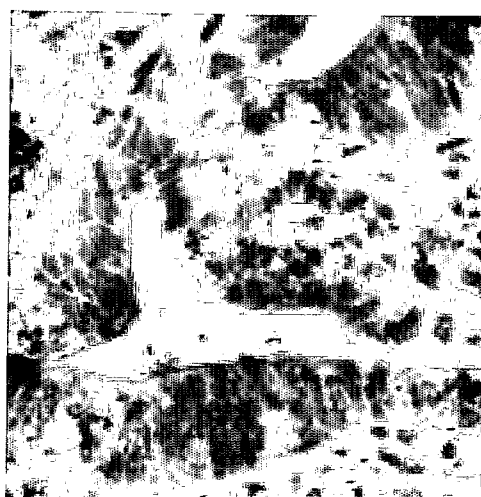
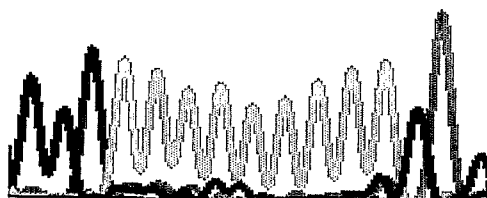
FIG. 1g

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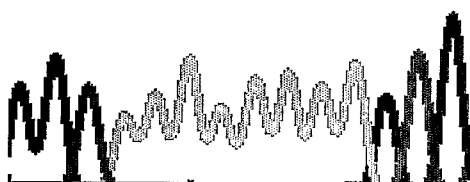
GGCAAAAAGTCT



GGCAAAAAGTCT



GGCAAAAAGTCT



GGCAAAAAGTCT

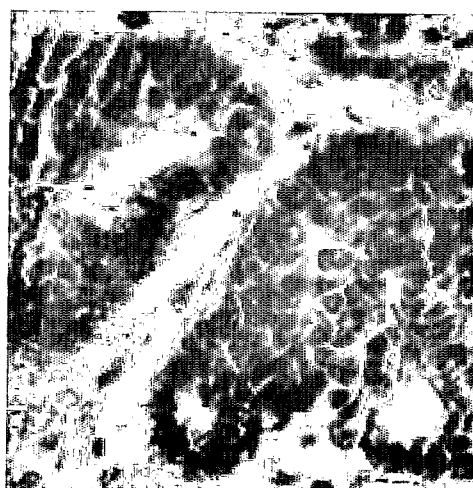
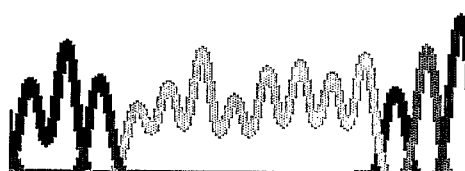


FIG. 1h

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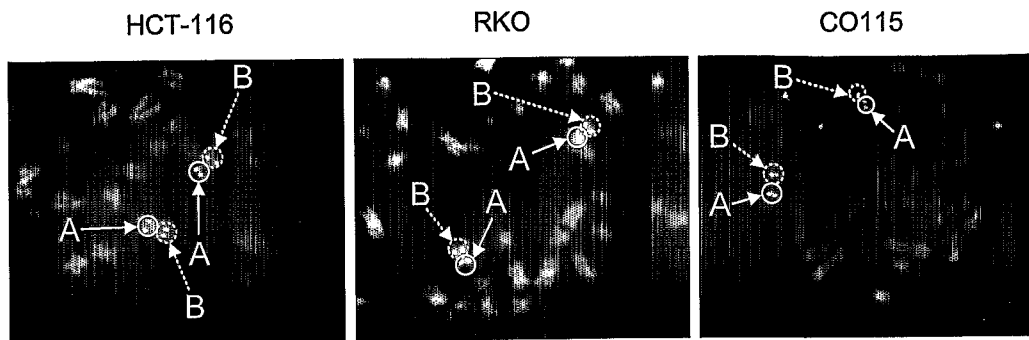


FIG. 1i

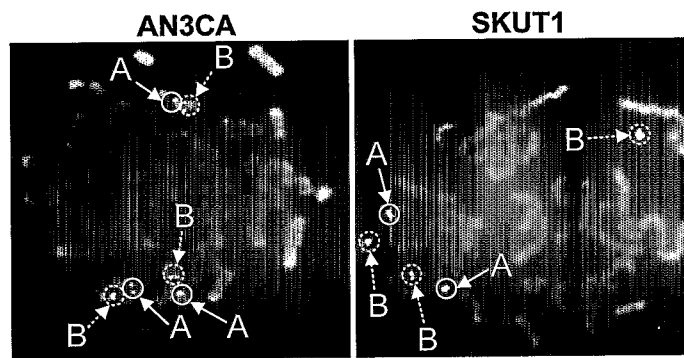


FIG. 2a

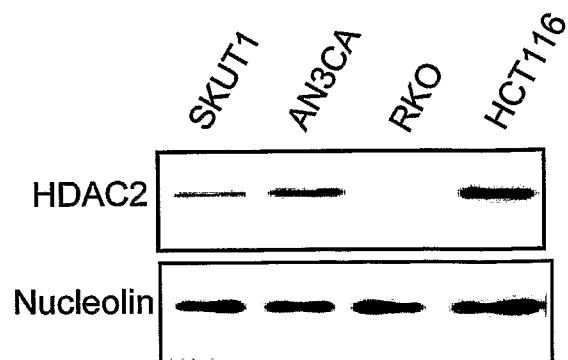


FIG. 2b

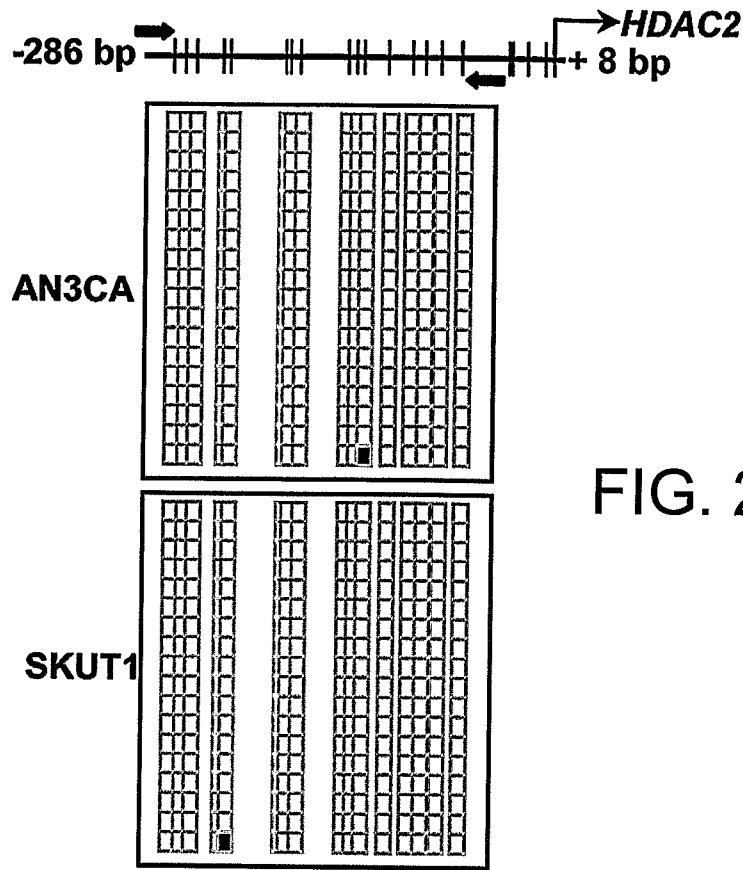


FIG. 2c

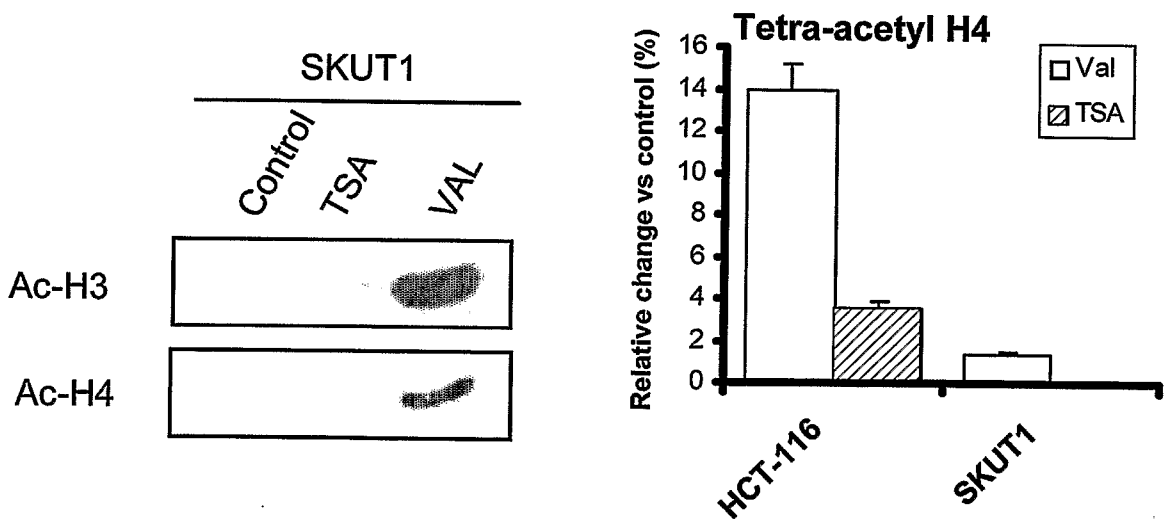


FIG. 2d

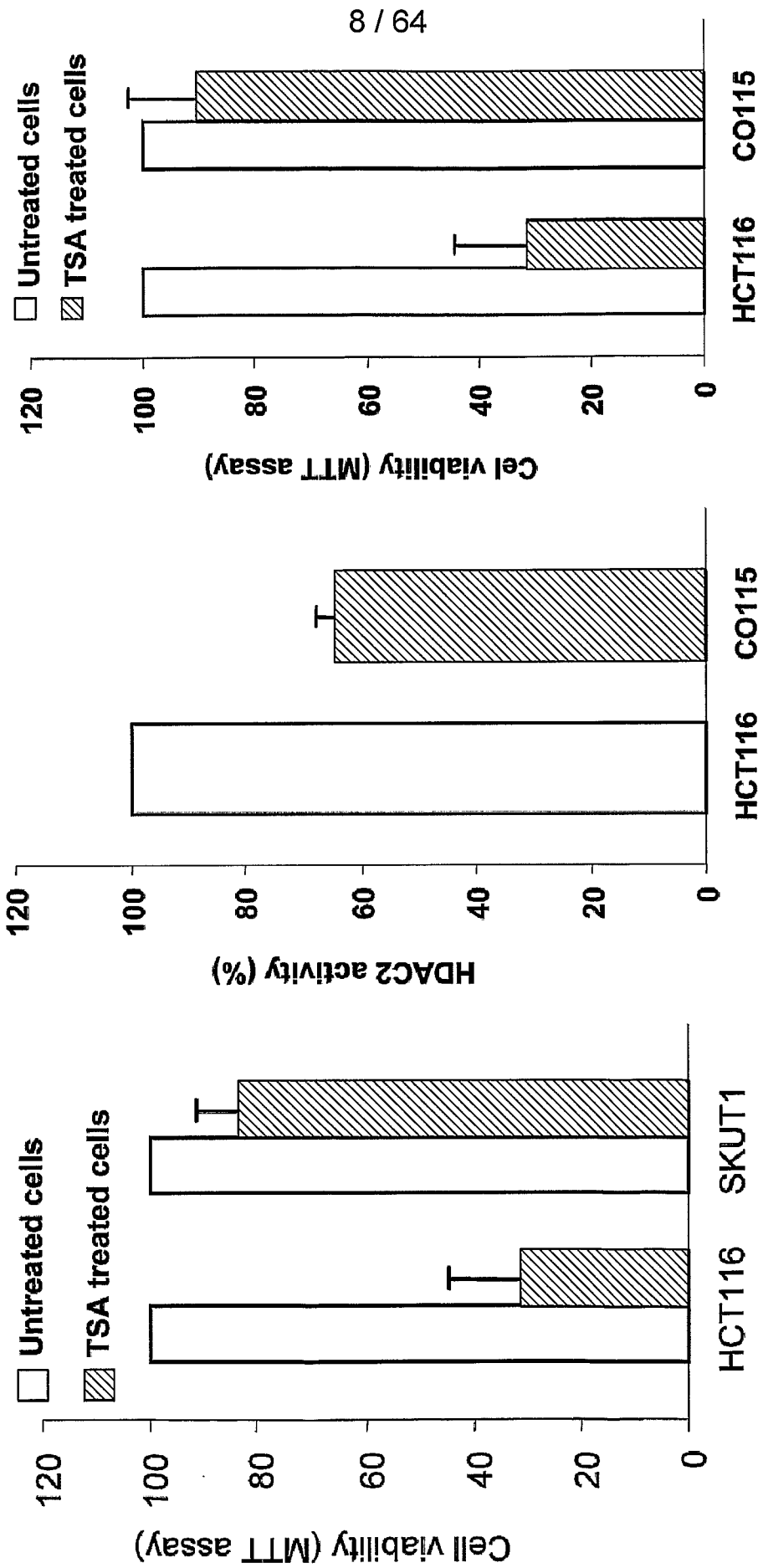


FIG. 2e

FIG. 3a

FIG. 3b

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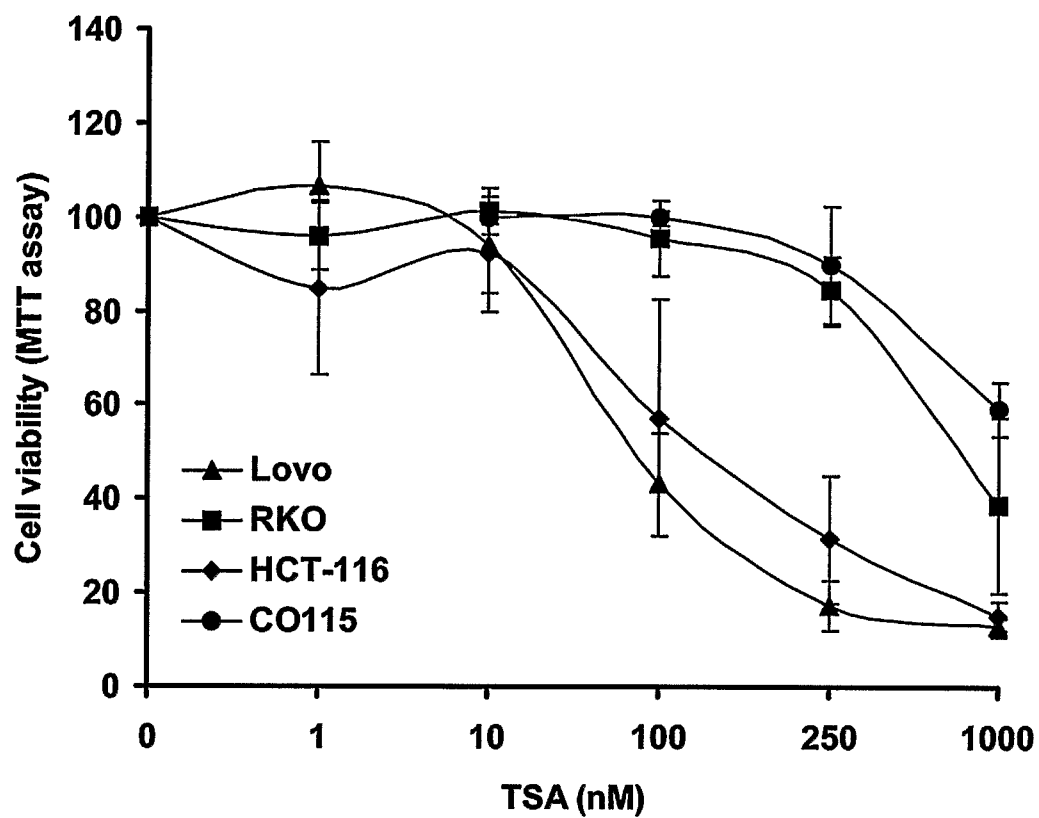


FIG. 3c



PBS BUT TSA

RKO/HCT116 RKO/HCT116 RKO/HCT116

FIG. 4a

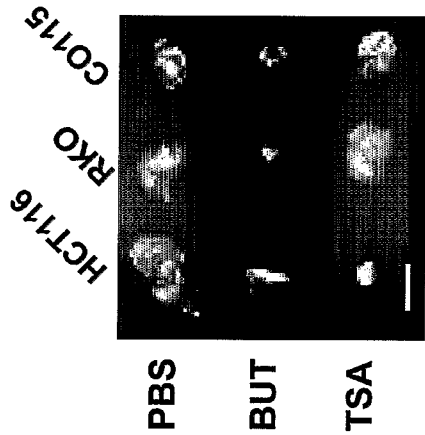


FIG. 4b

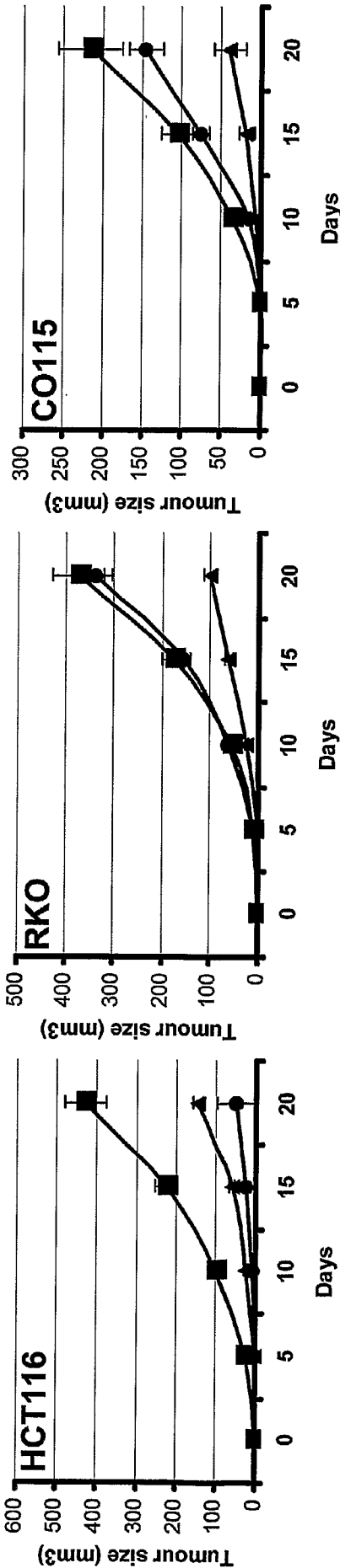


FIG. 4c

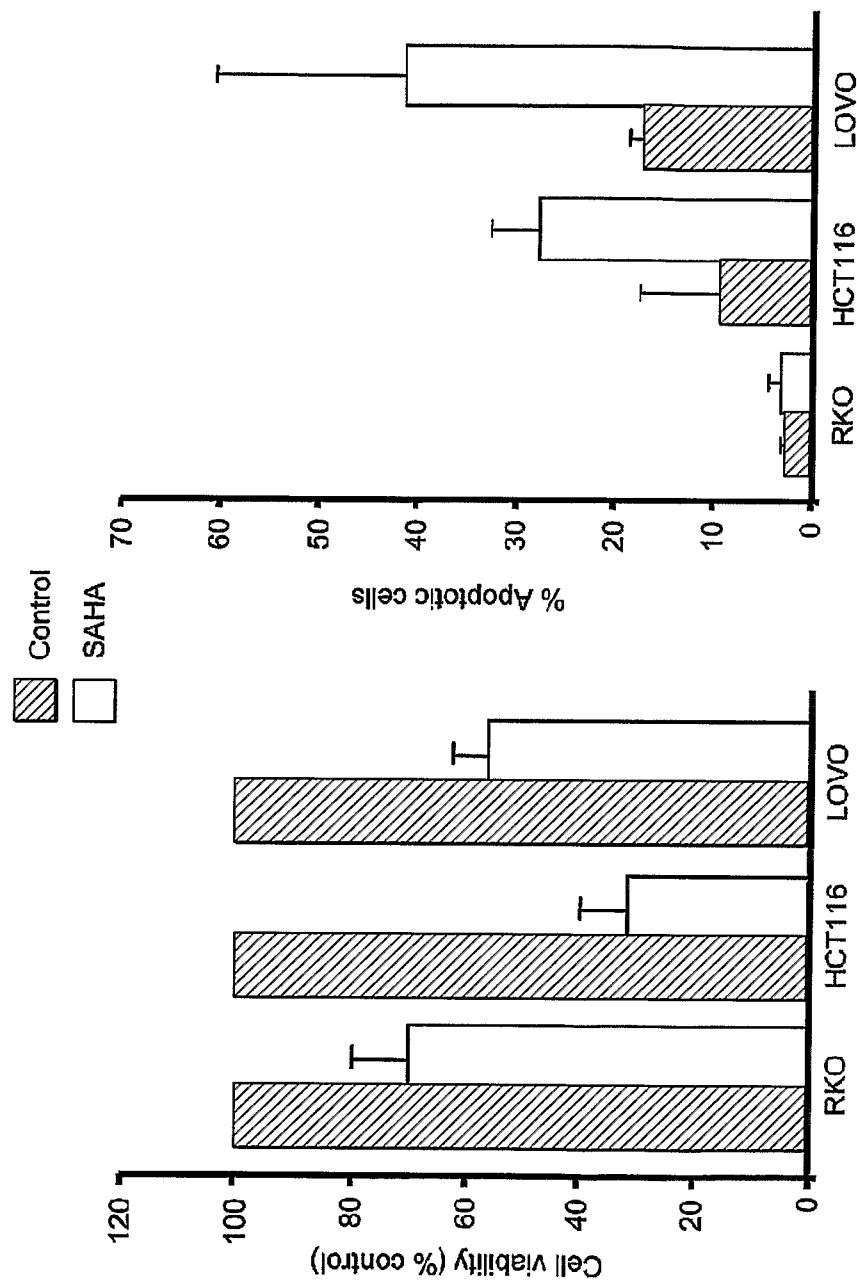


FIG. 5

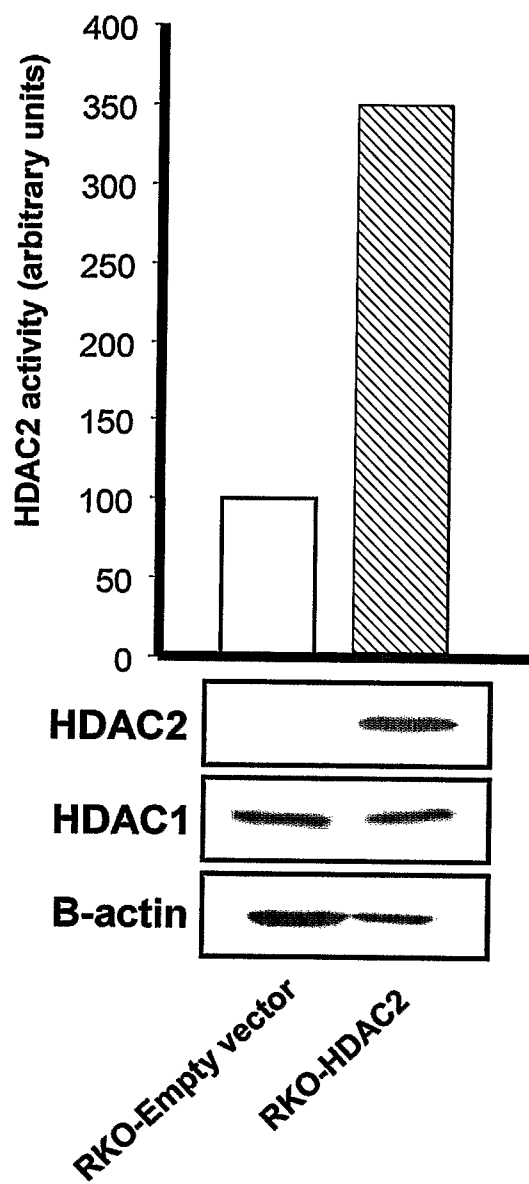


FIG. 6a

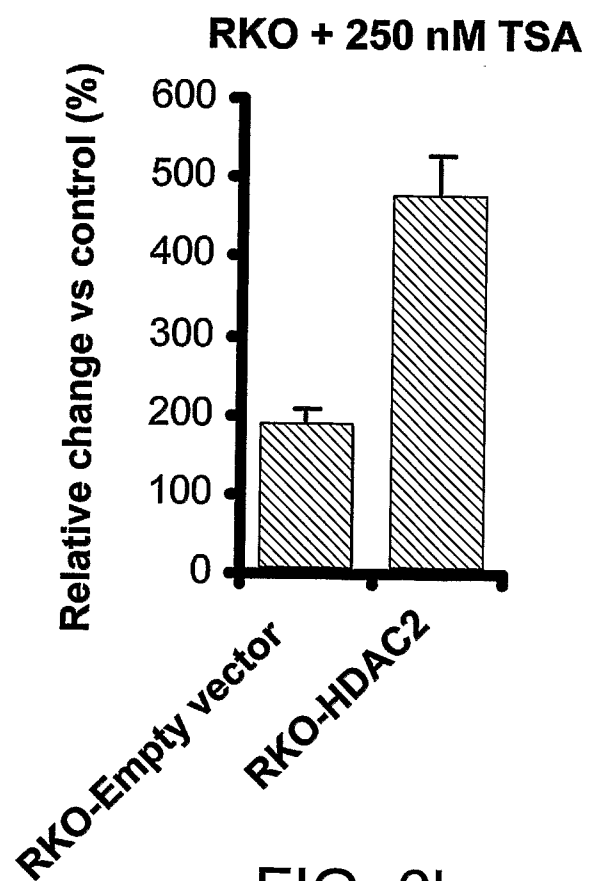


FIG. 6b

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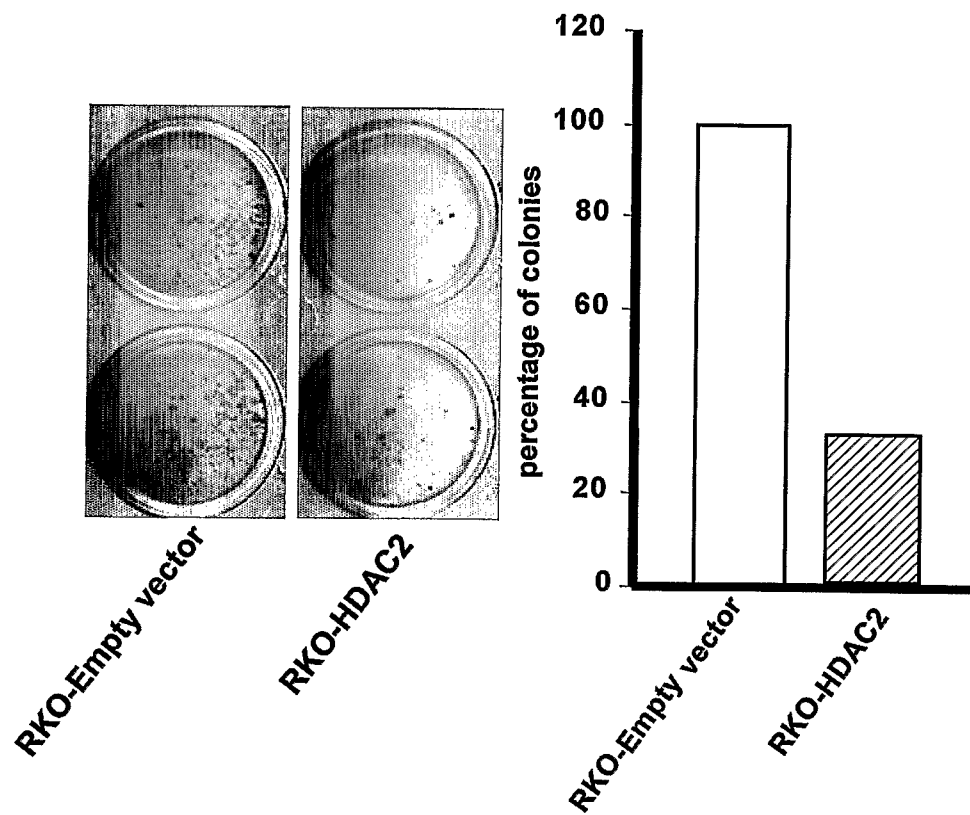


FIG. 6c

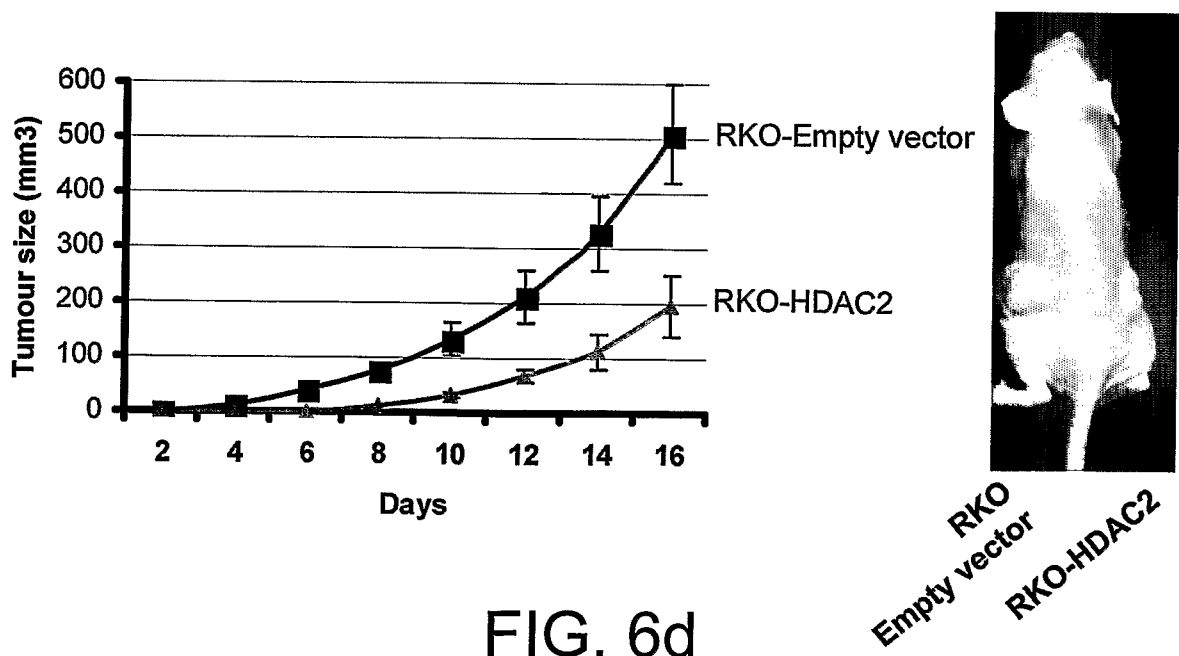


FIG. 6d

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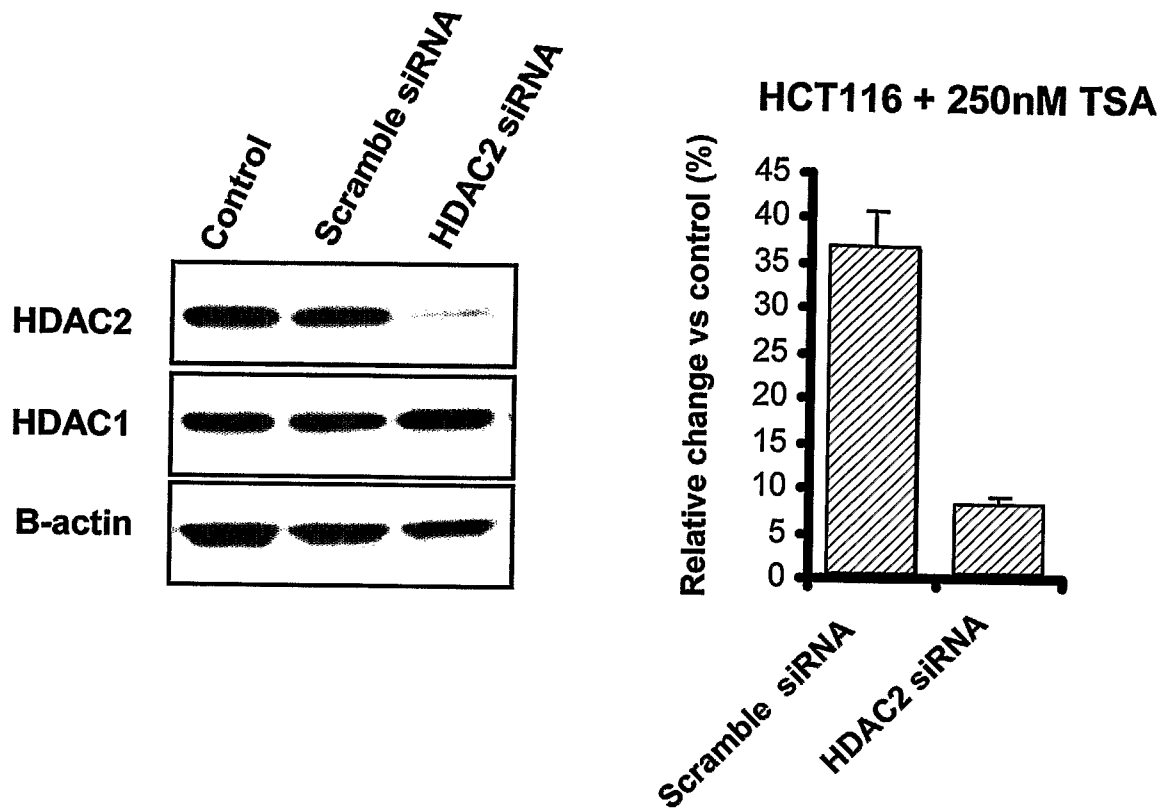


FIG. 6e

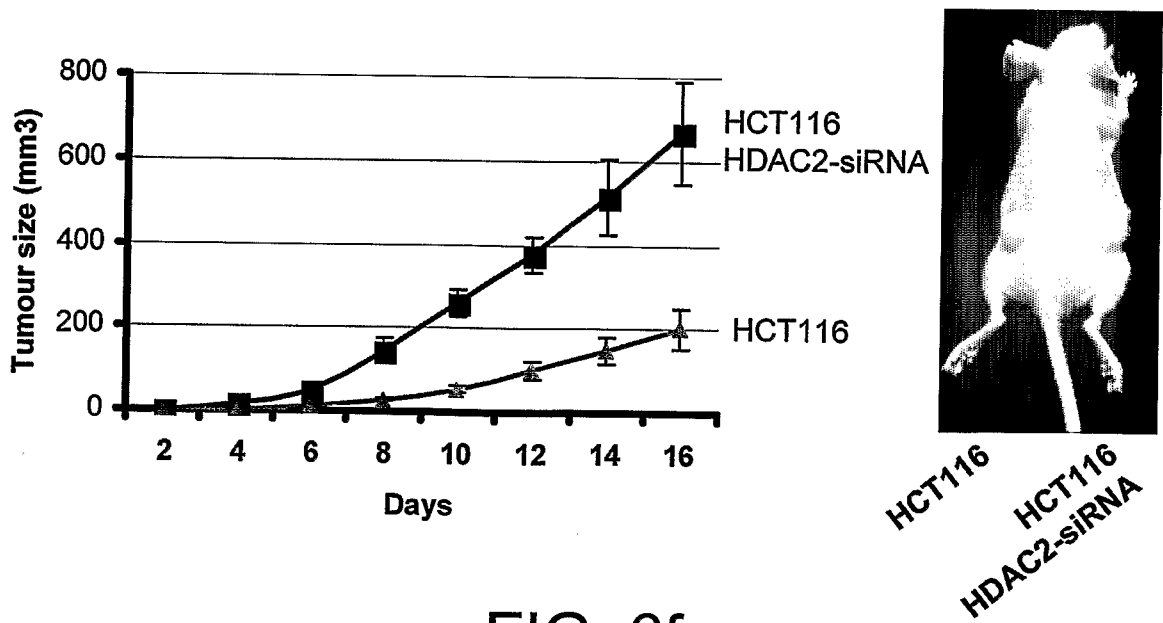


FIG. 6f

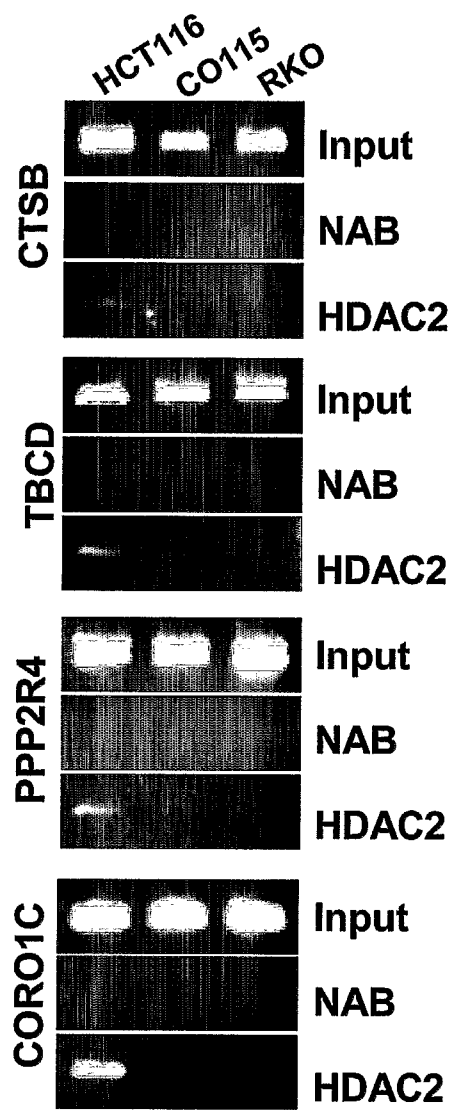


FIG. 7a

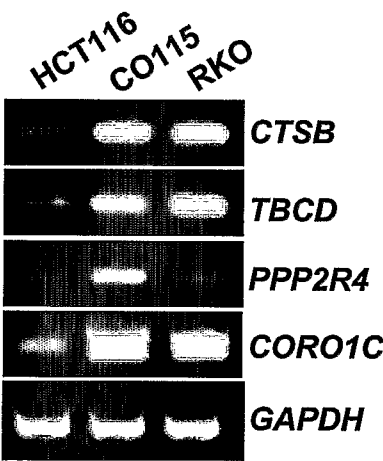


FIG. 7b

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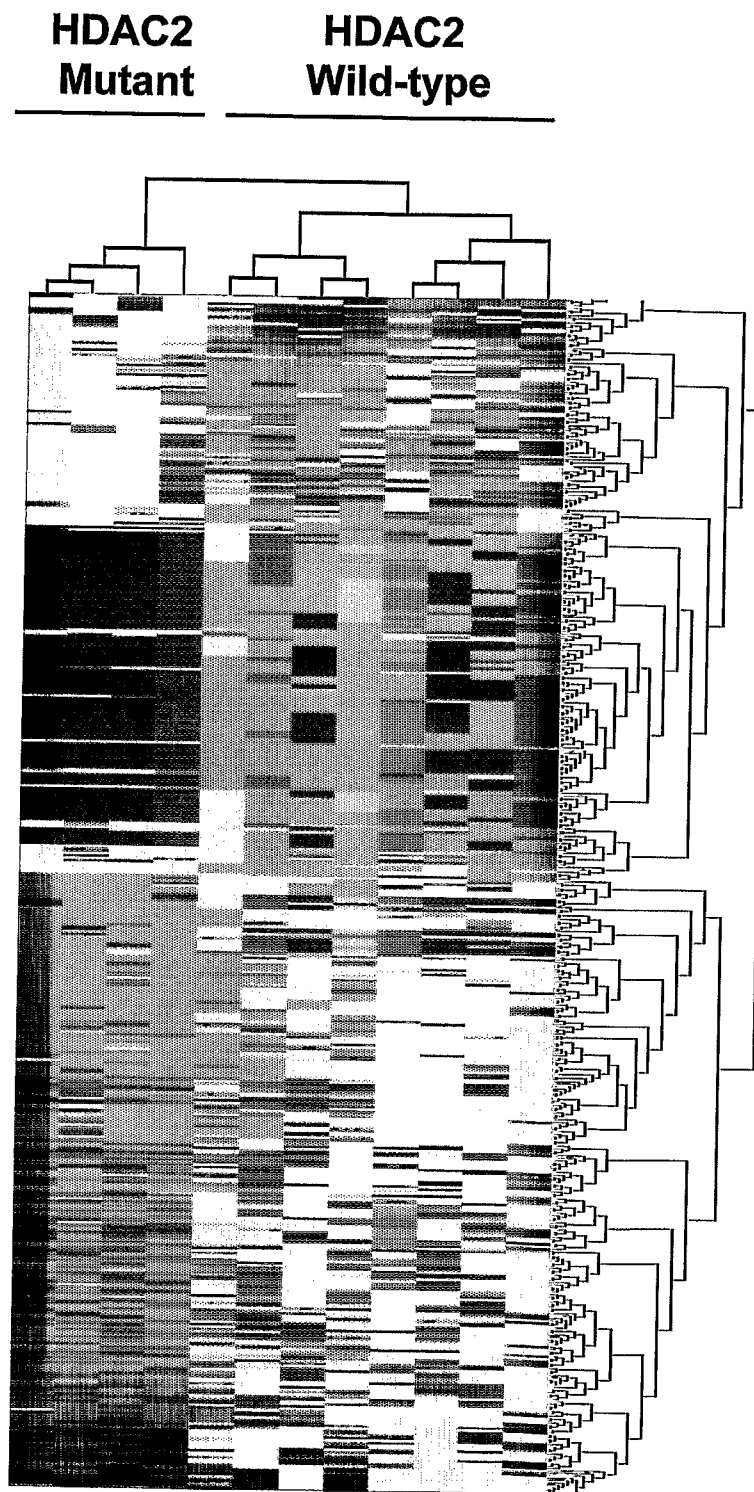


FIG. 7c

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ProbeName	GENE Symbol	mean mut	mean WT	FC MUT- m/WT-m	TTEST MUT- m vsWT-m	FC all MUT/WT	TTEST all MUT vsWT	ttest	FC
A_23_P407112	LOC132671	0.297446343	3.260318904	0.091232285	0.072447551	0.091232285	0.004535985	p<0.01	FC<-10
A_23_P18493	PTPN13	0.166259794	2.855205785	0.058230407	0.020833164	0.058230407	3.47740E-04	p<0.01	FC<-15
A_23_P213562	F2R	0.12770304	0.379702656	0.336323798	0.038674703	0.336323798	0.001575734	p<0.01	FC<-2
A_23_P84018	PPIC	0.39120698	1.157989868	0.337832818	0.059934594	0.337832818	0.002159501	p<0.01	FC<-2
A_23_P70660	FAM46A	0.274902991	0.802498258	0.342558988	0.065582387	0.342558988	0.003569743	p<0.01	FC<-2
A_23_P32175	LHX6	0.420877437	1.153528593	0.364860862	0.019258578	0.364860862	2.96751E-04	p<0.01	FC<-2
A_23_P120703	TTC3	0.566490478	1.502209239	0.377104909	0.075193083	0.377104909	0.009073593	p<0.01	FC<-2
A_23_P92794	C5orf13	0.044980486	0.117841617	0.381702894	0.064864439	0.381702894	0.007830429	p<0.01	FC<-2
A_23_P145965	TPST1	0.41058498	1.069658609	0.383846749	0.138201139	0.383846749	0.005484647	p<0.01	FC<-2
A_23_P252388	FLJ23577	0.089854035	0.233911294	0.384137223	0.021325626	0.384137223	0.003686822	p<0.01	FC<-2
A_23_P52031	PGM1	0.706353252	1.831821976	0.385601473	0.07832659	0.385601473	0.007822613	p<0.01	FC<-2
A_23_P318904	SERTAD4	0.190106934	0.479993716	0.396061298	0.002561177	0.396061298	7.63619E-04	p<0.01	FC<-2
A_23_P135517	PXMP2	0.646890201	1.619358675	0.399473082	0.00405771	0.399473082	1.90072E-05	p<0.01	FC<-2
A_23_P157330	EPHA1	0.376730942	0.926488224	0.406622483	0.069973992	0.406622483	0.004610824	p<0.01	FC<-2
A_23_P140434	MYO5C	2.997015544	7.263314438	0.412623682	0.075872909	0.412623682	0.008447251	p<0.01	FC<-2
A_23_P362148	DNER	0.079424457	0.191387249	0.414993458	0.058828731	0.414993458	0.009618807	p<0.01	FC<-2
A_23_P141235	POLR2A	0.91482583	2.171652568	0.421257913	3.68962E-04	0.421257913	8.92855E-06	p<0.01	FC<-2
A_23_P7212	IF	0.081188595	0.192033525	0.422783446	0.019121927	0.422783446	0.005784239	p<0.01	FC<-2
A_23_P152415	KIAA0182	0.373254003	0.882792506	0.42281057	0.039375578	0.42281057	0.001335365	p<0.01	FC<-2
A_23_P216609	EDG2	0.186921289	0.441328828	0.423541988	0.042306433	0.423541988	0.001588892	p<0.01	FC<-2
A_23_P203391	ASRGL1	0.351828072	0.828791438	0.424507368	0.021434209	0.424507368	3.41029E-04	p<0.01	FC<-2
A_23_P89762	PLEKHE1	1.49058961	3.43337676	0.434146822	0.127032201	0.434146822	0.00781686	p<0.01	FC<-2
A_23_P207493	CROP	0.371313665	0.850769196	0.436444651	0.032057391	0.436444651	0.003004676	p<0.01	FC<-2
A_23_P39237	ZFP36	1.24922588	2.818138056	0.443280583	0.034170696	0.443280583	0.001573456	p<0.01	FC<-2
A_23_P127128	DNAJC1	0.499694544	1.119475079	0.446365045	0.050721733	0.446365045	8.12353E-04	p<0.01	FC<-2
A_23_P124122	PXMP2	0.788576916	1.760854418	0.447837656	0.007646325	0.447837656	7.79800E-05	p<0.01	FC<-2
A_23_P150714	IPO7	1.065216205	2.365399873	0.450332401	0.045887845	0.450332401	0.001150437	p<0.01	FC<-2
A_23_P2601	TRA1	0.643908463	1.426723004	0.451319886	0.0470969	0.451319886	0.005537923	p<0.01	FC<-2
A_23_P203183	APOC3	0.063220209	0.139900588	0.451893806	0.001427778	0.451893806	0.003920614	p<0.01	FC<-2
A_23_P19291	TUBB2	0.336639518	0.740572624	0.454566516	0.020126743	0.454566516	4.67084E-04	p<0.01	FC<-2
A_23_P139260	SLC22A18	0.774086129	1.691107377	0.457739195	0.044086163	0.457739195	0.005130019	p<0.01	FC<-2
A_23_P52410	PLEKHK1	1.446874372	3.146266513	0.459870251	0.095727931	0.459870251	0.003124948	p<0.01	FC<-2
A_23_P114457	CD24	0.194362981	0.419409899	0.463420108	0.043191232	0.463420108	0.001790099	p<0.01	FC<-2
A_23_P36972	ZIC2	0.896483033	1.931324445	0.464180441	0.027840926	0.464180441	5.28158E-04	p<0.01	FC<-2
A_23_P148410	FTHL17	0.641795597	1.379779036	0.465143751	0.014806583	0.465143751	2.00633E-04	p<0.01	FC<-2
A_23_P103232	DUSP23	0.34823662	0.746379139	0.466567996	0.039383883	0.466567996	3.70257E-04	p<0.01	FC<-2
A_23_P21574	DPP7	0.553844472	1.182761356	0.468263922	0.001370808	0.468263922	2.07328E-05	p<0.01	FC<-2
A_23_P257231	AGXT2L1	0.588777126	1.255556609	0.468937141	0.08088675	0.468937141	0.00723414	p<0.01	FC<-2
A_23_P158318	ROR2	0.381483723	0.810070311	0.470926681	0.076620671	0.470926681	0.008607551	p<0.01	FC<-2
A_23_P360769	MAN2A1	0.262814106	0.554681049	0.473811223	0.072284391	0.473811223	0.004719745	p<0.01	FC<-2
A_23_P55276	HOXB7	0.666828101	1.386949087	0.480787728	0.043701899	0.480787728	0.005589034	p<0.01	FC<-2
A_23_P3934	FLJ20315	0.926944854	1.925247067	0.481467999	0.135462447	0.481467999	0.006211742	p<0.01	FC<-2
A_23_P45011	PPP1R14C	0.55104418	1.143174686	0.482029726	0.038165184	0.482029726	0.007212738	p<0.01	FC<-2
A_23_P23356	CGI-115	0.948128509	1.965161482	0.482468498	0.00175647	0.482468498	8.54172E-05	p<0.01	FC<-2
A_23_P151267	EPLIN	1.914948461	3.959498564	0.483634084	0.128181028	0.483634084	0.008034542	p<0.01	FC<-2
A_23_P131139	DIRC1	0.767399953	1.576659798	0.486725135	0.092941077	0.486725135	0.006573242	p<0.01	FC<-2
A_23_P116091	DPP3	0.842389184	1.727206945	0.487717576	0.077583149	0.487717576	0.008960258	p<0.01	FC<-2
A_23_P326852	CACNB2	0.735046171	1.49874885	0.490439857	0.062382913	0.490439857	0.004284611	p<0.01	FC<-2
A_23_P111194	SPDEF	0.722107384	1.472045304	0.490546984	0.013628753	0.490546984	1.66190E-04	p<0.01	FC<-2
A_23_P122304	HDAC2	1.349155098	2.745605883	0.491387022	0.02177901	0.491387022	0.001529985	p<0.01	FC<-2

FIG. 8

: A_23_P122001	MSH3	0.474696859	0.958537771	0.495230207	0.0378371	0.495230207	0.00118879	p<0.01	FC<-2
: A_23_P46936	EGR2	1.281859576	2.586987129	0.495502881	0.087639456	0.495502881	0.007641718	p<0.01	FC<-2
: A_23_P74112	IL28RA	4.318361738	8.709950988	0.49579633	0.094310781	0.49579633	0.002571565	p<0.01	FC<-2
: A_23_P72117	SMPDL3A	1.184662883	2.373996572	0.499016257	0.080263117	0.499016257	0.006367744	p<0.01	FC<-2
: A_23_P134454	CAV1	0.248919506	0.97937908	0.25416053	0.098082936	0.25416053	0.009427841	p<0.01	FC<-3
: A_23_P15353	LGALS3BP	0.623184797	2.432835034	0.256155797	0.079351834	0.256155797	0.002553602	p<0.01	FC<-3
: A_23_P111125	HCP5	0.908380469	3.44984534	0.263310491	0.078685984	0.263310491	0.006507972	p<0.01	FC<-3
: A_23_P108823	OSBP16	0.235623185	0.878611955	0.26817662	0.007280877	0.26817662	1.80085E-05	p<0.01	FC<-3
: A_23_P363316	HOXB5	0.846846681	3.155069246	0.268408271	0.03872757	0.268408271	0.002155009	p<0.01	FC<-3
: A_23_P43742	CLTB	14.86463856	54.85397631	0.270985616	0.1534887	0.270985616	0.003736143	p<0.01	FC<-3
: A_23_P320897	FLJ20054	0.43052369	1.58769403	0.271162883	0.086517398	0.271162883	0.006075283	p<0.01	FC<-3
: A_23_P415401	KLF9	0.371009065	1.366563875	0.271490467	0.035758322	0.271490467	0.002981901	p<0.01	FC<-3
: A_23_P13822	STYK1	1.05765604	3.893841822	0.271622754	0.003001901	0.271622754	2.32136E-05	p<0.01	FC<-3
: A_23_P128230	NR4A1	0.57610709	2.112287846	0.272740806	0.087056975	0.272740806	0.007817815	p<0.01	FC<-3
: A_23_P91081	TACSTD1	3.513558311	12.62580663	0.278283868	0.142732948	0.278283868	0.009886188	p<0.01	FC<-3
: A_23_P169978	ZNF608	0.442643042	1.578025572	0.280504353	0.052318062	0.280504353	1.87207E-04	p<0.01	FC<-3
: A_23_P87199	FTH1	0.444327718	1.57743549	0.281677267	0.005497038	0.281677267	6.45003E-04	p<0.01	FC<-3
: A_23_P15104	YPEL3	0.279969366	0.991242042	0.28244299	0.047747027	0.28244299	0.006844879	p<0.01	FC<-3
: A_23_P61886	TM4SF9	0.416377538	1.451588267	0.286842727	0.087231737	0.286842727	0.008625187	p<0.01	FC<-3
: A_23_P88119	HSPH1	0.104924517	0.347660662	0.301801521	0.031648227	0.301801521	0.001287552	p<0.01	FC<-3
: A_23_P145760	ARL4A	0.53213979	1.738975764	0.306007594	0.055407123	0.306007594	0.002714138	p<0.01	FC<-3
: A_23_P216468	SLC1A1	2.125694474	6.8664456	0.309577123	0.02300206	0.309577123	2.90315E-04	p<0.01	FC<-3
: A_23_P132378	CELSR1	0.53442083	1.693662666	0.315541485	0.150420187	0.315541485	0.006982156	p<0.01	FC<-3
: A_23_P161686	RICS	1.371635179	4.250026307	0.322735691	0.068798699	0.322735691	0.004677148	p<0.01	FC<-3
: A_23_P139934	ITM2B	1.064067955	3.275623674	0.324844384	0.01284345	0.324844384	2.31190E-04	p<0.01	FC<-3
: A_23_P29096	PDE9A	0.374973687	1.162290333	0.325415979	0.079620416	0.325415979	0.006470114	p<0.01	FC<-3
: A_23_P112974	SHOX2	0.178539552	0.546770288	0.326534847	0.06652736	0.326534847	0.004598445	p<0.01	FC<-3
: A_23_P210763	JAG1	0.486618238	1.479632135	0.328877852	0.079228551	0.328877852	0.006640637	p<0.01	FC<-3
: A_23_P166826	DCP1A	0.550876201	1.662069471	0.331439937	0.018648181	0.331439937	1.23988E-04	p<0.01	FC<-3
: A_23_P160689	RIF1	0.154668667	0.753727974	0.205204891	0.023378469	0.205204891	5.55936E-05	p<0.01	FC<-4
: A_23_P154526	EIF3S6	0.645571896	3.08516372	0.20925045	0.053470607	0.20925045	0.002979907	p<0.01	FC<-4
: A_23_P252677	CLTB	25.76808104	122.2334578	0.210810375	0.022525884	0.210810375	8.74708E-04	p<0.01	FC<-4
: A_23_P70148	NNT	0.163810683	0.770803138	0.212519481	0.051877519	0.212519481	0.002308843	p<0.01	FC<-4
: A_23_P42975	PRKAR2B	0.211308223	0.982969286	0.214969304	0.053480364	0.214969304	0.002432008	p<0.01	FC<-4
: A_23_P59470	ZNF467	0.265551438	1.204583405	0.220450852	0.02069477	0.220450852	0.001248104	p<0.01	FC<-4
: A_23_P137381	ID3	0.489883668	2.185374214	0.22416466	0.027398257	0.22416466	4.30078E-04	p<0.01	FC<-4
: A_23_P256473	SEMA3C	0.114100814	0.503620454	0.226561119	0.017213919	0.226561119	3.09452E-04	p<0.01	FC<-4
: A_23_P143906	MLF1	0.337568585	1.446895357	0.233305459	0.055615523	0.233305459	0.003242315	p<0.01	FC<-4
: A_23_P69537	NMU	0.685980729	2.933325167	0.233857718	0.064530622	0.233857718	8.14920E-04	p<0.01	FC<-4
: A_23_P79482	CHN1	0.198482586	1.116828712	0.177719809	0.024155949	0.177719809	4.12570E-04	p<0.01	FC<-5
: A_23_P31143	TPD52L1	0.975780397	5.428611754	0.179747685	0.035487401	0.179747685	5.63402E-04	p<0.01	FC<-5
: A_23_P415510	LAD1	3.537555425	19.59670867	0.180517835	0.071107413	0.180517835	0.004444398	p<0.01	FC<-5
: A_23_P208029	DSC3	1.102925367	5.977466335	0.184513857	0.009307343	0.184513857	1.69250E-04	p<0.01	FC<-5
: A_23_P204947	GJB2	10.23450644	54.96566536	0.186198173	0.056899157	0.186198173	0.002354688	p<0.01	FC<-5
: A_23_P92623	PPP3CA	0.717321917	3.810474946	0.188250002	0.077162442	0.188250002	0.004948992	p<0.01	FC<-5
: A_23_P363255	SE57-1	2.008186115	10.4355216	0.192437541	0.03520295	0.192437541	8.45078E-04	p<0.01	FC<-5
: A_23_P209978	VSNL1	0.122135676	6.294900615	0.01940232	0.041722259	0.01940232	0.001373323	p<0.01	FC<-5
: A_23_P211910	PL0D2	0.050636755	0.333643692	0.151768955	0.085213835	0.151768955	0.007138111	p<0.01	FC<-6
: A_23_P415622	EPM2AIP1	0.195854674	1.272467258	0.15391726	0.059158734	0.15391726	0.002728298	p<0.01	FC<-6
: A_23_P167291	SCOC	0.189988967	1.157008169	0.164207109	0.021088818	0.164207109	1.41660E-04	p<0.01	FC<-6
: A_23_P259065	PDE8B	0.114117225	0.692875535	0.164700902	0.049548721	0.164700902	0.003562564	p<0.01	FC<-6
: A_23_P143143	ID2	0.521596263	3.687388882	0.141454096	0.030583787	0.141454096	8.36441E-04	p<0.01	FC<-7
: A_23_P54140	BMP4	1.136863019	8.035022527	0.141488467	0.04218643	0.141488467	0.002228296	p<0.01	FC<-7

FIG. 8
CONT'D

: A_23_P253896		0.507924977	4.532512046	0.112062576	0.05389398	0.112062576	0.002325012	p<0.01	FC<-8
: A_23_P218918	FGF2	0.219846412	2.098590376	0.104759087	0.092273034	0.104759087	0.008094806	p<0.01	FC<-9
: A_23_P203027	RDX	0.049007747	0.449893462	0.108931894	0.040246618	0.108931894	0.001626667	p<0.01	FC<-9
: A_23_P41854	CARD6	2.217936915	1.081203902	2.051358592	0.174013192	2.051358592	0.008445495	p<0.01	FC>2
: A_23_P216241	TOP1MT	1.678673234	0.813876491	2.062565086	0.106418095	2.062565086	0.005905161	p<0.01	FC>2
: A_23_P116533	SWAP70	1.374709279	0.663773676	2.071051216	2.52191E-04	2.071051216	0.007785455	p<0.01	FC>2
: A_23_P17269	KIAA1212	1.041534017	0.502824135	2.071368388	0.047547994	2.071368388	0.001466044	p<0.01	FC>2
: A_23_P500271	IRF5	4.738498244	2.274549025	2.083269339	0.030832076	2.083269339	0.002086504	p<0.01	FC>2
: A_23_P83492	CGI-90	2.41881387	1.154345629	2.095398302	6.31314E-04	2.095398302	1.32587E-06	p<0.01	FC>2
: A_23_P63343	UTS2	1.248242758	0.595636779	2.095644195	0.057040917	2.095644195	0.004941419	p<0.01	FC>2
: A_23_P46604	DJ462O23.2	1.351695582	0.633873801	2.132436425	2.39692E-04	2.132436425	0.008966089	p<0.01	FC>2
: A_23_P200303	HHLA3	3.472850639	1.613674078	2.152138828	0.084281999	2.152138828	8.09593E-04	p<0.01	FC>2
: A_23_P140394	NFATC4	1.871693819	0.866911494	2.1590368	0.107862711	2.1590368	0.009602987	p<0.01	FC>2
: A_23_P392235	DKFZp686H1423	1.432286674	0.663059709	2.160117189	0.112352017	2.160117189	0.004923518	p<0.01	FC>2
: A_23_P329890	MGC17839	1.938027162	0.880712541	2.200521817	0.007568708	2.200521817	1.52893E-05	p<0.01	FC>2
: A_23_P94301	TSTA3	1.833379817	0.826069228	2.219402145	0.044514039	2.219402145	0.00520429	p<0.01	FC>2
: A_23_P332374	ZNF175	1.692419191	0.744897831	2.272015194	0.011058373	2.272015194	6.43422E-05	p<0.01	FC>2
: A_23_P119023		10.96181793	4.786481356	2.290162045	0.024258235	2.290162045	0.003217102	p<0.01	FC>2
: A_23_P28664	KIAA1212	1.387364173	0.60325808	2.299785478	0.081529352	2.299785478	0.001693893	p<0.01	FC>2
: A_23_P50887	LANCL1	1.430305693	0.619745909	2.307890494	0.001333784	2.307890494	0.004559679	p<0.01	FC>2
: A_23_P385768	FLJ38819	1.359465091	0.586253272	2.318904057	0.014097271	2.318904057	6.72587E-04	p<0.01	FC>2
: A_23_P336506	TAS2R9	1.30717952	0.553276402	2.362615713	0.026128752	2.362615713	0.008753358	p<0.01	FC>2
: A_23_P202458	ZNF22	1.393403927	0.587143456	2.373191618	0.080908582	2.373191618	0.005402164	p<0.01	FC>2
: A_23_P424645	SYT12	1.187676367	0.498302445	2.383444789	5.52908E-06	2.383444789	0.00979219	p<0.01	FC>2
: A_23_P116166	KIAA1826	1.568680196	0.657754539	2.384902121	0.022246936	2.384902121	0.002831094	p<0.01	FC>2
: A_23_P43150	ZHX1	2.542259166	1.065932853	2.385008735	0.022504834	2.385008735	7.20146E-04	p<0.01	FC>2
: A_23_P96099	BAIAP1	1.644900013	0.686879115	2.394744542	0.098712326	2.394744542	0.009974473	p<0.01	FC>2
: A_23_P150316		1.426673234	0.581135413	2.454975558	6.57545E-04	2.454975558	0.004110376	p<0.01	FC>2
: A_23_P384512	ZNF22	0.941582	0.376706612	2.499510147	0.101774898	2.499510147	0.003718806	p<0.01	FC>2
: A_23_P125375	HMP19	1.349435322	0.514508808	2.622764277	0.050729202	2.622764277	0.009475533	p<0.01	FC>2
: A_23_P61466	M160	2.714280373	1.018293487	2.665518739	0.080562612	2.665518739	0.005612296	p<0.01	FC>2
: A_23_P17095	TFPI	1.332438114	0.479335334	2.779761934	0.174596858	2.779761934	0.008379324	p<0.01	FC>2
: A_23_P150693	FJX1	1.727083199	0.597357885	2.891203487	0.126503091	2.891203487	0.006940178	p<0.01	FC>2
: A_23_P165598		1.603568198	0.518452005	3.092992566	0.093287226	3.092992566	0.007767318	p<0.01	FC>3
: A_23_P119362	EMP3	0.926623001	0.280303609	3.305783345	0.15406483	3.305783345	0.007267473	p<0.01	FC>3
: A_23_P217384	AP1S2	0.80402278	0.193525663	4.154605473	0.125451189	4.154605473	0.005827208	p<0.01	FC>4
: A_23_P69310	CCRL2	8.277575986	1.421690741	5.822346413	0.02463099	5.822346413	0.007471221	p<0.01	FC>5
: A_23_P119279	ZNF44	1.31804423	0.878420094	1.500471403	0.042127763	1.500471403	3.02719E-04	p<0.01	FC>1.5
: A_23_P91293	VAPB	1.125084194	0.74883136	1.502453361	0.019182061	1.502453361	2.66505E-04	p<0.01	FC>1.5
: A_23_P28797		2.172084801	1.443972023	1.504242995	0.064023548	1.504242995	0.0033073	p<0.01	FC>1.5
: A_23_P141315	FLJ10458	2.287192635	1.519145468	1.505578421	0.123773796	1.505578421	0.009551962	p<0.01	FC>1.5
: A_23_P3775	FLJ10826	1.751035682	1.159340724	1.510371925	0.004284177	1.510371925	0.001399115	p<0.01	FC>1.5
: A_23_P395464	ZNF582	3.282421131	2.168512036	1.513674389	0.044596565	1.513674389	0.00219994	p<0.01	FC>1.5
: A_23_P103091	RBM9	1.007260471	0.665200646	1.514220525	0.009116417	1.514220525	4.06660E-05	p<0.01	FC>1.5
: A_23_P25913	C14orf168	1.076722486	0.710887577	1.514617108	0.021498085	1.514617108	0.002591448	p<0.01	FC>1.5
: A_23_P218835	KPNA4	1.387293505	0.912908481	1.519641381	0.04027973	1.519641381	0.0067336	p<0.01	FC>1.5
: A_23_P171310	FUNDC2	0.803344917	0.528595106	1.519773657	0.014456589	1.519773657	0.002063839	p<0.01	FC>1.5
: A_23_P255916	MGC29784	2.219558864	1.458448579	1.521862955	0.0252105	1.521862955	0.007122258	p<0.01	FC>1.5
: A_23_P141908	DEDD2	1.362954775	0.894182158	1.524247339	0.016562392	1.524247339	5.37754E-04	p<0.01	FC>1.5
: A_23_P323094	PHC1	0.822785953	0.538180764	1.528828245	0.003407474	1.528828245	0.001344216	p<0.01	FC>1.5
: A_23_P79882	CSTF1	1.606225335	1.050391988	1.529167542	0.001741781	1.529167542	0.004959575	p<0.01	FC>1.5
: A_23_P144348	SLIT2	2.268830588	1.482966183	1.529927394	0.070555426	1.529927394	0.002594954	p<0.01	FC>1.5
: A_23_P23443	EFHD2	2.709620393	1.768999119	1.531725123	0.073976705	1.531725123	0.00116106	p<0.01	FC>1.5

FIG. 8
CONT'D

: A_23_P368777	MGC17986	1.758430069	1.144150129	1.536887533	0.144595047	1.536887533	0.008245218	p<0.01	FC>1.5
: A_23_P357900	ODF3L1	0.920389069	0.598714067	1.537276506	0.003965024	1.537276506	0.001027533	p<0.01	FC>1.5
: A_23_P254254	SGSH	0.901230612	0.585932946	1.5381122	0.109823684	1.5381122	0.009365815	p<0.01	FC>1.5
: A_23_P385843	DEFB127	4.488237723	2.917594267	1.538335119	0.023572141	1.538335119	9.78634E-04	p<0.01	FC>1.5
: A_23_P148798	UCHL5	2.816876916	1.829979814	1.539293983	0.002421524	1.539293983	1.12955E-05	p<0.01	FC>1.5
: A_23_P204593	LTA4H	3.326469356	2.159840062	1.54014615	0.076827928	1.54014615	0.007706206	p<0.01	FC>1.5
: A_23_P253817	MFN1	1.658511964	1.071770774	1.547450261	0.131001437	1.547450261	0.007258498	p<0.01	FC>1.5
: A_23_P53467	IKIP	1.279050206	0.825232466	1.549927153	0.036756526	1.549927153	0.003669021	p<0.01	FC>1.5
: A_23_P388670	LTA4H	3.220148075	2.074103545	1.552549333	0.033131357	1.552549333	0.002433185	p<0.01	FC>1.5
: A_23_P43141	EIF3S6	2.815272401	1.810002774	1.555396732	0.007390248	1.555396732	3.66978E-04	p<0.01	FC>1.5
: A_23_P152605	GSDM1	2.104326385	1.351900655	1.556568804	0.124131698	1.556568804	0.009968653	p<0.01	FC>1.5
: A_23_P272725	ZZANK1	0.610797557	0.391726083	1.559246583	0.055243848	1.559246583	0.009593913	p<0.01	FC>1.5
: A_23_P156443	KPNA5	2.858853692	1.820250934	1.570582186	0.068726358	1.570582186	0.00662602	p<0.01	FC>1.5
: A_23_P123544	CHRA1	2.134883553	1.359219524	1.570668693	0.117203079	1.570668693	0.007279357	p<0.01	FC>1.5
: A_23_P254645	FBXW2	0.765970056	0.487409713	1.571511678	0.005016926	1.571511678	0.004191573	p<0.01	FC>1.5
: A_23_P114968	PTGFRN	1.976391235	1.257291957	1.571942955	0.01470874	1.571942955	3.08753E-04	p<0.01	FC>1.5
: A_23_P90938	DUSP19	1.072288786	0.680233256	1.576354548	0.155930324	1.576354548	0.008639793	p<0.01	FC>1.5
: A_23_P28642	PLEKHB2	1.988643704	1.255586406	1.5838366	0.058030398	1.5838366	0.008420001	p<0.01	FC>1.5
: A_23_P165624	TNFAIP6	2.328996601	1.469958098	1.584396592	0.061601286	1.584396592	0.009319579	p<0.01	FC>1.5
: A_23_P57836		1.115132167	0.700717924	1.591413791	0.043307367	1.591413791	0.004404019	p<0.01	FC>1.5
: A_23_P210658	C20orf45	2.765983908	1.734970911	1.594253765	0.032285752	1.594253765	0.001537632	p<0.01	FC>1.5
: A_23_P95764	PRPS1	1.576158301	0.9868987	1.597082153	0.025274528	1.597082153	0.00341709	p<0.01	FC>1.5
: A_23_P49597	PLSCR3	0.891049929	0.557187369	1.599192621	0.131513277	1.599192621	0.009539101	p<0.01	FC>1.5
: A_23_P132914	LOC92689	1.119849592	0.699488993	1.600953844	0.103273771	1.600953844	0.004255296	p<0.01	FC>1.5
: A_23_P93236	TRIM38	1.747339816	1.085853353	1.609185817	0.032461262	1.609185817	0.001966222	p<0.01	FC>1.5
: A_23_P425104	BRD4	0.798537884	0.496012439	1.609915035	0.03340135	1.609915035	5.20081E-04	p<0.01	FC>1.5
: A_23_P146497	KIAA0649	2.28684344	1.419725651	1.610764332	0.028825506	1.610764332	0.001382274	p<0.01	FC>1.5
: A_23_P137578	FBXO28	2.851742602	1.768920355	1.612137366	0.001850313	1.612137366	0.002938577	p<0.01	FC>1.5
: A_23_P60458	PPP2R4	1.476274086	0.914226467	1.614779421	0.002454046	1.614779421	4.70558E-04	p<0.01	FC>1.5
: A_23_P73780	IRAK1	1.097467347	0.677874573	1.618982907	0.014485126	1.618982907	0.002698484	p<0.01	FC>1.5
: A_23_P118712	SSH2	2.29498784	1.41287764	1.624335876	0.083055339	1.624335876	0.007368561	p<0.01	FC>1.5
: A_23_P100925	EIF5A	2.543843455	1.565286604	1.625161455	0.013205503	1.625161455	0.001879909	p<0.01	FC>1.5
: A_23_P123732	C9orf103	2.561169053	1.573302697	1.627893385	0.071177709	1.627893385	0.006009401	p<0.01	FC>1.5
: A_23_P31838	EEF1D	1.650669372	1.011031182	1.632659211	0.015119426	1.632659211	8.85249E-05	p<0.01	FC>1.5
: A_23_P96641	PRPS2	3.274685019	1.999906151	1.637419345	0.003274655	1.637419345	3.77097E-06	p<0.01	FC>1.5
: A_23_P368691	ABCC9	1.168541523	0.712967394	1.638983119	0.043180754	1.638983119	0.006845595	p<0.01	FC>1.5
: A_23_P218108	WDFY2	1.280038104	0.778011264	1.645269373	1.29452E-04	1.645269373	4.09628E-05	p<0.01	FC>1.5
: A_23_P163373	MGC75360	3.589623333	2.179006862	1.647366695	0.031811213	1.647366695	0.00551169	p<0.01	FC>1.5
: A_23_P14853	LTK	0.885754959	0.536403922	1.651283524	0.002938252	1.651283524	0.001134477	p<0.01	FC>1.5
: A_23_P348015		1.363108885	0.823398478	1.65546685	0.082109492	1.65546685	0.003661443	p<0.01	FC>1.5
: A_23_P108342	ZNF571	1.794375333	1.083283326	1.656422922	0.01219423	1.656422922	0.001047232	p<0.01	FC>1.5
: A_23_P115523	FLJ12517	1.274516737	0.76919231	1.656954602	0.019704991	1.656954602	0.003821476	p<0.01	FC>1.5
: A_23_P90070		1.516248444	0.915080541	1.656956273	0.054070792	1.656956273	0.001750508	p<0.01	FC>1.5
: A_23_P167556	FLJ31951	2.001976493	1.20701527	1.65861737	0.143531289	1.65861737	0.009512806	p<0.01	FC>1.5
: A_23_P46337	MGC29875	1.850665036	1.115614308	1.658875314	0.048302973	1.658875314	0.008450654	p<0.01	FC>1.5
: A_23_P60000	KIAA0103	1.488242687	0.897021624	1.659093435	0.006557238	1.659093435	2.37269E-05	p<0.01	FC>1.5
: A_23_P218967	LARS	1.740167351	1.045587094	1.664296892	0.019430288	1.664296892	0.002121704	p<0.01	FC>1.5
: A_23_P160188	PEX19	1.902626756	1.139545272	1.66963683	0.134893118	1.66963683	0.009029147	p<0.01	FC>1.5
: A_23_P202740	GPR83	2.073175221	1.239984041	1.671937019	0.038971116	1.671937019	0.001487854	p<0.01	FC>1.5
: A_23_P216068	ATAD2	2.935321559	1.752975641	1.674479377	0.042363694	1.674479377	0.002882933	p<0.01	FC>1.5
: A_23_P1863	OR5AK2	2.053896718	1.224626331	1.677161977	0.042006891	1.677161977	0.006834792	p<0.01	FC>1.5
: A_23_P161891	OR6Q1	2.847135164	1.68897908	1.685713694	0.061512126	1.685713694	0.007597193	p<0.01	FC>1.5
: A_23_P88021	ITR	1.941013275	1.140649665	1.701673471	0.062848299	1.701673471	0.003748778	p<0.01	FC>1.5

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: A_23_P95027	MGC41816	1.545814872	0.908166159	1.702127807	0.002110168	1.702127807	0.004481732	p<0.01	FC>1.5
: A_23_P157669	NDUFB9	2.564449612	1.502343131	1.706966643	0.110836939	1.706966643	0.006863617	p<0.01	FC>1.5
: A_23_P253841	HSF1	1.64368526	0.962660036	1.707441047	0.111323599	1.707441047	0.003721173	p<0.01	FC>1.5
: A_23_P140050	FAM48A	1.914426476	1.11768948	1.712842887	0.063072294	1.712842887	0.003847278	p<0.01	FC>1.5
: A_23_P99754	RPL10L	1.648160011	0.960942932	1.715148689	0.066545357	1.715148689	0.001224145	p<0.01	FC>1.5
: A_23_P81012	KIAA1223	0.695301387	0.400037714	1.738089592	0.032114344	1.738089592	0.004641467	p<0.01	FC>1.5
: A_23_P20223	RRM2B	1.851948489	1.063845212	1.74080634	0.012968515	1.74080634	5.06055E-04	p<0.01	FC>1.5
: A_23_P97697	LOC90806	3.986192965	2.289154957	1.741338197	0.076560981	1.741338197	0.001136079	p<0.01	FC>1.5
: A_23_P169077	LY6E	1.764814679	1.01026025	1.746891139	0.091512515	1.746891139	0.001551111	p<0.01	FC>1.5
: A_23_P4425	FLII	1.808404687	1.031660405	1.752906943	0.124187672	1.752906943	0.006706179	p<0.01	FC>1.5
: A_23_P122012	IL3	4.186622152	2.387921083	1.753249796	0.018187546	1.753249796	7.56901E-04	p<0.01	FC>1.5
: A_23_P85993	FLJ21168	1.873944993	1.056656261	1.773466984	0.008856622	1.773466984	1.05511E-04	p<0.01	FC>1.5
: A_23_P140219	BCL2L2	2.022055046	1.132028457	1.786222806	0.122033263	1.786222806	0.006076945	p<0.01	FC>1.5
: A_23_P86822	PIG8	1.384261223	0.76728238	1.804109229	0.014977754	1.804109229	0.001117358	p<0.01	FC>1.5
: A_23_P44244	SMARCA1	0.957390387	0.52919525	1.809143953	0.014442442	1.809143953	0.002281333	p<0.01	FC>1.5
: A_23_P211619	SCUBE1	1.463899479	0.807270928	1.813393035	0.105176535	1.813393035	0.001539835	p<0.01	FC>1.5
: A_23_P371871	CDYL2	4.007562482	2.197432093	1.823748044	0.008602598	1.823748044	6.76650E-04	p<0.01	FC>1.5
: A_23_P96060	GDPD1	3.096689988	1.689008406	1.833436694	0.081972618	1.833436694	0.005033014	p<0.01	FC>1.5
: A_23_P145419	SERAC1	3.44503199	1.873807863	1.838519337	0.052472412	1.838519337	0.001907786	p<0.01	FC>1.5
: A_23_P202637	C11orf23	5.695302482	3.070474454	1.854860728	5.23504E-04	1.854860728	0.001194461	p<0.01	FC>1.5
: A_23_P15727	FKBP10	0.733150751	0.395027247	1.855949825	0.107316768	1.855949825	0.007242824	p<0.01	FC>1.5
: A_23_P108463	WDR35	1.817606516	0.978911418	1.856763014	0.135542888	1.856763014	0.003580063	p<0.01	FC>1.5
: A_23_P167138	PPM1K	1.163483882	0.626069919	1.858392885	0.021483195	1.858392885	0.001103306	p<0.01	FC>1.5
: A_23_P259090	NUDT12	4.460960406	2.39804698	1.860247294	0.047955147	1.860247294	0.002222546	p<0.01	FC>1.5
: A_23_P213344	DIAPH1	1.210278584	0.6416372	1.886235062	1.54321E-04	1.886235062	0.009016209	p<0.01	FC>1.5
: A_23_P84344	SIGIRR	1.629302282	0.85919533	1.896311846	0.049961032	1.896311846	1.05531E-04	p<0.01	FC>1.5
: A_23_P251412	SCGN	1.165973516	0.61452521	1.897356685	0.004379778	1.897356685	0.002466788	p<0.01	FC>1.5
: A_23_P157795	CTNNAL1	3.054186452	1.605052649	1.902857488	0.020157602	1.902857488	2.24818E-04	p<0.01	FC>1.5
: A_23_P150249	DIPA	1.369691218	0.709694204	1.929973799	0.002620182	1.929973799	2.65205E-04	p<0.01	FC>1.5
: A_23_P347048	SGPP1	1.617366044	0.831449451	1.945236769	0.01402098	1.945236769	0.003129776	p<0.01	FC>1.5
: A_23_P311039	LOC196549	2.244858039	1.134069816	1.979470759	0.005787986	1.979470759	6.18568E-06	p<0.01	FC>1.5
: A_23_P77612	KREMEN2	3.302363428	1.656347899	1.993761956	9.62604E-04	1.993761956	0.007345052	p<0.01	FC>1.5
: A_23_P332744	FMNL2	1.854969057	0.929881201	1.994845207	0.091027493	1.994845207	0.004156998	p<0.01	FC>1.5
: A_23_P88589	NR2F2	1.143676109	2.281128358	0.501364206	0.087402723	0.501364206	0.008439617	p<0.01	
: A_23_P101121		0.540257954	1.077176519	0.501550065	0.021188031	0.501550065	0.001211802	p<0.01	
: A_23_P255897	LOC129293	0.604949288	1.204885572	0.502080282	0.001704099	0.502080282	4.20886E-04	p<0.01	
: A_23_P205746	EML1	0.278469101	0.554055336	0.502601605	0.060733074	0.502601605	0.004604377	p<0.01	
: A_23_P250888	CDKN2A	1.073088208	2.130468905	0.503686398	0.057004849	0.503686398	0.004397159	p<0.01	
: A_23_P108042	NCR1	1.05799293	2.095028641	0.505001654	0.080285793	0.505001654	8.53129E-04	p<0.01	
: A_23_P107693	ZNF586	0.691563409	1.361808595	0.507827173	0.066987626	0.507827173	0.002699888	p<0.01	
: A_23_P75585		0.636605027	1.250161378	0.50921828	0.023395239	0.50921828	0.001756715	p<0.01	
: A_23_P334709	FKBP9	0.623167532	1.223140672	0.50948149	0.089987891	0.50948149	0.005158628	p<0.01	
: A_23_P81825	GUCA1B	0.457419773	0.897336876	0.509752564	0.06295219	0.509752564	0.003517892	p<0.01	
: A_23_P148047	PTGER4	0.541894562	1.053974483	0.514143911	0.089091113	0.514143911	0.006865614	p<0.01	
: A_23_P79231	CREB1	0.849443981	1.650341084	0.514708135	0.081980298	0.514708135	6.95747E-04	p<0.01	
: A_23_P212617	TFRC	0.680087499	1.315072516	0.517148287	0.034474698	0.517148287	0.001439213	p<0.01	
: A_23_P68102	TMSB10	1.113994304	2.139755605	0.520617542	7.33885E-04	0.520617542	0.00646616	p<0.01	
: A_23_P67977	KLF7	0.811674948	1.554380575	0.522185468	0.049377812	0.522185468	0.007615853	p<0.01	
: A_23_P430201	C14orf145	1.891959805	3.621094381	0.522482876	0.158110954	0.522482876	0.009864905	p<0.01	
: A_23_P250097	NAG8	0.542902159	1.037829366	0.523113122	0.07846012	0.523113122	0.008815155	p<0.01	
: A_23_P315320	IL27	0.812174204	1.55105086	0.523628351	0.067200735	0.523628351	0.009576894	p<0.01	
: A_23_P58201	AFP	0.003202492	0.006067928	0.527773575	0.005579505	0.527773575	0.001383826	p<0.01	
: A_23_P28307	DHX57	0.486484435	0.920627394	0.528427068	0.064319017	0.528427068	0.009175486	p<0.01	

FIG. 8
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: A_23_P218358	FBXW10	0.842615214	1.591006385	0.52961146	0.085055698	0.52961146	0.007289928	p<0.01
: A_23_P306755	CRYAA	0.472204615	0.890985346	0.529980225	0.011198984	0.529980225	3.46759E-06	p<0.01
: A_23_P126162	HPCA	0.783192857	1.47021657	0.532705775	0.067755782	0.532705775	0.004923333	p<0.01
: A_23_P310421	CHST12	0.573279669	1.070869047	0.535340592	0.010249751	0.535340592	2.50949E-04	p<0.01
: A_23_P159897	LOC340529	1.416149597	2.643171768	0.535776605	0.045051027	0.535776605	0.006466363	p<0.01
: A_23_P48771	C14orf159	1.175975415	2.181446682	0.539080522	0.023137598	0.539080522	4.70502E-04	p<0.01
: A_23_P48570	DHRS2	0.021971427	0.040575608	0.541493464	0.058917168	0.541493464	0.004800666	p<0.01
: A_23_P13753	NFE2	0.057640478	0.106370453	0.54188429	0.036369573	0.54188429	0.005016133	p<0.01
: A_23_P200710	PIK3C2B	1.496566945	2.7533923	0.543535676	0.063142111	0.543535676	0.004261906	p<0.01
: A_23_P133900	PSORS1C1	0.435061546	0.798198169	0.545054553	0.046347918	0.545054553	0.002829563	p<0.01
: A_23_P133095	RAPGEF2	1.416997191	2.590009936	0.547101064	0.119220458	0.547101064	0.006804102	p<0.01
: A_23_P21673	KIAA1797	1.664188778	3.037319565	0.547913626	0.001265801	0.547913626	2.90585E-05	p<0.01
: A_23_P115922	EIF4EBP2	1.162117967	2.116527381	0.549068241	0.084386849	0.549068241	0.005894646	p<0.01
: A_23_P63798	KLF6	0.568515701	1.03436919	0.549625517	0.013756568	0.549625517	3.78298E-04	p<0.01
: A_23_P94800	S100A4	0.400869321	0.725723234	0.552372175	0.059322262	0.552372175	0.003362468	p<0.01
: A_23_P164368		1.015987764	1.837176319	0.553015926	0.085407887	0.553015926	0.003056874	p<0.01
: A_23_P385114	ZBTB10	0.652385215	1.178160361	0.553732104	0.034952297	0.553732104	0.001810983	p<0.01
: A_23_P148949	SPRR2A	0.596068739	1.068115771	0.558056304	0.106459852	0.558056304	0.007483929	p<0.01
: A_23_P120472	TFAP2C	0.49280244	0.87904508	0.560611113	0.090051703	0.560611113	0.009062743	p<0.01
: A_23_P421326	C1orf24	0.324910914	0.576336023	0.56375257	0.103413044	0.56375257	0.009280733	p<0.01
: A_23_P99604	KIAA1333	0.675708733	1.195874163	0.565033307	0.043258557	0.565033307	0.003352339	p<0.01
: A_23_P257617	PPP1R14C	0.685539299	1.205247591	0.568795411	0.043665164	0.568795411	0.004820268	p<0.01
: A_23_P400217	MUM1	1.475826905	2.589276077	0.56997665	0.047645318	0.56997665	0.002416391	p<0.01
: A_23_P143324	BMP2	0.402640713	0.704179691	0.571786887	0.041784301	0.571786887	0.001586819	p<0.01
: A_23_P140347	PAPLN	0.712004616	1.244224379	0.572247761	0.011103242	0.572247761	0.001595731	p<0.01
: A_23_P118142	ARL6IP	1.528389991	2.658421794	0.574923812	0.05140596	0.574923812	0.008632411	p<0.01
: A_23_P16516	ARID3A	0.441472241	0.767444676	0.575249598	0.027236406	0.575249598	0.002177716	p<0.01
: A_23_P206441	FANCA	1.277756741	2.219857564	0.57560303	0.038169707	0.57560303	0.001173726	p<0.01
: A_23_P51327	KIAA0040	1.18027032	2.046956332	0.576597703	0.050441044	0.576597703	0.002070305	p<0.01
: A_23_P422724	PPIC	0.639277208	1.105855977	0.578083603	0.092319602	0.578083603	0.004124026	p<0.01
: A_23_P35871	FLJ23311	1.864438107	3.218223877	0.579337603	0.012109465	0.579337603	1.79468E-04	p<0.01
: A_23_P170518	DYM	0.946181942	1.630812999	0.580190336	0.029206698	0.580190336	9.44565E-04	p<0.01
: A_23_P150566	BSCL2	0.627163947	1.078069867	0.581747034	0.018338738	0.581747034	4.64466E-04	p<0.01
: A_23_P121795	ARGBP2	0.470440485	0.804915846	0.584459217	0.025260362	0.584459217	0.002941359	p<0.01
: A_23_P4494	DSC2	1.761420286	2.999567115	0.587224829	0.010943429	0.587224829	3.88918E-05	p<0.01
: A_23_P72830	DPP7	0.578888528	0.985352947	0.587493578	0.006153058	0.587493578	2.25501E-05	p<0.01
: A_23_P254512	EFNA1	0.446928652	0.759186501	0.588694149	0.080259999	0.588694149	0.007970738	p<0.01
: A_23_P168637	MGC10911	1.095031428	1.85997069	0.588735851	0.084213785	0.588735851	0.007953854	p<0.01
: A_23_P48951	MFGE8	0.864231851	1.467465765	0.588928118	0.04729136	0.588928118	0.006448187	p<0.01
: A_23_P203030	DLAT	1.35068126	2.286112278	0.590820177	0.093667332	0.590820177	0.008736312	p<0.01
: A_23_P356125	KIAA1468	1.627669217	2.754268899	0.590962349	0.076653912	0.590962349	0.005432714	p<0.01
: A_23_P74458	KIAA0907	0.460641189	0.778761278	0.591505	0.033508049	0.591505	0.003788579	p<0.01
: A_23_P52888	C11orf8	0.336585743	0.567187163	0.593429763	0.041049458	0.593429763	0.006547694	p<0.01
: A_23_P49878	FLJ10156	1.151945911	1.939724338	0.593870937	0.101007449	0.593870937	0.004069528	p<0.01
: A_23_P359174	MGC4308	0.6430861	1.082711527	0.593958856	0.019473791	0.593958856	0.002846024	p<0.01
: A_23_P202587	KIAA1598	0.911788694	1.534912229	0.594033116	0.045548835	0.594033116	0.002763499	p<0.01
: A_23_P384090	RANBP2L1	1.289977266	2.162096796	0.596632523	0.104529411	0.596632523	0.004896148	p<0.01
: A_23_P200843		0.329900591	0.552507436	0.597097105	0.018218332	0.597097105	0.002511574	p<0.01
: A_23_P99985	HMGB1	2.021042253	3.379254902	0.598073336	0.033240133	0.598073336	0.003011302	p<0.01
: A_23_P58443	ANKHD1	1.303870169	2.179372628	0.598277758	0.014962366	0.598277758	4.57153E-04	p<0.01
: A_23_P501080	ZNF92	1.528540102	2.553716914	0.598555029	0.024463434	0.598555029	4.69871E-04	p<0.01
: A_23_P91669	PIB5PA	0.654436269	1.09167507	0.599478991	0.101520141	0.599478991	0.005884394	p<0.01
: A_23_P327910	ZIC3	0.206314038	0.344048272	0.599665962	7.19615E-04	0.599665962	0.008452668	p<0.01

FIG. 8
CONT'D

: A_23_P419712	BTBD11	0.462088462	0.769252886	0.600697729	0.058417026	0.600697729	0.001871285	p<0.01
: A_23_P166100	DJ971N18.2	0.517738003	0.861040479	0.601293453	0.082497747	0.601293453	0.006637766	p<0.01
: A_23_P140405	CHES1	0.56889709	0.943805283	0.602769555	0.035570027	0.602769555	3.43486E-04	p<0.01
: A_23_P91390	THBD	0.45818831	0.759044524	0.603638253	0.13497795	0.603638253	0.008409448	p<0.01
: A_23_P130116	ASGR2	0.482651558	0.7982206	0.604659361	0.04709917	0.604659361	0.00167997	p<0.01
: A_23_P155711	FLJ10858	1.043304583	1.723324438	0.605402303	0.020808136	0.605402303	2.17673E-04	p<0.01
: A_23_P257407	NDOR1	0.498011062	0.82088454	0.606676138	0.009570357	0.606676138	1.70904E-04	p<0.01
: A_23_P254756	CD164	1.330906473	2.188865614	0.608034803	0.105797266	0.608034803	0.009977235	p<0.01
: A_23_P130773	GLTSCR1	0.634004066	1.042073287	0.608406408	0.032549167	0.608406408	0.001125607	p<0.01
: A_23_P120566	RRBP1	0.382587472	0.628421967	0.608806649	0.137724463	0.608806649	0.008718629	p<0.01
: A_23_P218637	RANBP2L1	1.28886457	2.115615861	0.609214836	0.103367274	0.609214836	0.007897026	p<0.01
: A_23_P382705	DKFZp762A217	0.973945005	1.598611801	0.609244223	0.00409478	0.609244223	0.00124181	p<0.01
: A_23_P205841	MYO9A	0.660073287	1.081696886	0.610220197	0.087631094	0.610220197	0.007941253	p<0.01
: A_23_P12572	CASP7	1.373269071	2.250277333	0.610266588	0.095176163	0.610266588	0.008882076	p<0.01
: A_23_P324327	GPRC5B	0.556541659	0.911903947	0.610307326	0.046239018	0.610307326	0.004589169	p<0.01
: A_23_P166553	PP2447	0.504321441	0.825271928	0.611097292	0.029606387	0.611097292	6.84955E-04	p<0.01
: A_23_P47168	FLRT1	1.271861063	2.076671882	0.612451622	0.035023743	0.612451622	0.00633365	p<0.01
: A_23_P1355	SFRP5	1.718396253	2.804198283	0.612794132	0.031386283	0.612794132	0.001466794	p<0.01
: A_23_P31315	CBX3	0.982853562	1.603122765	0.613086897	0.055430033	0.613086897	0.003698192	p<0.01
: A_23_P218608	EIF5B	1.083888057	1.767508302	0.613229401	0.098231724	0.613229401	0.004625181	p<0.01
: A_23_P153549	GRIN2D	0.500888549	0.816579935	0.613398062	0.060156592	0.613398062	0.003619872	p<0.01
: A_23_P252991	HNRPH1	1.225527734	1.992184341	0.615167838	0.031786227	0.615167838	0.004262162	p<0.01
: A_23_P70060	PPAP2A	0.357691588	0.579850853	0.616868262	0.092152207	0.616868262	0.004959277	p<0.01
: A_23_P208674	LOC284361	2.031730511	3.29143115	0.617278752	0.082150302	0.617278752	0.009958142	p<0.01
: A_23_P167338	USP53	1.5357464	2.487075823	0.617490784	0.072588753	0.617490784	0.005801091	p<0.01
: A_23_P157751	BICD2	0.637912392	1.030466968	0.619051762	0.084842868	0.619051762	0.00680413	p<0.01
: A_23_P10807	UBE2E2	0.688893851	1.110731432	0.620216401	0.094587689	0.620216401	0.008428444	p<0.01
: A_23_P82402	GLCC1	0.352442316	0.56811443	0.620372055	0.041843457	0.620372055	0.001661305	p<0.01
: A_23_P46507	CGI-143	0.671301056	1.080973153	0.621015475	0.007545207	0.621015475	1.26663E-04	p<0.01
: A_23_P89789	FECH	1.714370576	2.754751574	0.622332188	0.083652026	0.622332188	0.006507181	p<0.01
: A_23_P96205	MBNL3	0.517162676	0.829989171	0.623095692	0.034916666	0.623095692	0.006017239	p<0.01
: A_23_P41054	PTPRG	1.318957177	2.115696522	0.623415109	0.037990467	0.623415109	0.001959215	p<0.01
: A_23_P86710	FRMPD2	1.285165955	2.058181796	0.624418094	0.048423049	0.624418094	0.007329878	p<0.01
: A_23_P375524	LCE1D	0.787648469	1.2597602	0.625236826	0.010240746	0.625236826	0.004353974	p<0.01
: A_23_P128396	RNF34	1.556734176	2.472937106	0.629508196	0.096353511	0.629508196	0.005084882	p<0.01
: A_23_P166627	ITGB5	0.583958453	0.925383747	0.631044639	0.03957693	0.631044639	0.001108059	p<0.01
: A_23_P206741		0.239719445	0.379641767	0.631435912	0.008958963	0.631435912	0.0082566	p<0.01
: A_23_P118815	BIRC5	0.99796044	1.580108158	0.631577297	0.01133654	0.631577297	3.22002E-04	p<0.01
: A_23_P258493	LMNB1	0.860501802	1.362254654	0.631674702	0.142745531	0.631674702	0.007968191	p<0.01
: A_23_P44235		0.637540591	1.009109946	0.631785063	0.041757598	0.631785063	0.001851813	p<0.01
: A_23_P27107	TM4SF5	0.172346073	0.272728329	0.631933153	0.073165247	0.631933153	0.006815276	p<0.01
: A_23_P98085	PTEN	1.326871353	2.094896005	0.633382922	0.028495967	0.633382922	0.001034767	p<0.01
: A_23_P120594	ACAS2L	0.449826899	0.708316292	0.635065017	0.053663719	0.635065017	0.006774512	p<0.01
: A_23_P11283	HNRPH2	1.522402754	2.390074403	0.63696877	0.085703506	0.63696877	0.009199614	p<0.01
: A_23_P4944	CALM3	0.850847373	1.334955832	0.637359943	0.047117752	0.637359943	0.00158697	p<0.01
: A_23_P145904	H2AFV	0.82925434	1.2997143	0.638028172	0.134113882	0.638028172	0.009490109	p<0.01
: A_23_P65110	RACGAP1	1.519842979	2.379125796	0.638824135	0.010289982	0.638824135	2.58043E-04	p<0.01
: A_23_P28530	FLJ20160	0.881526852	1.378190742	0.63962616	0.076186301	0.63962616	0.009016164	p<0.01
: A_23_P105583	MGC13204	0.688329765	1.075232956	0.640168032	0.014507483	0.640168032	8.82255E-04	p<0.01
: A_23_P66149	VPS35	1.173928402	1.824493062	0.643427167	0.054435935	0.643427167	0.002492902	p<0.01
: A_23_P331700	FLJ37078	0.744077213	1.15598697	0.643672664	0.010880877	0.643672664	0.004055326	p<0.01
: A_23_P425704	PPARBP	0.64536489	0.99998792	0.645372686	0.124229836	0.645372686	0.003870237	p<0.01
: A_23_P35995	ASAM	0.154523853	0.238905907	0.646797957	0.11663517	0.646797957	0.002967481	p<0.01

FIG. 8
CONT'D

: A_23_P20075	NPC1L1	0.569544934	0.879370517	0.647673448	0.041487779	0.647673448	0.001475677	p<0.01
: A_23_P69171	SUCNR1	0.690911421	1.065978098	0.648147858	0.035546315	0.648147858	0.007031044	p<0.01
: A_23_P103199	EPHA8	0.664606591	1.023567122	0.649304356	0.032248452	0.649304356	0.002314305	p<0.01
: A_23_P16562		0.622725357	0.957964426	0.650050607	0.029119909	0.650050607	6.52097E-04	p<0.01
: A_23_P2935	C14orf24	0.51369701	0.789817374	0.650399734	0.077174608	0.650399734	0.003885067	p<0.01
: A_23_P302568	SLC30A3	0.332324721	0.510868232	0.650509663	0.075790178	0.650509663	0.006173568	p<0.01
: A_23_P69100	SCEF	0.804055925	1.233542438	0.651826723	0.027961096	0.651826723	0.002079546	p<0.01
: A_23_P153709	MIDN	0.975251761	1.488662982	0.65511924	0.034323116	0.65511924	0.006606469	p<0.01
: A_23_P132803	RPN1	1.752342797	2.673672454	0.655406684	0.064712789	0.655406684	0.009043188	p<0.01
: A_23_P76610	PSPC1	0.721793108	1.099752419	0.656323274	0.087084288	0.656323274	0.004941462	p<0.01
: A_23_P92765	MGC39633	1.359885783	2.070825946	0.65668763	0.062964798	0.65668763	0.005071002	p<0.01
: A_23_P359654	ZFOC1	2.587720683	3.933227542	0.657912784	0.045113269	0.657912784	0.006589111	p<0.01
: A_23_P401568	MAT2A	0.657451491	0.998066947	0.658724841	0.015775747	0.658724841	0.002526916	p<0.01
: A_23_P353541		0.424145194	0.64382803	0.658786468	0.056454378	0.658786468	0.009003276	p<0.01
: A_23_P43334	FREM1	0.262922937	0.398956735	0.659026191	0.00991348	0.659026191	0.001534612	p<0.01
: A_23_P309865	ZNF449	0.86224619	1.301639685	0.662430779	0.010477079	0.662430779	9.12434E-04	p<0.01
: A_23_P324994	KLHL7	0.852712617	1.286769508	0.662677046	0.105858821	0.662677046	0.001109503	p<0.01
: A_23_P23803	SRRM1	2.15345689	3.249623863	0.662678815	0.051078933	0.662678815	0.003414272	p<0.01
: A_23_P212854	GYPA	0.358893654	0.541387582	0.662914456	0.063228054	0.662914456	0.005208124	p<0.01
: A_23_P116202	FLJ21827	0.766345801	1.153423081	0.66409976	0.034329861	0.66409976	0.001999013	p<0.01
: A_23_P417415	THEA	0.743130701	1.118011378	0.664689748	0.091800393	0.664689748	0.006838151	p<0.01
: A_23_P110005	NICN1	0.953592258	1.432308563	0.665772922	0.02170636	0.665772922	0.009932436	p<0.01
: A_23_P30283	UNQ1912	1.413635922	2.122562575	0.666004356	0.083368227	0.666004356	0.007935972	p<0.01
: A_23_P215024	LRRC1	3.593931491	5.383009455	0.66764354	0.073902951	0.66764354	0.004996464	p<0.01
: A_23_P91912	PLSCR4	0.599976515	0.898567055	0.667703664	0.021249203	0.667703664	0.001049637	p<0.01
: A_23_P87401	PP1665	0.565889239	0.845648625	0.669177744	0.023107043	0.669177744	4.37356E-04	p<0.01
: A_23_P132948	ELF2	0.67254168	1.001826171	0.671315743	0.041327005	0.671315743	0.001047755	p<0.01
: A_23_P109682	AZI2	1.052738892	1.565284821	0.672554207	0.021654684	0.672554207	2.13991E-04	p<0.01
: A_23_P212715	CBLB	0.512518299	0.76154866	0.672994814	0.053060815	0.672994814	0.006222571	p<0.01
: A_23_P310372	IFNK	0.969014438	1.437906013	0.673906659	0.051573037	0.673906659	0.007198225	p<0.01
: A_23_P415561	GNA14	0.66838522	0.987764967	0.676664229	0.039671006	0.676664229	0.002428285	p<0.01
: A_23_P341418		2.020511247	2.985753622	0.676717339	0.128578306	0.676717339	0.008768354	p<0.01
: A_23_P392501	TNRC6C	0.667198522	0.983201026	0.678598277	0.153902349	0.678598277	0.004811161	p<0.01
: A_23_P7873	MCM3	1.108816192	1.628525279	0.680871342	0.009491459	0.680871342	0.002069953	p<0.01
: A_23_P206901	NDE1	0.846901998	1.240714293	0.68259228	0.089441948	0.68259228	0.003061748	p<0.01
: A_23_P51690	RHBG	0.528474263	0.773974825	0.682805494	0.13715298	0.682805494	0.008631839	p<0.01
: A_23_P314712	CABYR	0.630964732	0.922354268	0.684080677	0.021881487	0.684080677	0.002051621	p<0.01
: A_23_P126135	MFN2	1.501392697	2.190016391	0.685562311	0.033738538	0.685562311	0.002519395	p<0.01
: A_23_P384559	PHF13	0.952428448	1.388482017	0.68594943	0.061265109	0.68594943	0.005898076	p<0.01
: A_23_P213288	SCD4	0.445580267	0.646817762	0.68888069	0.028157053	0.68888069	0.004789056	p<0.01
: A_23_P167432		0.407421607	0.588368739	0.692459643	0.057676237	0.692459643	0.009179167	p<0.01
: A_23_P26704	ET	0.768406927	1.107472795	0.693838197	0.125163276	0.693838197	0.002728834	p<0.01
: A_23_P65040		0.943587925	1.357374643	0.695156588	0.07397533	0.695156588	0.004480751	p<0.01
: A_23_P74162	IQCC	0.517332833	0.744144798	0.695204528	0.019693722	0.695204528	1.95501E-04	p<0.01
: A_23_P85585	LCN7	0.609650675	0.876222071	0.695771877	0.026343076	0.695771877	0.004478553	p<0.01
: A_23_P428326	TBC1D16	0.834735222	1.199237421	0.696055015	0.099119328	0.696055015	0.008164814	p<0.01
: A_23_P106472	DNM1DN8-2	0.736880478	1.053722951	0.699311405	0.076838612	0.699311405	0.008233116	p<0.01
: A_23_P10591	METRNL	0.47020313	0.671056809	0.700690499	0.150391754	0.700690499	0.002550859	p<0.01
: A_23_P101875	FBXO17	0.495077018	0.706071317	0.701171406	0.034390485	0.701171406	9.20334E-04	p<0.01
: A_23_P113184	FTO	1.333905564	1.898234093	0.702708675	0.077499413	0.702708675	0.002144472	p<0.01
: A_23_P257198	NDUFS4	1.082680353	1.539494228	0.703270161	0.130100715	0.703270161	0.00882162	p<0.01
: A_23_P259103		0.999142465	1.418937724	0.704148214	0.005607961	0.704148214	6.26236E-04	p<0.01
: A_23_P402778	TRIM40	0.406254985	0.57669702	0.704451334	0.028425511	0.704451334	0.002139028	p<0.01

FIG. 8
CONT'D

: A_23_P330618	C20orf179	0.626430179	0.885263868	0.707619729	0.005372986	0.707619729	9.09938E-04	p<0.01
: A_23_P151120	ACRBP	0.434175201	0.613127922	0.70813151	0.013585969	0.70813151	0.003779512	p<0.01
: A_23_P136671	UGT2B7	0.453711869	0.639941134	0.708990006	0.06427996	0.708990006	0.001899793	p<0.01
: A_23_P133315	ZNF131	0.980165275	1.382280051	0.709093121	0.023951707	0.709093121	9.19999E-04	p<0.01
: A_23_P85853	FLJ22353	0.471684622	0.665179215	0.709109081	0.056516095	0.709109081	0.00492856	p<0.01
: A_23_P113172	DIAPH2	0.78625441	1.107840225	0.709718236	0.032624468	0.709718236	0.001845365	p<0.01
: A_23_P314151	NOLC1	1.392652447	1.959180961	0.710834004	0.050920512	0.710834004	0.009515841	p<0.01
: A_23_P206183	NUSAP1	1.417012725	1.993252286	0.710904854	0.088696254	0.710904854	0.009678171	p<0.01
: A_23_P40856	HT017	0.554342205	0.779534374	0.711119642	0.079674618	0.711119642	0.007884365	p<0.01
: A_23_P54556	MKL2	1.34993396	1.896148523	0.711934716	0.072933634	0.711934716	0.006242235	p<0.01
: A_23_P31386	TRA2A	1.366760586	1.917991909	0.712599766	0.115637914	0.712599766	0.002846918	p<0.01
: A_23_P206059	PRC1	1.961136212	2.749166141	0.713356746	0.048294367	0.713356746	0.004176907	p<0.01
: A_23_P252641	GOSR1	0.587002709	0.820696103	0.715249782	0.062674947	0.715249782	0.001551556	p<0.01
: A_23_P366454	WIRE	0.762448194	1.064045372	0.716556092	0.030787134	0.716556092	0.004487592	p<0.01
: A_23_P43786	LMLN	1.044400804	1.45402163	0.718284227	0.017552272	0.718284227	9.18109E-04	p<0.01
: A_23_P427119	ART5	0.595921323	0.829366973	0.718525505	0.03909785	0.718525505	0.003085728	p<0.01
: A_23_P19510	HLA-DQB2	0.400655694	0.556269961	0.720254052	0.072260995	0.720254052	0.008480452	p<0.01
: A_23_P112596	ADK	1.545947411	2.143582833	0.721197887	0.0812524	0.721197887	0.008162559	p<0.01
: A_23_P64630	RNF26	0.801313047	1.110760497	0.721409385	0.068369033	0.721409385	0.008531993	p<0.01
: A_23_P44617	COPG	0.864056631	1.195105034	0.722996395	0.068100748	0.722996395	0.006941543	p<0.01
: A_23_P26311		0.685661331	0.948197663	0.723120672	0.029198769	0.723120672	0.004100184	p<0.01
: A_23_P30870	BAT2	0.946263118	1.304065542	0.725625429	0.041500605	0.725625429	0.004432073	p<0.01
: A_23_P141263		0.692502976	0.952831731	0.726784125	0.040036379	0.726784125	0.007845987	p<0.01
: A_23_P40455	DSCR4	0.401542994	0.551699337	0.727829393	0.189830061	0.727829393	0.005348697	p<0.01
: A_23_P163361	RLBP1	0.400113876	0.549018072	0.728780885	0.037709533	0.728780885	0.001315371	p<0.01
: A_23_P347528	TFCP2	0.626464388	0.859397549	0.728957616	0.068678017	0.728957616	0.003690167	p<0.01
: A_23_P71787	AEGP	0.426137475	0.58371753	0.730040565	0.134271988	0.730040565	0.002078798	p<0.01
: A_23_P86610	ZNF365	0.545866571	0.745432843	0.732281353	0.054949788	0.732281353	0.007716702	p<0.01
: A_23_P213228	PHOX2B	0.722636259	0.985204753	0.733488401	0.030953968	0.733488401	0.007419951	p<0.01
: A_23_P205768	ARPP-19	2.259786268	3.080304311	0.733624357	0.029877412	0.733624357	0.003698589	p<0.01
: A_23_P162317	WNT10B	0.39245125	0.534665452	0.734012734	0.020429776	0.734012734	0.002046514	p<0.01
: A_23_P502320	AGRP	0.440493594	0.599574789	0.734676643	0.146895617	0.734676643	0.00851908	p<0.01
: A_23_P55242	PPP1R9B	0.681266362	0.926045655	0.735672543	0.032907104	0.735672543	9.19233E-04	p<0.01
: A_23_P35521	P4HA1	0.324786813	0.441212143	0.736123922	0.025312623	0.736123922	0.005003291	p<0.01
: A_23_P114656	HDAC1	2.353391513	3.194155034	0.736780616	0.011863817	0.736780616	0.009978427	p<0.01
: A_23_P49816	CENTA2	0.320816677	0.434912671	0.73765769	0.053440909	0.73765769	0.00793059	p<0.01
: A_23_P315345	PIN4	0.803902234	1.089473651	0.737881301	0.028901319	0.737881301	0.008464188	p<0.01
: A_23_P72949		0.456330364	0.615204998	0.741753342	0.07421578	0.741753342	0.005477368	p<0.01
: A_23_P37484	CHSY1	0.812362909	1.09429976	0.742358665	0.063473611	0.742358665	0.005539433	p<0.01
: A_23_P31253	FTSJ2	0.834714398	1.120905068	0.74467894	0.027942448	0.74467894	0.005993094	p<0.01
: A_23_P42224	RFP	0.818299216	1.097825709	0.74538172	0.065854904	0.74538172	0.002190764	p<0.01
: A_23_P36698	TAPBPL	0.405637462	0.544119265	0.745493659	0.054476747	0.745493659	0.0033876	p<0.01
: A_23_P76823	ADSSL1	0.675575255	0.90445154	0.746944668	0.018017262	0.746944668	0.00319248	p<0.01
: A_23_P390744	FLJ31153	1.442413113	1.930138559	0.747310656	0.080980447	0.747310656	0.00720132	p<0.01
: A_23_P5342	LRP1B	0.827156794	1.104833828	0.748670771	0.032320577	0.748670771	0.003365922	p<0.01
: A_23_P166536	BRD1	1.098682799	1.461200416	0.751904247	0.010237766	0.751904247	0.00592425	p<0.01
: A_23_P91930	QTRTD1	1.431118595	1.902909291	0.752068741	0.014772796	0.752068741	0.001187078	p<0.01
: A_23_P18023		0.816794559	1.081670515	0.755123255	0.030167247	0.755123255	0.009737501	p<0.01
: A_23_P380881	FLJ25555	0.472520115	0.624009968	0.757231679	0.123714238	0.757231679	0.006265102	p<0.01
: A_23_P70998		1.315744444	1.733342465	0.759079334	0.036896357	0.759079334	0.001968455	p<0.01
: A_23_P316974	SYNJ2	0.543089657	0.714768035	0.759812456	0.052198159	0.759812456	0.002950399	p<0.01
: A_23_P167624		0.564676757	0.742458654	0.760549768	0.050702488	0.760549768	0.008057548	p<0.01
: A_23_P209426	ALS2CR3	0.872582985	1.144689477	0.762287941	0.06098567	0.762287941	0.007842001	p<0.01

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: A_23_P431330	FLJ34443	1.294066912	1.697341199	0.762408237	0.011289258	0.762408237	0.001824999	p<0.01
: A_23_P82176	SOX4	0.511516849	0.666711698	0.76722345	0.068968051	0.76722345	0.004405628	p<0.01
: A_23_P162589	VDR	0.582009657	0.757385602	0.768445631	0.067791866	0.768445631	0.007311422	p<0.01
: A_23_P17955	FBXL2	0.62122031	0.808014627	0.7688231	0.093707608	0.7688231	0.009271248	p<0.01
: A_23_P371106	D4S234E	0.689841155	0.895774637	0.770105701	0.127351399	0.770105701	0.006135933	p<0.01
: A_23_P251075	CXorf6	0.796012162	1.032103951	0.771251928	7.07525E-04	0.771251928	0.0034033	p<0.01
: A_23_P43695	KIF24	0.63305749	0.819967437	0.772051987	0.040637419	0.772051987	0.006309605	p<0.01
: A_23_P42347	ETV7	0.434404543	0.562498525	0.772276768	0.10140202	0.772276768	0.009475203	p<0.01
: A_23_P128375	FLJ14721	0.432482192	0.55908634	0.773551706	0.046539017	0.773551706	0.003262074	p<0.01
: A_23_P150960	MGC13168	0.39892423	0.51554299	0.773794307	0.105037695	0.773794307	0.009817264	p<0.01
: A_23_P201816	CAP350	0.916900956	1.18463777	0.773992674	0.074771589	0.773992674	0.003588277	p<0.01
: A_23_P17420	BCAS1	0.454468432	0.58562591	0.776038807	0.012413431	0.776038807	0.003342285	p<0.01
: A_23_P129556	IL4R	0.665237652	0.857067997	0.776178383	0.002548112	0.776178383	0.001693183	p<0.01
: A_23_P22693	CTAG2	0.602092774	0.775012261	0.776881611	0.065991524	0.776881611	0.004657896	p<0.01
: A_23_P72680	CDV1	0.589400378	0.758225839	0.777341456	6.49657E-04	0.777341456	0.007898306	p<0.01
: A_23_P34879	RBM15	0.902610493	1.159954262	0.778143176	0.049416091	0.778143176	0.005904708	p<0.01
: A_23_P91850	MGC34923	0.489779778	0.629400198	0.778169089	0.021586639	0.778169089	0.009539582	p<0.01
: A_23_P125687	ING2	0.765085293	0.978269487	0.782080299	0.069008356	0.782080299	0.007393115	p<0.01
: A_23_P99349	BTBD11	0.540172886	0.68985031	0.783029127	0.076977225	0.783029127	0.008097814	p<0.01
: A_23_P217968	SUV420H1	0.560776832	0.715997854	0.783210213	0.066233006	0.783210213	0.004040029	p<0.01
: A_23_P158925		1.538984216	1.964393329	0.783439953	0.046382587	0.783439953	0.007713274	p<0.01
: A_23_P52556	CTSD	0.377244659	0.481482902	0.783505826	0.013309714	0.783505826	0.007755963	p<0.01
: A_23_P122068	C1QTNF3	0.70747382	0.900041108	0.786046119	0.045179843	0.786046119	0.00821503	p<0.01
: A_23_P158129	MTA1	1.056347786	1.337207723	0.789965364	0.010815018	0.789965364	0.00445332	p<0.01
: A_23_P259846	TNK2	0.44598118	0.563200259	0.791869628	0.08961242	0.791869628	0.003845442	p<0.01
: A_23_P392529	C21orf81	0.602794585	0.756721147	0.796587471	0.025392056	0.796587471	0.00989772	p<0.01
: A_23_P11295	MTCP1	0.915658092	1.14768917	0.797827597	0.072653235	0.797827597	0.005701472	p<0.01
: A_23_P2711	TDRD3	0.758943319	0.948876186	0.799833878	0.041175248	0.799833878	0.00306933	p<0.01
: A_23_P253774		1.289728084	1.611810908	0.800173319	0.029549418	0.800173319	0.009517754	p<0.01
: A_23_P139725		0.60021984	0.748787389	0.801589141	0.026372495	0.801589141	0.004938916	p<0.01
: A_23_P100196	USP10	1.626340964	2.024010157	0.803524112	0.089785519	0.803524112	0.009674692	p<0.01
: A_23_P4662	BCL3	0.428818745	0.533250533	0.804159994	0.034061502	0.804159994	0.007445357	p<0.01
: A_23_P106562	GALNS	0.567308683	0.705049209	0.804637003	0.018596354	0.804637003	0.001027456	p<0.01
: A_23_P379778	DIRAS2	0.490379109	0.607746357	0.806881199	0.056140416	0.806881199	0.005792344	p<0.01
: A_23_P51639	KIAA0467	0.59711829	0.738069651	0.809027019	0.091397731	0.809027019	0.0095249	p<0.01
: A_23_P114814	RHOU	1.250777626	1.54445143	0.809852354	0.010833397	0.809852354	0.002775092	p<0.01
: A_23_P50297		0.60936653	0.752398778	0.809898351	0.001888488	0.809898351	0.007862214	p<0.01
: A_23_P252175		1.015369423	1.252198821	0.810869174	0.045317352	0.810869174	0.007473682	p<0.01
: A_23_P46315	FLJ37099	1.034308601	1.266616544	0.816591735	0.054081382	0.816591735	0.005369631	p<0.01
: A_23_P112078	MFHAS1	0.750840024	0.916378262	0.819355996	0.013814978	0.819355996	0.001076673	p<0.01
: A_23_P114343	GAGED4	0.538973516	0.654389234	0.823628337	0.023050516	0.823628337	0.001485429	p<0.01
: A_23_P92253	PIK3CB	1.102553775	1.336869938	0.824727779	0.022488151	0.824727779	0.009671095	p<0.01
: A_23_P9571	ECT2	1.59440984	1.930422861	0.825938126	0.078297702	0.825938126	0.005024625	p<0.01
: A_23_P80345	MAP3K7IP1	0.502819667	0.607748159	0.827348729	0.058788308	0.827348729	0.009013716	p<0.01
: A_23_P110557		0.697505864	0.84196725	0.828423984	0.078688593	0.828423984	0.009187026	p<0.01
: A_23_P96395	ASB12	0.638158209	0.769088829	0.829758781	0.003676233	0.829758781	0.009895354	p<0.01
: A_23_P57513	C1QTNF6	0.746900709	0.897635973	0.832075286	0.125126648	0.832075286	0.008032093	p<0.01
: A_23_P169553	FGF12	0.684988091	0.820360184	0.834984565	0.057249861	0.834984565	0.007308164	p<0.01
: A_23_P250173	CNTN3	0.791645196	0.947617249	0.835406064	0.018284799	0.835406064	0.004641076	p<0.01
: A_23_P377212	LOC150678	0.5755201	0.687620221	0.836973786	0.062093196	0.836973786	0.007843165	p<0.01
: A_23_P251621	SUPT3H	0.565141868	0.674228977	0.838204656	0.060123993	0.838204656	0.005323821	p<0.01
: A_23_P339705	C19orf14	0.606312076	0.723267963	0.83829522	0.014204264	0.83829522	0.008933483	p<0.01
: A_23_P51187	PRKCZ	0.529622049	0.627713829	0.843731689	0.047467477	0.843731689	0.007559056	p<0.01

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: A_23_P213415	SEMA5A	0.665631652	0.788699402	0.843961148	0.00337505	0.843961148	0.006244083	p<0.01
: A_23_P33675	TRIM6	0.728361007	0.859712589	0.847214542	0.033390401	0.847214542	0.007000012	p<0.01
: A_23_P258592	CIDEA	0.471554877	0.554084088	0.851052913	0.036937572	0.851052913	0.008275932	p<0.01
: A_23_P124664	ATR	1.318387811	1.5308432	0.861216754	0.070509143	0.861216754	0.005703791	p<0.01
: A_23_P372860	HIST1H2AC	0.72105821	0.828727196	0.870079096	0.041651953	0.870079096	0.002573636	p<0.01
: A_23_P48740	DIO2	0.638673963	0.725938742	0.879790436	0.047012784	0.879790436	0.001646749	p<0.01
: A_23_P423957	FBXL18	0.489921934	0.544643426	0.899527858	0.003740107	0.899527858	0.002887489	p<0.01
: A_23_P73150	DKFZP434H0115	0.682269532	0.757981498	0.900113702	0.024134301	0.900113702	0.004023582	p<0.01
: A_23_P110175	CTSO	0.784916925	0.862068197	0.910504444	0.007553301	0.910504444	0.006130427	p<0.01
: A_23_P160237	ACP6	0.641975037	0.578670494	1.109396527	9.60365E-04	1.109396527	0.003085505	p<0.01
: A_23_P336670	C3orf17	2.194310314	1.9207995	1.142394255	1.36403E-04	1.142394255	0.00526542	p<0.01
: A_23_P157428	SLC10A5	0.734871107	0.641324294	1.145865071	0.006906872	1.145865071	0.001483434	p<0.01
: A_23_P60758		0.701237485	0.607050219	1.15515564	0.009922287	1.15515564	6.58634E-04	p<0.01
: A_23_P35168	ALG6	1.299466532	1.124635597	1.155455631	0.036042796	1.155455631	0.002194109	p<0.01
: A_23_P154130	MAP4K3	1.092846855	0.939827151	1.162816857	0.021564084	1.162816857	0.003445154	p<0.01
: A_23_P201419	ITLN2	0.599191944	0.511012453	1.172558399	0.001730955	1.172558399	0.001380125	p<0.01
: A_23_P42507	PPIL4	1.412717409	1.198164864	1.179067632	6.47729E-05	1.179067632	0.001787079	p<0.01
: A_23_P346206	RAE1	1.290260809	1.092611542	1.180896191	0.044412719	1.180896191	0.007037239	p<0.01
: A_23_P63153	DDX20	1.544470863	1.302583549	1.185698118	0.006311161	1.185698118	0.006224874	p<0.01
: A_23_P105461	CMKLR1	0.52751871	0.444663107	1.18633343	0.046640723	1.18633343	0.009690683	p<0.01
: A_23_P252184	GRM2	1.125289917	0.941557173	1.195137108	0.021946327	1.195137108	0.001133579	p<0.01
: A_23_P60947	DC12	1.512537278	1.263769525	1.196845824	0.073224066	1.196845824	0.008198858	p<0.01
: A_23_P113983		1.156284153	0.965353361	1.197783319	0.007636704	1.197783319	0.005590673	p<0.01
: A_23_P155197	PTPLB	2.292550429	1.913679768	1.197980178	0.013068182	1.197980178	0.003480752	p<0.01
: A_23_P103734	KIAA1639	0.809554751	0.674920756	1.19948119	0.025809479	1.19948119	0.007675577	p<0.01
: A_23_P23206	MAD2L2	0.920456114	0.764016218	1.204759915	0.050893101	1.204759915	0.009776043	p<0.01
: A_23_P304410	FLJ35382	2.571904307	2.129533302	1.207731433	0.008895994	1.207731433	0.004761928	p<0.01
: A_23_P403385	OTOR	0.81664013	0.674961352	1.209906504	0.027911534	1.209906504	0.00913233	p<0.01
: A_23_P502427	MRPL47	2.504002557	2.067388769	1.211190945	0.006914114	1.211190945	0.003749261	p<0.01
: A_23_P73451		1.293049323	1.066289776	1.212662217	0.005525064	1.212662217	0.002524073	p<0.01
: A_23_P95231	CASC1	1.225989629	1.008008752	1.216248992	0.096488991	1.216248992	0.005123552	p<0.01
: A_23_P23522	LOC128387	1.112083546	0.913772865	1.217024043	0.061160776	1.217024043	0.006676241	p<0.01
: A_23_P67323	SBB154	0.889585766	0.730604187	1.217602885	0.015224675	1.217602885	0.001255927	p<0.01
: A_23_P40975	EDEM1	1.556496542	1.274373583	1.221381676	0.038873581	1.221381676	0.005190391	p<0.01
: A_23_P85570	YARS	1.60123907	1.306034099	1.226031595	0.04787771	1.226031595	0.003914632	p<0.01
: A_23_P14915	CSNK2A2	1.559626639	1.271374065	1.226725227	0.003543045	1.226725227	0.009964405	p<0.01
: A_23_P66095	MC1R	0.829920095	0.675175341	1.229191952	0.068263873	1.229191952	0.004968639	p<0.01
: A_23_P162127	MDS025	0.962922867	0.781992383	1.231371159	0.095363648	1.231371159	0.007925146	p<0.01
: A_23_P54198	C14orf118	1.206721516	0.9797465	1.231667085	0.014463033	1.231667085	6.74973E-04	p<0.01
: A_23_P79043	NIFIE14	2.026284049	1.644936062	1.231831495	0.057821326	1.231831495	0.004500724	p<0.01
: A_23_P44514		1.545077274	1.25369092	1.2324228	0.042668196	1.2324228	0.004749763	p<0.01
: A_23_P47444	OR5T1	1.378727575	1.118434124	1.232730248	0.038263475	1.232730248	0.004677527	p<0.01
: A_23_P143867	TMF1	2.066962068	1.675496562	1.233641486	0.057088433	1.233641486	0.005351937	p<0.01
: A_23_P2873	KNS2	1.423210548	1.153476113	1.233844839	0.048495831	1.233844839	0.003716879	p<0.01
: A_23_P256903		1.441870051	1.167089373	1.235440991	0.065966481	1.235440991	0.006943408	p<0.01
: A_23_P130266	LLGL1	1.454409164	1.177184476	1.235498084	0.072433753	1.235498084	0.007408336	p<0.01
: A_23_P159277		1.152185367	0.931292683	1.237189326	0.025194371	1.237189326	0.007576563	p<0.01
: A_23_P202496	C10orf117	2.970246434	2.397370005	1.238960372	0.031471734	1.238960372	0.005666571	p<0.01
: A_23_P200535	TRAPPC3	1.332157634	1.071433152	1.243341809	0.040170363	1.243341809	0.006671895	p<0.01
: A_23_P88177	SERPINA12	2.995511754	2.408671056	1.243636713	0.060393006	1.243636713	0.005982178	p<0.01
: A_23_P82664	ARPC1A	1.28636911	1.033920304	1.244166601	0.084826568	1.244166601	0.009373136	p<0.01
: A_23_P65609	GTF2A1	0.749035647	0.602024155	1.244195338	0.002890395	1.244195338	4.73861E-04	p<0.01
: A_23_P150069	ANKRD16	1.534864261	1.232947399	1.244874082	0.058095666	1.244874082	0.007461663	p<0.01

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: A_23_P303085	PTN	0.710602678	0.570787238	1.244951938	0.050622404	1.244951938	0.00587757	p<0.01
: A_23_P141146	FBXL20	2.420955706	1.941037677	1.247248178	0.002916951	1.247248178	6.91099E-04	p<0.01
: A_23_P201591	AMPD2	1.169474681	0.937082383	1.247995589	0.040330055	1.247995589	0.00203198	p<0.01
: A_23_P17115	CHRNA	0.596043305	0.477196978	1.249050881	0.011852069	1.249050881	8.08467E-04	p<0.01
: A_23_P100155	FLJ20507	1.054283324	0.843809318	1.249433138	0.032391011	1.249433138	0.008931089	p<0.01
: A_23_P212025	FLJ35036	0.776518492	0.621016451	1.250399231	0.029392055	1.250399231	0.007904011	p<0.01
: A_23_P75310	ARHGAP22	0.585234702	0.467819508	1.250983962	0.071844731	1.250983962	0.006071995	p<0.01
: A_23_P257988	SEN2	0.710862013	0.567936251	1.251658106	0.097190698	1.251658106	0.003653331	p<0.01
: A_23_P133011	LOC401137	1.456866379	1.16197046	1.253789515	0.047907414	1.253789515	0.002355176	p<0.01
: A_23_P99961	BBS4	1.486892232	1.185897864	1.253811376	0.087945017	1.253789515	0.001988186	p<0.01
: A_23_P156109	ETEA	2.394366507	1.907655014	1.255136012	0.046761808	1.255136012	0.003400518	p<0.01
: A_23_P372255	ITPKB	0.591914661	0.470841553	1.257141935	0.03997912	1.257141935	0.007420698	p<0.01
: A_23_P73023	TBC1D1	0.93313416	0.741786173	1.257955722	0.098284706	1.257955722	0.005521395	p<0.01
: A_23_P147154		2.371110892	1.873655187	1.265500134	0.062838124	1.265500134	0.008829089	p<0.01
: A_23_P264400	HSRG1	1.27039171	1.002654316	1.267028616	0.005043568	1.267028616	0.002390476	p<0.01
: A_23_P67737	ZNF568	0.780400076	0.615652673	1.267597967	0.063914503	1.267597967	0.001537387	p<0.01
: A_23_P74178	HCRTR1	0.745493116	0.588039829	1.267759562	0.057760996	1.267759562	0.003483396	p<0.01
: A_23_P501805	LIPT1	3.31385088	2.611794578	1.268802266	0.181335203	1.268802266	0.004773692	p<0.01
: A_23_P100872	HOXB3	0.758506895	0.597099388	1.270319332	0.041204338	1.270319332	0.005494918	p<0.01
: A_23_P33256	GP9	0.459502196	0.361502704	1.271089237	0.004003707	1.271089237	2.45026E-04	p<0.01
: A_23_P132820	XRNI	1.68899724	1.32431474	1.275374493	0.009696307	1.275374493	0.004951853	p<0.01
: A_23_P104680	SF3A1	2.063727807	1.613252296	1.279234384	0.013392341	1.279234384	3.02032E-04	p<0.01
: A_23_P15466	SCO1	1.461160877	1.141355885	1.280197435	0.025585416	1.280197435	0.001625463	p<0.01
: A_23_P151264	GRIN2B	1.195234911	0.932976642	1.281098429	0.115289028	1.281098429	0.009532853	p<0.01
: A_23_P103905	Ufc1	1.065624624	0.831271246	1.28192167	0.114736555	1.28192167	0.008288197	p<0.01
: A_23_P167256	PHF17	0.758126938	0.589356165	1.28636465	0.022274425	1.28636465	0.002698613	p<0.01
: A_23_P119618	SF4	1.437595509	1.116861062	1.287174886	0.029733334	1.287174886	0.001495373	p<0.01
: A_23_P135157	PLAA	1.072898748	0.832981266	1.288022662	0.080115868	1.288022662	0.006128167	p<0.01
: A_23_P320185	NDUFA11	1.222011562	0.946442581	1.291162914	0.041992265	1.291162914	5.23962E-04	p<0.01
: A_23_P341325	RPL10L	1.418296111	1.098036321	1.291665935	0.062080265	1.291665935	0.008449635	p<0.01
: A_23_P217643	F8	1.468593582	1.136841954	1.2918186	0.004792101	1.2918186	0.006528172	p<0.01
: A_23_P33343	SAGE1	1.524320148	1.179661447	1.292167471	0.015431791	1.292167471	0.001524537	p<0.01
: A_23_P107673	ZFP28	0.970430226	0.75100549	1.29217461	0.046068893	1.29217461	0.004735821	p<0.01
: A_23_P334218	MGC21654	2.271834751	1.757423709	1.292707467	0.061988352	1.292707467	0.003932103	p<0.01
: A_23_P119652		2.33158602	1.801733055	1.294079616	0.040645578	1.294079616	0.00674912	p<0.01
: A_23_P25644	FLJ11305	0.91685697	0.708443985	1.294184141	0.050761447	1.294184141	0.00103742	p<0.01
: A_23_P383435	TRIP3	2.152130088	1.662403463	1.294589512	0.023003435	1.294589512	0.001224149	p<0.01
: A_23_P203983	RHOF	0.556429267	0.428786755	1.297682964	0.010670507	1.297682964	0.006371439	p<0.01
: A_23_P13273	OR5AR1	3.058397793	2.355770977	1.298257692	0.037927544	1.298257692	0.002609097	p<0.01
: A_23_P41912	C5orf3	1.528028042	1.175662205	1.299716905	0.006584518	1.299716905	4.43174E-04	p<0.01
: A_23_P154056	EIF2B4	1.173382248	0.902251561	1.300504535	0.015975276	1.300504535	0.002470631	p<0.01
: A_23_P28683	CPSF3	1.163979783	0.894480415	1.301291525	0.079905625	1.301291525	0.006149465	p<0.01
: A_23_P87329	FLJ10774	0.9501862	0.729841591	1.301907443	0.016411457	1.301907443	5.67071E-04	p<0.01
: A_23_P138665	GLUD1	0.880586576	0.675520305	1.303567886	0.02180062	1.303567886	2.09137E-04	p<0.01
: A_23_P202693	KBTBD4	1.185242634	0.908826448	1.304146283	0.039546396	1.304146283	0.001666992	p<0.01
: A_23_P358470	FLJ33167	1.605448058	1.230806069	1.304387505	0.078275903	1.304387505	0.00866412	p<0.01
: A_23_P37535	RAB8B	1.694894555	1.296696257	1.307086795	0.007702169	1.307086795	0.001750311	p<0.01
: A_23_P426944	PAX9	1.983228499	1.516216968	1.308011017	0.017542072	1.308011017	0.003905556	p<0.01
: A_23_P501795	SURF5	1.379505119	1.053888081	1.308967379	0.014361129	1.308967379	3.49644E-04	p<0.01
: A_23_P46708		3.862162613	2.948874228	1.309707473	0.030462252	1.309707473	6.52435E-04	p<0.01
: A_23_P259555	OR12D3	0.897181657	0.684496968	1.310716773	0.007083189	1.310716773	0.002790396	p<0.01
: A_23_P397899	C9orf80	2.98553254	2.272064307	1.314017623	0.088050756	1.314017623	0.007264248	p<0.01
: A_23_P103110	MAFF	0.811179714	0.61701703	1.314679619	0.010844422	1.314679619	0.001580906	p<0.01

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: A_23_P53370	RND1	2.059097536	1.565264597	1.315494863	0.038269699	1.315494863	0.003831492	p<0.01
: A_23_P74059	NPPA	2.661998101	2.0234834	1.315552231	0.062580558	1.315552231	0.007938655	p<0.01
: A_23_P83149	C9orf77	1.367785553	1.0383293	1.317294574	0.012740737	1.317294574	0.004017519	p<0.01
: A_23_P54636	ATP6V0D1	0.73769959	0.559612154	1.318233681	0.156981259	1.318233681	0.009662185	p<0.01
: A_23_P216188	IKBKB	0.901885889	0.683468176	1.319572616	0.015793811	1.319572616	7.00515E-04	p<0.01
: A_23_P201097	GUK1	1.618714862	1.22466666	1.321759557	0.093031989	1.321759557	0.009487454	p<0.01
: A_23_P20298	COH1	2.100633174	1.588656518	1.322270201	0.043655266	1.322270201	0.006879754	p<0.01
: A_23_P77440	NFATC3	1.764502385	1.334207711	1.322509509	0.003490727	1.322509509	0.002960019	p<0.01
: A_23_P409888	C20orf128	2.370429396	1.787813157	1.325882062	0.118059991	1.325882062	0.008131903	p<0.01
: A_23_P106236	CHES1	1.562231361	1.17731693	1.326942067	0.100983336	1.326942067	0.00574586	p<0.01
: A_23_P86369		2.598037077	1.95169428	1.331170104	0.018424483	1.331170104	0.001485465	p<0.01
: A_23_P363769	KRTHB1	1.577260237	1.182293016	1.334068809	0.056512654	1.334068809	0.002563616	p<0.01
: A_23_P31426	LEP	4.101229088	3.066726594	1.337331178	0.045867668	1.337331178	0.006037722	p<0.01
: A_23_P136857		0.757514638	0.566234703	1.337810336	0.039466838	1.337810336	0.0086019	p<0.01
: A_23_P70348	SERPINB6	0.684191669	0.51074381	1.339598554	0.079438835	1.339598554	0.008329198	p<0.01
: A_23_P118042	FLJ11004	0.730478842	0.54471527	1.341028759	0.01968882	1.341028759	0.001329526	p<0.01
: A_23_P123672	TDRD7	1.09026811	0.812129781	1.34248015	0.011896285	1.34248015	0.005592375	p<0.01
: A_23_P86350	OR1C1	1.603669899	1.194205714	1.342875754	0.035490842	1.342875754	0.009061296	p<0.01
: A_23_P90814	FBXO11	0.814800881	0.606270381	1.343956272	0.092395431	1.343956272	0.007159181	p<0.01
: A_23_P68949	ST13	1.089342894	0.810149067	1.344620314	0.012509265	1.344620314	1.30793E-04	p<0.01
: A_23_P36513	PRKAG1	1.569921003	1.167541775	1.344637971	0.096503107	1.344637971	0.006870105	p<0.01
: A_23_P258531	PHKA1	1.834591891	1.363592521	1.345410643	0.033664205	1.345410643	0.002037652	p<0.01
: A_23_P112061	FLJ32731	1.76343588	1.309865107	1.346272888	0.066487971	1.346272888	0.005127968	p<0.01
: A_23_P119788		1.724859068	1.280782815	1.346722526	0.060487734	1.346722526	0.007544902	p<0.01
: A_23_P56354	PSG3	2.600158082	1.927603092	1.348907404	0.039934613	1.348907404	0.005597701	p<0.01
: A_23_P135576	PTPRT	1.74885732	1.295893947	1.349537378	0.034683238	1.349537378	0.007934242	p<0.01
: A_23_P67042	MOCOS	1.491009228	1.104342081	1.35013349	0.025539522	1.35013349	6.44265E-04	p<0.01
: A_23_P53439	SDSL	1.11796827	0.826861587	1.352062168	0.063555104	1.352062168	0.005194887	p<0.01
: A_23_P129569	FLJ21816	1.736571791	1.282973886	1.35355194	0.088644306	1.35355194	0.002191965	p<0.01
: A_23_P113803	KATNA1	2.210449918	1.63287389	1.353717474	0.031562935	1.353717474	0.001238954	p<0.01
: A_23_P147976	BRDT	1.310802672	0.966414958	1.356355944	0.057085402	1.356355944	0.009010928	p<0.01
: A_23_P24926	FNTA	1.559401387	1.149478473	1.356616435	0.099475202	1.356616435	0.006870779	p<0.01
: A_23_P62672	RAB3B	1.152808868	0.847354787	1.36047956	0.080682538	1.36047956	0.00998869	p<0.01
: A_23_P148541	CTAG1B	0.678555943	0.49848509	1.361236187	0.084593371	1.361236187	0.006970433	p<0.01
: A_23_P258367	GLE1L	1.083944411	0.795155107	1.363186128	0.017538328	1.363186128	5.23907E-05	p<0.01
: A_23_P106949	ADCY7	1.283494907	0.941342333	1.363473056	0.103410664	1.363473056	0.004594306	p<0.01
: A_23_P126992	ABI1	2.423011435	1.776755039	1.363728472	0.170435487	1.363728472	0.007996732	p<0.01
: A_23_P132444	TCEA1	2.95018632	2.163280268	1.363755942	0.057607656	1.363755942	0.007064636	p<0.01
: A_23_P205659	BTBD5	1.718702094	1.260267104	1.36376018	0.058091013	1.36376018	0.006203406	p<0.01
: A_23_P149398		0.874895012	0.640309273	1.366363177	0.077315392	1.366363177	0.006569595	p<0.01
: A_23_P158524		2.491301254	1.82307559	1.366537552	0.025760023	1.366537552	0.005694775	p<0.01
: A_23_P205449	CDCA4	1.91111211	1.397207481	1.367808386	0.038722645	1.367808386	0.007960304	p<0.01
: A_23_P118038	NUTF2	2.600284647	1.898267194	1.369820147	0.059897789	1.369820147	0.001497481	p<0.01
: A_23_P146611	OR1B1	1.969008341	1.437166146	1.370063124	0.019054633	1.370063124	0.001858985	p<0.01
: A_23_P10743	PDE6B	1.245814784	0.90926322	1.370136564	0.078787954	1.370136564	0.00257857	p<0.01
: A_23_P40588	HSC20	1.063657422	0.775985603	1.370717986	0.041039832	1.370717986	0.002212315	p<0.01
: A_23_P70384	RNF8	1.589187925	1.159343941	1.370764851	0.062045228	1.370764851	0.001845241	p<0.01
: A_23_P254382		0.680593996	0.49628499	1.371377352	0.035917054	1.371377352	3.52434E-04	p<0.01
: A_23_P11884	ALDH9A1	2.369104636	1.726713398	1.372031189	0.056254834	1.372031189	0.003320184	p<0.01
: A_23_P130130	BCL6B	0.671722152	0.488104613	1.376184805	0.014293784	1.376184805	0.001159259	p<0.01
: A_23_P50575	PPP1R12C	1.177933821	0.853944739	1.379402866	0.041589015	1.379402866	0.002834223	p<0.01
: A_23_P133728	GCM1	1.206938056	0.874925043	1.379475952	0.003841911	1.379475952	0.002230929	p<0.01
: A_23_P3716	ARHGAP17	0.410571508	0.297493815	1.380100988	0.057212447	1.380100988	0.004822732	p<0.01

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: A_23_P32294	C9orf10	0.975734612	0.70692757	1.380246935	0.06875936	1.380246935	0.006637574	p<0.01
: A_23_P63205	DR1	2.502453757	1.81215685	1.380925584	0.008498223	1.380925584	0.004358219	p<0.01
: A_23_P68208	SPR	2.05390358	1.484400826	1.383658339	0.038170782	1.383658339	0.002156232	p<0.01
: A_23_P123814	RAB9P40	1.379553006	0.996233792	1.384768332	0.040301766	1.384768332	0.006777129	p<0.01
: A_23_P164421	TTC19	1.350168978	0.974037983	1.386156394	0.063571589	1.386156394	0.004972169	p<0.01
: A_23_P110725	PRKAA1	1.130040116	0.814089761	1.388102602	0.019437564	1.388102602	0.002179316	p<0.01
: A_23_P103180	LOC127253	2.092720645	1.506019363	1.389570875	0.06024076	1.389570875	0.008439774	p<0.01
: A_23_P42335	FANCE	2.022929723	1.452349972	1.392866569	0.020268194	1.392866569	3.21534E-04	p<0.01
: A_23_P11107	BMP15	1.376025365	0.987748895	1.393092284	0.02280114	1.393092284	0.007198477	p<0.01
: A_23_P23191	HSPG2	0.778038475	0.558089396	1.394110838	0.081898254	1.394110838	0.004905957	p<0.01
: A_23_P50456	POLD1	1.487865914	1.066594499	1.394968675	0.064362192	1.394968675	0.007380241	p<0.01
: A_23_P165325	SLC3A1	1.32487655	0.948900777	1.39622243	0.047062044	1.39622243	8.25127E-04	p<0.01
: A_23_P169925	PRUNE	0.975582717	0.698612623	1.39645733	0.168457134	1.39645733	0.00741349	p<0.01
: A_23_P135914	SF3B3	1.851830814	1.323087758	1.399628106	0.044904728	1.399628106	0.002058355	p<0.01
: A_23_P57133	OXT	0.881990564	0.62963525	1.40079604	0.088743658	1.40079604	0.001827377	p<0.01
: A_23_P13344	EEF1G	1.505810782	1.072518368	1.403995332	0.048123873	1.403995332	0.008211462	p<0.01
: A_23_P54728	MGC2494	1.346408527	0.958895883	1.404123796	0.050496922	1.404123796	0.009793221	p<0.01
: A_23_P202392	SUV39H2	2.415179414	1.718762585	1.405185007	0.034477916	1.405185007	0.002746369	p<0.01
: A_23_P23318	WDR3	2.495576145	1.772023704	1.408319843	0.001918932	1.408319843	8.39414E-05	p<0.01
: A_23_P251089	PLP2	1.125832596	0.798637424	1.40969176	0.11953489	1.40969176	0.007501912	p<0.01
: A_23_P24361	GRM5	3.29654329	2.338380417	1.409754917	0.047736805	1.409754917	0.004241611	p<0.01
: A_23_P146050	FLJ14007	2.555901127	1.811840909	1.410665315	0.149823444	1.410665315	0.009463901	p<0.01
: A_23_P206484	GFER	1.110516861	0.786679887	1.411650253	0.003744058	1.411650253	0.001063144	p<0.01
: A_23_P153867	LASS4	2.639178621	1.868144124	1.412727523	0.015070895	1.412727523	3.83730E-04	p<0.01
: A_23_P158048	C9orf16	1.483277838	1.047079958	1.416585073	0.019817355	1.416585073	0.004650837	p<0.01
: A_23_P18223	ITIH1	2.518599536	1.776356152	1.41784604	0.046236215	1.41784604	0.006724576	p<0.01
: A_23_P75111	CYP17A1	2.655969669	1.87211746	1.4186982	0.062913108	1.4186982	0.008349669	p<0.01
: A_23_P138881	ACTN3	1.816666536	1.280164617	1.419088227	0.037711021	1.419088227	0.002264404	p<0.01
: A_23_P303293	FLJ39378	0.825515946	0.581416937	1.419834706	0.109902081	1.420007466	0.005518555	p<0.01
: A_23_P149887	GALNACT-2	1.223777911	0.861810899	1.420007466	0.038365194	1.419834706	0.002304131	p<0.01
: A_23_P148150	COBRA1	0.858054809	0.604237196	1.420062873	0.032870361	1.420062873	0.005145479	p<0.01
: A_23_P144257	COPS8	1.420182966	0.997700613	1.423456042	0.098988614	1.423456042	0.006165035	p<0.01
: A_23_P254441	LOC155060	1.058945216	0.743632396	1.424017056	0.049055054	1.424017056	0.002060689	p<0.01
: A_23_P111432	DGKI	1.947689225	1.36684693	1.424950506	0.022990109	1.424950506	2.65283E-04	p<0.01
: A_23_P98616	SLC22A6	0.967882993	0.679220354	1.424991149	0.052310967	1.424991149	0.007295641	p<0.01
: A_23_P110116	SH3BP2	1.300171362	0.911937882	1.425723602	0.087272873	1.425723602	0.004405077	p<0.01
: A_23_P337896	RTTN	1.428196805	1.000900188	1.426912316	0.014571834	1.426912316	0.001678979	p<0.01
: A_23_P108708	LOC51255	1.220593962	0.855053576	1.427505826	0.038597843	1.427505826	0.004911695	p<0.01
: A_23_P96559	FLNA	1.207177305	0.845128849	1.428394388	0.0310134	1.428394388	0.00134381	p<0.01
: A_23_P47377	HSD17B12	3.5490113	2.481608564	1.430125343	0.05260564	1.430125343	0.003375867	p<0.01
: A_23_P255226	EBAG9	1.766362187	1.227086435	1.439476582	0.012448332	1.439476582	6.08615E-04	p<0.01
: A_23_P157715	PPP1R16A	1.571014823	1.091231535	1.439671392	0.033258882	1.439671392	0.001137749	p<0.01
: A_23_P13018	FIBP	1.354752904	0.940718638	1.440125505	0.002027031	1.440125505	5.14927E-06	p<0.01
: A_23_P216995	SH3GLB2	1.332092877	0.921657949	1.445322398	0.100638866	1.445322398	0.006333049	p<0.01
: A_23_P134786	PHF20L1	1.016941029	0.703155799	1.44625278	0.040786059	1.44625278	0.001414698	p<0.01
: A_23_P434419	C10orf9	1.513842094	1.046432067	1.446670205	0.098793178	1.446670205	0.0011035	p<0.01
: A_23_P32183	CEP1	1.042303182	0.719475124	1.448699402	0.162516535	1.448699402	0.004492046	p<0.01
: A_23_P130418	NDUFV2	2.228175144	1.53787814	1.448863266	0.015790544	1.448863266	5.68477E-04	p<0.01
: A_23_P55854	LOC147804	0.787923456	0.543346618	1.450130413	0.035162081	1.450130413	0.001385978	p<0.01
: A_23_P57033	TOMM34	1.08010265	0.744490813	1.450793793	0.005363744	1.450793793	1.35296E-05	p<0.01
: A_23_P217776	MSL3L1	2.803519597	1.931762697	1.451275356	0.045456857	1.451275356	0.004082016	p<0.01
: A_23_P32217	TOPORS	3.37056643	2.321557346	1.45185577	0.083395027	1.45185577	0.003923364	p<0.01
: A_23_P372874	S100A13	1.098226731	0.754866535	1.454862124	0.040632316	1.454862124	0.003003692	p<0.01

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: A_23_P201030	GBA	1.094985539	0.752444416	1.455237777	0.039210018	1.455237777	0.001330759	p<0.01	
: A_23_P68700	C21orf55	2.339996445	1.606190817	1.456860804	0.012757813	1.456860804	0.007481138	p<0.01	
: A_23_P29034	IFNGR2	1.604976272	1.101286688	1.457364636	0.030784075	1.457364636	0.001959578	p<0.01	
: A_23_P37251	SNAPC1	1.249550963	0.855703021	1.460262418	0.009003161	1.460262418	1.25909E-04	p<0.01	
: A_23_P139244	OR56B1	3.203752942	2.192621182	1.461152053	0.022527638	1.461152053	0.003607187	p<0.01	
: A_23_P126446	APOA1BP	1.456911871	0.994193394	1.465420994	0.028727207	1.465420994	6.62771E-04	p<0.01	
: A_23_P314642	SUHW3	4.655063861	3.173930984	1.466655666	0.075108715	1.466655666	0.002830831	p<0.01	
: A_23_P405148	C2orf33	1.790587693	1.220781245	1.466755572	0.008638955	1.466755572	2.11535E-05	p<0.01	
: A_23_P98261	SSSCA1	1.236712648	0.84186741	1.469011193	0.006171772	1.469011193	7.56693E-04	p<0.01	
: A_23_P256413	CKLFSF7	5.101864019	3.470353075	1.470128229	0.114267596	1.470128229	0.005147603	p<0.01	
: A_23_P217068	NBEAL1	2.658719714	1.807483079	1.470951371	0.024795108	1.470951371	0.00812521	p<0.01	
: A_23_P49725		1.317906982	0.895256079	1.472100568	0.110661068	1.472100568	0.00977115	p<0.01	
: A_23_P426472	ZNF45	1.336359847	0.90759165	1.472424131	0.049022279	1.472424131	0.002181401	p<0.01	
: A_23_P131322	LOC400986	1.035268868	0.702995803	1.472652984	0.003559812	1.472652984	1.22165E-04	p<0.01	
: A_23_P37237	CHURC1	2.94259878	1.997185143	1.473373057	0.040021298	1.473373057	0.001806052	p<0.01	
: A_23_P210920	GSS	1.582582806	1.072620806	1.475435492	0.024256016	1.475435492	6.67556E-04	p<0.01	
: A_23_P32770	CD96	2.558382154	1.729258722	1.479467544	0.028863119	1.479467544	0.004049489	p<0.01	
: A_23_P57293	C21orf61	1.313526153	0.887570272	1.479912289	0.007526118	1.479912289	0.005481783	p<0.01	
: A_23_P216043	DERL1	1.776812455	1.199646497	1.481113361	0.030905919	1.481113361	0.002566865	p<0.01	
: A_23_P47426	ACAD8	1.097668409	0.740655978	1.482021938	0.038051753	1.482021938	0.00345482	p<0.01	
: A_23_P157679	MGC14595	2.085819158	1.406915329	1.482547751	0.021570042	1.482547751	0.009540305	p<0.01	
: A_23_P88961	ALDOA	0.600442855	0.404933803	1.482817317	0.075422715	1.482817317	0.00855916	p<0.01	
: A_23_P20502	SLC39A4	2.207260278	1.486621541	1.48474929	0.004674182	1.48474929	4.49969E-04	p<0.01	
: A_23_P8930	JRK	1.267646367	0.853741636	1.484812633	0.063788314	1.484812633	8.96648E-04	p<0.01	
: A_23_P56529	AAMP	1.428140448	0.961544073	1.485257398	0.066125471	1.485257398	0.002957608	p<0.01	
: A_23_P422849	FERD3L	0.961271392	0.646019661	1.487990925	0.073892887	1.487990925	0.001473436	p<0.01	
: A_23_P208615	PRKCSH	1.676065227	1.125530406	1.489133673	0.043395356	1.489133673	0.006047517	p<0.01	
: A_23_P73577	TCTE1L	1.217584424	0.817128076	1.490077822	0.100043368	1.490077822	0.009749887	p<0.01	
: A_23_P166994	EPHB1	2.29054624	1.533902737	1.493279974	0.029491871	1.493279974	0.006851919	p<0.01	
: A_23_P43255	FAM49B	3.073982654	2.057664058	1.493918622	0.038514042	1.493918622	0.001735756	p<0.01	
: A_23_P65000	HSU79274	1.207131585	0.807348112	1.495181035	0.080654152	1.495181035	0.006313207	p<0.01	
: A_23_P983	PRDX6	2.117204785	1.415926097	1.495279159	0.071940326	1.495279159	0.003261038	p<0.01	
: A_23_P210134	LOC400986	0.885147508	0.591790983	1.495709689	0.00655753	1.495709689	3.50330E-05	p<0.01	
: A_23_P212229	ARL10C	1.096029575	0.731531194	1.49826772	0.039077486	1.49826772	0.004940644	p<0.01	
: A_23_P54078	OSGEP	1.580780849	1.054785459	1.498675237	0.058122841	1.498675237	0.003336887	p<0.01	
: A_23_P22297	LOR	2.781154173	1.855510225	1.498862219	0.01798522	1.498862219	0.008008916	p<0.01	
: A_23_P365149	BCKDK	1.684080379	1.122946002	1.49969845	0.045413092	1.49969845	0.002856153	p<0.01	
: A_23_P96652	CYorf15B	0.136244277	1.829627442	0.074465584	0.175704155	0.074465584	0.0309491	p<0.05	FC<-10
: A_23_P94358	MTUS1	0.81340525	10.73750957	0.075753623	0.159395338	0.075753623	0.02571681	p<0.05	FC<-10
: A_23_P100059	RBPMS2	0.14247065	1.738922338	0.081930427	0.187150278	0.081930427	0.036011831	p<0.05	FC<-10
: A_23_P24129	DKK1	0.305326932	3.619860921	0.084347697	0.147727685	0.084347697	0.022994985	p<0.05	FC<-10
: A_23_P64792	KCNMB4	0.294395276	3.149350611	0.093478089	0.077663921	0.093478089	0.011604435	p<0.05	FC<-10
: A_23_P130824	NALP2	0.266249468	2.748961353	0.096854569	0.179635117	0.096854569	0.034931054	p<0.05	FC<-10
: A_23_P27315	EMILIN2	0.217251299	2.190242287	0.099190532	0.194697196	0.099190532	0.038698743	p<0.05	FC<-10
: A_23_P14216		12.15119639	121.5127698	0.099999337	0.158989946	0.099999337	0.028790495	p<0.05	FC<-10
: A_23_P136041	PRKG1	0.709044625	2.120711618	0.334342783	0.155386959	0.334342783	0.042248645	p<0.05	FC<-2
: A_23_P50919	SERPINE2	0.071464839	0.210349771	0.33974289	0.133075398	0.33974289	0.017288201	p<0.05	FC<-2
: A_23_P37127	FOXA1	0.480376837	1.399617378	0.343220114	0.148879767	0.343220114	0.023029975	p<0.05	FC<-2
: A_23_P27795	SPINT2	3.390421127	9.860169488	0.343850187	0.24126159	0.343850187	0.042856156	p<0.05	FC<-2

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: A_23_P254924	PTPRK	0.645829454	1.818904576	0.355065056	0.149581372	0.355065056	0.024159977	p<0.05	FC<-2
: A_23_P129458	HSPC105	0.831567069	2.338751785	0.355560207	0.123727572	0.355560207	0.021086807	p<0.05	FC<-2
: A_23_P65789	MCTP2	0.640756514	1.801387632	0.355701628	0.213416715	0.355701628	0.036550304	p<0.05	FC<-2
: A_23_P25605	KBTBD7	0.705729344	1.966152949	0.358939188	0.168989423	0.358939188	0.018783246	p<0.05	FC<-2
: A_23_P251364	DKFZp762K222	0.613588702	1.704056651	0.360075295	0.103228342	0.360075295	0.025670616	p<0.05	FC<-2
: A_23_P111888	TBX1	0.26660716	0.734116018	0.363167611	0.200991234	0.363167611	0.047083924	p<0.05	FC<-2
: A_23_P79289	COBL1	0.487394406	1.339282428	0.36392205	0.184115325	0.36392205	0.036629031	p<0.05	FC<-2
: A_23_P31031	DSP	1.014305482	2.753800519	0.368329323	0.178238598	0.368329323	0.028369883	p<0.05	FC<-2
: A_23_P503072	CCL28	0.260861575	0.704494159	0.370282098	0.080811732	0.370282098	0.012545299	p<0.05	FC<-2
: A_23_P127014	TCF7L2	3.27182243	8.72561838	0.374967399	0.188461658	0.374967399	0.043228611	p<0.05	FC<-2
: A_23_P155556	C3orf4	0.892489034	2.371660083	0.376314059	0.109086754	0.376314059	0.01678842	p<0.05	FC<-2
: A_23_P111888	CTHRC1	0.179942853	0.476060677	0.377983021	0.143070804	0.377983021	0.025445823	p<0.05	FC<-2
: A_23_P250914	ATP6V1C2	2.982846954	7.875818502	0.378734852	0.134863368	0.378734852	0.028471907	p<0.05	FC<-2
: A_23_P413075	MTAC2D1	1.291614389	3.408526126	0.378936332	0.170066378	0.378936332	0.028942726	p<0.05	FC<-2
: A_23_P167812	RBM24	0.489304123	1.289716277	0.379388964	0.067560773	0.379388964	0.01516217	p<0.05	FC<-2
: A_23_P366890	FLJ20972	0.227674289	0.599209147	0.379957966	0.093006533	0.379957966	0.021785723	p<0.05	FC<-2
: A_23_P419038	CLOCK	0.510734293	1.339786465	0.381205742	0.112347689	0.381205742	0.011916003	p<0.05	FC<-2
: A_23_P22232	KLRC3	0.096595607	0.253148882	0.381576274	0.154887383	0.381576274	0.037692725	p<0.05	FC<-2
: A_23_P118894	MGC11242	0.891269826	2.324368424	0.383446022	0.137483796	0.383446022	0.019896557	p<0.05	FC<-2
: A_23_P70007	HMMR	1.195789902	3.106260429	0.384961251	0.179120591	0.384961251	0.024960053	p<0.05	FC<-2
: A_23_P151805	FBLN5	0.243393025	0.631287915	0.385549951	0.186147214	0.385549951	0.04178121	p<0.05	FC<-2
: A_23_P155688	SPINK2	0.741029608	1.908123204	0.388355221	0.126766424	0.388355221	0.03040061	p<0.05	FC<-2
: A_23_P133684	RRAGD	0.344750073	0.883475042	0.3902205	0.144530302	0.3902205	0.022694226	p<0.05	FC<-2
: A_23_P89431	CCL2	0.175560206	0.447912368	0.391952129	0.029017145	0.391952129	0.011823501	p<0.05	FC<-2
: A_23_P95184	PSCD1	1.260987038	3.18155464	0.39634304	0.150187889	0.39634304	0.047863223	p<0.05	FC<-2
: A_23_P21618	PDZRN3	0.106075037	0.267132004	0.397088461	0.173530895	0.397088461	0.048610519	p<0.05	FC<-2
: A_23_P258912	MYOM2	0.635705668	1.586779441	0.400626358	0.184871128	0.400626358	0.049057861	p<0.05	FC<-2
: A_23_P253046	UGP2	0.424146172	1.058434394	0.400729771	0.158064223	0.400729771	0.017155758	p<0.05	FC<-2
: A_23_P72737	IFITM1	0.385688319	0.961902765	0.400963936	0.152911458	0.400963936	0.024425335	p<0.05	FC<-2
: A_23_P208119	PSTPIP2	0.588927309	1.466431775	0.401605665	0.094929658	0.401605665	0.011307055	p<0.05	FC<-2
: A_23_P49155	CDH3	2.435106525	6.029870052	0.403840631	0.291322347	0.403840631	0.044628783	p<0.05	FC<-2
: A_23_P93442	SASH1	0.318886689	0.788960916	0.40418566	0.12947313	0.40418566	0.016552383	p<0.05	FC<-2
: A_23_P66682	HOXB6	0.898970034	2.194496347	0.409647542	0.076068185	0.409647542	0.010534741	p<0.05	FC<-2
: A_23_P58636	PITX1	2.581377378	6.239347339	0.413725545	0.182321596	0.413725545	0.046256712	p<0.05	FC<-2
: A_23_P36397	CYP27B1	77.69259969	187.1310628	0.415177462	0.260701356	0.415177462	0.042770187	p<0.05	FC<-2
: A_23_P205713	STXBP6	1.356046197	3.262098203	0.41569754	0.120353363	0.41569754	0.019262028	p<0.05	FC<-2
: A_23_P408249	PCK1	0.222011355	0.534063954	0.415701815	0.152005268	0.415701815	0.03122325	p<0.05	FC<-2
: A_23_P31073	MYB	0.324138753	0.779536478	0.415809602	0.106112257	0.415809602	0.012896228	p<0.05	FC<-2
: A_23_P22382	DKFZP434P1750	0.443441991	1.064850973	0.416435729	0.161758844	0.416435729	0.026808224	p<0.05	FC<-2
: A_23_P328501	TCF7L2	2.876806185	6.900419165	0.416903106	0.161291746	0.416903106	0.031565093	p<0.05	FC<-2
: A_23_P165369	GALNT13	0.83769498	1.996137014	0.419658057	0.010208452	0.419658057	0.010011137	p<0.05	FC<-2
: A_23_P8196	ME1	1.053326343	2.49629698	0.421955541	0.240532145	0.421955541	0.030474918	p<0.05	FC<-2
: A_23_P347471	FZD3	0.768529893	1.816787434	0.423015857	0.19464885	0.423015857	0.040865552	p<0.05	FC<-2
: A_23_P202435	ADD3	0.772506319	1.820459935	0.424346784	0.118495743	0.424346784	0.013690209	p<0.05	FC<-2
: A_23_P108676	FLJ13391	0.108477154	0.254642639	0.425997604	0.082611673	0.425997604	0.013286393	p<0.05	FC<-2
: A_23_P200780	TGFB3	0.262397377	0.614409919	0.427072169	0.143671338	0.427072169	0.021510984	p<0.05	FC<-2
: A_23_P101208	CYB5	1.471865151	3.445416424	0.42719514	0.1383356	0.42719514	0.019056713	p<0.05	FC<-2
: A_23_P58697		1.294080835	2.989422169	0.432886612	0.169523568	0.432886612	0.038128797	p<0.05	FC<-2
: A_23_P41487	KIAA0882	0.195251817	0.450638842	0.433277825	0.167482418	0.433277825	0.035090575	p<0.05	FC<-2
: A_23_P9688	DNCL12	0.21418404	0.492415661	0.434965939	0.171450435	0.434965939	0.031456877	p<0.05	FC<-2
: A_23_P66454	GSDML	0.447367066	1.022207463	0.437648013	0.097524573	0.437648013	0.014876769	p<0.05	FC<-2
: A_23_P53193	SYTL2	0.274859662	0.625890518	0.439149746	0.190514432	0.439149746	0.042945587	p<0.05	FC<-2
: A_23_P85780	PHGDH	0.482043487	1.085912716	0.443906292	0.288510539	0.443906292	0.048755148	p<0.05	FC<-2

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: A_23_P209449	FZD7	0.903238638	2.03262443	0.444370649	0.110741567	0.444370649	0.01338883	p<0.05	FC<-2
: A_23_P202658	GSTP1	1.225958918	2.749541464	0.445877589	0.087719752	0.445877589	0.015717031	p<0.05	FC<-2
: A_23_P46245	HEYL	0.599895651	1.335732772	0.449113523	0.161294111	0.449113523	0.028034217	p<0.05	FC<-2
: A_23_P29735	BSN	0.670855165	1.49345834	0.449195767	0.069701041	0.449195767	0.020268049	p<0.05	FC<-2
: A_23_P137035	PIR	0.448224292	0.989253332	0.453093537	0.115189626	0.453093537	0.019058053	p<0.05	FC<-2
: A_23_P95802	CNTNAP2	0.904019454	1.979501908	0.456690367	0.115450627	0.456690367	0.039437661	p<0.05	FC<-2
: A_23_P96285	C2orf23	1.106094534	2.42129834	0.456818772	0.187852837	0.456818772	0.01911144	p<0.05	FC<-2
: A_23_P87539	IFITM3	0.970401847	2.118792206	0.457997648	0.199443251	0.457997648	0.039350501	p<0.05	FC<-2
: A_23_P105862	13CDNA73	0.566209936	1.233151084	0.459156987	0.179145831	0.459156987	0.046250369	p<0.05	FC<-2
: A_23_P167067	UGDH	0.456016977	0.989994624	0.460625711	0.104848036	0.460625711	0.011035105	p<0.05	FC<-2
: A_23_P370586	HOXB8	0.580710139	1.244615461	0.466577957	0.169849829	0.466577957	0.044957282	p<0.05	FC<-2
: A_23_P19652	LRP11	0.341611632	0.720021955	0.474446133	0.19977134	0.474446133	0.01159258	p<0.05	FC<-2
: A_23_P164196	DLX4	0.509850624	1.068133119	0.477328729	0.146238574	0.477328729	0.03733585	p<0.05	FC<-2
: A_23_P214798	SYNCRIP	1.414809363	2.963034076	0.4774867	0.127979532	0.4774867	0.020852196	p<0.05	FC<-2
: A_23_P39594	NCOA1	0.528262734	1.105945748	0.477657005	0.122506243	0.477657005	0.016708841	p<0.05	FC<-2
: A_23_P76364	CD9	1.470275949	3.065276861	0.479655188	0.110884786	0.479655188	0.013244081	p<0.05	FC<-2
: A_23_P167818	C6orf60	0.484001388	1.008325884	0.480004922	0.116430964	0.480004922	0.02121237	p<0.05	FC<-2
: A_23_P500501	FGFR3	0.26227847	0.53984593	0.485839488	0.168988454	0.485839488	0.024337329	p<0.05	FC<-2
: A_23_P35546		0.632374467	1.298631692	0.486954439	0.134175178	0.486954439	0.046273002	p<0.05	FC<-2
: A_23_P349416	ERBB3	0.838147802	1.720496084	0.487154728	0.128071817	0.487154728	0.016954663	p<0.05	FC<-2
: A_23_P134125	MAP3K5	0.931090494	1.910306482	0.487403724	0.185961885	0.487403724	0.040373577	p<0.05	FC<-2
: A_23_P166797	IFRG28	0.595302941	1.215566607	0.489732884	0.038047419	0.489732884	0.040336999	p<0.05	FC<-2
: A_23_P254626	SGCE	0.276409454	0.557263874	0.496011793	0.180028375	0.496011793	0.040791524	p<0.05	FC<-2
: A_23_P61438	LOC148418	0.611560475	1.230319377	0.49707457	0.163476344	0.49707457	0.029016988	p<0.05	FC<-2
: A_23_P135417	GSTA1	0.308821061	0.621118088	0.497201848	0.103231375	0.497201848	0.047400864	p<0.05	FC<-2
: A_23_P145388	MTCH1	0.75653356	1.517778462	0.498447948	0.216010376	0.498447948	0.04558591	p<0.05	FC<-2
: A_23_P202810	OVOL1	0.169190745	0.339297335	0.498650378	0.149578015	0.498650378	0.025664963	p<0.05	FC<-2
: A_23_P2502	PAH	0.063928927	0.12814193	0.498891557	0.139511848	0.498891557	0.038495867	p<0.05	FC<-2
: A_23_P97431	RBP7	0.641095755	14.25043758	0.044987794	0.183114067	0.044987794	0.037341092	p<0.05	FC<-20
: A_23_P31922	ASS	0.271787961	1.085434972	0.250395434	0.085427026	0.250395434	0.017696286	p<0.05	FC<-3
: A_23_P365189	CAMTA2	1.563397253	6.207896127	0.251840111	0.144354854	0.251840111	0.025741016	p<0.05	FC<-3
: A_23_P309361	FLJ30525	0.380518018	1.495130414	0.254504901	0.199530901	0.254504901	0.04197727	p<0.05	FC<-3
: A_23_P323930	TM4SF9	0.479049354	1.866129188	0.256707498	0.104392852	0.256707498	0.011805124	p<0.05	FC<-3
: A_23_P154338	EFHD1	0.227552336	0.867578502	0.262284433	0.099139454	0.262284433	0.010416604	p<0.05	FC<-3
: A_23_P206359	CDH1	1.317155455	4.932958324	0.267011267	0.127152668	0.267011267	0.012935907	p<0.05	FC<-3
: A_23_P138635		0.065618871	0.244224406	0.268682693	0.171090227	0.268682693	0.042486819	p<0.05	FC<-3
: A_23_P146233	LPL	0.253934551	0.928178842	0.273583645	0.144486718	0.273583645	0.02684909	p<0.05	FC<-3
: A_23_P51231	RUNX3	0.18895914	0.686546193	0.275231502	0.210015652	0.275231502	0.049635186	p<0.05	FC<-3
: A_23_P347070	PAG	0.354162547	1.272443356	0.278332663	0.131331103	0.278332663	0.017482937	p<0.05	FC<-3
: A_23_P102391	SLC40A1	0.252636072	0.876586619	0.288204345	0.145024726	0.288204345	0.02069653	p<0.05	FC<-3
: A_23_P358545	SLC43A3	0.105796723	0.364636692	0.290142835	0.112158385	0.290142835	0.012287159	p<0.05	FC<-3
: A_23_P133606	SLC12A2	2.43726885	8.391831375	0.290433487	0.095628014	0.290433487	0.014452788	p<0.05	FC<-3
: A_23_P88439	MTAC2D1	3.444204992	11.77754908	0.292438178	0.187363147	0.292438178	0.028522002	p<0.05	FC<-3
: A_23_P19944	CLDN4	1.332487293	4.553272581	0.292643866	0.154822999	0.292643866	0.02855361	p<0.05	FC<-3
: A_23_P105405	MAP3K12	7.480121511	25.32347041	0.295382955	0.19145411	0.295382955	0.040344197	p<0.05	FC<-3
: A_23_P145935	EPHB6	0.151213095	0.510033119	0.296477012	0.068725599	0.296477012	0.012770419	p<0.05	FC<-3
: A_23_P214950	PERP	1.896874394	6.381232793	0.297258297	0.131738919	0.297258297	0.028889563	p<0.05	FC<-3
: A_23_P252306	ID1	0.665352619	2.225016727	0.299032637	0.202457432	0.299032637	0.046873895	p<0.05	FC<-3
: A_23_P32838	MID1	0.603271966	1.994274347	0.302501994	0.159262217	0.302501994	0.025038238	p<0.05	FC<-3
: A_23_P1043	FLJ10901	1.381577858	4.50123824	0.306932845	0.136848494	0.306932845	0.012349513	p<0.05	FC<-3
: A_23_P97725	STX6	90.62064475	287.8034579	0.314869896	0.161351222	0.314869896	0.024418699	p<0.05	FC<-3
: A_23_P65817	GABARAPL1	0.292913238	0.913699352	0.320579453	0.156750147	0.320579453	0.03306333	p<0.05	FC<-3
: A_23_P104492	PAPSS2	0.69742425	2.169953901	0.321400491	0.199684986	0.321400491	0.044350382	p<0.05	FC<-3

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: A_23_P369298	PERP	1.474901097	4.579305143	0.322079672	0.125348042	0.322079672	0.01786863	p<0.05	FC<-3
: A_23_P9809	UBE1L	1.544092511	4.660357276	0.331324922	0.115461625	0.331324922	0.019929713	p<0.05	FC<-3
: A_23_P107744	EDG8	0.734440226	2.2142138	0.331693455	0.200121987	0.331693455	0.04255331	p<0.05	FC<-3
: A_23_P412335	TGFB1	1.788993696	8.469708633	0.211222578	0.160848116	0.211222578	0.030828297	p<0.05	FC<-4
: A_23_P170037	MID1	0.556694141	2.598868059	0.214206388	0.162066221	0.214206388	0.025530699	p<0.05	FC<-4
: A_23_P55518	SMAD7	0.443192155	2.040439559	0.217204255	0.105741568	0.217204255	0.01120865	p<0.05	FC<-4
: A_23_P212400	HYAL3	5.522955456	24.95124531	0.221349892	0.136416809	0.221349892	0.022294707	p<0.05	FC<-4
: A_23_P83298	PRRX2	0.301492312	1.35175263	0.223038081	0.201527788	0.223038081	0.043714187	p<0.05	FC<-4
: A_23_P204654	KITLG	1.188921787	5.295041642	0.224534927	0.181878736	0.224534927	0.038763718	p<0.05	FC<-4
: A_23_P144179	CPOX	1.106275241	4.821587056	0.229442138	0.183972741	0.229442138	0.034152437	p<0.05	FC<-4
: A_23_P420863	CARD15	0.814684053	3.510912603	0.232043387	0.115064813	0.232043387	0.023017814	p<0.05	FC<-4
: A_23_P148014	AXIN2	1.015974394	4.289042025	0.236876764	0.18304932	0.236876764	0.034523299	p<0.05	FC<-4
: A_23_P214315	ICK	15.99302503	67.4042582	0.237270248	0.150832849	0.237270248	0.026134609	p<0.05	FC<-4
: A_23_P159395	AXIN2	0.80551252	3.360461216	0.239702966	0.194348082	0.239702966	0.043453144	p<0.05	FC<-4
: A_23_P139277	LIN7C	11.08302763	45.71955756	0.242413274	0.09267177	0.242413274	0.012862885	p<0.05	FC<-4
: A_23_P122976	GNAI1	1.225095462	4.951850269	0.247401556	0.164716294	0.247401556	0.027338329	p<0.05	FC<-4
: A_23_P128918	LGALS3	0.863424766	3.46978712	0.248840847	0.193491802	0.248840847	0.046859431	p<0.05	FC<-4
: A_23_P101960	ZFP36L2	0.255057419	1.023384087	0.249229416	0.157123732	0.249229416	0.024561517	p<0.05	FC<-4
: A_23_P32165	LHX2	0.240796618	1.375832724	0.175018818	0.181890972	0.175018818	0.035888205	p<0.05	FC<-5
: A_23_P83028	RECK	0.089346076	0.503860283	0.177323117	0.1143507	0.177323117	0.01829905	p<0.05	FC<-5
: A_23_P25674	CKB	0.151750549	0.837306516	0.181236556	0.15759226	0.181236556	0.027701077	p<0.05	FC<-5
: A_23_P134058	C6orf114	78.83277022	427.4757197	0.184414615	0.114258362	0.184414615	0.015944975	p<0.05	FC<-5
: A_23_P95029	SNTB1	0.185424863	0.992842258	0.186761655	0.137738731	0.186761655	0.019025591	p<0.05	FC<-5
: A_23_P53891	KLF5	2.544867476	13.39336502	0.190009566	0.152702533	0.190009566	0.023772113	p<0.05	FC<-5
: A_23_P39885	DPP4	0.760705983	3.842139397	0.197990209	0.125927801	0.197990209	0.025490637	p<0.05	FC<-5
: A_23_P129397	LOC146177	4.853744472	24.40620058	0.198873416	0.185012377	0.198873416	0.04277769	p<0.05	FC<-5
: A_23_P59926	LAPTM4B	0.029331869	1.482546914	0.19784783	0.154792543	0.19784783	0.024294331	p<0.05	FC<-50
: A_23_P41664		16.74634636	116.8937585	0.143261253	0.169767876	0.143261253	0.034365501	p<0.05	FC<-6
: A_23_P258462	PROM1	0.205664679	1.389478199	0.148015765	0.093048383	0.148015765	0.010183697	p<0.05	FC<-6
: A_23_P171296	MPP1	0.046116752	0.302770794	0.152315721	0.125856436	0.152315721	0.020180894	p<0.05	FC<-6
: A_23_P120105	KCNK3	0.47191213	2.99046207	0.157805757	0.135441962	0.157805757	0.019050908	p<0.05	FC<-6
: A_23_P58396	PDGFC	0.050267857	0.311793357	0.161221705	0.104223453	0.161221705	0.023719382	p<0.05	FC<-6
: A_23_P22526	HEPH	0.162329762	1.28946329	0.125889402	0.203571755	0.125889402	0.045195743	p<0.05	FC<-7
: A_23_P46894	CHAT	69.22470123	546.5113907	0.12666653	0.169600416	0.12666653	0.038790227	p<0.05	FC<-7
: A_23_P108143	GAMT	0.200088619	1.529976895	0.13077885	0.156495032	0.13077885	0.025031649	p<0.05	FC<-7
: A_23_P156498	ELOVL5	0.05852766	0.441919825	0.132439543	0.177954802	0.132439543	0.033950867	p<0.05	FC<-7
: A_23_P159974	KLHL13	0.140521501	1.04359327	0.134651597	0.180353982	0.134651597	0.036888162	p<0.05	FC<-7
: A_23_P10031	MID1	0.403374852	2.856699853	0.141203092	0.167893731	0.141203092	0.030300652	p<0.05	FC<-8
: A_23_P117782	FLJ11196	0.098847071	0.859454305	0.115011432	0.135817374	0.115011432	0.023392097	p<0.05	FC<-8
: A_23_P156431	MAN1A1	0.089953845	0.753197554	0.119429284	0.110565835	0.119429284	0.012819995	p<0.05	FC<-8
: A_23_P96410	MAOA	0.158464669	1.324994928	0.119596434	0.177972162	0.119596434	0.034564779	p<0.05	FC<-8
: A_23_P217797	DDX3Y	0.129844042	1.062853736	0.122165484	0.177488185	0.122165484	0.031938455	p<0.05	FC<-8
: A_23_P87049	SORL1	0.219754615	2.101847292	0.104553083	0.141993804	0.104553083	0.019741902	p<0.05	FC<-9
: A_23_P1186	C1QL3	141.014125	1326.968859	0.106267848	0.191371462	0.106267848	0.039411205	p<0.05	FC<-9
: A_23_P111712	MTERF	0.10915017	1.019533283	0.107058957	0.212230199	0.107058957	0.048939151	p<0.05	FC<-9
: A_23_P338890	PTPN1	0.888432891	0.591681511	1.501539044	0.164241185	1.501539044	0.013802717	p<0.05	FC>1.5
: A_23_P9523	RBKS	1.320562676	0.877380945	1.505118937	0.216358032	1.505118937	0.03676067	p<0.05	FC>1.5
: A_23_P413089	DEFB119	3.706464036	2.46154746	1.50574551	0.112080315	1.50574551	0.036340857	p<0.05	FC>1.5
: A_23_P343837	PARP11	1.607582829	1.067483949	1.505955036	0.040282001	1.505955036	0.043310308	p<0.05	FC>1.5
: A_23_P99879	SLC12A1	1.841090402	1.221316177	1.507464191	0.013730117	1.507464191	0.019321185	p<0.05	FC>1.5
: A_23_P102832	CEP2	1.3402828	0.88655419	1.511788918	0.221728745	1.511788918	0.029817716	p<0.05	FC>1.5
: A_23_P157117	CREB5	0.894432753	0.591348615	1.512530392	0.195983271	1.512530392	0.01896692	p<0.05	FC>1.5
: A_23_P214544	GPX5	0.58634271	0.387606374	1.512727211	0.196158238	1.512727211	0.019782142	p<0.05	FC>1.5

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: A_23_P252253	STATH	0.845456536	0.558865383	1.51280892	0.276424271	1.51280892	0.034253594	p<0.05	FC>1.5
: A_23_P3819	MGC2474	0.830737733	0.548222365	1.515329883	0.073030388	1.515329883	0.017005831	p<0.05	FC>1.5
: A_23_P164889	AP2A1	1.122467388	0.739747195	1.517366198	0.013553294	1.517366198	0.030819511	p<0.05	FC>1.5
: A_23_P40809	KLF15	1.709996219	1.126912898	1.517416495	0.212498051	1.517416495	0.022156272	p<0.05	FC>1.5
: A_23_P305173	ZMYND19	0.900070701	0.592330605	1.519541103	0.139479417	1.519541103	0.029103092	p<0.05	FC>1.5
: A_23_P38887	EIF3S4	1.018358472	0.669835645	1.52031096	0.222115173	1.52031096	0.021489156	p<0.05	FC>1.5
: A_23_P80436	COL8A1	2.926638076	1.924956154	1.520366097	0.126523244	1.520366097	0.038128058	p<0.05	FC>1.5
: A_23_P63668	IFIT5	4.796677894	3.15376568	1.520936677	0.223306101	1.520936677	0.033431942	p<0.05	FC>1.5
: A_23_P30995	NCB5OR	1.988971586	1.307027404	1.521752016	0.189036797	1.521752016	0.011061547	p<0.05	FC>1.5
: A_23_P365694	DMRT2	1.295544847	0.851222191	1.521981994	0.026621913	1.521981994	0.046339119	p<0.05	FC>1.5
: A_23_P2180		1.566200403	1.023923703	1.529606551	0.094585605	1.529606551	0.010810533	p<0.05	FC>1.5
: A_23_P82558	TRY1	2.048719035	1.339330557	1.529658996	0.09387994	1.529658996	0.033162637	p<0.05	FC>1.5
: A_23_P347432	DVL1	2.476183441	1.617566451	1.530807862	0.036928606	1.530807862	0.024178441	p<0.05	FC>1.5
: A_23_P9869	CNDP1	1.227506263	0.800245692	1.533911741	0.031224352	1.533911741	0.03797205	p<0.05	FC>1.5
: A_23_P210482	ADA	0.59562975	0.388220936	1.534254583	0.228685383	1.534254583	0.037604712	p<0.05	FC>1.5
: A_23_P208520	LENG1	1.043456054	0.679843713	1.534846957	0.244393365	1.534846957	0.037526325	p<0.05	FC>1.5
: A_23_P25534		2.744065262	1.786852466	1.535697722	0.130485469	1.535697722	0.041206207	p<0.05	FC>1.5
: A_23_P256375	STX4A	1.723744649	1.122213008	1.536022696	0.247447731	1.536022696	0.042542821	p<0.05	FC>1.5
: A_23_P106753	FLJ11171	2.084509693	1.35510617	1.538263008	0.200759922	1.538263008	0.016758575	p<0.05	FC>1.5
: A_23_P165636	CAPG	0.987526117	0.641517589	1.539359379	0.169872212	1.539359379	0.016314969	p<0.05	FC>1.5
: A_23_P43684	BNC2	1.336671468	0.86770844	1.540461528	0.106304835	1.540461528	0.037718878	p<0.05	FC>1.5
: A_23_P138885	LOC387758	1.303759559	0.846075995	1.540948529	0.199083705	1.540948529	0.01402491	p<0.05	FC>1.5
: A_23_P39561	NCE2	1.241286525	0.805139559	1.541703561	0.106600647	1.541703561	0.010560509	p<0.05	FC>1.5
: A_23_P310460	MDGA1	5.104502349	3.309454632	1.542399856	0.223184976	1.542399856	0.030242107	p<0.05	FC>1.5
: A_23_P24375	OTUB1	1.359319474	0.878562439	1.547208729	0.179870745	1.547208729	0.01172903	p<0.05	FC>1.5
: A_23_P339633	FLJ38348	1.974401334	1.273422426	1.55046848	0.203232509	1.55046848	0.02823312	p<0.05	FC>1.5
: A_23_P8116	ZBTB9	1.324850891	0.851740617	1.555462854	5.95055E-04	1.555462854	0.020788381	p<0.05	FC>1.5
: A_23_P156417	CAP2	1.168636467	0.751008152	1.556090255	0.202477471	1.556090255	0.022754293	p<0.05	FC>1.5
: A_23_P52957	OR1S1	1.422575376	0.912345301	1.559251059	5.43261E-04	1.559251059	0.014994206	p<0.05	FC>1.5
: A_23_P34382	CLCA3	3.041462481	1.947956564	1.561360524	0.131934588	1.561360524	0.020463446	p<0.05	FC>1.5
: A_23_P94020		2.429210918	1.554277031	1.562920167	0.114188619	1.562920167	0.045967088	p<0.05	FC>1.5
: A_23_P80635	IRAK2	2.311523139	1.476921898	1.565095041	0.087525616	1.565095041	0.023292862	p<0.05	FC>1.5
: A_23_P74155	CITED4	0.935587245	0.596929153	1.567333812	0.282201854	1.567333812	0.049078223	p<0.05	FC>1.5
: A_23_P50597	FLJ21369	2.103239105	1.341051544	1.568350684	0.048108698	1.568350684	0.013236911	p<0.05	FC>1.5
: A_23_P154234	POLE4	1.115983501	0.70649579	1.579603893	0.226631615	1.579603893	0.043312075	p<0.05	FC>1.5
: A_23_P22957	SH3GLB1	1.154663722	0.728122249	1.585810245	0.243702125	1.585810245	0.026980414	p<0.05	FC>1.5
: A_23_P41365	PROL5	0.70640866	0.445161264	1.586860127	0.130849125	1.586860127	0.026112389	p<0.05	FC>1.5
: A_23_P102048	DKFZp547E052	2.153370115	1.354529564	1.589754976	0.194722508	1.589754976	0.014449608	p<0.05	FC>1.5
: A_23_P132468	SLC4A7	1.647633618	1.036113343	1.590205965	0.056465834	1.590205965	0.012827271	p<0.05	FC>1.5
: A_23_P348264	LETM2	3.138735627	1.969844858	1.593392299	0.009058243	1.593392299	0.020414459	p<0.05	FC>1.5
: A_23_P369393	RABL3	2.563784543	1.608611697	1.593787082	0.129067182	1.593787082	0.035099424	p<0.05	FC>1.5
: A_23_P24856	OR51T1	0.949959075	0.594507231	1.597893221	0.06839449	1.597893221	0.044922364	p<0.05	FC>1.5
: A_23_P154108	DNCI2	1.710226606	1.068619258	1.600407809	0.167273451	1.600407809	0.023771544	p<0.05	FC>1.5
: A_23_P60510	FLJ20534	0.712428137	0.445054592	1.600765726	0.060596668	1.600765726	0.046149109	p<0.05	FC>1.5
: A_23_P130285	FLJ10979	1.686110968	1.052920161	1.6013664	0.064770621	1.6013664	0.011425642	p<0.05	FC>1.5
: A_23_P135946		3.453052638	2.155543269	1.601940767	0.024585247	1.601940767	0.02001293	p<0.05	FC>1.5
: A_23_P151351	WASF3	2.653792495	1.655645496	1.602874831	0.104640164	1.602874831	0.021774599	p<0.05	FC>1.5
: A_23_P108170	PSG6	1.308230648	0.8149066	1.605374957	0.007645689	1.605374957	0.03626776	p<0.05	FC>1.5
: A_23_P62471	CDY1	0.904323137	0.562786328	1.606867636	0.00437343	1.606867636	0.017625652	p<0.05	FC>1.5
: A_23_P49338	TNFRSF12A	1.625921752	1.011634974	1.607221769	0.177924153	1.607221769	0.025033738	p<0.05	FC>1.5
: A_23_P23983	C10orf97	1.506110175	0.932606699	1.614946768	0.289153747	1.614946768	0.043098576	p<0.05	FC>1.5
: A_23_P129614	CPSF5	2.279818066	1.409129722	1.617890837	0.241269956	1.617890837	0.028457086	p<0.05	FC>1.5
: A_23_P368259	FLJ38944	1.50317629	0.927549173	1.620589327	0.192904832	1.620589327	0.029000612	p<0.05	FC>1.5

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: A_23_P150238	Bles03	1.693374658	1.044660967	1.620980119	0.237596248	1.620980119	0.029271392	p<0.05	FC>1.5
: A_23_P168993	ADRB3	1.36066869	0.839298513	1.621197547	0.065528372	1.621197547	0.014173176	p<0.05	FC>1.5
: A_23_P37137	DNAJC8	1.579243058	0.967898371	1.631620742	0.242220887	1.631620742	0.032205917	p<0.05	FC>1.5
: A_23_P28233	SNX17	2.38180984	1.455258973	1.636691396	0.130520899	1.636691396	0.033354793	p<0.05	FC>1.5
: A_23_P216176	MSR1	3.746370256	2.284667181	1.639788187	0.182020637	1.639788187	0.033459985	p<0.05	FC>1.5
: A_23_P378588	ARL8	2.206118038	1.342846423	1.642866973	0.160594317	1.642866973	0.037199886	p<0.05	FC>1.5
: A_23_P71709		2.748504241	1.665134266	1.650620192	0.060732643	1.650620192	0.020377317	p<0.05	FC>1.5
: A_23_P206877	RRN3	1.226401055	0.742434611	1.651864065	0.220981405	1.651864065	0.037331306	p<0.05	FC>1.5
: A_23_P150343	SLN	1.182554393	0.714529544	1.655011193	0.076595746	1.655011193	0.043777593	p<0.05	FC>1.5
: A_23_P52597	C1QTNF4	0.946181221	0.571445428	1.655768292	0.030946146	1.655768292	0.025521194	p<0.05	FC>1.5
: A_23_P15414	SCARF1	0.597042356	0.360131977	1.657843219	0.3086227	1.657843219	0.049031649	p<0.05	FC>1.5
: A_23_P1196	NUDT5	3.452565258	2.077969647	1.661508994	0.239925186	1.661508994	0.021880584	p<0.05	FC>1.5
: A_23_P7361	ELOVL6	3.251003122	1.954733823	1.663143638	0.074479585	1.663143638	0.010147785	p<0.05	FC>1.5
: A_23_P94141	RAD54B	1.574226253	0.945111044	1.665652162	0.249659815	1.665652162	0.041371449	p<0.05	FC>1.5
: A_23_P361333	C3orf20	1.675954593	1.00273381	1.671385343	0.009414513	1.671385343	0.010895321	p<0.05	FC>1.5
: A_23_P147664	OLFML1	3.4560333	2.064114875	1.67434155	0.106481299	1.67434155	0.032881996	p<0.05	FC>1.5
: A_23_P310582	ST7L	4.071882844	2.427541243	1.677369172	0.262329173	1.677369172	0.038942016	p<0.05	FC>1.5
: A_23_P169587		1.708944992	1.016710433	1.680857141	0.292441775	1.680857141	0.045867749	p<0.05	FC>1.5
: A_23_P383385	POLE4	1.038398974	0.617426745	1.681817286	0.211584322	1.681817286	0.02883013	p<0.05	FC>1.5
: A_23_P51906	PFND2	2.290181194	1.353827111	1.691634904	0.244773037	1.691634904	0.024209879	p<0.05	FC>1.5
: A_23_P43296	FBXL6	1.959720615	1.157677114	1.692804144	0.034132208	1.692804144	0.030782702	p<0.05	FC>1.5
: A_23_P215956	MYC	4.013519233	2.368598345	1.694470167	0.25798112	1.694470167	0.031507512	p<0.05	FC>1.5
: A_23_P12386	FMO1	2.812835914	1.658983917	1.695517289	0.094425597	1.695517289	0.010071271	p<0.05	FC>1.5
: A_23_P253614	KIAA1446	1.314640365	0.77494591	1.696428548	0.013538619	1.696428548	0.01195664	p<0.05	FC>1.5
: A_23_P363936	HSPA4L	5.784052524	3.407936161	1.697230303	0.264365348	1.697230303	0.032020364	p<0.05	FC>1.5
: A_23_P256868	DCP2	2.17657274	1.280660726	1.699570149	0.146554314	1.699570149	0.025185454	p<0.05	FC>1.5
: A_23_P31866	THRAP6	4.374473706	2.553524446	1.713112131	0.217694589	1.713112131	0.02854541	p<0.05	FC>1.5
: A_23_P158699		3.864185254	2.255110846	1.713523574	0.002381161	1.713523574	0.012038447	p<0.05	FC>1.5
: A_23_P51339	DNAJB4	1.117817291	0.651580686	1.715547	0.186372214	1.715547	0.021015084	p<0.05	FC>1.5
: A_23_P110777	LECT2	2.703118265	1.574831072	1.716449664	0.095062613	1.716449664	0.046044585	p<0.05	FC>1.5
: A_23_P101721	ZNF45	2.127678957	1.237790122	1.718933541	0.241830036	1.718933541	0.041502461	p<0.05	FC>1.5
: A_23_P210400	KCNQ2	3.79641431	2.201659613	1.724342077	0.183651779	1.724342077	0.03037446	p<0.05	FC>1.5
: A_23_P124095	CALML5	0.952988706	0.552651132	1.724394741	0.172018706	1.724394741	0.018483349	p<0.05	FC>1.5
: A_23_P55889	RAD23A	3.521102456	2.040210176	1.725852806	0.2713142	1.725852806	0.035533311	p<0.05	FC>1.5
: A_23_P406478	FLJ32784	2.058812751	1.190717988	1.729051524	0.044861275	1.729051524	0.04854041	p<0.05	FC>1.5
: A_23_P155959	FLJ13220	1.059202352	0.610992586	1.733576439	0.074585147	1.733576439	0.021056791	p<0.05	FC>1.5
: A_23_P12896	FANCF	2.997304035	1.728483335	1.734065914	0.19406418	1.734065914	0.024195019	p<0.05	FC>1.5
: A_23_P124703		3.97844354	2.280009214	1.744924326	0.062409258	1.744924326	0.014527768	p<0.05	FC>1.5
: A_23_P90089	GCDH	1.807805559	1.029356808	1.756247731	0.189846828	1.756247731	0.015176259	p<0.05	FC>1.5
: A_23_P131308	CYP27A1	3.266402399	1.859309506	1.756782498	0.217369718	1.756782498	0.024748271	p<0.05	FC>1.5
: A_23_P78405	LIPG	1.28633929	0.730255899	1.761491132	0.054495856	1.761491132	0.014802547	p<0.05	FC>1.5
: A_23_P68628	APBA2BP	1.158675541	0.656354798	1.765318918	0.018283876	1.765318918	0.016087736	p<0.05	FC>1.5
: A_23_P214739	FBXL4	3.054760341	1.726097415	1.769749676	0.174866647	1.769749676	0.017607073	p<0.05	FC>1.5
: A_23_P43434	PSMD5	1.170248619	0.658908269	1.776041786	0.145310437	1.776041786	0.018806388	p<0.05	FC>1.5
: A_23_P118124	RGS11	0.564785288	0.317427443	1.779257906	0.294758015	1.779257906	0.042654885	p<0.05	FC>1.5
: A_23_P157809	LTB4DH	1.207713259	0.67812111	1.78096986	0.274260461	1.78096986	0.039038499	p<0.05	FC>1.5
: A_23_P55688	FLJ20557	3.16717105	1.761019716	1.798486991	0.286629052	1.798486991	0.049588383	p<0.05	FC>1.5
: A_23_P409866	JARID1B	0.536670238	0.297895331	1.801539608	0.254237035	1.801539608	0.030640123	p<0.05	FC>1.5
: A_23_P133049		2.387178101	1.322007148	1.805722537	0.231524665	1.805722537	0.021390649	p<0.05	FC>1.5
: A_23_P167212	QDPR	2.279698738	1.25625712	1.814675277	0.226218715	1.814675277	0.018844018	p<0.05	FC>1.5
: A_23_P86424	NCOA4	1.326108032	0.728611526	1.820048111	0.203330483	1.820048111	0.013182376	p<0.05	FC>1.5
: A_23_P381577	ZNF25	4.321523616	2.370028142	1.823406034	0.164808853	1.823406034	0.044696032	p<0.05	FC>1.5
: A_23_P213279	FLJ21934	0.985401007	0.536606975	1.836355194	0.010605889	1.836355194	0.012621121	p<0.05	FC>1.5

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: A_23_P71368	RP1	6.98115033	3.79627829	1.838945882	0.029420816	1.838945882	0.039280985	p<0.05	FC>1.5
: A_23_P411215	FLJ23790	2.144487423	1.161948794	1.845595464	0.120118363	1.845595464	0.03026288	p<0.05	FC>1.5
: A_23_P150619	TRIM3	2.169821012	1.170943219	1.853053997	0.275492144	1.853053997	0.031096347	p<0.05	FC>1.5
: A_23_P123702	C9orf27	1.202298633	0.647199756	1.857693274	0.012238432	1.857693274	0.025971005	p<0.05	FC>1.5
: A_23_P143258	C20orf43	1.247106533	0.660443788	1.888285658	0.189721392	1.888285658	0.04899973	p<0.05	FC>1.5
: A_23_P418516	PRPS1L1	3.205733951	1.680528113	1.907575319	0.149313759	1.907575319	0.023295571	p<0.05	FC>1.5
: A_23_P37949	MGC2655	1.475927932	0.769394069	1.918299076	0.23381168	1.918299076	0.023606021	p<0.05	FC>1.5
: A_23_P169376	OR1N1	2.847031636	1.482676021	1.920198071	0.077603898	1.920198071	0.010156671	p<0.05	FC>1.5
: A_23_P112159	EIF2C2	1.440321544	0.747880985	1.92586999	0.039977791	1.92586999	0.013020552	p<0.05	FC>1.5
: A_23_P90682	ALS2CR2	1.708385863	0.882251047	1.936394259	0.251532704	1.936394259	0.026632845	p<0.05	FC>1.5
: A_23_P71316	RBPMS	1.224869188	0.631060508	1.940969484	0.175625047	1.940969484	0.015613413	p<0.05	FC>1.5
: A_23_P36432	RBMS2	4.983483721	2.526463446	1.972513685	0.139889339	1.972513685	0.041558877	p<0.05	FC>1.5
: A_23_P65843		1.21623382	0.60960272	1.995125315	0.146106974	1.995125315	0.034490562	p<0.05	FC>1.5
: A_23_P61268	LOC51236	2.244476128	1.121903422	2.00059656	0.171564951	2.00059656	0.018280161	p<0.05	FC>2
: A_23_P20372		1.237497641	0.614743	2.013032504	0.048310808	2.013032504	0.013638411	p<0.05	FC>2
: A_23_P9061	EIF3S3	2.858287735	1.418816096	2.014558295	0.223864339	2.014558295	0.021433363	p<0.05	FC>2
: A_23_P7791	OGFRL1	3.026341319	1.486301929	2.036155144	0.153510496	2.036155144	0.011262637	p<0.05	FC>2
: A_23_P118234	FLJ31547	1.392634269	0.680288334	2.04712355	0.095241709	2.04712355	0.030907455	p<0.05	FC>2
: A_23_P138524	CPXM2	0.874857707	0.42250531	2.070643102	0.007412048	2.070643102	0.014112704	p<0.05	FC>2
: A_23_P16354	ZNF382	1.40246964	0.675265732	2.076915165	0.184878055	2.076915165	0.023289744	p<0.05	FC>2
: A_23_P156025	IRX2	1.944826419	0.930495541	2.090097515	0.170657473	2.090097515	0.041146423	p<0.05	FC>2
: A_23_P215875	DKFZP564O0463	3.53413785	1.687862336	2.093854323	0.208213466	2.093854323	0.018758836	p<0.05	FC>2
: A_23_P340640		1.263773985	0.598746278	2.110700361	0.010888536	2.110700361	0.018439957	p<0.05	FC>2
: A_23_P80788		1.174955532	0.55539985	2.115512874	0.015809833	2.115512874	0.014574271	p<0.05	FC>2
: A_23_P96369	FLJ10178	4.511871809	2.108958397	2.13938398	0.259209715	2.13938398	0.035281056	p<0.05	FC>2
: A_23_P32966		1.342760897	0.623804438	2.152535018	0.127272214	2.152535018	0.014800821	p<0.05	FC>2
: A_23_P257031	SCHIP1	3.642079986	1.670055275	2.180814038	0.243288215	2.180814038	0.036840925	p<0.05	FC>2
: A_23_P69206	SLC6A6	1.28316332	0.585195536	2.19270866	0.047432467	2.19270866	0.01496129	p<0.05	FC>2
: A_23_P120064	C2orf3	2.479833398	1.114185514	2.225691652	0.038778411	2.225691652	0.01159539	p<0.05	FC>2
: A_23_P251528	OR1K1	1.284403781	0.567326384	2.263959192	0.126248023	2.263959192	0.013918421	p<0.05	FC>2
: A_23_P39790	CD207	1.483393888	0.654895486	2.265084917	6.58537E-04	2.265084917	0.010213129	p<0.05	FC>2
: A_23_P5246	THSD6	1.083088256	0.475435145	2.278098849	0.210395435	2.278098849	0.02223445	p<0.05	FC>2
: A_23_P168008	HIST1H2AI	1.813094788	0.791234353	2.291476326	0.214221117	2.291476326	0.018723391	p<0.05	FC>2
: A_23_P59825	TAS2R16	1.49040853	0.642814506	2.318567047	7.64150E-04	2.318567047	0.020382888	p<0.05	FC>2
: A_23_P63319	SOAT1	1.317963358	0.561218176	2.348397495	0.244007885	2.348397495	0.026980848	p<0.05	FC>2
: A_23_P151127	NET-5	1.340099564	0.567141613	2.362901139	0.086965537	2.362901139	0.012439545	p<0.05	FC>2
: A_23_P5831	HPCAL1	1.227546331	0.516967317	2.374514386	0.068775601	2.374514386	0.011259213	p<0.05	FC>2
: A_23_P97541	C4BPA	1.049168037	0.440178595	2.383505351	0.159382305	2.383505351	0.013013912	p<0.05	FC>2
: A_23_P100602	TBCD	1.371471101	0.555220028	2.470139824	0.030753289	2.470139824	0.01253471	p<0.05	FC>2
: A_23_P361509	CTAG3	1.377628871	0.553215717	2.490220052	0.001717712	2.490220052	0.010331348	p<0.05	FC>2
: A_23_P320846	DEFB125	3.978369938	1.54137445	2.581053512	0.002625067	2.581053512	0.024057318	p<0.05	FC>2
: A_23_P68978	FLJ23588	5.815274475	2.227081987	2.611163176	0.095041664	2.611163176	0.014460952	p<0.05	FC>2
: A_23_P430747	CXorf1	3.041215321	1.111514412	2.736100665	0.190864987	2.736100665	0.046616442	p<0.05	FC>2
: A_23_P252163	DAPK1	2.457621976	0.882986671	2.783305861	0.214010965	2.783305861	0.018511244	p<0.05	FC>2
: A_23_P131455	SIAT2	1.344136053	0.474156609	2.834793459	0.118304924	2.834793459	0.011206579	p<0.05	FC>2
: A_23_P84475		4.720574391	1.631813018	2.892840257	0.295579465	2.892840257	0.040758208	p<0.05	FC>2
: A_23_P103812	DBCOR1L	1.362794915	0.469746337	2.901129415	0.079918696	2.901129415	0.010603306	p<0.05	FC>2
: A_23_P95417	TNFRSF10D	2.929847119	1	2.929847119	0.120363221	2.929847119	0.019020713	p<0.05	FC>2
: A_23_P53456	CORO1C	3.202804553	1.075730354	2.977330277	0.290007519	2.977330277	0.038917509	p<0.05	FC>2
: A_23_P128866	OR11H1	1.671847649	0.521551184	3.20552939	0.141760376	3.20552939	0.027696828	p<0.05	FC>3
: A_23_P147950	FLJ32731	4.633809006	1.440667167	3.216432713	0.159293797	3.216432713	0.021225008	p<0.05	FC>3
: A_23_P107701	ERCC1	3.757977265	1.116952595	3.36449128	0.241769897	3.36449128	0.022931687	p<0.05	FC>3
: A_23_P354827	ZNF550	1.279124184	0.350176571	3.652797733	0.272504257	3.652797733	0.033789028	p<0.05	FC>3

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: A_23_P124381	IQCG	4.294818428	1.003294397	4.280716051	0.202167415	4.280716051	0.033716998	p<0.05	FC>4
: A_23_P12282	DYRK3	4.598758266	1.05778011	4.347556002	0.213051744	4.347556002	0.016406135	p<0.05	FC>4
: A_23_P35617	PLCE1	0.791972325	1.574714725	0.502930666	0.178907317	0.502930666	0.032355531	p<0.05	
: A_23_P254242	PTPRK	0.627430413	1.240389243	0.505833485	0.189895357	0.505833485	0.0376022	p<0.05	
: A_23_P151046	KLRC1	0.16285047	0.318948934	0.510584776	0.123168399	0.510584776	0.019774832	p<0.05	
: A_23_P8763	PTPN12	1.330601981	2.598489876	0.51206741	0.170325094	0.51206741	0.035019607	p<0.05	
: A_23_P62932	ATP1B1	1.097265083	2.139059298	0.512966183	0.200638977	0.512966183	0.049096114	p<0.05	
: A_23_P210235	CGREF1	0.890292659	1.733003203	0.513728224	0.09496091	0.513728224	0.01227801	p<0.05	
: A_23_P329870	RHBDL6	1.143736041	2.22428115	0.514204799	0.172939148	0.514204799	0.013388935	p<0.05	
: A_23_P67771	BARD1	0.402283919	0.781662255	0.514651842	0.139511536	0.514651842	0.018664756	p<0.05	
: A_23_P61112		0.558152558	1.080936711	0.516360072	0.191542575	0.516360072	0.048208447	p<0.05	
: A_23_P205607	C14orf101	0.964758611	1.867296818	0.516660555	0.175440165	0.516660555	0.031547375	p<0.05	
: A_23_P3748	PTP205	0.729363773	1.399892481	0.521088584	0.093604752	0.521088584	0.015871569	p<0.05	
: A_23_P29152	VPREB1	0.446026335	0.855244587	0.521519039	0.109861045	0.521519039	0.019180796	p<0.05	
: A_23_P60550	KIF12	0.788051724	1.50888144	0.522275444	0.22510942	0.522275444	0.024167717	p<0.05	
: A_23_P102000	CXCR4	0.120613156	0.23089514	0.522371999	0.086666098	0.522371999	0.036457449	p<0.05	
: A_23_P319617	CHST7	0.673920604	1.284041912	0.524843152	0.168077317	0.524843152	0.044217981	p<0.05	
: A_23_P403955	TARDBP	0.659468724	1.251935477	0.526759354	0.220115287	0.526759354	0.047595909	p<0.05	
: A_23_P134854	CLDN23	1.717677951	3.260743744	0.526774897	0.115896956	0.526774897	0.038861159	p<0.05	
: A_23_P73699	MED12	1.71428093	3.247643474	0.527853794	0.149759271	0.527853794	0.02517305	p<0.05	
: A_23_P46588	IRF2BP2	0.735404033	1.387529423	0.530009686	0.113035499	0.530009686	0.01698412	p<0.05	
: A_23_P138655	CYP26A1	0.632114644	1.192204149	0.530206713	0.156180007	0.530206713	0.026960703	p<0.05	
: A_23_P9293	TJP2	0.791204515	1.486777993	0.532160496	0.181063643	0.532160496	0.024803162	p<0.05	
: A_23_P137470	SIPA1L2	0.27889088	0.522600411	0.533659895	0.159228083	0.533659895	0.027709384	p<0.05	
: A_23_P165727	GDF8	0.860559362	1.610055309	0.534490559	0.106340392	0.534490559	0.03972547	p<0.05	
: A_23_P63402	GPSM2	1.00196984	1.873508126	0.534809444	0.150338875	0.534809444	0.013554646	p<0.05	
: A_23_P165061	AES	0.747454749	1.393706877	0.536306996	0.101882932	0.536306996	0.014231665	p<0.05	
: A_23_P171038	SLC6A14	0.244497045	0.455744008	0.536478901	0.080700338	0.536478901	0.031103651	p<0.05	
: A_23_P32249	FNBP1	0.44334052	0.82524564	0.537222493	0.120592918	0.537222493	0.015950389	p<0.05	
: A_23_P151756	KIAA0998	0.539720968	1.003794999	0.537680471	0.07530545	0.537680471	0.02324064	p<0.05	
: A_23_P3221	SQRDL	1.320464284	2.454940804	0.537880295	0.169844526	0.537880295	0.033783541	p<0.05	
: A_23_P212888	PCDH7	0.93411594	1.736275746	0.537999763	0.116606179	0.537999763	0.014189749	p<0.05	
: A_23_P434305	PTMA	2.205762528	4.094917193	0.538658641	0.096429228	0.538658641	0.029709791	p<0.05	
: A_23_P202140	NOLC1	1.592303572	2.955945448	0.538678267	0.220094112	0.538678267	0.01717661	p<0.05	
: A_23_P121676	CXXC4	0.465506829	0.862691758	0.539598095	0.087076361	0.539598095	0.028853419	p<0.05	
: A_23_P331598	IPO7	0.501220092	0.924581803	0.542104647	0.028748918	0.542104647	0.013091918	p<0.05	
: A_23_P103864	TTC13	1.140057829	2.10219523	0.54231777	0.17402063	0.54231777	0.023533744	p<0.05	
: A_23_P206212	THBS1	0.230834361	0.424946127	0.543208529	0.115695745	0.543208529	0.015644317	p<0.05	
: A_23_P324461	MIDN	0.435043244	0.799479037	0.544158413	0.186303113	0.544158413	0.037907165	p<0.05	
: A_23_P257457	RDHE2	0.772419653	1.417095265	0.545072496	0.228344282	0.545072496	0.046551794	p<0.05	
: A_23_P152696	USP43	1.549997459	2.834541309	0.546824791	0.172773484	0.546824791	0.046202202	p<0.05	
: A_23_P62768	BCLP	3.780379177	6.907906782	0.547253936	0.119057798	0.547253936	0.015468222	p<0.05	
: A_23_P399880	FLJ33996	0.845397741	1.543739307	0.54762986	0.148466318	0.54762986	0.043622369	p<0.05	
: A_23_P48669	CDKN3	1.901261797	3.470843828	0.547780854	0.139033811	0.547780854	0.021488783	p<0.05	
: A_23_P35564	SEC31L2	0.642318153	1.172170616	0.547973259	0.150733164	0.547973259	0.02160298	p<0.05	
: A_23_P30796	HIST1H3F	0.899630264	1.63413847	0.550522664	0.09952055	0.550522664	0.011688887	p<0.05	
: A_23_P431268	PLEKHA6	1.353663082	2.456370121	0.551082701	0.128872858	0.551082701	0.026567777	p<0.05	
: A_23_P213424	ENC1	1.285737109	2.326968292	0.552537443	0.096201947	0.552537443	0.021601054	p<0.05	
: A_23_P19964	POR	1.189489473	2.152754979	0.552542897	0.132405101	0.552542897	0.020712129	p<0.05	
: A_23_P210224	DPYSL5	0.717823429	1.299056201	0.552573036	0.16068039	0.552573036	0.049125247	p<0.05	
: A_23_P69058	MLH1	0.524537708	0.949218432	0.552599581	0.124605618	0.552599581	0.014783727	p<0.05	
: A_23_P42220	HIST1H2AK	0.522588083	0.945337563	0.552805795	0.098636836	0.552805795	0.01247942	p<0.05	
: A_23_P518	B7-H4	0.772693079	1.397020517	0.553100738	0.116700334	0.553100738	0.045354741	p<0.05	

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: A_23_P87899	DYRK4	0.681186514	1.230975926	0.553371109	0.250917107	0.553371109	0.038500827	p<0.05
: A_23_P335239	GAB1	0.633070797	1.139564536	0.555537468	0.06851398	0.555537468	0.021773354	p<0.05
: A_23_P85441	IGSF9	0.597922231	1.076150539	0.555612072	0.184272989	0.555612072	0.024635639	p<0.05
: A_23_P7528	DPYSL3	0.329290568	0.591932209	0.55629777	0.085454026	0.55629777	0.033285285	p<0.05
: A_23_P415652	GALNT12	1.256404028	2.257602073	0.556521472	0.196325694	0.556521472	0.019400289	p<0.05
: A_23_P413193	C10orf78	1.31809067	2.365257818	0.557271457	0.089359915	0.557271457	0.011842545	p<0.05
: A_23_P216630	CDW92	1.430321622	2.561536954	0.558384145	0.186651862	0.558384145	0.021044788	p<0.05
: A_23_P67820	ACVR1C	1.047299256	1.872693646	0.559247509	0.113164637	0.559247509	0.028517574	p<0.05
: A_23_P162640	GABARAPL1	0.411855907	0.735408039	0.560037266	0.110774458	0.560037266	0.016704417	p<0.05
: A_23_P133786	EGFL9	1.021591401	1.811768677	0.563864148	0.101250864	0.563864148	0.018029267	p<0.05
: A_23_P212354	CCR2	0.313130128	0.553892005	0.56532704	0.028402937	0.56532704	0.015545324	p<0.05
: A_23_P53033	MYOD1	0.56343947	0.996337535	0.565510633	0.140252523	0.565510633	0.016379371	p<0.05
: A_23_P124542	CR2	0.472262488	0.834943963	0.565621777	0.141196538	0.565621777	0.030152332	p<0.05
: A_23_P40025	DAZAP2	1.269672552	2.244721683	0.565625824	0.149003616	0.565625824	0.017234883	p<0.05
: A_23_P7882	C6orf85	0.382847731	0.67631782	0.566076657	0.114197103	0.566076657	0.017786999	p<0.05
: A_23_P42800	ERP70	1.224300125	2.15562522	0.567955929	0.162825144	0.567955929	0.047223789	p<0.05
: A_23_P59388	DST	0.726546276	1.278334889	0.568353631	0.122854703	0.568353631	0.022282742	p<0.05
: A_23_P61860	SLC35E2	1.303191384	2.291413691	0.568728113	0.114589066	0.568728113	0.041743862	p<0.05
: A_23_P215922	FZD3	0.679738233	1.191181152	0.5706422	0.186144016	0.5706422	0.035879859	p<0.05
: A_23_P137238	SMCY	0.424868926	0.743802022	0.571212383	0.145694491	0.571212383	0.023343255	p<0.05
: A_23_P57417	MMP11	0.65847421	1.152389122	0.571399189	0.145294057	0.571399189	0.030407107	p<0.05
: A_23_P114607	LCE1C	0.700679995	1.22496634	0.571999386	0.172622748	0.571999386	0.026111738	p<0.05
: A_23_P99891	MESDC1	0.9072308	1.58488187	0.572428026	0.109777939	0.572428026	0.012669034	p<0.05
: A_23_P20168		1.157512408	2.022020613	0.572453318	0.011663308	0.572453318	0.022422956	p<0.05
: A_23_P92954	HSD17B4	0.863803442	1.506182558	0.573505142	0.149006147	0.573505142	0.018229629	p<0.05
: A_23_P304897	BDKRB2	0.667913097	1.163087617	0.574258626	0.169220802	0.574258626	0.036127959	p<0.05
: A_23_P257731	GALNT12	1.425771306	2.48042608	0.574809029	0.272433349	0.574809029	0.047481976	p<0.05
: A_23_P348257	ARK5	0.687716324	1.192971868	0.576473211	0.20237438	0.576473211	0.047063648	p<0.05
: A_23_P96611	LUZP4	0.81821817	1.418817127	0.576690367	0.014449415	0.576690367	0.010249344	p<0.05
: A_23_P136935	SYN	0.474666634	0.820442483	0.578549556	0.234190066	0.578549556	0.049485383	p<0.05
: A_23_P98069	LHFP	0.390495777	0.673307734	0.579966272	0.203335984	0.579966272	0.043579696	p<0.05
: A_23_P154889	CSTB	1.130194227	1.94744782	0.580346346	0.277600251	0.580346346	0.041477676	p<0.05
: A_23_P422703	NR2F2	0.661324654	1.133888982	0.583235806	0.145930234	0.583235806	0.023668102	p<0.05
: A_23_P203009	CUL5	0.919735319	1.576536969	0.58338963	0.163042109	0.58338963	0.026265902	p<0.05
: A_23_P57779	CLDN1	0.48929984	0.835276818	0.585793631	0.190505997	0.585793631	0.037589358	p<0.05
: A_23_P256956	KIF20A	0.885239229	1.503144371	0.588924954	0.151992645	0.588924954	0.016076538	p<0.05
: A_23_P118002	UQCRC2	1.141993288	1.934489417	0.59033318	0.116633201	0.59033318	0.016674751	p<0.05
: A_23_P76499	NDUFA9	1.409886062	2.386336951	0.590816004	0.179201193	0.590816004	0.035216619	p<0.05
: A_23_P306105	GALNT1	1.373858813	2.3227628	0.591476156	0.150260843	0.591476156	0.014913459	p<0.05
: A_23_P48747	DHRS1	0.750137967	1.263318585	0.593783687	0.202241243	0.593783687	0.049343394	p<0.05
: A_23_P73828	MOSPD1	0.692786996	1.160905864	0.596764145	0.125006285	0.596764145	0.019852554	p<0.05
: A_23_P432360	PMM2	1.380980762	2.313290561	0.596976785	0.119749179	0.596976785	0.016422404	p<0.05
: A_23_P251173	EIF2AK1	1.395243034	2.336029345	0.597271193	0.140961806	0.597271193	0.02364675	p<0.05
: A_23_P213139	LNK	0.805429158	1.348111903	0.597449779	0.148109899	0.597449779	0.029715367	p<0.05
: A_23_P43810	LTBP1	0.149911106	0.250896903	0.597500825	0.272836281	0.597500825	0.045876709	p<0.05
: A_23_P114185	TM4SF2	0.156234952	0.261389996	0.597708232	0.140595993	0.597708232	0.044099827	p<0.05
: A_23_P139919	CHST11	0.342272737	0.571682142	0.598711613	0.11733192	0.598711613	0.040773622	p<0.05
: A_23_P211468	TIMP3	0.444957564	0.742150645	0.599551543	0.119771727	0.599551543	0.024337786	p<0.05
: A_23_P68488	BMP7	0.484924578	0.808611303	0.599700469	0.195290461	0.599700469	0.047454711	p<0.05
: A_23_P34007		2.758732182	4.595634876	0.60029403	0.128708661	0.60029403	0.035328355	p<0.05
: A_23_P17854	HRIHFB2122	0.518695422	0.863551388	0.6006538	0.202015299	0.6006538	0.032233835	p<0.05
: A_23_P144596	ENPEP	0.966254224	1.608128234	0.600856451	0.112368445	0.600856451	0.016164567	p<0.05
: A_23_P2492	C1S	0.179165161	0.298179777	0.600862884	0.099813293	0.600862884	0.023541136	p<0.05

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: A_23_P129204	IDH2	0.660100487	1.098581656	0.600866111	0.176241518	0.600866111	0.033739007	p<0.05
: A_23_P428738	RNASE4	0.410352235	0.682539687	0.601213736	0.160480172	0.601213736	0.029910848	p<0.05
: A_23_P357270	SLC17A4	1.231979748	2.043814627	0.602784485	0.192611709	0.602784485	0.046479002	p<0.05
: A_23_P402765	NRAP	0.698445463	1.158649673	0.602809873	0.078386119	0.602809873	0.026634447	p<0.05
: A_23_P80068	BTG3	1.60237214	2.651205905	0.604393697	0.224037853	0.604393697	0.026397015	p<0.05
: A_23_P150950	MGC23401	0.752505451	1.2449919	0.604425981	0.135064579	0.604425981	0.022360354	p<0.05
: A_23_P160214	C1orf34	3.382461428	5.589018087	0.605197796	0.164259448	0.605197796	0.041788365	p<0.05
: A_23_P56678	ATP5G3	1.608468653	2.657583328	0.605237335	0.203638305	0.605237335	0.02688636	p<0.05
: A_23_P354175	LOC92305	1.385660649	2.289167855	0.605311946	0.180796209	0.605311946	0.040134934	p<0.05
: A_23_P122617	C6orf111	0.537578266	0.886523542	0.60638916	0.095642082	0.60638916	0.011279825	p<0.05
: A_23_P1253281	TBC1D8	1.288966308	2.125170303	0.606523772	0.153747649	0.606523772	0.027613013	p<0.05
: A_23_P84995	MTMR8	0.66313459	1.09137873	0.607611796	0.108957324	0.607611796	0.020115298	p<0.05
: A_23_P310900		0.244660357	0.402619804	0.607670946	0.124842349	0.607670946	0.017638685	p<0.05
: A_23_P209020	UBA2	1.043720756	1.71611658	0.60818756	0.138174366	0.60818756	0.021705493	p<0.05
: A_23_P127915	STK33	0.847877695	1.393700108	0.608364518	0.096491862	0.608364518	0.010937356	p<0.05
: A_23_P212050	BCHE	0.190909358	0.313486763	0.608986983	0.282346645	0.608986983	0.039023823	p<0.05
: A_23_P28707	OGFR	0.970370797	1.593051952	0.6091269	0.188394207	0.6091269	0.040110075	p<0.05
: A_23_P214969	CITED2	0.359040407	0.588879262	0.609701224	0.124414635	0.609701224	0.029749542	p<0.05
: A_23_P144994	KIAA1961	0.663029726	1.087276796	0.609807667	0.250282329	0.609807667	0.041090175	p<0.05
: A_23_P212204	FLJ10707	0.638567948	1.046265046	0.610330958	0.036886784	0.610330958	0.010270177	p<0.05
: A_23_P93311		1.097342154	1.797930057	0.610336398	0.268849507	0.610336398	0.043218739	p<0.05
: A_23_P4373	GOSR1	0.420149378	0.688294414	0.610421019	0.13758381	0.610421019	0.018991287	p<0.05
: A_23_P207999	PMAIP1	0.653361551	1.069164568	0.611095402	0.146633018	0.611095402	0.022248753	p<0.05
: A_23_P48698	ADAM20	0.691559064	1.131403077	0.611240218	0.06675668	0.611240218	0.017747298	p<0.05
: A_23_P21382	LAMB2	0.858028091	1.402731833	0.611683624	0.159920868	0.611683624	0.03614639	p<0.05
: A_23_P153945	GTDC1	1.041720112	1.702426444	0.611903155	0.150781609	0.611903155	0.027237125	p<0.05
: A_23_P68730	PDXK	0.540459419	0.882246207	0.612594778	0.114561001	0.612594778	0.016720825	p<0.05
: A_23_P19673	SGK	0.126111874	0.205785065	0.612832973	0.156729715	0.612832973	0.03129124	p<0.05
: A_23_P336992	LOC90637	0.711429045	1.160638188	0.612963671	0.078533695	0.612963671	0.016797104	p<0.05
: A_23_P337201	SRP72	0.732694475	1.195053433	0.613106037	0.308115303	0.613106037	0.048599701	p<0.05
: A_23_P141688	RAB31	0.16667728	0.271805	0.613223744	0.105613512	0.613223744	0.033232867	p<0.05
: A_23_P152593	SLC9A3R1	1.266042894	2.06037558	0.614471898	0.185938894	0.614471898	0.033810036	p<0.05
: A_23_P63897	CTBP2	2.194203964	3.570559593	0.614526633	0.159245481	0.614526633	0.031751447	p<0.05
: A_23_P149707	DLGAP3	0.538006703	0.871858996	0.617079948	0.119566788	0.617079948	0.021970218	p<0.05
: A_23_P308519	SLC9A3R1	1.289156567	2.086901116	0.617737255	0.22658943	0.617737255	0.038404843	p<0.05
: A_23_P142916	FLJ38973	1.321763074	2.138226405	0.618158616	0.240495872	0.618158616	0.02836939	p<0.05
: A_23_P35634	RHOBTB1	0.644982224	1.04272618	0.618553784	0.128619346	0.618553784	0.040340808	p<0.05
: A_23_P66958	ZCCHC2	1.78830429	2.890383708	0.618708265	0.156897064	0.618708265	0.0119499	p<0.05
: A_23_P76998	KIAA1036	0.480724654	0.774354574	0.620806889	0.101512196	0.620806889	0.012101535	p<0.05
: A_23_P146456	CTSL2	0.82187851	1.323758753	0.62086729	0.179066236	0.62086729	0.029614585	p<0.05
: A_23_P111797		1.001420398	1.611451613	0.621439942	0.081813195	0.621439942	0.012555342	p<0.05
: A_23_P94517	DBC1	0.408651374	0.657108344	0.621893448	0.038281873	0.621893448	0.043229955	p<0.05
: A_23_P73530	MTMR1	0.494216168	0.792917604	0.623288177	0.100505111	0.623288177	0.018494587	p<0.05
: A_23_P157726	C9orf55	0.675936971	1.084304218	0.623383142	0.194932505	0.623383142	0.04039919	p<0.05
: A_23_P100660	SERPINF1	0.144729072	0.231476243	0.625243743	0.099437557	0.625243743	0.017334062	p<0.05
: A_23_P374777	SH3KBP1	0.789625251	1.261345176	0.62601837	0.144484912	0.62601837	0.015046203	p<0.05
: A_23_P71627	C9orf19	0.80464396	1.28462928	0.626362774	0.038580942	0.626362774	0.015262842	p<0.05
: A_23_P126706	ANGPTL1	0.855624936	1.365188214	0.626745036	0.028308749	0.626745036	0.013109685	p<0.05
: A_23_P64184		1.419968961	2.26524374	0.626850407	0.095604706	0.626850407	0.033571758	p<0.05
: A_23_P142631	FKBP1B	0.386655067	0.616732144	0.626941649	0.149156511	0.626941649	0.027334346	p<0.05
: A_23_P28434	VAMP8	0.648067744	1.030010326	0.629185677	0.121643533	0.629185677	0.013553922	p<0.05
: A_23_P79652	HOXD3	1.013683429	1.608896921	0.630048709	0.127066379	0.630048709	0.034470896	p<0.05
: A_23_P2922	MBIP	1.730936783	2.741952226	0.631278972	0.111284108	0.631278972	0.011388427	p<0.05

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: A_23_P74145	CD48	0.203715355	0.322485459	0.631704001	0.030610785	0.631704001	0.030030777	p<0.05
: A_23_P26468	RHBDL1	0.596415192	0.942727879	0.632648302	0.152514291	0.632648302	0.033106939	p<0.05
: A_23_P377114	MCC	0.335833016	0.530563195	0.632974582	0.124720143	0.632974582	0.041717815	p<0.05
: A_23_P206937	PMM2	1.569511584	2.47915521	0.633083228	0.166807502	0.633083228	0.039155942	p<0.05
: A_23_P73559	FGD1	0.843155784	1.331547534	0.633214934	0.163102182	0.633214934	0.035318388	p<0.05
: A_23_P104892	EIF4G2	1.559867463	2.46021439	0.634037208	0.093663863	0.634037208	0.036786279	p<0.05
: A_23_P54649	TRADD	0.801130908	1.262710597	0.634453302	0.134947193	0.634453302	0.026497574	p<0.05
: A_23_P149388	CGN	0.898674232	1.414727727	0.635227694	0.169023208	0.635227694	0.044867133	p<0.05
: A_23_P155815	HCAP-G	1.030431176	1.622124883	0.635235417	0.21318855	0.635235417	0.042744585	p<0.05
: A_23_P128073	SMARCC2	0.506754429	0.796441159	0.636273532	0.135131786	0.636273532	0.018376526	p<0.05
: A_23_P124773	CAPS2	1.590549246	2.491854718	0.63829935	0.12975214	0.63829935	0.024321055	p<0.05
: A_23_P46767	NHLRC2	1.379138144	2.160568548	0.638321865	0.196643604	0.638321865	0.031220932	p<0.05
: A_23_P161647	PC	0.390736918	0.610198471	0.640343981	0.140724049	0.640343981	0.026039436	p<0.05
: A_23_P119992	VRK2	2.479701685	3.871530697	0.640496455	0.19447165	0.640496455	0.027526523	p<0.05
: A_23_P50031	OR3A1	1.01425451	1.583213432	0.640630309	0.125205031	0.640630309	0.031079051	p<0.05
: A_23_P99883	GRP58	1.007535583	1.570104997	0.641699652	0.13559442	0.641699652	0.023000908	p<0.05
: A_23_P132784	FXR1	0.768853787	1.194281769	0.643779221	0.138306491	0.643779221	0.014755993	p<0.05
: A_23_P150057	MMRN2	0.42953629	0.666743921	0.64422978	0.262386875	0.64422978	0.040011186	p<0.05
: A_23_P168598	PON1	0.840009277	1.301529294	0.645401744	0.168729475	0.645401744	0.041348614	p<0.05
: A_23_P397347	MCMDC1	0.978765954	1.514299232	0.646349105	0.189595597	0.646349105	0.038929547	p<0.05
: A_23_P71752	ZA20D2	1.491880527	2.307250929	0.646605234	0.104040133	0.646605234	0.010143773	p<0.05
: A_23_P16583	KIRREL2	0.631123602	0.975982419	0.646654683	0.163022654	0.646654683	0.021564165	p<0.05
: A_23_P77776	SFRS2	1.98502659	3.067165589	0.647185987	0.125238495	0.647185987	0.015234255	p<0.05
: A_23_P3973	MRPS7	1.173520711	1.811435331	0.647840246	0.125545509	0.647840246	0.01755689	p<0.05
: A_23_P90579	HS6ST1	0.323798423	0.499058271	0.648818869	0.242268135	0.648818869	0.04632025	p<0.05
: A_23_P258144		0.904518834	1.393450993	0.649121382	0.097455134	0.649121382	0.01431025	p<0.05
: A_23_P203649	ZF	0.907499345	1.396327158	0.649918853	0.149461409	0.649918853	0.026299174	p<0.05
: A_23_P47777	MARCH-IX	0.698047634	1.071871424	0.651241948	0.269672615	0.651241948	0.048920558	p<0.05
: A_23_P40724	PPARA	0.677423359	1.038776544	0.652135787	0.228979192	0.652135787	0.044496289	p<0.05
: A_23_P361448	SESN3	0.618495751	0.946017803	0.653788701	0.167704235	0.653788701	0.040625664	p<0.05
: A_23_P125265	KPNA2	1.185448953	1.810386428	0.654804375	0.264628712	0.654804375	0.048019887	p<0.05
: A_23_P204937	RGC32	1.030680313	1.57286614	0.655288004	0.107421308	0.655288004	0.02324126	p<0.05
: A_23_P36795	SYT1	1.993186728	3.041653024	0.655297206	0.153691445	0.655297206	0.046436102	p<0.05
: A_23_P150996		0.537103214	0.819209561	0.655635919	0.115412496	0.655635919	0.030657429	p<0.05
: A_23_P141738	SS18	0.491116366	0.748874809	0.655805697	0.173209931	0.655805697	0.029095074	p<0.05
: A_23_P202053	ITI12	0.208239147	0.317451382	0.655971777	0.143005632	0.655971777	0.045490792	p<0.05
: A_23_P42695	C7orf24	1.359413975	2.070731703	0.656489671	0.142875756	0.656489671	0.034166577	p<0.05
: A_23_P169828		0.65926841	1.003700555	0.656837745	0.006044015	0.656837745	0.019798031	p<0.05
: A_23_P349928	SP100	1.897935315	2.889186083	0.65691003	0.052648149	0.65691003	0.020217229	p<0.05
: A_23_P50399	LOC90379	0.621651341	0.945978787	0.65715146	0.059157258	0.65715146	0.015767395	p<0.05
: A_23_P250347	CAMK4	0.809383219	1.231259207	0.657362165	0.068351813	0.657362165	0.030856419	p<0.05
: A_23_P64689	USP52	0.368408229	0.560171883	0.657669976	0.125691839	0.657669976	0.024363227	p<0.05
: A_23_P210283	PTMA	0.840010701	1.276857909	0.65787328	0.113671364	0.65787328	0.0283595	p<0.05
: A_23_P140884	TUBB4Q	0.60911807	0.925155611	0.658395261	0.196961502	0.658395261	0.044908827	p<0.05
: A_23_P166280		0.955647221	1.450805126	0.658701299	0.105182706	0.658701299	0.019923847	p<0.05
: A_23_P98995	KIAA1536	0.748120802	1.133738517	0.659870676	0.226218015	0.659870676	0.031094803	p<0.05
: A_23_P28295	LRP2	1.328131321	2.010162971	0.660708281	0.061836434	0.660708281	0.016322488	p<0.05
: A_23_P57568	A4GALT	0.520017122	0.786181696	0.661446488	0.205779501	0.661446488	0.047497174	p<0.05
: A_23_P205188	C13orf11	1.243949154	1.879643328	0.661800638	0.152086178	0.661800638	0.032917881	p<0.05
: A_23_P168507	HIBADH	1.097057821	1.65721354	0.661989415	0.112817637	0.661989415	0.022846441	p<0.05
: A_23_P15226		0.702799811	1.061147119	0.662301954	0.13460966	0.662301954	0.036517225	p<0.05
: A_23_P129053	USP8	1.351711275	2.038073718	0.663229825	0.213526226	0.663229825	0.020924776	p<0.05
: A_23_P215318	VPS41	1.864152901	2.808264684	0.663809545	0.168043252	0.663809545	0.036494589	p<0.05

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: A_23_P109322	PCP4	0.895523119	1.348101525	0.664284627	0.12177639	0.664284627	0.019877028	p<0.05
: A_23_P133470	PJA2	0.650012758	0.977069374	0.665267764	0.138853965	0.665267764	0.034587224	p<0.05
: A_23_P162805	HMGB1	1.867259294	2.805575407	0.665553059	0.088763912	0.665553059	0.030323857	p<0.05
: A_23_P70849	NOS3	0.747934104	1.123234978	0.665875012	0.282952664	0.665875012	0.041611742	p<0.05
: A_23_P209689	ROCK2	0.483616272	0.726199343	0.665955259	0.167297546	0.665955259	0.028866601	p<0.05
: A_23_P104522	NEBL	1.058718203	1.587736855	0.666809616	0.156511054	0.666809616	0.038439422	p<0.05
: A_23_P74299	ADORA1	0.754456699	1.131217566	0.66694217	0.095906665	0.66694217	0.044564142	p<0.05
: A_23_P129096	HEXA	0.406839144	0.609577088	0.667412133	0.068239526	0.667412133	0.01252446	p<0.05
: A_23_P339079	ZNF573	0.285251674	0.427350695	0.667488497	0.174545621	0.667488497	0.044965985	p<0.05
: A_23_P78018	ABCA5	0.635549709	0.951584433	0.667885777	0.212399248	0.667885777	0.049303116	p<0.05
: A_23_P104781		0.810112418	1.212821327	0.667956936	0.131164741	0.667956936	0.033300655	p<0.05
: A_23_P61778	NXN	1.056478551	1.579762185	0.668757969	0.112887902	0.668757969	0.015578921	p<0.05
: A_23_P7684	FLJ14166	0.524885678	0.78321345	0.670169388	0.12836364	0.670169388	0.018761811	p<0.05
: A_23_P94838	RYR3	0.703519438	1.048528765	0.670958644	0.160286583	0.670958644	0.040228902	p<0.05
: A_23_P15639	NJMU-R1	0.713018873	1.061769458	0.671538315	0.106809406	0.671538315	0.010509	p<0.05
: A_23_P26094	FLJ13213	0.990851346	1.474998081	0.671764499	0.206828627	0.671764499	0.046328251	p<0.05
: A_23_P99437	ING1	1.59947118	2.378083696	0.672588262	0.105454566	0.672588262	0.01171413	p<0.05
: A_23_P415511	C2orf15	1.366975317	2.029291936	0.673621815	0.167198003	0.673621815	0.040773897	p<0.05
: A_23_P200001	NEXN	0.690538078	1.024316231	0.674145403	0.041458246	0.674145403	0.016918421	p<0.05
: A_23_P78068	TBC1D3	1.211497732	1.796798323	0.674253596	0.112489993	0.674253596	0.019400685	p<0.05
: A_23_P304991	HLCS	1.336731106	1.980700433	0.674877979	0.166678551	0.674877979	0.027922218	p<0.05
: A_23_P256329		0.700111365	1.037199801	0.675001445	0.088225542	0.675001445	0.031352122	p<0.05
: A_23_P27894	SAFB2	1.085375685	1.607195985	0.675322546	0.095625069	0.675322546	0.021684816	p<0.05
: A_23_P204019	CACNB3	1.81920145	2.692873255	0.675561483	0.212541464	0.675561483	0.036337847	p<0.05
: A_23_P204541	CNTN1	0.668491498	0.989475148	0.67560211	0.089662896	0.67560211	0.03121463	p<0.05
: A_23_P56197	CRLF1	0.413599281	0.612139154	0.67566219	0.147184366	0.67566219	0.033198889	p<0.05
: A_23_P327551	CPNE4	0.980609008	1.451092908	0.675772725	0.135922554	0.675772725	0.025019864	p<0.05
: A_23_P116802	COPZ1	1.206682369	1.784769185	0.676099957	0.158385087	0.676099957	0.026011388	p<0.05
: A_23_P106973	Sep-09	0.901732775	1.331660965	0.677148913	0.151071098	0.677148913	0.028872937	p<0.05
: A_23_P60148	PDGFRL	1.113656333	1.643597154	0.677572561	0.186000361	0.677572561	0.042936532	p<0.05
: A_23_P205336	C14orf129	3.435742871	5.067286797	0.678024159	0.102217354	0.678024159	0.013127331	p<0.05
: A_23_P215302	RALA	1.282369817	1.891042207	0.678128607	0.202325999	0.678128607	0.026570231	p<0.05
: A_23_P307400	LOC90799	0.782581235	1.149370517	0.680878118	0.167639905	0.680878118	0.025909294	p<0.05
: A_23_P148519	TMEM29	0.586774789	0.861506459	0.68110318	0.117344915	0.68110318	0.015275604	p<0.05
: A_23_P7253	FLJ10378	1.593049007	2.338618953	0.681192207	0.235245403	0.681192207	0.045695311	p<0.05
: A_23_P27013	HOXB9	0.843688785	1.237179398	0.681945389	0.113181469	0.681945389	0.023113329	p<0.05
: A_23_P424	MARK1	1.115670493	1.635971777	0.681961944	0.098663365	0.681961944	0.016670731	p<0.05
: A_23_P83704	CSNK1G1	1.031344673	1.512104853	0.682058966	0.07822746	0.682058966	0.010376105	p<0.05
: A_23_P72058	FLJ20674	1.985617323	2.902894669	0.684012873	0.064501484	0.684012873	0.01838222	p<0.05
: A_23_P75071	MPHOSPH1	1.322508886	1.933152113	0.684120446	0.109478434	0.684120446	0.011433027	p<0.05
: A_23_P57676	SMARCA3	0.436010719	0.637116462	0.684350107	0.169830203	0.684350107	0.033309015	p<0.05
: A_23_P427148	PROCA1	0.409602772	0.59795167	0.68500983	0.076542329	0.68500983	0.011078985	p<0.05
: A_23_P408271	DHRS8	1.39198165	2.03082313	0.685427317	0.165577093	0.685427317	0.019338929	p<0.05
: A_23_P131383	FANCL	0.898128865	1.309432678	0.685891593	0.215970364	0.685891593	0.036593826	p<0.05
: A_23_P251339	DHRSX	0.977520761	1.425059058	0.685951053	0.185256756	0.685951053	0.034200174	p<0.05
: A_23_P130614	STXBP2	1.024323477	1.49222314	0.686441223	0.2242161	0.686441223	0.021273202	p<0.05
: A_23_P103149	ACO2	1.373481041	1.998327145	0.68731541	0.190751611	0.68731541	0.027984203	p<0.05
: A_23_P321351	FLJ33069	0.364391324	0.530040456	0.687478323	0.158006687	0.687478323	0.034757459	p<0.05
: A_23_P92349	FGFRL1	0.194803964	0.283010407	0.688327918	0.201453031	0.688327918	0.029172682	p<0.05
: A_23_P153137	GALNT1	1.49539528	2.170870848	0.688845806	0.216153144	0.688845806	0.017208005	p<0.05
: A_23_P213184	ADH1B	0.799073958	1.159061639	0.68941455	0.005830387	0.68941455	0.046307391	p<0.05
: A_23_P105794	EPSTI1	0.682741886	0.989796624	0.68977997	0.210034582	0.68977997	0.047063105	p<0.05
: A_23_P57347	PCNT2	1.034792147	1.499479086	0.690101087	0.149164048	0.690101087	0.027264822	p<0.05

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: A_23_P371280	RNF165	0.52327144	0.757893002	0.690429175	0.077841172	0.690429175	0.040431449	p<0.05
: A_23_P3651	HBZ	0.017590065	0.025436715	0.691522657	0.021528833	0.691522657	0.029492766	p<0.05
: A_23_P8625	LRRC4	1.631196349	2.355990118	0.692361287	0.093125724	0.692361287	0.011906623	p<0.05
: A_23_P104939	OR5M9	0.307887315	0.444357984	0.692881248	0.200896816	0.692881248	0.045940719	p<0.05
: A_23_P359630	PLGL	1.099464946	1.58538863	0.693498695	0.164004894	0.693498695	0.034737058	p<0.05
: A_23_P98844	GEFT	0.57803673	0.832788929	0.694097519	0.090261008	0.694097519	0.02373823	p<0.05
: A_23_P502731	PRRX1	0.615020782	0.885807438	0.69430528	0.158176182	0.69430528	0.017278639	p<0.05
: A_23_P259641	EZH2	1.032114848	1.485466068	0.694808767	0.306195609	0.694808767	0.043078407	p<0.05
: A_23_P21640	CHD3	0.670437499	0.96459626	0.69504468	0.116319947	0.69504468	0.037614452	p<0.05
: A_23_P128759	SERPINA10	0.248929945	0.358100742	0.695139428	0.116733528	0.695139428	0.011178724	p<0.05
: A_23_P250982	CGI-111	1.37967192	1.984352003	0.695275796	0.118509476	0.695275796	0.013409327	p<0.05
: A_23_P49539	KIAA1447	0.776551904	1.116437151	0.695562579	0.21019066	0.695562579	0.022423354	p<0.05
: A_23_P213877	FLJ13231	0.283355038	0.407260482	0.695758735	0.132545717	0.695758735	0.02253855	p<0.05
: A_23_P146744		0.908670512	1.305725212	0.695912512	0.125541137	0.695912512	0.02710972	p<0.05
: A_23_P873	C1orf38	0.494074271	0.709200089	0.696664141	0.036803008	0.696664141	0.016735582	p<0.05
: A_23_P9831	ETV5	1.167426973	1.673610517	0.697549975	0.185424323	0.697549975	0.047729037	p<0.05
: A_23_P117157	SUCLA2	1.282424966	1.837704727	0.697840598	0.138944286	0.697840598	0.029052023	p<0.05
: A_23_P213592	RNF44	0.642657888	0.919995129	0.698544881	0.138930033	0.698544881	0.036000862	p<0.05
: A_23_P89349	PPM1D	1.562158793	2.234283229	0.699176708	0.09878463	0.699176708	0.024582287	p<0.05
: A_23_P153098	HDHD2	0.929537174	1.327489921	0.700221644	0.08271659	0.700221644	0.011415547	p<0.05
: A_23_P6821	ITIH3	0.261520175	0.373457605	0.70026737	0.017864225	0.70026737	0.017851784	p<0.05
: A_23_P355860	PCP2	1.203897735	1.71571872	0.701687124	0.128414356	0.701687124	0.042203904	p<0.05
: A_23_P134167	C6orf210	1.515612607	2.154562512	0.70344332	0.131857582	0.70344332	0.01866784	p<0.05
: A_23_P166431	C22orf24	0.458641307	0.651982172	0.703456821	0.116145373	0.703456821	0.023852413	p<0.05
: A_23_P417942	FBNP1L	1.602370742	2.277025032	0.703712396	0.150505376	0.703712396	0.023414368	p<0.05
: A_23_P50096	TYMS	1.306301817	1.855368732	0.704065879	0.079967171	0.704065879	0.015650403	p<0.05
: A_23_P137427	ZMPSTE24	1.862183504	2.6407193	0.705180405	0.067203031	0.705180405	0.015353687	p<0.05
: A_23_P376686	BTNL2	0.310046508	0.439605494	0.705283515	0.204438213	0.705283515	0.025353826	p<0.05
: A_23_P56328	PLVAP	0.319920518	0.453528175	0.705403845	0.129050348	0.705403845	0.032760982	p<0.05
: A_23_P250571	DMXL1	1.182011839	1.675425106	0.705499658	0.123729673	0.705499658	0.016810855	p<0.05
: A_23_P88434	CHES1	0.547027636	0.775107014	0.70574466	0.23108265	0.70574466	0.049482734	p<0.05
: A_23_P162446	SRGAP1	0.715253744	1.012615705	0.706342732	0.210630908	0.706342732	0.031440776	p<0.05
: A_23_P66579	RPIP8	0.34069658	0.482107542	0.706681705	0.206596721	0.706681705	0.046642651	p<0.05
: A_23_P128319	ATP2B1	0.702852986	0.994388709	0.706819154	0.135898004	0.706819154	0.022932517	p<0.05
: A_23_P34650	FCGR2B	0.306436113	0.432920267	0.70783499	0.020166719	0.70783499	0.026972031	p<0.05
: A_23_P203299	RCN1	1.159486983	1.636965443	0.708314881	0.133906511	0.708314881	0.016876731	p<0.05
: A_23_P201565	FLJ10330	0.520446722	0.733804068	0.709244804	0.034826304	0.709244804	0.015122065	p<0.05
: A_23_P156898	TNFAIP3	0.461398269	0.650402132	0.709404607	0.166820288	0.709404607	0.032721871	p<0.05
: A_23_P110266	FLJ23191	1.192894565	1.681517065	0.709415676	0.033738002	0.709415676	0.010438814	p<0.05
: A_23_P206510	GLG1	0.865030967	1.21875622	0.709765376	0.138784146	0.709765376	0.031127376	p<0.05
: A_23_P374294	CCDC7	0.552126429	0.777871285	0.709791503	0.155352452	0.709791503	0.026412728	p<0.05
: A_23_P21128	NBEA	0.591440684	0.833189097	0.709851684	0.146035356	0.709851684	0.042510454	p<0.05
: A_23_P218863	PB1	0.734186391	1.034230769	0.709886432	0.09427803	0.709886432	0.014026202	p<0.05
: A_23_P215841	PAG	0.668721898	0.94153504	0.710246427	0.10945213	0.710246427	0.013073054	p<0.05
: A_23_P333605	ENPEP	1.010179824	1.421493603	0.71064676	0.116967418	0.71064676	0.024627728	p<0.05
: A_23_P213199	FLJ14281	1.066547653	1.499805484	0.711123985	0.112821727	0.711123985	0.023930393	p<0.05
: A_23_P128773	CTAGE5	1.357109436	1.90754005	0.711444793	0.112769795	0.711444793	0.011261581	p<0.05
: A_23_P46355	FLJ23467	0.394481538	0.553917071	0.712167144	0.117422155	0.712167144	0.030040833	p<0.05
: A_23_P39735	IL18R1	0.732222803	1.027606823	0.71255152	0.146550723	0.71255152	0.03272137	p<0.05
: A_23_P204119	RBM19	0.495337321	0.694522049	0.713206041	0.147893208	0.713206041	0.030047173	p<0.05
: A_23_P133245	IK	0.854518574	1.197505761	0.713582015	0.191382866	0.713582015	0.036065752	p<0.05
: A_23_P372888	SC5DL	1.696288463	2.376649419	0.713731041	0.126563765	0.713731041	0.022108295	p<0.05
: A_23_P129659	LOC115509	0.553607134	0.775593967	0.713784734	0.095111978	0.713784734	0.019445714	p<0.05

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: A_23_P17620	CYYR1	0.779711628	1.091971933	0.714039989	0.101635757	0.714039989	0.016770703	p<0.05
: A_23_P110031	ZNF589	0.796804326	1.115634416	0.714216337	0.165268768	0.714216337	0.043340537	p<0.05
: A_23_P251606	ELOVL2	0.625330369	0.875346452	0.714380423	0.087651981	0.714380423	0.013050645	p<0.05
: A_23_P48835	KIF23	1.376831859	1.926702699	0.714605247	0.152363502	0.714605247	0.019819697	p<0.05
: A_23_P81588	PDE6A	0.479078507	0.67040643	0.714609057	0.137016912	0.714609057	0.030196684	p<0.05
: A_23_P4221	NDP52	1.128842436	1.579200527	0.714818933	0.081882144	0.714818933	0.014298526	p<0.05
: A_23_P152237	IRX3	0.284257333	0.39764678	0.714848825	0.259145524	0.714848825	0.044860014	p<0.05
: A_23_P110811	COX7C	1.95852656	2.738175069	0.715267107	0.049123022	0.715267107	0.011816167	p<0.05
: A_23_P338919	APEG1	0.550415581	0.768925424	0.7158244	0.069681536	0.7158244	0.041527024	p<0.05
: A_23_P127990	CHRD2	0.735100888	1.026846068	0.715882264	0.09366041	0.715882264	0.027354068	p<0.05
: A_23_P407628	MYST3	0.35909139	0.501429999	0.716134636	0.156005896	0.716134636	0.034085205	p<0.05
: A_23_P162087	C11orf15	0.464834376	0.648677909	0.716587339	0.034114384	0.716587339	0.031486203	p<0.05
: A_23_P217236	HMGB3	0.82671232	1.153649803	0.716605956	0.203439968	0.716605956	0.020261727	p<0.05
: A_23_P50426	ANKRD25	0.877932271	1.224126212	0.717190975	0.017376904	0.717190975	0.021407768	p<0.05
: A_23_P218523		0.346351364	0.482768159	0.717427937	0.207416424	0.717427937	0.047899157	p<0.05
: A_23_P215449	BAZ1B	1.351345384	1.882880848	0.717700955	0.148998295	0.717700955	0.023002284	p<0.05
: A_23_P97481	FLJ23033	0.568088713	0.791162237	0.718043261	0.165398884	0.718043261	0.016128685	p<0.05
: A_23_P61937		0.169709983	0.23633905	0.718078468	0.207280291	0.718078468	0.047308217	p<0.05
: A_23_P254612	ASK	2.24728226	3.127735556	0.718501363	0.194647972	0.718501363	0.043305797	p<0.05
: A_23_P200015	AK5	0.343884934	0.477948276	0.719502404	0.095072148	0.719502404	0.033645329	p<0.05
: A_23_P27392	LOC147650	0.422586545	0.586396722	0.720649568	0.049306778	0.720649568	0.020922639	p<0.05
: A_23_P115872	C10orf3	2.624124595	3.638136753	0.721282561	0.189864871	0.721282561	0.040428639	p<0.05
: A_23_P209160	FSTL3	0.403890943	0.55923435	0.72222127	0.117195262	0.72222127	0.021406109	p<0.05
: A_23_P132793	ARMET	0.719725324	0.996118184	0.722530052	0.142708551	0.722530052	0.046046097	p<0.05
: A_23_P153086	C18orf22	1.699860578	2.350998909	0.723037587	0.255009734	0.723037587	0.047972654	p<0.05
: A_23_P422222	C6orf62	1.379099633	1.905118037	0.723891962	0.072599347	0.723891962	0.018220977	p<0.05
: A_23_P38271	MYH2	0.750614962	1.036576329	0.724128982	0.080299368	0.724128982	0.029213807	p<0.05
: A_23_P71241	SEC61G	1.338861399	1.848594845	0.72425897	0.053538371	0.72425897	0.02808775	p<0.05
: A_23_P23102	ZNF31	0.80413866	1.109825641	0.724563058	0.130349581	0.724563058	0.030581058	p<0.05
: A_23_P70045	H2AFY	1.859351986	2.565315657	0.724804365	0.170074475	0.724804365	0.035187797	p<0.05
: A_23_P88503	MESDC2	0.901142113	1.242845266	0.725063802	0.07240402	0.725063802	0.015330866	p<0.05
: A_23_P357811	MBNL1	1.861908477	2.566413449	0.725490461	0.088755262	0.725490461	0.010377906	p<0.05
: A_23_P34827	HCN3	0.845746521	1.165244835	0.725810143	0.119837412	0.725810143	0.01655512	p<0.05
: A_23_P203228		0.434259953	0.598128335	0.7260314	0.13076487	0.7260314	0.025553701	p<0.05
: A_23_P125602		0.865532705	1.192082205	0.726067968	0.085643071	0.726067968	0.011700422	p<0.05
: A_23_P164289	DERP6	0.7568866	1.042154131	0.726271266	0.129255494	0.726271266	0.031261202	p<0.05
: A_23_P59790	LUC7L2	0.810017158	1.115203182	0.726340429	0.093092282	0.726340429	0.011350998	p<0.05
: A_23_P24332	MUC15	0.579288799	0.796626502	0.727177413	0.138525191	0.727177413	0.039812925	p<0.05
: A_23_P127353	NDUFV1	0.843688197	1.159334679	0.727734805	0.152914469	0.727734805	0.044173627	p<0.05
: A_23_P103070	YWHAH	1.925510503	2.645054811	0.727966201	0.099583443	0.727966201	0.013032077	p<0.05
: A_23_P56709	RNF103	1.079866265	1.482639305	0.728340508	0.129054111	0.728340508	0.024583339	p<0.05
: A_23_P37564	MAN2A2	0.680544759	0.932480149	0.729822249	0.187080746	0.729822249	0.031723894	p<0.05
: A_23_P41340		0.400154078	0.548140093	0.730021546	0.194386252	0.730021546	0.045683139	p<0.05
: A_23_P29800	CLDN11	0.941846493	1.290116001	0.730047912	0.065318955	0.730047912	0.01972964	p<0.05
: A_23_P42963	RNF133	1.514727299	2.073642628	0.730466898	0.070857512	0.730466898	0.026311432	p<0.05
: A_23_P6293	UBASH3A	0.300841046	0.411829678	0.730498703	0.101888308	0.730498703	0.027543657	p<0.05
: A_23_P365874	PB1	0.94187494	1.28883245	0.73079704	0.126501902	0.73079704	0.03720467	p<0.05
: A_23_P66900	CDK5RAP3	0.618058091	0.845468611	0.73102429	0.215204137	0.73102429	0.022758755	p<0.05
: A_23_P211572	Sep-03	0.891189966	1.218893875	0.73114648	0.134934071	0.73114648	0.046869368	p<0.05
: A_23_P71179		0.922541239	1.261477548	0.731318001	0.144803735	0.731318001	0.047323719	p<0.05
: A_23_P43841	CALML5	0.553442365	0.756416765	0.731663272	0.037954726	0.731663272	0.011509301	p<0.05
: A_23_P35219	NEK2	0.494234892	0.675469816	0.731690566	0.083480762	0.731690566	0.027436085	p<0.05
: A_23_P368225	EME1	1.415701977	1.93357998	0.732166237	0.114332688	0.732166237	0.022471521	p<0.05

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: A_23_P127095	USMG5	3.355229018	4.579978156	0.732586249	0.145462207	0.732586249	0.034295171	p<0.05
: A_23_P88740	BM039	0.750905685	1.024386214	0.733029862	0.210867421	0.733029862	0.041549038	p<0.05
: A_23_P86493	LBX1	0.646055892	0.881287213	0.733082113	0.214994559	0.733082113	0.041539413	p<0.05
: A_23_P335329	GNG4	0.356746703	0.486311964	0.73357583	0.111786055	0.73357583	0.013021422	p<0.05
: A_23_P45712		1.343020187	1.829684285	0.734017447	0.043148946	0.734017447	0.020882697	p<0.05
: A_23_P88331	DLG7	1.167492387	1.590055507	0.734246309	0.172640773	0.734246309	0.018165244	p<0.05
: A_23_P38167	GPRC5C	0.426156111	0.580373138	0.734279522	0.095798462	0.734279522	0.010999509	p<0.05
: A_23_P38244	APOH	0.012672894	0.017243744	0.734927048	0.027325726	0.734927048	0.01270455	p<0.05
: A_23_P110445	APBB3	0.761557787	1.036180098	0.734966622	0.114678177	0.734966622	0.026699229	p<0.05
: A_23_P87513	ATP6V0A2	1.429613386	1.943917824	0.73542892	0.183784841	0.73542892	0.045654547	p<0.05
: A_23_P30055		1.140752299	1.550605855	0.735681666	0.080148692	0.735681666	0.014349072	p<0.05
: A_23_P340340	LCE3E	0.478696335	0.650019286	0.736434049	0.286947153	0.736434049	0.043852435	p<0.05
: A_23_P23506	FLJ23506	0.406273107	0.551264948	0.736983383	0.180943669	0.736983383	0.019779859	p<0.05
: A_23_P213680	CXXC5	0.943343668	1.279953513	0.737014007	0.157944093	0.737014007	0.028605803	p<0.05
: A_23_P165879	RAB10	1.982508693	2.688292466	0.737460198	0.243180177	0.737460198	0.032388867	p<0.05
: A_23_P407090	HOZFP	1.55791261	2.111573131	0.737797137	0.260439237	0.737797137	0.039787688	p<0.05
: A_23_P377264	RABGAP1L	0.786959581	1.065942977	0.738275497	0.024139451	0.738275497	0.014403137	p<0.05
: A_23_P101992	MARCO	0.531047455	0.718933098	0.738660463	0.160479504	0.738660463	0.034253932	p<0.05
: A_23_P379614	OIP5	1.40547047	1.901985371	0.738949148	0.153464709	0.738949148	0.02572447	p<0.05
: A_23_P49898	PELP1	0.622580405	0.842341031	0.739107299	0.107034349	0.739107299	0.040205859	p<0.05
: A_23_P207336	PPY	0.53569725	0.724671249	0.739227962	0.004737267	0.739227962	0.025175826	p<0.05
: A_23_P428139	EFNB2	1.320261779	1.785532218	0.739421986	0.19315696	0.739421986	0.049533662	p<0.05
: A_23_P258340	PPIA	1.349444859	1.823276385	0.740120845	0.035065635	0.740120845	0.026435932	p<0.05
: A_23_P154566	C20orf100	0.366924372	0.49550528	0.740505472	0.149588178	0.740505472	0.021639363	p<0.05
: A_23_P358599	POPDC3	1.046965353	1.413587452	0.740644204	0.174865328	0.740644204	0.047425637	p<0.05
: A_23_P75509	PPFIA1	0.876882585	1.183832702	0.740714953	0.231251056	0.740714953	0.036691901	p<0.05
: A_23_P55256	ZNF652	0.511225253	0.690032835	0.740870909	0.135605691	0.740870909	0.021584105	p<0.05
: A_23_P63281	MGC10334	0.393117984	0.530239344	0.741397235	0.247121774	0.741397235	0.045946637	p<0.05
: A_23_P98446	SC5DL	1.40761935	1.898446921	0.741458365	0.135917677	0.741458365	0.034872871	p<0.05
: A_23_P326700	OVOL1	1.090801357	1.470011864	0.742035751	0.024423731	0.742035751	0.046917481	p<0.05
: A_23_P11051	THOC2	0.821248155	1.106316855	0.742326351	0.047212379	0.742326351	0.013912432	p<0.05
: A_23_P114616	DKFZP566D1346	1.394209008	1.876091684	0.743145455	0.164349416	0.743145455	0.029222953	p<0.05
: A_23_P58993	MOCS1	0.77937583	1.048002045	0.743677776	0.127709184	0.743677776	0.039226104	p<0.05
: A_23_P159053	RAD17	0.782183267	1.051646244	0.743770323	0.101145364	0.743770323	0.011621561	p<0.05
: A_23_P162106	MRPL48	1.061203492	1.425015088	0.74469632	0.109453307	0.74469632	0.017608294	p<0.05
: A_23_P54406		0.567248279	0.761092559	0.745307876	0.212874546	0.745307876	0.020493166	p<0.05
: A_23_P120002	SP110	0.87920843	1.179601385	0.745343674	0.183297239	0.745343674	0.048326778	p<0.05
: A_23_P347040	DTX3L	0.744766526	0.998967732	0.745536119	0.125227282	0.745536119	0.03794131	p<0.05
: A_23_P393015	MYLC2PL	0.853664192	1.144494976	0.745887234	0.051354546	0.745887234	0.024451917	p<0.05
: A_23_P50535	DMPK	0.675141231	0.905031654	0.745986318	0.065109763	0.745986318	0.014661714	p<0.05
: A_23_P380815	KIAA1279	2.048851204	2.746388057	0.746016645	0.170566894	0.746016645	0.036591735	p<0.05
: A_23_P365117	FLJ23754	0.457532244	0.613066302	0.746301408	0.098169112	0.746301408	0.034993915	p<0.05
: A_23_P210253	DGKD	1.367107043	1.830684836	0.746773566	0.129245941	0.746773566	0.024091666	p<0.05
: A_23_P103996	GCLM	1.574905346	2.108410285	0.746963415	0.045028419	0.746963415	0.013714511	p<0.05
: A_23_P325562	SLC1A7	0.370946535	0.496475793	0.747159358	0.044532996	0.747159358	0.013497682	p<0.05
: A_23_P252371	RBBP8	1.377146935	1.842986329	0.747236652	0.136072569	0.747236652	0.043281679	p<0.05
: A_23_P130764	KCNJ14	0.672855004	0.900437127	0.747253732	0.077114251	0.747253732	0.028329963	p<0.05
: A_23_P206677	PDPR	0.885184021	1.184578774	0.747256359	0.058005719	0.747256359	0.021125588	p<0.05
: A_23_P81717	FRMD1	0.500738593	0.669685057	0.747722512	0.169114788	0.747722512	0.04233729	p<0.05
: A_23_P13364	NUCB2	0.832848008	1.113611597	0.74788015	0.122638866	0.74788015	0.020700319	p<0.05
: A_23_P166698	SS18L2	1.355958539	1.809203986	0.749477974	0.13396238	0.749477974	0.029098302	p<0.05
: A_23_P354326	FLJ31713	0.555894608	0.741545196	0.749643596	0.182021467	0.749643596	0.049056128	p<0.05
: A_23_P99373	TDRD4	0.943594804	1.258437753	0.749814444	0.063825397	0.749814444	0.015364674	p<0.05

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: A_23_P200288	S100A8	0.702226419	0.934921162	0.751107631	0.163179055	0.751107631	0.036292073	p<0.05
: A_23_P42514		1.405867655	1.871209981	0.751314748	0.077286738	0.751314748	0.015713786	p<0.05
: A_23_P211479	APOL4	0.553256476	0.736105458	0.751599475	0.145681383	0.751599475	0.030381652	p<0.05
: A_23_P355525	HECTD2	1.046521018	1.392183746	0.751711849	0.032937129	0.751711849	0.016406593	p<0.05
: A_23_P133257		0.503858971	0.670261355	0.751735076	0.016919323	0.751735076	0.02692475	p<0.05
: A_23_P34433	ZCCHC11	1.096776479	1.458614449	0.751930354	0.257823814	0.751930354	0.04836228	p<0.05
: A_23_P169599	LMAN2	0.462905284	0.615297231	0.752327917	0.166187539	0.752327917	0.020955631	p<0.05
: A_23_P131036		0.542642172	0.721158793	0.75245865	0.159887911	0.75245865	0.039413152	p<0.05
: A_23_P61854	KIAA0372	0.587780511	0.781011981	0.75258834	0.073892873	0.75258834	0.012823958	p<0.05
: A_23_P53081	OSBPL5	1.516657824	2.01473004	0.752784638	0.009842168	0.752784638	0.02842676	p<0.05
: A_23_P107509	CBX1	0.655788439	0.870780011	0.753104608	0.098692397	0.753104608	0.012268566	p<0.05
: A_23_P203692	MOGAT2	0.641845944	0.851642747	0.753656326	0.003547567	0.753656326	0.026930719	p<0.05
: A_23_P44132	FASN	0.461606506	0.612247338	0.753954288	0.009174583	0.753954288	0.024691557	p<0.05
: A_23_P79429	DKFZp762E1312	1.072791472	1.421659419	0.754605117	0.148006327	0.754605117	0.043543143	p<0.05
: A_23_P28869	PTPRA	0.859834608	1.13923306	0.754748645	0.278201348	0.754748645	0.043236836	p<0.05
: A_23_P137797	RYR2	0.898789403	1.190754034	0.754806936	0.060318668	0.754806936	0.016992388	p<0.05
: A_23_P66219	PDPK1	0.828362738	1.09664449	0.755361236	0.066394005	0.755361236	0.021037924	p<0.05
: A_23_P255444	DAPP1	0.358620822	0.474672335	0.755512373	0.038745775	0.755512373	0.024568108	p<0.05
: A_23_P349310	TNRC6A	0.714479831	0.945630962	0.755558838	0.22704681	0.755558838	0.042660783	p<0.05
: A_23_P45140	KRAS2	1.975862595	2.612339928	0.756357384	0.200852157	0.756357384	0.043340084	p<0.05
: A_23_P214554	TRIM15	0.895921928	1.184260464	0.756524393	0.059352883	0.756524393	0.011983874	p<0.05
: A_23_P24397	RCOR2	0.612038208	0.80858333	0.756926572	0.207209197	0.756926572	0.019020348	p<0.05
: A_23_P131375	C2orf22	2.016858555	2.664421101	0.756959384	0.180566979	0.756959384	0.0414139	p<0.05
: A_23_P14243	TFDP1	2.204152748	2.910298359	0.757363155	0.171349397	0.757363155	0.032832355	p<0.05
: A_23_P95302	RFC5	1.770998649	2.337689193	0.757585163	0.179006058	0.757585163	0.038390354	p<0.05
: A_23_P56630	STAT1	0.700812309	0.924145344	0.758335595	0.134658539	0.758335595	0.01877354	p<0.05
: A_23_P148737	MYBPH	0.53795606	0.709314876	0.758416435	0.222899622	0.758416435	0.044429871	p<0.05
: A_23_P48358	PCCA	0.483903597	0.637964788	0.758511451	0.24028141	0.758511451	0.04124716	p<0.05
: A_23_P39309	PSG9	0.995806962	1.312801076	0.758536065	0.184963371	0.758536065	0.047587875	p<0.05
: A_23_P52017	ASPM	1.031988354	1.360290157	0.758653107	0.14469067	0.758653107	0.021991829	p<0.05
: A_23_P109676		1.193221562	1.572642012	0.758736924	0.026114242	0.758736924	0.020125508	p<0.05
: A_23_P88450	DEGS2	0.425139318	0.560132388	0.758997921	0.08307931	0.758997921	0.013970663	p<0.05
: A_23_P167738	FLJ32112	1.891513857	2.491944379	0.759051395	0.156764902	0.759051395	0.041734497	p<0.05
: A_23_P372962	FLJ25179	0.469016663	0.61760392	0.759413352	0.169870519	0.759413352	0.033229973	p<0.05
: A_23_P29124	GP1BB	0.368522054	0.484938917	0.759934995	0.232975666	0.759934995	0.037725551	p<0.05
: A_23_P163107	PRPF39	1.527135665	2.008565825	0.760311485	0.157042696	0.760311485	0.02043745	p<0.05
: A_23_P65240	COL4A1	0.390236294	0.512856285	0.760907695	0.214946885	0.760907695	0.045379445	p<0.05
: A_23_P92899	C1QTNF2	0.435593791	0.572404729	0.760989155	0.217614377	0.760989155	0.025752789	p<0.05
: A_23_P5882	TFCP2L2	1.569673184	2.06235673	0.761106535	0.180405251	0.761106535	0.048911941	p<0.05
: A_23_P9513	MTA1	0.940108928	1.235053521	0.761188816	0.16830066	0.761188816	0.045725391	p<0.05
: A_23_P428835	PHF20	0.406581691	0.533872039	0.761571429	0.138724583	0.761571429	0.032321158	p<0.05
: A_23_P64280	FLJ23342	0.944543221	1.23920174	0.762219089	0.090598241	0.762219089	0.030265897	p<0.05
: A_23_P380998	R3HDM	1.670897314	2.191459511	0.762458674	0.183749351	0.762458674	0.04286185	p<0.05
: A_23_P322550	REC8L1	0.635506298	0.833430383	0.762518755	0.046422345	0.762518755	0.027573989	p<0.05
: A_23_P56508	ACCN4	0.475651169	0.623679251	0.762653509	0.149138131	0.762653509	0.015132601	p<0.05
: A_23_P360324	AIM1L	0.74449277	0.9756609	0.763065087	0.088755298	0.763065087	0.020517569	p<0.05
: A_23_P128254	SLCO1B1	0.609173249	0.798208616	0.763175486	0.134835751	0.763175486	0.038022759	p<0.05
: A_23_P135837		0.904828934	1.183689964	0.764413792	0.176981855	0.764413792	0.032004195	p<0.05
: A_23_P2283	TAC3	1.152126384	1.504416248	0.765829528	0.0857583	0.765829528	0.010051993	p<0.05
: A_23_P73820		0.436643023	0.569811298	0.766294077	0.122455319	0.766294077	0.032209067	p<0.05
: A_23_P218058	KLRC4	0.273528075	0.356799409	0.766615831	0.132144279	0.766615831	0.027770772	p<0.05
: A_23_P253154	EP400	0.689562457	0.898947264	0.767077764	0.076269055	0.767077764	0.011609383	p<0.05
: A_23_P28466	FLJ25955	0.906981434	1.182206388	0.767193819	0.093780402	0.767193819	0.044246656	p<0.05

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: A_23_P141459	GIP	0.532341869	0.692813623	0.768376734	0.091839499	0.768376734	0.022194493	p<0.05
: A_23_P140301	PSMA3	2.345012006	3.050697062	0.768680717	0.150134068	0.768680717	0.042420653	p<0.05
: A_23_P3042	PPP2R5E	1.309306764	1.702820077	0.768904937	0.195461268	0.768904937	0.022659859	p<0.05
: A_23_P340171	P53AIP1	1.229832989	1.599306271	0.768979032	0.042692353	0.768979032	0.023608366	p<0.05
: A_23_P367014	FLJ40873	0.868366089	1.128613323	0.769409745	0.026001484	0.769409745	0.026949316	p<0.05
: A_23_P405048	PTPRJ	0.717927492	0.932365303	0.770006659	0.051453521	0.770006659	0.01147558	p<0.05
: A_23_P74993	FLJ39739	0.579350534	0.752334661	0.770070242	0.049553524	0.770070242	0.011341807	p<0.05
: A_23_P42657	MAD1L1	0.652928582	0.846404557	0.771414303	0.114219483	0.771414303	0.045139518	p<0.05
: A_23_P157963	C9orf39	0.844812247	1.094763755	0.771684523	0.111590535	0.771684523	0.035128301	p<0.05
: A_23_P25926	EIF2B2	1.184488215	1.534573482	0.771868033	0.110278331	0.771868033	0.019238856	p<0.05
: A_23_P54983	PIP5K2B	0.824400085	1.067837754	0.772027475	0.092997564	0.772027475	0.021699165	p<0.05
: A_23_P110604	MAML1	1.369035708	1.772775391	0.772255591	0.167576893	0.772255591	0.034737151	p<0.05
: A_23_P82088	NRN1	0.357318763	0.462460635	0.772646872	0.285852865	0.772646872	0.048014434	p<0.05
: A_23_P75609	Cep164	0.591862924	0.765670819	0.772999191	0.187625569	0.772999191	0.029461375	p<0.05
: A_23_P166109	FLRT3	0.810869185	1.047922643	0.773787255	0.11974715	0.773787255	0.039089265	p<0.05
: A_23_P200661	PAI-RBP1	1.695499434	2.189760521	0.774285324	0.062597972	0.774285324	0.026094997	p<0.05
: A_23_P205027	C13orf6	1.984761929	2.563183716	0.774334636	0.135288952	0.774334636	0.029420201	p<0.05
: A_23_P201951	ARID4B	0.990623923	1.279160738	0.774432714	0.050651955	0.774432714	0.012507747	p<0.05
: A_23_P202232	MKI67	1.060181265	1.368760119	0.774555929	0.121056902	0.774555929	0.01535905	p<0.05
: A_23_P129103	LOC388152	0.701583302	0.903132094	0.77683354	0.148506612	0.77683354	0.024055239	p<0.05
: A_23_P76388	UNG	1.781861211	2.29354447	0.776902839	0.257940899	0.776902839	0.024678302	p<0.05
: A_23_P63644		0.629906765	0.810538137	0.777146363	0.014780454	0.777146363	0.029626409	p<0.05
: A_23_P252145	C1GALT1	0.997073003	1.282576271	0.777398605	0.213052052	0.777398605	0.048574051	p<0.05
: A_23_P253949	RAB2	0.431663669	0.555231748	0.777447742	0.073357498	0.777447742	0.042881398	p<0.05
: A_23_P6344	SDF2L1	0.753621598	0.968847645	0.777853568	0.169142461	0.777853568	0.043240618	p<0.05
: A_23_P156087	GHR	0.464643298	0.597327588	0.777870146	0.292135509	0.777870146	0.048360927	p<0.05
: A_23_P72271	IGLC2	0.384207061	0.493830603	0.778013874	0.082908871	0.778013874	0.011056677	p<0.05
: A_23_P211167	C21orf2	0.804418255	1.033019347	0.778705895	0.09326159	0.778705895	0.01207202	p<0.05
: A_23_P8083	LY6G6C	0.492350571	0.632001199	0.779034234	0.266837046	0.779034234	0.044229321	p<0.05
: A_23_P20573		0.443431991	0.56920604	0.77903599	0.128199104	0.77903599	0.011537399	p<0.05
: A_23_P88303	HSPA2	0.78206224	1.003837859	0.779072271	0.190841772	0.779072271	0.035690435	p<0.05
: A_23_P38545	NPB	0.366291527	0.470144733	0.779103756	0.104428111	0.779103756	0.017821856	p<0.05
: A_23_P211015	C21orf91	1.155360696	1.481451804	0.779884093	0.156682927	0.779884093	0.0466683	p<0.05
: A_23_P324490	KIAA0355	0.774389401	0.992462571	0.780270636	0.083362017	0.780270636	0.023366198	p<0.05
: A_23_P24294	SLC17A6	0.647472312	0.829279709	0.780764686	0.185056183	0.780764686	0.045536989	p<0.05
: A_23_P140142	BDKRB2	0.4441985	0.56884765	0.780874282	0.051092577	0.780874282	0.037210238	p<0.05
: A_23_P156471	CDC5L	1.183443688	1.51547983	0.780903622	0.117287783	0.780903622	0.02022139	p<0.05
: A_23_P129466	ATF7IP2	0.697935068	0.893427017	0.781188675	0.026050097	0.781188675	0.015804806	p<0.05
: A_23_P201918	ABCB10	1.660454899	2.125458963	0.78122181	0.195726598	0.78122181	0.0451223	p<0.05
: A_23_P79360	NOSTRIN	0.820591186	1.049922281	0.781573266	0.133639017	0.781573266	0.017995909	p<0.05
: A_23_P31176	FLJ11000	0.342616216	0.438326967	0.781645305	0.077430835	0.781645305	0.044629564	p<0.05
: A_23_P410746	LMTK2	0.683547791	0.874235769	0.781880375	0.015242717	0.781880375	0.031084481	p<0.05
: A_23_P164100	LOC124773	1.239293159	1.58458258	0.782094398	0.091714754	0.782094398	0.029316187	p<0.05
: A_23_P255091		1.017632462	1.300802135	0.782311494	0.023376693	0.782311494	0.025301521	p<0.05
: A_23_P593	SP192	1.048550728	1.339977635	0.782513603	0.20248509	0.782513603	0.019894499	p<0.05
: A_23_P41818	ZFR	1.442214359	1.842173418	0.782887401	0.28541537	0.782887401	0.0377181	p<0.05
: A_23_P139327	OR51E2	0.544820385	0.695802044	0.783010613	0.02476515	0.783010613	0.020418323	p<0.05
: A_23_P37994	TP53TG3	0.847833489	1.080635735	0.784569177	0.066923516	0.784569177	0.039782192	p<0.05
: A_23_P105313	EIF2B1	1.23908395	1.577764902	0.785341307	0.188849443	0.785341307	0.01379653	p<0.05
: A_23_P98173	PTPRCAP	0.301305952	0.383548302	0.785574986	0.187909396	0.785574986	0.030149743	p<0.05
: A_23_P150931	LIMR	0.31149548	0.396446259	0.785719307	0.077391086	0.785719307	0.012170582	p<0.05
: A_23_P15942	ELAC1	1.977248509	2.515190722	0.786122695	0.166421813	0.786122695	0.039563726	p<0.05
: A_23_P123022	YWHAG	0.857336199	1.090397394	0.786260315	0.166845672	0.786260315	0.039622949	p<0.05

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: A_23_P42565		0.752351245	0.956387558	0.786659382	0.062947862	0.786659382	0.022091432	p<0.05
: A_23_P502158	ADAM11	0.618412419	0.785653731	0.787131015	0.081193563	0.787131015	0.033652453	p<0.05
: A_23_P76192	LYZ	0.229453759	0.291426316	0.787347421	0.15828878	0.787347421	0.042084268	p<0.05
: A_23_P125333	ADK	1.240528697	1.574382556	0.787946165	0.129663757	0.787946165	0.022108862	p<0.05
: A_23_P216004	MSCP	0.461058715	0.585092248	0.788010294	0.040072871	0.788010294	0.032435611	p<0.05
: A_23_P161815	OR6T1	0.420659265	0.53366945	0.788239358	0.093949408	0.788239358	0.044718767	p<0.05
: A_23_P10513	TFDP3	1.244868632	1.577572991	0.789103667	0.023893343	0.789103667	0.012933556	p<0.05
: A_23_P159693		1.204059033	1.525339118	0.789371372	0.127761279	0.789371372	0.04200931	p<0.05
: A_23_P129602	PRSS21	0.402146088	0.50942949	0.789404808	0.199667509	0.789404808	0.033201273	p<0.05
: A_23_P155407	RTP1	0.839029228	1.062492899	0.789679844	0.032729054	0.789679844	0.025566627	p<0.05
: A_23_P141028	COX4I1	0.702704958	0.889525238	0.789977539	0.063371418	0.789977539	0.021578111	p<0.05
: A_23_P335920	RPS6KA2	0.732072349	0.92662725	0.790039737	0.163363421	0.790039737	0.035106708	p<0.05
: A_23_P163732	GGA2	0.486245569	0.615444473	0.7900722	0.095769129	0.7900722	0.0256493	p<0.05
: A_23_P140364	C14orf58	0.412484727	0.521855316	0.790419708	0.182742229	0.790419708	0.021118645	p<0.05
: A_23_P211083	IFNAR2	0.509431622	0.644115275	0.79090132	0.204438854	0.79090132	0.027649164	p<0.05
: A_23_P34396	NPD014	0.575946892	0.726918239	0.792313166	0.088506396	0.792313166	0.014871508	p<0.05
: A_23_P162776	FLJ10154	1.497732582	1.890310243	0.792321042	0.226025472	0.792321042	0.030368009	p<0.05
: A_23_P102664	ATP9A	0.945822209	1.193617494	0.792399754	0.063492667	0.792399754	0.047287089	p<0.05
: A_23_P341547	NKX2-8	0.917159815	1.156918859	0.792760709	0.100371851	0.792760709	0.048541582	p<0.05
: A_23_P13244	OR8U1	0.506999898	0.639384005	0.79295055	0.157828291	0.79295055	0.026822452	p<0.05
: A_23_P404108	KIAA1128	1.125867861	1.419455493	0.793168836	0.27391563	0.793168836	0.047873804	p<0.05
: A_23_P6849	CCR1	0.997343006	1.257142862	0.793341024	0.029412168	0.793341024	0.015215147	p<0.05
: A_23_P259201	FLJ10916	0.439706011	0.554112853	0.793531514	0.154179929	0.793531514	0.043806099	p<0.05
: A_23_P388331	BAGE	0.5521106	0.69542321	0.793920295	0.107932311	0.793920295	0.032442637	p<0.05
: A_23_P49972	CDC6	0.927462515	1.168193934	0.793928549	0.143045199	0.793928549	0.041957292	p<0.05
: A_23_P152984	THOC4	3.401764102	4.281080769	0.794604046	0.065002759	0.794604046	0.039338963	p<0.05
: A_23_P104970		0.865064927	1.088518754	0.794717523	0.051277456	0.794717523	0.042902113	p<0.05
: A_23_P29634	NCKIPSD	0.912427764	1.14733863	0.795255856	0.245388731	0.795255856	0.04705408	p<0.05
: A_23_P23783	MYOC	1.017943366	1.279793725	0.795396434	0.040244215	0.795396434	0.048741241	p<0.05
: A_23_P157835		0.541566154	0.680855713	0.795419857	0.101910225	0.795419857	0.03368166	p<0.05
: A_23_P46649		0.654569054	0.822029072	0.796284554	0.082254448	0.796284554	0.012490536	p<0.05
: A_23_P114783	PARP1	1.568910594	1.968593658	0.796970257	0.041325315	0.796970257	0.014352865	p<0.05
: A_23_P211459	ZNF278	0.880549911	1.104810347	0.79701454	0.152628945	0.79701454	0.025732349	p<0.05
: A_23_P51082		0.694049555	0.870642139	0.797169726	0.107470251	0.797169726	0.048151165	p<0.05
: A_23_P122600	UNQ3045	0.492573411	0.61763655	0.797513377	0.060673156	0.797513377	0.029028956	p<0.05
: A_23_P58031	RPL4	0.570856138	0.715736239	0.797578923	0.022487027	0.797578923	0.035972652	p<0.05
: A_23_P143184	MYBL2	0.481023882	0.602774887	0.798015796	0.216657272	0.798015796	0.024212752	p<0.05
: A_23_P171143	TM4SF6	1.244265637	1.558577033	0.798334385	0.130582362	0.798334385	0.015188598	p<0.05
: A_23_P101516	KCNC3	0.583590738	0.730555773	0.798831191	0.25452898	0.798831191	0.035899478	p<0.05
: A_23_P154915	C21orf105	0.670979927	0.839043264	0.799696459	0.1724765	0.799696459	0.035887534	p<0.05
: A_23_P388932	LOC220070	0.603174673	0.753632495	0.800356509	0.152565713	0.800356509	0.013940015	p<0.05
: A_23_P120252	DUSP22	0.605168169	0.756087523	0.800394333	0.112618991	0.800394333	0.037021302	p<0.05
: A_23_P343843	MGC16385	0.640198886	0.799547726	0.800701278	0.144013249	0.800701278	0.029388025	p<0.05
: A_23_P92824	APG10L	0.775347915	0.968038713	0.800947219	0.060656486	0.800947219	0.017739635	p<0.05
: A_23_P28201	ITSN2	0.453646133	0.566277756	0.801101805	0.191991058	0.801101805	0.029743325	p<0.05
: A_23_P330581	MGC14816	0.599887235	0.748055405	0.801928883	0.048772622	0.801928883	0.026942673	p<0.05
: A_23_P212968	UGT2B28	0.359592039	0.448386192	0.801969475	0.239235003	0.801969475	0.046665627	p<0.05
: A_23_P25638	C13orf7	1.175347256	1.465278033	0.802132585	0.148450237	0.802132585	0.046945828	p<0.05
: A_23_P213959	PPARGC1B	0.574054705	0.715321402	0.802512973	0.094840243	0.802512973	0.025533368	p<0.05
: A_23_P381505	FLJ14712	1.007836733	1.255846523	0.802515844	0.051786045	0.802515844	0.016089876	p<0.05
: A_23_P154954	PCQAP	0.411428305	0.51265415	0.802545546	0.191658226	0.802545546	0.020224473	p<0.05
: A_23_P70571	SLC39A7	0.48648378	0.605883684	0.80293263	0.077454005	0.80293263	0.018917338	p<0.05
: A_23_P202029	SPFH1	0.972382146	1.210434907	0.803332869	0.112941157	0.803332869	0.016641368	p<0.05

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: A_23_P206806	ITGAL	0.502691458	0.625175323	0.804080775	0.260408498	0.804080775	0.046112374	p<0.05
: A_23_P211550	RBX1	1.592853013	1.980906299	0.804103159	0.093500439	0.804103159	0.03113968	p<0.05
: A_23_P95200	CART1	0.498008017	0.619160583	0.804327715	0.051191657	0.804327715	0.015800339	p<0.05
: A_23_P2262	SURB7	1.34252504	1.66838677	0.804684539	0.174900213	0.804684539	0.037805685	p<0.05
: A_23_P122736	MAP7	0.479436263	0.595552992	0.805027041	0.033760021	0.805027041	0.018091073	p<0.05
: A_23_P141965	MGC20533	0.88697553	1.101066793	0.805560149	0.121000564	0.805560149	0.0386071	p<0.05
: A_23_P212440	WDR10	0.478270477	0.593369486	0.806024725	0.161047223	0.806024725	0.031018228	p<0.05
: A_23_P22499	GNL3L	0.344001279	0.426755848	0.806084511	0.089847913	0.806084511	0.014846299	p<0.05
: A_23_P426270		0.43865285	0.543700815	0.806790864	0.102146595	0.806790864	0.03160241	p<0.05
: A_23_P162007	CCKBR	0.50106531	0.620952669	0.806929957	0.039535137	0.806929957	0.018624613	p<0.05
: A_23_P170050	RIT2	0.87954863	1.089909809	0.806992123	0.139619744	0.806992123	0.049558383	p<0.05
: A_23_P98960	LOC144438	1.80126234	2.231600878	0.807161513	0.184221263	0.807161513	0.041543536	p<0.05
: A_23_P65370	C1orf87	1.630279583	2.019702823	0.807187851	0.116553376	0.807187851	0.035312855	p<0.05
: A_23_P4308	PLD2	0.782857187	0.969342858	0.807616398	0.077105142	0.807616398	0.024718395	p<0.05
: A_23_P77731	CRYM	0.511766879	0.633082858	0.808372668	0.092953118	0.808372668	0.010327081	p<0.05
: A_23_P16408		0.708132246	0.875985717	0.808383325	0.18090824	0.808383325	0.01576305	p<0.05
: A_23_P157022	DKFZp762l137	0.791741276	0.978747056	0.808933494	0.067894385	0.808933494	0.021894305	p<0.05
: A_23_P88033	FGF14	0.802913897	0.991192103	0.810048722	0.180171497	0.810048722	0.046207218	p<0.05
: A_23_P256260		0.552916301	0.682348441	0.810313717	0.084972735	0.810313717	0.046629246	p<0.05
: A_23_P116249	GRIK4	0.963383093	1.188515376	0.810576887	0.150999668	0.810576887	0.032906434	p<0.05
: A_23_P6321	CLDN5	0.377152191	0.464923097	0.811214142	0.073704499	0.811214142	0.02680108	p<0.05
: A_23_P27128	KLHL10	0.833149787	1.026548184	0.811603196	0.142277681	0.811603196	0.039987521	p<0.05
: A_23_P142527	COL3A1	0.56628553	0.697703376	0.811642238	0.097805651	0.811642238	0.024360727	p<0.05
: A_23_P200325	RABGAP1L	1.195776037	1.469280924	0.813851195	0.153353678	0.813851195	0.042701203	p<0.05
: A_23_P282	C1orf27	0.794040391	0.975222313	0.814214749	0.165813797	0.814214749	0.046342468	p<0.05
: A_23_P91104	KCNK3	0.498113232	0.611542467	0.814519447	0.225639121	0.814519447	0.042896628	p<0.05
: A_23_P217508	ZBED1	1.037529176	1.273671197	0.814597345	0.10043522	0.814597345	0.021522842	p<0.05
: A_23_P90732		1.399944711	1.718467277	0.814647291	0.132879702	0.814647291	0.018266586	p<0.05
: A_23_P22613	Sep-06	0.604414344	0.741582558	0.815033118	0.035667909	0.815033118	0.012185408	p<0.05
: A_23_P59285	GCM2	0.39261456	0.481711351	0.815041122	0.089456056	0.815041122	0.020787683	p<0.05
: A_23_P258633	TH	0.522751546	0.641293898	0.815151287	0.011435729	0.815151287	0.015647429	p<0.05
: A_23_P46068		0.340628952	0.417622519	0.815638373	0.152727398	0.815638373	0.042151335	p<0.05
: A_23_P98147	CPN1	0.620683927	0.760663655	0.815976842	0.102086629	0.815976842	0.020538798	p<0.05
: A_23_P105545	VAMP1	0.673321339	0.824510153	0.816631956	0.16348694	0.816631956	0.020538798	p<0.05
: A_23_P123039	NUPL2	1.343102246	1.642784588	0.817576605	0.155412103	0.817576605	0.038292066	p<0.05
: A_23_P2152	NDUFC2	1.072205829	1.311230219	0.817709822	0.146924501	0.817709822	0.047055653	p<0.05
: A_23_P69329	HYAL1	0.351193983	0.429388022	0.817894225	0.037315018	0.817894225	0.017456587	p<0.05
: A_23_P420431	MGC57211	0.512385119	0.625839894	0.818715975	0.205659528	0.818715975	0.031746634	p<0.05
: A_23_P81759	QKI	0.530593865	0.647857427	0.818997889	0.07494516	0.818997889	0.020748788	p<0.05
: A_23_P61738	LOC51204	0.530802168	0.648066804	0.819054709	0.099914517	0.819054709	0.013377143	p<0.05
: A_23_P58557	FLJ90650	0.538643011	0.657200737	0.819601958	0.220877439	0.819601958	0.037333399	p<0.05
: A_23_P167497	EFNA5	0.528953301	0.644697928	0.820466885	0.08197591	0.820466885	0.045273193	p<0.05
: A_23_P78656	VN1R4	0.742585476	0.905046463	0.820494313	0.181371815	0.820494313	0.047042345	p<0.05
: A_23_P207557	TCF2	0.441127456	0.537583501	0.820574767	0.015438308	0.820574767	0.016652165	p<0.05
: A_23_P150189	MRE11A	0.688069512	0.838097456	0.820989859	0.172618064	0.820989859	0.012974276	p<0.05
: A_23_P156811		0.475849741	0.579289348	0.821437064	0.154615938	0.821437064	0.020260667	p<0.05
: A_23_P112187	FIBCD1	0.406968175	0.494855064	0.822398727	0.079530109	0.822398727	0.017408068	p<0.05
: A_23_P163858	ZNRF1	1.084776681	1.318368958	0.82281722	0.046018621	0.82281722	0.011883083	p<0.05
: A_23_P49616	GK001	1.354750629	1.644785411	0.82366406	0.035902585	0.82366406	0.011629663	p<0.05
: A_23_P48299	CDADC1	0.458295394	0.556221221	0.82394446	0.266289423	0.82394446	0.042912059	p<0.05
: A_23_P342709	FBXO15	0.556120309	0.674871838	0.824038399	0.004600669	0.824038399	0.016473105	p<0.05
: A_23_P152755	FLJ21019	0.9024211	1.094921561	0.824187898	0.194825904	0.824187898	0.026276702	p<0.05
: A_23_P87730	POLR3B	0.496650015	0.601923237	0.825105237	0.109940575	0.825105237	0.0343134	p<0.05

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: A_23_P36205		0.836242344	1.013103485	0.825426381	0.045734744	0.825426381	0.044156172	p<0.05
: A_23_P200699		1.013428993	1.227412736	0.825662764	0.084013952	0.825662764	0.033869229	p<0.05
: A_23_P108734	ALLC	0.772999128	0.936213663	0.825665293	0.088079684	0.825665293	0.015612618	p<0.05
: A_23_P169989	ADCY8	0.60273807	0.729940483	0.825735911	0.166611562	0.825735911	0.021939038	p<0.05
: A_23_P80831	TMEM41A	0.599566083	0.725804928	0.826070559	0.036347262	0.826070559	0.01004381	p<0.05
: A_23_P81640	KIAA1909	0.535244982	0.647846599	0.826190927	0.051516325	0.826190927	0.01165946	p<0.05
: A_23_P124485	PTPN9	0.683071707	0.826517111	0.826445935	0.087768876	0.826445935	0.014060647	p<0.05
: A_23_P62588	CAGLP	0.535600407	0.647539654	0.827131441	0.085146879	0.827131441	0.029930615	p<0.05
: A_23_P314086	RNF126	1.090546671	1.318213743	0.827291231	0.101373211	0.827291231	0.018217461	p<0.05
: A_23_P76901	PLEKHG3	0.849182893	1.025686215	0.827916843	0.199235486	0.827916843	0.043205851	p<0.05
: A_23_P304509	C10orf72	0.810536469	0.97827624	0.828535372	0.130907788	0.828535372	0.0227412	p<0.05
: A_23_P217659	CXorf53	0.940970635	1.135366747	0.828781218	0.090939968	0.828781218	0.046597285	p<0.05
: A_23_P384056	FLJ12892	1.374747487	1.657386715	0.82946694	0.135751021	0.82946694	0.045494967	p<0.05
: A_23_P171007		1.064656473	1.282983662	0.829828551	0.023722318	0.829828551	0.01742351	p<0.05
: A_23_P89310	EPN2	0.607886482	0.732155124	0.830270065	0.106434001	0.830270065	0.020390316	p<0.05
: A_23_P319512	KLF11	0.559100121	0.673280269	0.830412158	0.051518104	0.830412158	0.011908017	p<0.05
: A_23_P403424	PLA2G4B	1.069577041	1.287475419	0.83075531	0.083318149	0.83075531	0.032515664	p<0.05
: A_23_P119578	KCNN1	0.378873257	0.455861203	0.831115379	0.124683027	0.831115379	0.038919955	p<0.05
: A_23_P211126	DYRK1A	1.210010266	1.454988997	0.831628465	0.176199337	0.831628465	0.042847815	p<0.05
: A_23_P22013	R-spondin	0.631154364	0.758893012	0.83167766	0.102122691	0.83167766	0.042048941	p<0.05
: A_23_P4782	CACNG7	0.632950554	0.760857068	0.831891535	0.094263254	0.831891535	0.019667173	p<0.05
: A_23_P87219	SLC22A8	0.460017392	0.552635555	0.832406435	0.04388268	0.832406435	0.01163736	p<0.05
: A_23_P42304	HLA-DMA	0.307233937	0.369071219	0.832451627	0.119755448	0.832451627	0.045656125	p<0.05
: A_23_P321913	DEF6	0.425895843	0.511560773	0.832542027	0.117936272	0.832542027	0.042919826	p<0.05
: A_23_P210827	C20orf36	1.111035224	1.334214479	0.832726103	0.171333182	0.832726103	0.014821567	p<0.05
: A_23_P90612	MCM6	1.65597282	1.988349327	0.832837972	0.071757136	0.832837972	0.035744958	p<0.05
: A_23_P103756	OVGP1	0.482058048	0.578606144	0.833136761	0.081200139	0.833136761	0.028128044	p<0.05
: A_23_P217727		0.881485703	1.057906095	0.833236246	0.159258872	0.833236246	0.035013663	p<0.05
: A_23_P152428	MARVELD3	0.415415306	0.498353071	0.833576293	0.02666999	0.833576293	0.020575223	p<0.05
: A_23_P72434		0.856615074	1.027463147	0.833718539	0.204585109	0.833718539	0.02795477	p<0.05
: A_23_P136123	FRMD3	0.544872517	0.653525629	0.833743152	0.114934656	0.833743152	0.0285498	p<0.05
: A_23_P217218	KCND1	0.521438768	0.624711766	0.834686964	7.19793E-04	0.834686964	0.022685684	p<0.05
: A_23_P400406	LOC134548	0.520386282	0.623349624	0.834822485	0.085108781	0.834822485	0.04950298	p<0.05
: A_23_P206598		0.725025969	0.868262579	0.835030768	0.100145663	0.835030768	0.023315562	p<0.05
: A_23_P416821	MGC42090	1.681376007	2.013273683	0.835145276	0.077331206	0.835145276	0.02679809	p<0.05
: A_23_P161237	GBF1	1.225472003	1.465795082	0.836045923	0.176352726	0.836045923	0.045053905	p<0.05
: A_23_P70278	ROS1	0.569005497	0.680343301	0.836350554	0.00574889	0.836350554	0.012363585	p<0.05
: A_23_P101642	PTPRH	0.402366709	0.480479108	0.837428105	0.247687432	0.837428105	0.045879193	p<0.05
: A_23_P132428	MYLK	0.927449971	1.107452687	0.837462387	0.123827795	0.837462387	0.041030955	p<0.05
: A_23_P337753	LOC93349	0.801311024	0.956601598	0.837664317	0.0844771	0.837664317	0.027158774	p<0.05
: A_23_P89365	FMNL1	0.670320445	0.800199043	0.837692136	0.020369337	0.837692136	0.045843417	p<0.05
: A_23_P267	PIN1L	0.500566548	0.597369161	0.837951773	0.099163727	0.837951773	0.034924929	p<0.05
: A_23_P133868	ZNF307	0.470956354	0.561662864	0.838503636	0.105527297	0.838503636	0.012726543	p<0.05
: A_23_P61987	MGC4659	0.470139975	0.560136548	0.83933101	0.12686478	0.83933101	0.028907945	p<0.05
: A_23_P105908	ATP11A	0.827342212	0.985454727	0.839553751	0.075703633	0.839553751	0.019148703	p<0.05
: A_23_P435987	ILF3	0.520014356	0.619071579	0.839990679	0.088236196	0.839990679	0.02682014	p<0.05
: A_23_P55544	CCBE1	0.780805163	0.928571703	0.840866849	0.08111358	0.840866849	0.035389932	p<0.05
: A_23_P136724		0.762243199	0.905629877	0.841671877	0.120671142	0.841671877	0.033198278	p<0.05
: A_23_P305761	PHF12	0.933587494	1.108966561	0.841853602	0.13677507	0.841853602	0.033040874	p<0.05
: A_23_P60627	ALOX15B	0.858183426	1.018342758	0.842725515	0.079056747	0.842725515	0.037419344	p<0.05
: A_23_P206413	WWOX	0.618161767	0.733438224	0.842827313	0.066430045	0.842827313	0.014506255	p<0.05
: A_23_P77371	CNOT1	1.287239487	1.526635822	0.843187005	0.183751979	0.843187005	0.049025546	p<0.05
: A_23_P89249	ERBB2	0.567742929	0.673228082	0.84331439	0.051856472	0.84331439	0.011376472	p<0.05

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: A_23_P122077	C2GNT3	0.555574148	0.658014093	0.844319527	0.222692805	0.844319527	0.024496748	p<0.05
: A_23_P125990	E2F2	0.573221888	0.678497271	0.844840373	0.034914744	0.844840373	0.020677283	p<0.05
: A_23_P39550	DKFZP566N034	1.058745296	1.25262524	0.845221111	0.112784472	0.845221111	0.023184447	p<0.05
: A_23_P65617	TGM1	0.470263551	0.556149699	0.84557009	0.035609037	0.84557009	0.014216123	p<0.05
: A_23_P218170	SMAP-1	0.472574946	0.558771243	0.845739562	0.115713898	0.845739562	0.033198125	p<0.05
: A_23_P324931	TNK2	0.763926124	0.901943218	0.846978068	0.123812001	0.846978068	0.029635818	p<0.05
: A_23_P3562	FLJ13291	1.021310533	1.205160484	0.847447744	0.090129039	0.847447744	0.021585318	p<0.05
: A_23_P56978	PTK6	0.564595117	0.66490963	0.849130607	0.056106612	0.849130607	0.024971566	p<0.05
: A_23_P396765	PGM2L1	0.914045518	1.074991013	0.850282009	0.109387519	0.850282009	0.043725682	p<0.05
: A_23_P250528		0.432136833	0.507810021	0.850981301	0.156006007	0.850981301	0.041115127	p<0.05
: A_23_P87653	KRT6A	0.443427944	0.520978693	0.851144106	0.134361487	0.851144106	0.022556205	p<0.05
: A_23_P428840	LOC93109	0.526884829	0.618858805	0.851381325	0.014612045	0.851381325	0.013723952	p<0.05
: A_23_P163997	SENP3	0.798056676	0.937283918	0.851456704	0.136558187	0.851456704	0.036633192	p<0.05
: A_23_P40516	STK22B	0.588664602	0.689942268	0.853208492	0.213893226	0.853208492	0.032127149	p<0.05
: A_23_P161257	PDCD11	0.634163636	0.743051672	0.853458325	0.146523445	0.853458325	0.022372573	p<0.05
: A_23_P43504	ABCA2	0.412688109	0.483526784	0.853495861	0.109650315	0.853495861	0.033538428	p<0.05
: A_23_P155582		0.800099781	0.937192388	0.853719889	0.047036881	0.853719889	0.038904837	p<0.05
: A_23_P96271	MYOM1	0.636889502	0.745523696	0.854284719	0.190297518	0.854284719	0.031683225	p<0.05
: A_23_P61318	GDDR	0.488381447	0.571039778	0.855249434	0.192143039	0.855249434	0.036936107	p<0.05
: A_23_P168669	CROT	0.438341653	0.512464834	0.855359477	0.193601275	0.855359477	0.047115074	p<0.05
: A_23_P115792	PLEKHA1	0.896493414	1.047801084	0.855595043	0.172955292	0.855595043	0.040890449	p<0.05
: A_23_P26674		0.849066665	0.992260015	0.85568969	0.260435387	0.85568969	0.046184602	p<0.05
: A_23_P370682	MGC20410	0.904206541	1.055751128	0.856458039	0.013254217	0.856458039	0.024238796	p<0.05
: A_23_P401472	CHRM3	0.471760434	0.550339423	0.857217226	0.043969994	0.857217226	0.038316954	p<0.05
: A_23_P411188	CHRNA10	0.702293333	0.819005465	0.857495295	0.090893466	0.857495295	0.038774198	p<0.05
: A_23_P23837	LGR6	0.430176086	0.50159287	0.857620017	0.022644684	0.857620017	0.035249279	p<0.05
: A_23_P98115	KIAA0514	0.61048093	0.710943315	0.858691427	0.107375933	0.858691427	0.018877373	p<0.05
: A_23_P203231	ABCG4	0.518355421	0.603401014	0.859056264	0.102667917	0.859056264	0.022969682	p<0.05
: A_23_P38978		0.460201937	0.534719126	0.860642371	0.049926075	0.860642371	0.042579387	p<0.05
: A_23_P148475	KIF4A	0.776423203	0.901461767	0.861293547	0.030906598	0.861293547	0.010407997	p<0.05
: A_23_P143621	CRYBB1	0.550676797	0.639054299	0.861705802	0.091995716	0.861705802	0.030359396	p<0.05
: A_23_P97112	SELE	0.983718218	1.140929332	0.862207843	0.168662917	0.862207843	0.044774034	p<0.05
: A_23_P330561	LOC199675	0.361325445	0.418920742	0.862515051	0.067428223	0.862515051	0.030422542	p<0.05
: A_23_P27450	APOC4	0.465790321	0.539792501	0.862906246	0.065732553	0.862906246	0.022378345	p<0.05
: A_23_P318860	AGTRL1	0.448341129	0.518296237	0.865028718	0.042527213	0.865028718	0.022992235	p<0.05
: A_23_P30633	BACH2	0.72393202	0.836443047	0.865488717	0.087643558	0.865488717	0.041025418	p<0.05
: A_23_P75677	OR8A1	0.884101727	1.019053728	0.86757126	0.082417129	0.86757126	0.044839619	p<0.05
: A_23_P29378	RNF13	0.807177005	0.929988627	0.867942878	0.050748815	0.867942878	0.023915796	p<0.05
: A_23_P141555	TBX21	0.703306997	0.809844338	0.868447137	0.137400127	0.868447137	0.041151673	p<0.05
: A_23_P171188	VCX2	0.560078273	0.644595506	0.868883304	0.047617251	0.868883304	0.011363905	p<0.05
: A_23_P168882	TP53INP1	0.709259444	0.815829275	0.869372386	0.070609787	0.869372386	0.024620374	p<0.05
: A_23_P90058	BIRC8	1.141106286	1.312192303	0.869618183	0.117116343	0.869618183	0.019846494	p<0.05
: A_23_P18202	SRISNF2L	0.564815426	0.649333252	0.86983906	0.070183128	0.86983906	0.038335123	p<0.05
: A_23_P211829	MGC11349	0.927973145	1.066164666	0.870384449	0.108171909	0.870384449	0.048757641	p<0.05
: A_23_P62128	MTM1	1.101047943	1.264926201	0.870444412	0.059331115	0.870444412	0.036661224	p<0.05
: A_23_P125705	NAP1L2	0.722440043	0.829512146	0.870921598	0.15700786	0.870921598	0.039488669	p<0.05
: A_23_P5070	IGSF4C	0.531672368	0.610056957	0.871512671	0.126990987	0.871512671	0.036537625	p<0.05
: A_23_P214511		0.952967863	1.093311224	0.871634573	0.094382831	0.871634573	0.030615415	p<0.05
: A_23_P18186	GNB4	0.449003857	0.514834805	0.872131901	0.028265402	0.872131901	0.027850679	p<0.05
: A_23_P77813	FN3KRP	0.940283971	1.07733805	0.872784518	0.034662381	0.872784518	0.016222659	p<0.05
: A_23_P402670	CD1A	0.744135044	0.852514464	0.872870873	0.073734499	0.872870873	0.03494982	p<0.05
: A_23_P384600	IPO13	0.683538509	0.782935949	0.873045247	0.042911029	0.873045247	0.019454989	p<0.05
: A_23_P44054		0.512636659	0.586828315	0.873571785	0.053507535	0.873571785	0.043577519	p<0.05

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: A_23_P35970	SLC37A4	0.549400582	0.627909115	0.874968318	0.102724337	0.874968318	0.029768917	p<0.05
: A_23_P136054	ATR	1.439872228	1.645524637	0.875023196	0.189292493	0.875023196	0.029416163	p<0.05
: A_23_P416581	GNAZ	0.653004646	0.74584432	0.875524057	0.00410227	0.875524057	0.024041931	p<0.05
: A_23_P168909	ZFPM2	0.865775001	0.988783864	0.875595803	0.070392694	0.875595803	0.015435305	p<0.05
: A_23_P351270	PAPPA	0.686674031	0.784212164	0.875622775	0.078002769	0.875622775	0.010512195	p<0.05
: A_23_P502782	BVES	0.543892716	0.619679814	0.877699587	0.051152314	0.877699587	0.033753117	p<0.05
: A_23_P100177	MMP15	0.785947315	0.893946562	0.879188252	0.107315268	0.879188252	0.036366583	p<0.05
: A_23_P161253	SFXN2	0.970203995	1.102981682	0.879619318	0.088616721	0.879619318	0.029299732	p<0.05
: A_23_P204712	AQP6	0.791440045	0.899210498	0.880149916	0.071515352	0.880149916	0.025158658	p<0.05
: A_23_P54075	OR6S1	0.477999192	0.543027966	0.880247835	0.057779809	0.880247835	0.017099863	p<0.05
: A_23_P115805	C10orf94	0.783896506	0.889904419	0.880877193	0.171174621	0.880877193	0.039397194	p<0.05
: A_23_P81401	SQSTM1	0.714700983	0.810068989	0.882271749	0.205462973	0.882271749	0.036225952	p<0.05
: A_23_P113972	SEC3L1	0.470351842	0.532170404	0.883836903	0.095680747	0.883836903	0.01850592	p<0.05
: A_23_P104867		0.702006575	0.792971754	0.885285726	0.143896815	0.885285726	0.015179205	p<0.05
: A_23_P53119	OR52J3	0.727991606	0.822297589	0.885314047	0.053439172	0.885314047	0.017488087	p<0.05
: A_23_P71140	POLD2	0.964861441	1.085318549	0.889012209	0.04368501	0.889012209	0.032497415	p<0.05
: A_23_P93937	KIAA0363	0.455888686	0.512729823	0.889140177	0.122364833	0.889140177	0.038813079	p<0.05
: A_23_P51479	INSL5	0.652673249	0.73350386	0.889802065	0.050860068	0.889802065	0.020344676	p<0.05
: A_23_P8133	ZNF76	0.495807125	0.557200656	0.889817913	6.80945E-04	0.889817913	0.034353184	p<0.05
: A_23_P255418	SOX18	0.58706921	0.658756395	0.891178005	0.139439596	0.891178005	0.048379117	p<0.05
: A_23_P65388	C14orf27	0.637797276	0.715266632	0.891691639	0.018800667	0.891691639	0.01891479	p<0.05
: A_23_P10091		0.446660702	0.500316178	0.892756864	0.042923397	0.892756864	0.046988143	p<0.05
: A_23_P386254	BAPX1	0.862956885	0.965243474	0.894030271	0.074405781	0.894030271	0.030388801	p<0.05
: A_23_P145024	ADRB2	0.590384587	0.658935687	0.895966935	0.200437071	0.895966935	0.040762813	p<0.05
: A_23_P1575	TRIM49	0.686638463	0.765990389	0.896406108	0.214990051	0.896406108	0.037769217	p<0.05
: A_23_P257263	ODZ1	0.697119682	0.776737248	0.897497428	0.026760445	0.897497428	0.024035426	p<0.05
: A_23_P155348	BTB	0.741122276	0.823952932	0.899471616	0.127972566	0.899471616	0.020225066	p<0.05
: A_23_P315964	UMODL1	0.95206288	1.057889475	0.899964413	0.218380479	0.899964413	0.016936535	p<0.05
: A_23_P414913	C9orf19	0.466757121	0.518140378	0.900831398	0.05754414	0.900831398	0.04430459	p<0.05
: A_23_P348253	FLJ23834	0.66491054	0.736299527	0.903043552	0.091977924	0.903043552	0.045040454	p<0.05
: A_23_P19352	TNRC5	0.59065297	0.65391936	0.903250471	0.10818497	0.903250471	0.027988044	p<0.05
: A_23_P33429		0.749272409	0.829298474	0.903501492	0.118657576	0.903501492	0.039399702	p<0.05
: A_23_P23617	DKFZP434H2010	0.588634237	0.650875165	0.904373478	0.055183195	0.904373478	0.013924546	p<0.05
: A_23_P161156	LOC220929	0.838913498	0.926195123	0.905763242	0.096811448	0.905763242	0.035982736	p<0.05
: A_23_P86250	PIGC	0.72501502	0.799489302	0.906847681	0.151577619	0.906847681	0.028796012	p<0.05
: A_23_P99498		0.703174505	0.7744364	0.90798225	0.117759219	0.90798225	0.030249617	p<0.05
: A_23_P208158	DTNA	0.664943487	0.726770417	0.914929215	0.162355359	0.914929215	0.048350157	p<0.05
: A_23_P354320	GPR161	0.754058354	0.823893848	0.915237268	0.174285244	0.915237268	0.047061223	p<0.05
: A_23_P254594	GNRH1	0.678495914	0.736547569	0.921184106	0.063295417	0.921184106	0.013045633	p<0.05
: A_23_P89649	KRTAP3-3	0.848562484	0.91525035	0.927137023	0.087038477	0.927137023	0.018778138	p<0.05
: A_23_P130496		0.900260045	0.967458054	0.930541682	0.074597531	0.930541682	0.036985802	p<0.05
: A_23_P66758	RIP	1.254932948	1.334971173	0.940044978	0.135617716	0.940044978	0.049789123	p<0.05
: A_23_P114259	ASB11	1.01061644	0.957546453	1.055422885	0.041544027	1.055422885	0.044606111	p<0.05
: A_23_P81273		1.847917135	1.707289757	1.082368782	0.072746428	1.082368782	0.044338709	p<0.05
: A_23_P125286	OR52A1	0.992236049	0.900838282	1.101458573	0.092846658	1.101458573	0.025273178	p<0.05
: A_23_P107531	LOXHD1	1.116362746	1.011835334	1.103304766	0.121420148	1.103304766	0.049227848	p<0.05
: A_23_P98282	SPTBN2	0.865669532	0.781429662	1.107802243	0.057010148	1.107802243	0.045841805	p<0.05
: A_23_P24044	CNNM2	2.436952648	2.196615952	1.109412251	0.132748238	1.109412251	0.046642119	p<0.05
: A_23_P119068	ZNF71	0.545127413	0.490991666	1.110257976	0.146008402	1.110257976	0.049726238	p<0.05
: A_23_P17786	PITPNB	0.84351494	0.755731409	1.11615705	0.050547127	1.11615705	0.041157537	p<0.05
: A_23_P253062	ANAPC2	0.77706733	0.695652614	1.11703358	0.079972241	1.11703358	0.023453011	p<0.05
: A_23_P154561	SLC32A1	0.694449721	0.621571049	1.117249142	0.17184054	1.117249142	0.044479586	p<0.05
: A_23_P28964	C20orf178	0.668735841	0.597462277	1.119293831	0.101737065	1.119293831	0.037073606	p<0.05

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: A_23_P2258	TSP-NY	1.271049608	1.127107509	1.127709289	0.1307096	1.127709289	0.035967432	p<0.05
: A_23_P256021	FLJ12525	0.776324692	0.687337733	1.129466133	0.135984649	1.129466133	0.032256226	p<0.05
: A_23_P112645	ABO	1.224353917	1.083817552	1.129667917	0.067695056	1.129667917	0.038232658	p<0.05
: A_23_P208409	ADCK4	1.428131899	1.263723956	1.130097987	0.101807748	1.130097987	0.033606754	p<0.05
: A_23_P69229	FLJ22405	0.887731875	0.785200399	1.130580009	0.017805679	1.130580009	0.04772658	p<0.05
: A_23_P169341		0.878157713	0.774785407	1.133420563	0.244475886	1.133420563	0.029788694	p<0.05
: A_23_P28181	PTHR2	1.307205472	1.152913148	1.133828228	0.099743713	1.133828228	0.045520794	p<0.05
: A_23_P97221	LOC51058	0.720975443	0.635009792	1.13537689	0.076503947	1.13537689	0.045972885	p<0.05
: A_23_P72359		0.511627817	0.45021576	1.136405838	0.047750143	1.136405838	0.044473996	p<0.05
: A_23_P166491	RUTBC3	0.96005754	0.844138439	1.137322382	0.110200137	1.137322382	0.02913673	p<0.05
: A_23_P58102	EXOSC7	0.826931839	0.726696635	1.137932665	0.093975794	1.137932665	0.017421665	p<0.05
: A_23_P46560	FOX3	0.521642712	0.457274454	1.140765042	0.021612792	1.140765042	0.013317632	p<0.05
: A_23_P4678	ERF	2.002512931	1.755135492	1.140944924	0.113875674	1.140944924	0.04215065	p<0.05
: A_23_P27571	MCOLN1	0.892362441	0.781580338	1.141741159	0.083162868	1.141741159	0.010690963	p<0.05
: A_23_P313010	FLJ38377	1.289290585	1.127079705	1.143921392	0.124318293	1.143921392	0.036375003	p<0.05
: A_23_P57036	CD40	0.566675568	0.495370026	1.143943998	0.163868834	1.143943998	0.045297007	p<0.05
: A_23_P150080	RPP38	1.348024602	1.175704465	1.146567561	0.089813131	1.146567561	0.016388714	p<0.05
: A_23_P43726	NUP160	1.403588166	1.223195832	1.14747625	0.056130104	1.14747625	0.010903798	p<0.05
: A_23_P101684	CLC	0.868969546	0.75719203	1.147621093	0.032738026	1.147621093	0.026551369	p<0.05
: A_23_P214594	RPP21	1.24773016	1.086314003	1.148590699	0.016734004	1.148590699	0.010660415	p<0.05
: A_23_P114903	HSPA6	0.646808445	0.562797629	1.14927358	0.007013168	1.14927358	0.045353263	p<0.05
: A_23_P98273	MAP3K11	0.854468936	0.743412381	1.149387551	0.007112737	1.149387551	0.030652974	p<0.05
: A_23_P62981	TBX15	0.511412536	0.444823056	1.149698803	0.053300337	1.149698803	0.02606659	p<0.05
: A_23_P100788	STAT5B	0.629028837	0.546424659	1.151172128	0.040069981	1.151172128	0.011606357	p<0.05
: A_23_P23673		1.098341795	0.952539347	1.153067114	0.010965377	1.153067114	0.023360023	p<0.05
: A_23_P130064	EAP30	1.208225678	1.047347713	1.153605114	0.115570133	1.153605114	0.034315342	p<0.05
: A_23_P133087		1.164587273	1.009454939	1.153679306	0.055276702	1.153679306	0.031605047	p<0.05
: A_23_P388081	RYK	2.157050076	1.868016552	1.154727496	0.057497456	1.154727496	0.047080178	p<0.05
: A_23_P361542	RCP9	2.056449943	1.779387313	1.155706758	0.146235509	1.155706758	0.044537289	p<0.05
: A_23_P22001	RYK	2.094055093	1.810296572	1.15674698	0.042969986	1.15674698	0.039046392	p<0.05
: A_23_P303833	SCN4B	0.640630395	0.55369338	1.157012921	0.108642751	1.157012921	0.030096639	p<0.05
: A_23_P51861	DUSP10	0.626976937	0.5417773	1.157259519	0.077098281	1.157259519	0.011264102	p<0.05
: A_23_P9186	ACTL7B	0.830863655	0.71792711	1.157309207	0.147174139	1.157309207	0.041761769	p<0.05
: A_23_P211079	OLIG2	1.690819564	1.460219092	1.157921831	0.026049546	1.157921831	0.028696592	p<0.05
: A_23_P50000	CT120	1.155512848	0.997402406	1.158522219	0.107352724	1.158522219	0.047556357	p<0.05
: A_23_P33326		1.030553004	0.889261701	1.158886077	0.033498105	1.158886077	0.033791633	p<0.05
: A_23_P78682	FARSLA	1.055418268	0.910542151	1.159109731	0.124990308	1.159109731	0.048392253	p<0.05
: A_23_P69129		2.391629054	2.063291302	1.159133008	0.08724545	1.159133008	0.046035667	p<0.05
: A_23_P56450	CAPN14	0.661677385	0.570560835	1.159696468	0.180972962	1.159696468	0.049859777	p<0.05
: A_23_P114857	PLA2G2E	0.727631527	0.62736724	1.159817537	0.073210544	1.159817537	0.010121219	p<0.05
: A_23_P417294	C21orf86	0.711712637	0.613102495	1.160837941	2.85196E-04	1.160837941	0.029124807	p<0.05
: A_23_P7901	TTL2	0.763211467	0.657364447	1.161017256	0.012746669	1.161017256	0.017900253	p<0.05
: A_23_P31437	CYP2W1	0.67779354	0.583653856	1.16129369	0.164267898	1.16129369	0.038328765	p<0.05
: A_23_P211699	CCR8	1.585724591	1.364838186	1.161840728	0.064400045	1.161840728	0.034975372	p<0.05
: A_23_P35667	ZNFN1A5	3.364239518	2.893819066	1.162560423	0.159674017	1.162560423	0.021320932	p<0.05
: A_23_P345708	FLJ35155	1.340674821	1.153121527	1.162648332	0.107572176	1.162648332	0.046661104	p<0.05
: A_23_P308097	PPP2CB	1.427303778	1.226475976	1.163743771	0.066409276	1.163743771	0.039632542	p<0.05
: A_23_P207614	KIAA0100	0.904596552	0.776971038	1.164260324	0.057027686	1.164260324	0.019878982	p<0.05
: A_23_P114895		1.057047548	0.907747552	1.164473036	0.161954743	1.164473036	0.032217005	p<0.05
: A_23_P128432	DKFZP586A0522	2.051567978	1.761096587	1.164937797	0.030382789	1.164937797	0.047800915	p<0.05
: A_23_P214839	MAK	1.17284554	1.006751406	1.164980285	0.022645907	1.164980285	0.01674686	p<0.05
: A_23_P96976	PS1D	0.74014029	0.633930188	1.167542268	0.138441578	1.167542268	0.022940853	p<0.05
: A_23_P44380	EMR4	1.043380485	0.89256517	1.168968407	0.046069619	1.168968407	0.031383481	p<0.05

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: A_23_P11136	SYTL4	0.739980249	0.632821728	1.169334452	0.055103516	1.169334452	0.020005361	p<0.05
: A_23_P15202	DHODH	1.714449817	1.465552489	1.169831739	0.128735319	1.169831739	0.044913497	p<0.05
: A_23_P91885	LOC116441	1.110778549	0.949083349	1.170369863	0.011918372	1.170369863	0.025531402	p<0.05
: A_23_P202769	DNAJC4	0.712819883	0.608900556	1.170667159	0.153670164	1.170667159	0.039506965	p<0.05
: A_23_P63534	XPR1	1.77471991	1.515230006	1.171254465	0.202181638	1.171254465	0.014025273	p<0.05
: A_23_P3527	POLR2C	1.677770333	1.431139236	1.172332007	0.100324523	1.172332007	0.045544479	p<0.05
: A_23_P387722	SFXN4	1.426896705	1.216845896	1.172619072	0.180713859	1.172619072	0.045620454	p<0.05
: A_23_P350093	CRK7	2.575553036	2.196402815	1.172623263	0.148240701	1.172623263	0.033325438	p<0.05
: A_23_P17655	KCNJ15	2.195520661	1.871571834	1.173089176	0.106153642	1.173089176	0.047793869	p<0.05
: A_23_P79416	FBXO11	1.544297251	1.316252328	1.173253197	0.297256891	1.173253197	0.036552986	p<0.05
: A_23_P150590	SLC22A9	1.325274096	1.129554218	1.173271787	0.141660602	1.173271787	0.04260543	p<0.05
: A_23_P66497	CACNG5	0.451176396	0.38448894	1.173444407	0.124050662	1.173444407	0.0137068	p<0.05
: A_23_P255038	IL1RAPL2	1.516908334	1.292594709	1.173537478	0.099915638	1.173537478	0.018268603	p<0.05
: A_23_P377197	MRAS	2.69566745	2.294648061	1.174762917	0.103779605	1.174762917	0.023290062	p<0.05
: A_23_P203737	MGC16733	1.755764669	1.492852777	1.176113744	0.095644206	1.176113744	0.042959877	p<0.05
: A_23_P343366	FLJ38716	2.060419673	1.751728332	1.176221012	0.149749745	1.176221012	0.04708786	p<0.05
: A_23_P106061	TRA@	0.773682557	0.65765572	1.176424889	0.141419135	1.176424889	0.016631916	p<0.05
: A_23_P98244	MGC11134	0.739038686	0.627916494	1.176969697	0.112271068	1.176969697	0.022496997	p<0.05
: A_23_P14464	SEC10L1	0.818585836	0.695309432	1.177297183	0.158200823	1.177297183	0.042057251	p<0.05
: A_23_P389569	SEZ6	0.818912757	0.695187973	1.177973135	0.087097609	1.177973135	0.016243607	p<0.05
: A_23_P92476	GRPEL1	0.722611833	0.613341236	1.178156285	0.179425124	1.178156285	0.040172068	p<0.05
: A_23_P138125	TOSO	0.428037645	0.363272572	1.178282311	0.025676046	1.178282311	0.023951807	p<0.05
: A_23_P78554	FBXL12	1.340528832	1.13751902	1.17846718	0.009585959	1.17846718	0.045566001	p<0.05
: A_23_P1102	ACTA1	1.610919505	1.366861671	1.178553426	0.095435537	1.178553426	0.01958176	p<0.05
: A_23_P92754	FGFR4	0.784424325	0.665331935	1.178996954	0.107846749	1.178996954	0.042459348	p<0.05
: A_23_P170209	TCBA1	3.763201649	3.189384724	1.179914615	0.066303215	1.179914615	0.037911932	p<0.05
: A_23_P144704	FLJ10246	0.532656769	0.45138185	1.180058013	0.102898864	1.180058013	0.032771568	p<0.05
: A_23_P158533	DEAF1	1.447414855	1.224952737	1.181608735	0.07572786	1.181608735	0.010566899	p<0.05
: A_23_P29296		0.908034153	0.767395845	1.183266966	0.128844549	1.183266966	0.037325862	p<0.05
: A_23_P252936	SLC9A8	1.745768923	1.475275055	1.183351482	0.087370484	1.183351482	0.026071641	p<0.05
: A_23_P416234	MS4A6E	0.743449555	0.628158908	1.183537389	0.224198296	1.183537389	0.040075234	p<0.05
: A_23_P364517	SELK	1.27165402	1.073723168	1.184340674	0.145710867	1.184340674	0.03254379	p<0.05
: A_23_P98598	SCGB1D4	1.161167185	0.979985009	1.1848826	0.006589721	1.1848826	0.042639874	p<0.05
: A_23_P210872	TM9SF4	0.808341676	0.682049856	1.185165086	0.039850521	1.185165086	0.017601742	p<0.05
: A_23_P47004	DHX32	2.183810163	1.842122254	1.185486011	0.085957096	1.185486011	0.017366956	p<0.05
: A_23_P49646	PRPSAP2	1.118405693	0.942984425	1.186027747	0.133858243	1.186027747	0.04326004	p<0.05
: A_23_P2294	HELB	1.606683527	1.354056398	1.18657061	0.144813859	1.18657061	0.046188665	p<0.05
: A_23_P92802	LTC4S	0.404266781	0.340679653	1.186647861	0.192864878	1.186647861	0.022418744	p<0.05
: A_23_P155868	PGRMC2	1.109838187	0.934681026	1.187397793	0.06826259	1.187397793	0.024057076	p<0.05
: A_23_P23266	BLZF1	1.259740898	1.05875957	1.189827165	0.175214228	1.189827165	0.042154417	p<0.05
: A_23_P81247	NDFIP1	1.643703946	1.381019202	1.190210783	0.248797923	1.190210783	0.028544184	p<0.05
: A_23_P141479	SUPT6H	0.638473434	0.536381223	1.19033517	0.02245622	1.19033517	0.036056455	p<0.05
: A_23_P259344	CECR6	2.466258154	2.069803941	1.191541916	0.162374993	1.191541916	0.038251032	p<0.05
: A_23_P2006	CNGA4	1.029146796	0.863672872	1.191593287	0.057638012	1.191593287	0.049878302	p<0.05
: A_23_P117447	C14orf119	1.427748439	1.197989947	1.191786661	0.15322746	1.191786661	0.03169296	p<0.05
: A_23_P17984		2.214481094	1.857868356	1.191947259	0.197216775	1.191947259	0.043540755	p<0.05
: A_23_P126225	PAX7	0.85185332	0.714610786	1.192052143	0.164296959	1.192052143	0.043317968	p<0.05
: A_23_P391725	DR1	1.937893598	1.624102903	1.193208629	0.118714847	1.193208629	0.041141021	p<0.05
: A_23_P17144	XAB1	1.612911309	1.3511361	1.193744515	0.218908029	1.193744515	0.038696374	p<0.05
: A_23_P126508	BMP8A	1.218015544	1.020295147	1.193787452	0.061444384	1.193787452	0.027107549	p<0.05
: A_23_P96931	C1orf26	0.941343821	0.788012289	1.194580128	0.283494067	1.194580128	0.034592984	p<0.05
: A_23_P129225	TRPM1	1.45571963	1.21858341	1.194599909	0.066732184	1.194599909	0.01446085	p<0.05
: A_23_P7005	ALG3	1.563451244	1.308236243	1.195083267	0.090593126	1.195083267	0.026146227	p<0.05

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: A_23_P36057	OR5D14	2.102623956	1.758900125	1.195419755	0.107870035	1.195419755	0.023474925	p<0.05
: A_23_P108761	C2orf29	1.267339806	1.06003457	1.195564599	0.094356159	1.195564599	0.010534939	p<0.05
: A_23_P44177	MGC26717	1.422325654	1.188940048	1.196297203	0.050552188	1.196297203	0.012352327	p<0.05
: A_23_P207088	SHBG	0.785185447	0.656309128	1.19636527	0.275862172	1.19636527	0.04517192	p<0.05
: A_23_P111737	RAMP3	1.286753571	1.075350335	1.196590106	0.088791931	1.196590106	0.020751019	p<0.05
: A_23_P157996	OR1J2	0.95185328	0.794775851	1.197637396	0.085923595	1.197637396	0.017422551	p<0.05
: A_23_P126207	CLSPN	1.418552852	1.184196436	1.197903328	0.208800417	1.197903328	0.049545905	p<0.05
: A_23_P161125	MOV10	1.56110083	1.302769238	1.198294207	0.079702914	1.198294207	0.017008258	p<0.05
: A_23_P155997		0.856441353	0.714667086	1.198378055	0.162974524	1.198378055	0.022244932	p<0.05
: A_23_P139147	MS4A8B	1.60012075	1.334735412	1.198829923	0.218018865	1.198829923	0.04952965	p<0.05
: A_23_P77724	BCAR1	0.344305729	0.287197267	1.198847515	0.227087677	1.198847515	0.049059461	p<0.05
: A_23_P254202	SSX4	0.752156969	0.627160635	1.199305134	0.104328902	1.199305134	0.013024291	p<0.05
: A_23_P60101	FLJ14129	1.429915269	1.192069724	1.199523183	0.020805482	1.199523183	0.015698772	p<0.05
: A_23_P84922	HDAC8	1.639042957	1.366083814	1.199811417	0.063840469	1.199811417	0.044937387	p<0.05
: A_23_P42045	ORC3L	1.177598465	0.979466759	1.202285278	0.218449459	1.202285278	0.040078858	p<0.05
: A_23_P84084	GFRA2	1.369274654	1.13875222	1.202434235	0.174627261	1.202434235	0.048581066	p<0.05
: A_23_P135454	AFG3L2	0.912012709	0.758379186	1.202581407	0.168142431	1.202581407	0.03626441	p<0.05
: A_23_P131534	GPR45	1.082645027	0.899761852	1.203257312	0.0865537	1.203257312	0.021206751	p<0.05
: A_23_P255942	PBOV1	2.473273846	2.055131782	1.20346241	0.0720869	1.20346241	0.04701036	p<0.05
: A_23_P250564	PRKCE	1.499372118	1.245565716	1.203767973	0.174977325	1.203767973	0.043085457	p<0.05
: A_23_P201939	PPP2CZ	0.694482085	0.576246066	1.205183213	0.069074987	1.205183213	0.045176334	p<0.05
: A_23_P63067	DAP3	1.654156965	1.372426051	1.205279486	0.128144149	1.205279486	0.020570923	p<0.05
: A_23_P427075	CTNS	2.005528593	1.663798292	1.205391664	0.138730205	1.205391664	0.044348282	p<0.05
: A_23_P256716	SMARCA5	1.94250895	1.611314344	1.205543138	0.124637833	1.205543138	0.021716063	p<0.05
: A_23_P430785	FRS2	2.190396525	1.814146906	1.207397547	0.065226843	1.207397547	0.037104296	p<0.05
: A_23_P104086	CROCC	0.771045013	0.638549041	1.207495372	0.048124783	1.207495372	0.012427096	p<0.05
: A_23_P155968	PLK4	1.424384105	1.178774565	1.208360061	0.08030798	1.208360061	0.037545777	p<0.05
: A_23_P54597	CSIG	0.806101588	0.667061216	1.2084372	0.111943518	1.2084372	0.018709921	p<0.05
: A_23_P339098	SLC35F2	2.810783536	2.325333929	1.208765546	0.020063152	1.208765546	0.014642616	p<0.05
: A_23_P382043	NT5C2L1	1.121721724	0.927729856	1.209103832	0.137888657	1.209103832	0.041992322	p<0.05
: A_23_P348828	IL3	1.248395352	1.032381095	1.209238873	0.152103883	1.209238873	0.043332717	p<0.05
: A_23_P218283	ZNF434	0.961974843	0.795462313	1.209327994	0.004769949	1.209327994	0.040345955	p<0.05
: A_23_P381532	KIR2DS5	0.729649926	0.602946246	1.210140922	0.140187409	1.210140922	0.043340636	p<0.05
: A_23_P72169		0.890194774	0.735607662	1.210148861	0.182414517	1.210148861	0.043814577	p<0.05
: A_23_P59976	GML	1.320951441	1.091535768	1.210176964	0.277271645	1.210176964	0.040744952	p<0.05
: A_23_P138975	RBM7	1.723928351	1.423750716	1.21083581	0.110186668	1.21083581	0.013177715	p<0.05
: A_23_P50182	SIGLEC7	1.863089924	1.537335857	1.211895185	0.091504868	1.211895185	0.017912384	p<0.05
: A_23_P215594	SRPK2	1.288684091	1.063237768	1.212037542	0.103557312	1.212037542	0.027622017	p<0.05
: A_23_P103912	B4GALT3	1.150470024	0.948963618	1.212343658	0.109357826	1.212343658	0.018789169	p<0.05
: A_23_P166135	XRN2	1.127541788	0.929225384	1.213421208	0.163719268	1.213421208	0.036925025	p<0.05
: A_23_P117172	PARP4	1.574397239	1.297224262	1.213666199	0.077127461	1.213666199	0.03359969	p<0.05
: A_23_P208981	PTBP1	1.021213839	0.840959624	1.214343483	0.025710844	1.214343483	0.013033759	p<0.05
: A_23_P33148		1.050478122	0.864738206	1.214793234	0.11259278	1.214793234	0.016013048	p<0.05
: A_23_P81683	GPRC6A	3.48052577	2.864641913	1.214995059	0.053662948	1.214995059	0.029946147	p<0.05
: A_23_P6479	KIAA0063	1.186483684	0.975837764	1.21586162	0.076363147	1.21586162	0.043507426	p<0.05
: A_23_P28625	WDR12	2.059155291	1.691744365	1.21717875	0.153487021	1.21717875	0.019816929	p<0.05
: A_23_P147296	HIRIP5	1.840997998	1.511732992	1.217806324	0.14140257	1.217806324	0.028797427	p<0.05
: A_23_P141336	ARHGAP27	0.615147253	0.505037102	1.218023886	0.183301369	1.218023886	0.03966372	p<0.05
: A_23_P500390	DONSON	1.031722861	0.847034403	1.21804127	0.12867065	1.21804127	0.036045623	p<0.05
: A_23_P7612	PRDM9	0.532332911	0.436807349	1.218690371	0.228512736	1.218690371	0.045097165	p<0.05
: A_23_P205228	ATP7B	0.948099582	0.777484729	1.219444635	0.089225435	1.219444635	0.02389784	p<0.05
: A_23_P138680	IL15RA	1.059419136	0.868516888	1.219802575	0.082307506	1.219802575	0.035733813	p<0.05
: A_23_P166910		1.550621259	1.271088069	1.219916462	0.217474195	1.219916462	0.025568614	p<0.05

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: A_23_P160148	GALE	0.966087648	0.791535633	1.220523255	0.119325541	1.220523255	0.015222497	p<0.05
: A_23_P435974	OVCH1	1.966698908	1.610603806	1.221094164	0.074037361	1.221094164	0.029769715	p<0.05
: A_23_P170925		0.724999002	0.593678828	1.221197333	0.046450139	1.221197333	0.010793041	p<0.05
: A_23_P73809	LRCH2	1.486272349	1.216629749	1.22163078	0.040019556	1.22163078	0.012092321	p<0.05
: A_23_P61643	HAL	1.678880033	1.373789681	1.222079374	0.210798846	1.222079374	0.040650881	p<0.05
: A_23_P164520		3.754974367	3.071262838	1.222615766	0.112211109	1.222615766	0.037142945	p<0.05
: A_23_P156993	CNOT4	1.319965145	1.079499215	1.222756929	0.049496162	1.222756929	0.012129386	p<0.05
: A_23_P142455	SIRT2	1.33626067	1.092459803	1.223166899	0.174590626	1.223166899	0.036934736	p<0.05
: A_23_P302410	KIAA1984	2.402577161	1.963979649	1.223320803	0.057161924	1.223320803	0.012474998	p<0.05
: A_23_P27414	ZNF497	1.082572543	0.884341329	1.224156904	0.059666702	1.224156904	0.02067607	p<0.05
: A_23_P84555		1.152690437	0.941541184	1.224259179	0.126999049	1.224259179	0.028909418	p<0.05
: A_23_P171107	CCNB3	0.703039866	0.574068921	1.224661082	0.065615492	1.224661082	0.014434029	p<0.05
: A_23_P119957	SLC8A1	2.862215277	2.336395263	1.225056103	0.098956816	1.225056103	0.023518731	p<0.05
: A_23_P18267	TUSC4	0.712050831	0.580625011	1.226352323	0.015086319	1.226352323	0.019781488	p<0.05
: A_23_P1912	ZP1	1.131080205	0.922177239	1.226532338	0.170778685	1.226532338	0.030366465	p<0.05
: A_23_P103968	AKR7A3	1.077622194	0.878072784	1.227258393	0.301802557	1.227258393	0.047011659	p<0.05
: A_23_P325501	ZCWCC3	2.094580468	1.706073203	1.227720161	0.091387521	1.227720161	0.012601626	p<0.05
: A_23_P126939	RAB7L1	1.739683331	1.415036794	1.229426216	0.037617752	1.229426216	0.017589883	p<0.05
: A_23_P27784	GP6	1.973962115	1.60487342	1.229979941	0.041861153	1.229979941	0.031263546	p<0.05
: A_23_P157416	ZNF394	1.077759989	0.875976401	1.230352768	6.10384E-04	1.230352768	0.044542898	p<0.05
: A_23_P208535	RPS9	1.394470307	1.132796937	1.230997597	0.010690233	1.230997597	0.021698681	p<0.05
: A_23_P36183	GTF2H1	1.198303472	0.973204159	1.231297113	0.157110591	1.231297113	0.036427499	p<0.05
: A_23_P205575	GPR135	1.112191203	0.903088919	1.231541191	0.145486411	1.231541191	0.04090407	p<0.05
: A_23_P130735	SLC6A16	3.007546743	2.439797289	1.232703535	0.130629756	1.232703535	0.012278421	p<0.05
: A_23_P122563	HKE2	0.824560009	0.668318721	1.233782599	0.192993225	1.233782599	0.049664867	p<0.05
: A_23_P152768	TUBG1	0.950282247	0.770216038	1.233786627	0.136208959	1.233786627	0.03891157	p<0.05
: A_23_P148546	ARD1	1.063808649	0.861883305	1.234283855	0.031788259	1.234283855	0.030821955	p<0.05
: A_23_P28555	STAMPB	1.887718053	1.52795732	1.235452083	0.206406905	1.235452083	0.047986552	p<0.05
: A_23_P154166		1.348010497	1.091034497	1.235534257	0.100921726	1.235534257	0.027780646	p<0.05
: A_23_P217666	RPL10	1.393423291	1.127222462	1.236156427	0.012076505	1.236156427	0.039346683	p<0.05
: A_23_P121885	ROPN1L	2.01482442	1.629768453	1.236264217	0.043101849	1.236264217	0.011778355	p<0.05
: A_23_P346813	PAK3	1.198432417	0.968879888	1.236925682	0.013664942	1.236925682	0.013855285	p<0.05
: A_23_P208325	ZNF235	0.516589149	0.417615079	1.236998314	0.07817046	1.236998314	0.039277522	p<0.05
: A_23_P57181	RBBP9	2.103532263	1.700492438	1.237013594	0.039105298	1.237013594	0.031717095	p<0.05
: A_23_P81121	EXOSC9	1.022809646	0.82677213	1.237111906	0.145150229	1.237111906	0.028187305	p<0.05
: A_23_P252653	STK25	0.793475031	0.641255217	1.237377895	0.271366655	1.237377895	0.044998782	p<0.05
: A_23_P94711		2.120913879	1.714007272	1.237400747	0.084354922	1.237400747	0.036488829	p<0.05
: A_23_P115861	ZNF485	1.20880432	0.976391443	1.23803248	0.072476543	1.23803248	0.012348588	p<0.05
: A_23_P157168	WBSCR18	1.169167389	0.944268935	1.238172035	0.187403444	1.238172035	0.033478988	p<0.05
: A_23_P83266	ENDOG	1.046452047	0.844923377	1.238517096	0.155429741	1.238517096	0.02486636	p<0.05
: A_23_P28733	RBL1	1.323315642	1.068376401	1.238623055	0.041978495	1.238623055	0.029237957	p<0.05
: A_23_P61202	C21orf70	0.648137011	0.523268721	1.23863129	0.145962485	1.23863129	0.02398989	p<0.05
: A_23_P210784		0.604173126	0.487737157	1.238726879	0.055730084	1.238726879	0.048120677	p<0.05
: A_23_P98669		0.639730163	0.51641453	1.238791952	0.286752285	1.238791952	0.04015947	p<0.05
: A_23_P29058	KCNJ6	1.964255411	1.585360504	1.238996056	0.125276441	1.238996056	0.039095765	p<0.05
: A_23_P107154	USP32	0.692109323	0.558588317	1.239032937	0.11870548	1.239032937	0.016083517	p<0.05
: A_23_P31829		1.537300945	1.240338229	1.239420756	0.059600857	1.239420756	0.010792895	p<0.05
: A_23_P413696	C21orf129	2.069536003	1.668556824	1.240314968	0.129402335	1.240314968	0.025228802	p<0.05
: A_23_P253409	SLC31A1	1.277026602	1.028862146	1.241202825	0.112972992	1.241202825	0.038151609	p<0.05
: A_23_P214529	ZNF192	1.95336954	1.573038614	1.241781049	0.078757501	1.241781049	0.028382517	p<0.05
: A_23_P55504	OR3A2	3.797466982	3.057224145	1.242129069	0.142212406	1.242129069	0.044279799	p<0.05
: A_23_P127995	CLNS1A	1.600636978	1.288541081	1.242208728	0.093826502	1.242208728	0.024163243	p<0.05
: A_23_P77310	ZFP106	1.717543396	1.381289513	1.243434761	0.136493686	1.243434761	0.02107547	p<0.05
: A_23_P148204	USP47	1.136329146	0.91354129	1.243872782	0.169794347	1.243872782	0.035131693	p<0.05

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: A_23_P52543	IDI2	1.89232529	1.521032837	1.244105482	0.121016062	1.244105482	0.043263614	p<0.05
: A_23_P403898	PTPN3	1.696494792	1.363127133	1.244560944	0.11319213	1.244560944	0.035676977	p<0.05
: A_23_P253421	AUP1	1.554204753	1.248585214	1.244772672	0.115725736	1.244772672	0.048034017	p<0.05
: A_23_P250865	THG-1	1.36803196	1.098476312	1.245390498	0.09399317	1.245390498	0.03978769	p<0.05
: A_23_P93613	MKLN1	1.680281251	1.348914136	1.245654714	0.196749677	1.245654714	0.041040393	p<0.05
: A_23_P29866		0.941769885	0.755629841	1.246337603	0.03438604	1.246337603	0.020896433	p<0.05
: A_23_P303320	LOC90353	1.01032265	0.810512248	1.246523606	0.05683812	1.246523606	0.015455574	p<0.05
: A_23_P201396	FLJ20729	1.529452927	1.226792137	1.246709105	0.188856315	1.246709105	0.025046064	p<0.05
: A_23_P10753		1.977024271	1.585637828	1.246832181	0.147240942	1.246832181	0.032565284	p<0.05
: A_23_P126623	PGD	1.649720485	1.322796053	1.247146513	0.135812605	1.247146513	0.036818058	p<0.05
: A_23_P142950	TNRC15	1.217950278	0.976330794	1.24747707	0.020675442	1.24747707	0.011111061	p<0.05
: A_23_P91015	SMYD5	0.837741864	0.671168156	1.248184759	0.084047468	1.248184759	0.035116117	p<0.05
: A_23_P148114	EHBP1L1	0.95687183	0.766410586	1.248510717	0.196742365	1.248510717	0.031902307	p<0.05
: A_23_P9455	PAF53	0.799506607	0.640327394	1.248590353	0.04738098	1.248590353	0.015800887	p<0.05
: A_23_P312181	TCEB2	1.37608173	1.101990026	1.248724305	0.148330358	1.248724305	0.028251832	p<0.05
: A_23_P61580	NSUN6	1.456757755	1.165853912	1.249519979	0.103988489	1.249519979	0.018641676	p<0.05
: A_23_P258410	WNT7A	1.186463868	0.949470786	1.249605449	0.156649446	1.249605449	0.043490556	p<0.05
: A_23_P45756	P29	1.879507624	1.503203209	1.250335026	0.132131358	1.250335026	0.025258093	p<0.05
: A_23_P113825	BTBD14A	2.396382056	1.916535974	1.25037155	0.003486745	1.25037155	0.03702022	p<0.05
: A_23_P806	GALNT2	1.113450125	0.889772357	1.251387635	0.120676431	1.251387635	0.049367297	p<0.05
: A_23_P156484	CD2AP	1.547540756	1.236572574	1.251475884	0.107453846	1.251475884	0.021137546	p<0.05
: A_23_P169934	FLJ39378	1.127486769	0.900454309	1.252131017	0.104553172	1.252131017	0.015031164	p<0.05
: A_23_P422193	SUV39H1	1.204217289	0.95965162	1.254848389	0.202305439	1.254848389	0.039818099	p<0.05
: A_23_P51951	IL24	1.317872691	1.049584748	1.255613416	0.129210489	1.255613416	0.037277717	p<0.05
: A_23_P150974	HOXC6	1.932565378	1.538729031	1.255949123	0.196431377	1.255949123	0.048087851	p<0.05
: A_23_P59048	SLC17A2	1.973795301	1.57078507	1.25656612	0.021792874	1.25656612	0.04097886	p<0.05
: A_23_P45361	GLUD2	0.450996765	0.358795448	1.256974601	0.052124131	1.256974601	0.017661411	p<0.05
: A_23_P201921	CDC14A	0.779776842	0.620203604	1.257291697	0.074675696	1.257291697	0.020491142	p<0.05
: A_23_P148446	UBE2A	1.818955797	1.445654087	1.258223398	0.117368701	1.258223398	0.032797311	p<0.05
: A_23_P55136	RANGNRF	0.946192343	0.751792035	1.258582559	0.014961454	1.258582559	0.012893226	p<0.05
: A_23_P208973	RANBP3	1.58169874	1.253319219	1.262007887	0.023589609	1.262007887	0.015842101	p<0.05
: A_23_P251209	TUFM	1.880119044	1.488753727	1.262881167	0.181979568	1.262881167	0.034819695	p<0.05
: A_23_P62303	NLGN3	2.523374777	1.997914232	1.263004556	0.092339138	1.263004556	0.012777127	p<0.05
: A_23_P80377	PACSIN2	1.398467381	1.10664091	1.263704756	0.15016313	1.263704756	0.031203506	p<0.05
: A_23_P211355	DGCR8	0.923682469	0.730687523	1.264127879	0.051130651	1.264127879	0.032488056	p<0.05
: A_23_P85171	EMD	0.958026865	0.757766773	1.264276686	0.123188169	1.264276686	0.041610733	p<0.05
: A_23_P202408	HERC4	0.6745019	0.533489912	1.264319878	0.216605885	1.264319878	0.049011248	p<0.05
: A_23_P5027	EEF2	1.79603055	1.420423057	1.264433538	0.04185961	1.264433538	0.037799897	p<0.05
: A_23_P340333	KIAA1754	0.903012042	0.714007179	1.26471003	0.048911466	1.26471003	0.010375509	p<0.05
: A_23_P112825		1.047189455	0.827956733	1.264787655	0.165976063	1.264787655	0.034518931	p<0.05
: A_23_P117082	HEBP1	2.092297436	1.65408043	1.264930893	0.101050184	1.264930893	0.040909158	p<0.05
: A_23_P154675	SNRPB	0.951855384	0.752266674	1.265316432	0.137275318	1.265316432	0.038737187	p<0.05
: A_23_P60766	BRUNOL5	0.827726176	0.654141093	1.265363368	0.010654902	1.265363368	0.01025244	p<0.05
: A_23_P396842	C6orf89	1.372597203	1.084710349	1.265404357	0.288837579	1.265404357	0.040166405	p<0.05
: A_23_P86434	JMJD1C	2.339577989	1.848713602	1.265516729	0.225323854	1.265516729	0.032387939	p<0.05
: A_23_P367071	MGC42638	0.912051427	0.720407023	1.266022399	0.077448156	1.266022399	0.043461873	p<0.05
: A_23_P119543	HMG20B	0.748242873	0.590997501	1.266067744	0.15062232	1.266067744	0.03052707	p<0.05
: A_23_P83200	C9orf98	2.858280141	2.257328565	1.266222465	0.125279944	1.266222465	0.017615904	p<0.05
: A_23_P89012		1.018291443	0.803963087	1.266589796	0.071455256	1.266589796	0.01708704	p<0.05
: A_23_P147782	SCRT1	0.933757499	0.736962228	1.267035763	0.050570044	1.267035763	0.012528669	p<0.05
: A_23_P111448	PLXNA4	1.027928909	0.8111656	1.267224483	0.160721136	1.267224483	0.043763615	p<0.05
: A_23_P89334	MYH13	0.801355656	0.63219688	1.267572937	0.139964205	1.267572937	0.022884515	p<0.05
: A_23_P253245	GCET2	1.051882572	0.829791561	1.267646746	0.129524613	1.267646746	0.018808992	p<0.05
: A_23_P216850	RNF20	1.16890729	0.921904639	1.267926465	0.136787713	1.267926465	0.032012098	p<0.05

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: A_23_P111448	PLXNA4	1.027928909	0.8111656	1.267224483	0.160721136	1.267224483	0.043763615	p<0.05
: A_23_P89334	MYH13	0.801355656	0.63219688	1.267572937	0.139964205	1.267572937	0.022884515	p<0.05
: A_23_P253245	GCET2	1.051882572	0.829791561	1.267646746	0.129524613	1.267646746	0.018808992	p<0.05
: A_23_P216850	RNF20	1.16890729	0.921904639	1.267926465	0.136787713	1.267926465	0.032012098	p<0.05
: A_23_P13065	ZDHHC13	2.585616403	2.038918925	1.268131053	0.22965391	1.268131053	0.047959493	p<0.05
: A_23_P100355	PPP4C	0.981585127	0.773429801	1.269132797	0.101709414	1.269132797	0.01817912	p<0.05
: A_23_P157991	OR1L8	2.567328713	2.022710873	1.269251452	0.085159587	1.269251452	0.033136254	p<0.05
: A_23_P98830	UBQLN3	1.412000958	1.112123272	1.269644287	0.10371784	1.269644287	0.029718512	p<0.05
: A_23_P91520	SH3BGR	2.094283645	1.649248222	1.269841384	0.0506196	1.269841384	0.017011242	p<0.05
: A_23_P1775	DPAGT1	1.699087731	1.33786019	1.270003954	0.133281747	1.270003954	0.020813866	p<0.05
: A_23_P310552	FLJ35740	1.370231734	1.078815384	1.270126235	0.158984494	1.270126235	0.027721044	p<0.05
: A_23_P416836	LOC51333	5.157931773	4.058940182	1.270758262	0.064574511	1.270758262	0.011957868	p<0.05
: A_23_P359173	COH1	2.253704269	1.771434524	1.272248135	0.126721655	1.272248135	0.016220946	p<0.05
: A_23_P332246	ATOH1	1.760636821	1.383441632	1.272649875	0.100604368	1.272649875	0.021563827	p<0.05
: A_23_P49145	ZG16	1.963460299	1.542070527	1.273262321	0.159489341	1.273262321	0.031860338	p<0.05
: A_23_P322426	E2F7	0.831115607	0.652612057	1.273521685	0.044286673	1.273521685	0.021026694	p<0.05
: A_23_P1343	STAM	3.570700591	2.803647921	1.27359094	0.112415472	1.27359094	0.021707463	p<0.05
: A_23_P18153	ATP2B2	0.72434997	0.568429397	1.274300685	0.287677282	1.274300685	0.043262519	p<0.05
: A_23_P30923	HLA-DOA	0.813133279	0.638100307	1.274303225	0.067396499	1.274303225	0.040048221	p<0.05
: A_23_P2124	HT007	2.198777395	1.725036839	1.274626342	0.241808408	1.274626342	0.039768088	p<0.05
: A_23_P250537	IHPK1	1.125494907	0.882998312	1.274628605	0.197851134	1.274628605	0.013423094	p<0.05
: A_23_P372434	SCIRP10	2.08705309	1.636855351	1.275038194	0.124260122	1.275038194	0.035298494	p<0.05
: A_23_P1320	MYOZ1	1.320712173	1.035751456	1.275124612	0.056053408	1.275124612	0.014575652	p<0.05
: A_23_P80242	SEZ6L	1.846668423	1.448128854	1.275220934	0.08129826	1.275220934	0.037613368	p<0.05
: A_23_P124213	LCMT1	1.189842974	0.932439926	1.276053224	0.199482605	1.276053224	0.028704193	p<0.05
: A_23_P304554	C21orf61	1.646659735	1.289497804	1.276977541	0.154472527	1.276977541	0.034702488	p<0.05
: A_23_P97043	ALPL	0.885771165	0.693582237	1.277096094	0.227400727	1.277096094	0.034287933	p<0.05
: A_23_P157435	OAZIN	2.023944803	1.584342324	1.277466853	0.102787776	1.277466853	0.014715498	p<0.05
: A_23_P121646	SLC34A2	1.170029068	0.915475677	1.278055876	0.141899805	1.278055876	0.03128192	p<0.05
: A_23_P135826	ZNF505	0.534954981	0.418392565	1.278595811	0.12756348	1.278595811	0.036096141	p<0.05
: A_23_P106362	AQP9	1.707386183	1.333072846	1.280789859	0.05502784	1.280789859	0.010536012	p<0.05
: A_23_P87007	HTR3B	1.667827533	1.301760321	1.281209379	0.123762439	1.281209379	0.012221351	p<0.05
: A_23_P250824	RABGEF1	1.968519625	1.536397747	1.281256516	0.083851036	1.281256516	0.029395737	p<0.05
: A_23_P105691	GPRC5D	0.638428899	0.498214975	1.281432577	0.045310098	1.281432577	0.014875151	p<0.05
: A_23_P305581		4.2541263	3.318238969	1.282043379	0.138467767	1.282043379	0.040135678	p<0.05
: A_23_P218015	OR51A4	1.170244282	0.91264337	1.282258021	0.064141251	1.282258021	0.049922715	p<0.05
: A_23_P105873	TRPC4	1.178578756	0.918994984	1.282464842	0.060017673	1.282464842	0.034791181	p<0.05
: A_23_P113263		0.974786564	0.759876057	1.282823107	0.014685886	1.282823107	0.025293555	p<0.05
: A_23_P47774	OR51B6	1.250780751	0.9747671	1.283158563	0.092288618	1.283158563	0.036413865	p<0.05
: A_23_P167640	SLC36A1	2.506638706	1.953469925	1.283172407	0.078030579	1.283172407	0.014106937	p<0.05
: A_23_P147215	AGTRAP	0.487676224	0.380036532	1.283235117	0.040681878	1.283235117	0.017126062	p<0.05
: A_23_P17482	C20orf30	1.403302155	1.093218518	1.283642869	0.091487762	1.283642869	0.020898977	p<0.05
: A_23_P146679		0.704856258	0.548908372	1.284105497	0.212509421	1.284105497	0.02923551	p<0.05
: A_23_P38696	DSC1	3.564495236	2.773248844	1.285313881	0.120061608	1.285313881	0.018692344	p<0.05
: A_23_P149826	POLR3A	2.177073758	1.693414984	1.285611488	0.007064632	1.285611488	0.01906861	p<0.05
: A_23_P408323	FIS	2.445831863	1.901549868	1.286230723	0.020142178	1.286230723	0.023576393	p<0.05
: A_23_P39110	RUVBL2	0.872597149	0.678322788	1.286404003	0.092037268	1.286404003	0.019495333	p<0.05
: A_23_P388681	ELAVL1	1.862770069	1.447736283	1.286677753	0.155015571	1.286677753	0.040374474	p<0.05
: A_23_P123393	KCNQ3	2.387370316	1.85484202	1.2871017	0.071705649	1.2871017	0.013440907	p<0.05
: A_23_P21425	GPR119	0.791665177	0.614503533	1.288300448	0.24145216	1.288300448	0.04999244	p<0.05
: A_23_P413826	SEC10L1	1.599792071	1.241749247	1.288337461	0.081244791	1.288337461	0.013404578	p<0.05
: A_23_P57910	TMEM7	2.170323728	1.684437261	1.288456256	0.09583363	1.288456256	0.012196141	p<0.05
: A_23_P403968	C20orf116	0.733256717	0.56780795	1.29138156	0.1858976	1.29138156	0.018134202	p<0.05

FIG. 8
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: A_23_P333552	GGN	1.213449555	0.93948163	1.291616053	0.090436649	1.291616053	0.043544372	p<0.05
: A_23_P53378	OR8S1	0.598012903	0.462737799	1.292336404	0.159385846	1.292336404	0.038083416	p<0.05
: A_23_P76718	NEK3	1.408622626	1.089979022	1.292339208	0.205198638	1.292339208	0.033274649	p<0.05
: A_23_P213334	FGF1	0.922467919	0.713371717	1.293109744	0.013502897	1.293109744	0.040350063	p<0.05
: A_23_P213001	WDR1	1.08902717	0.842141856	1.293163571	0.275157126	1.293163571	0.041547128	p<0.05
: A_23_P207759	MAFG	0.88503471	0.684354827	1.293239522	0.152044503	1.293239522	0.022849561	p<0.05
: A_23_P56356	PLB1	0.931423281	0.718283742	1.29673446	0.147129958	1.29673446	0.029064051	p<0.05
: A_23_P145357	BAK1	1.204036248	0.928458842	1.296811655	0.063048801	1.296811655	0.034204505	p<0.05
: A_23_P126528	KCNA10	1.061798112	0.818635922	1.297033375	0.236902071	1.297033375	0.026725207	p<0.05
: A_23_P45913	HPRP8BP	1.134748916	0.874525172	1.297560038	0.106471518	1.297560038	0.020370486	p<0.05
: A_23_P93352	C6orf29	1.291122156	0.994252621	1.29858562	0.173760263	1.29858562	0.037416582	p<0.05
: A_23_P74022	DBT	1.152387451	0.887371746	1.298652403	0.158375983	1.298652403	0.045663379	p<0.05
: A_23_P60899	NCOA6IP	0.932342559	0.717683983	1.299099019	0.007789886	1.299099019	0.028842147	p<0.05
: A_23_P80987	MTNR1A	1.022193763	0.786766679	1.299233674	0.038181527	1.299233674	0.015135637	p<0.05
: A_23_P170058	PSMB2	2.08728604	1.606116001	1.299586106	0.211890423	1.299586106	0.025792221	p<0.05
: A_23_P155666	ASAH1	2.105766347	1.620114811	1.299763655	0.133993811	1.299763655	0.026133465	p<0.05
: A_23_P207600	PSMD11	1.574772589	1.211533721	1.299817381	0.169942454	1.299817381	0.028920435	p<0.05
: A_23_P92524	ANP32C	0.937880962	0.721408252	1.300069633	0.128217943	1.300069633	0.035928142	p<0.05
: A_23_P111303	RBM16	1.914870048	1.472339267	1.30056305	0.059024743	1.30056305	0.03419422	p<0.05
: A_23_P39263	LOC126295	0.755163832	0.580464976	1.300963647	0.188339456	1.300963647	0.03324548	p<0.05
: A_23_P302094	IMP4	2.031073631	1.560525536	1.301531814	0.019842348	1.301531814	0.010649097	p<0.05
: A_23_P73441	ADAM2	1.055980585	0.811256713	1.301660212	0.028667527	1.301660212	0.039704766	p<0.05
: A_23_P103631	EBNA1BP2	1.926130849	1.479276619	1.30207618	0.116990523	1.30207618	0.023060292	p<0.05
: A_23_P58686	MYOZ3	1.376462696	1.056897655	1.302361387	0.10958899	1.302361387	0.014690247	p<0.05
: A_23_P77274	LOC92912	1.383199941	1.06184648	1.302636461	0.178007053	1.302636461	0.042131585	p<0.05
: A_23_P115366	UMP-CMPK	1.945630318	1.492416735	1.303677634	0.097324833	1.303677634	0.017983851	p<0.05
: A_23_P105423	KIAA0748	1.615501918	1.238896965	1.303984079	0.08010374	1.303984079	0.029022864	p<0.05
: A_23_P414842	CRYGB	1.173882352	0.900146899	1.304100867	0.015704135	1.304100867	0.023866117	p<0.05
: A_23_P17356	GDAP1L1	1.085635623	0.831303506	1.305943755	0.151728624	1.305943755	0.025015133	p<0.05
: A_23_P161634	MUS81	1.343238618	1.028507557	1.306007533	0.080942072	1.306007533	0.018692406	p<0.05
: A_23_P307430	FLJ30656	2.833031153	2.168760314	1.306290572	0.076782852	1.306290572	0.047078969	p<0.05
: A_23_P67529	KCNNA	1.085831951	0.831119711	1.306468775	0.254255796	1.306468775	0.04211711	p<0.05
: A_23_P126825	SLC16A1	1.762160213	1.348511587	1.306744584	0.066817284	1.306744584	0.01833933	p<0.05
: A_23_P8959	DNAJC5B	1.558093081	1.192094528	1.307021418	0.024512347	1.307021418	0.016507444	p<0.05
: A_23_P11774	CGI-94	2.423538553	1.853630995	1.307454698	0.048260865	1.307454698	0.01808597	p<0.05
: A_23_P200741	DPT	0.415024118	0.317117106	1.308740874	0.190464487	1.308740874	0.012545096	p<0.05
: A_23_P87438	RHPN1	0.546194957	0.417308051	1.30885315	0.116366536	1.30885315	0.015409514	p<0.05
: A_23_P51105	CRIM1	0.637506224	0.486907141	1.309297339	0.089236941	1.309297339	0.018205339	p<0.05
: A_23_P90829	SPP2	0.749825313	0.572674238	1.309340045	0.103715314	1.309340045	0.039267716	p<0.05
: A_23_P73264		1.400230064	1.069289771	1.309495426	0.212438487	1.309495426	0.035321051	p<0.05
: A_23_P47879	STAT6	1.284302733	0.980628727	1.309672761	0.191488662	1.309672761	0.045741749	p<0.05
: A_23_P117115	IL22	3.60786353	2.75464202	1.309739525	0.090459175	1.309739525	0.045631092	p<0.05
: A_23_P402164	LOC142937	1.356361792	1.035311987	1.310099573	0.127244553	1.310099573	0.035504426	p<0.05
: A_23_P51414	SMYD3	1.194856461	0.911289975	1.311170422	0.225113072	1.311170422	0.024185417	p<0.05
: A_23_P218905	FLJ10808	1.245074772	0.949440714	1.31137706	0.165758057	1.31137706	0.010748493	p<0.05
: A_23_P252276	FLJ20184	1.458118644	1.111633719	1.31168983	0.0205014	1.31168983	0.033952834	p<0.05
: A_23_P147544	WNT7B	2.759133797	2.101224524	1.313107555	0.084492191	1.313107555	0.017195536	p<0.05
: A_23_P212825	NARG1	2.591843794	1.973275822	1.313472635	0.033692249	1.313472635	0.015068513	p<0.05
: A_23_P400344	MGC10067	3.036407675	2.311524437	1.313595317	0.139293347	1.313595317	0.02918549	p<0.05
: A_23_P259874	SEC22L2	1.720575672	1.309296444	1.314122314	0.203455163	1.314122314	0.036326293	p<0.05
: A_23_P81092		0.642472683	0.488779699	1.31444224	0.127990832	1.31444224	0.045094368	p<0.05
: A_23_P122104	LOC285590	1.190778353	0.905875566	1.314505434	0.073315819	1.314505434	0.019120787	p<0.05
: A_23_P51745	PROK1	2.49346002	1.896819971	1.314547536	0.061197299	1.314547536	0.042302304	p<0.05

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: A_23_P2023	TSSC4	0.784949977	0.596896404	1.315052278	0.128708241	1.315052278	0.02990473	p<0.05
: A_23_P502363	EYA1	1.741065572	1.323867555	1.315135766	0.082152544	1.315135766	0.037647394	p<0.05
: A_23_P10081	ARL2L1	3.035627088	2.307381519	1.315615586	0.164039943	1.315615586	0.034494367	p<0.05
: A_23_P309711	TXNDC	1.78057767	1.353235397	1.315793006	0.212239494	1.315793006	0.044092239	p<0.05
: A_23_P169257	TNFSF8	1.543558279	1.172305127	1.316686453	0.104875399	1.316686453	0.016939714	p<0.05
: A_23_P53614	BRAP	1.204213336	0.914242454	1.31717066	0.145435863	1.31717066	0.032399239	p<0.05
: A_23_P75998	SERPINH1	0.56994456	0.432333844	1.318297349	0.046789328	1.318297349	0.038430269	p<0.05
: A_23_P86124	RASAL2	1.160870221	0.880516494	1.318396905	0.210896821	1.318396905	0.025405053	p<0.05
: A_23_P169612	PRKDC	0.889611331	0.674707616	1.318513842	0.239353897	1.318513842	0.033900997	p<0.05
: A_23_P59338	PDE7B	0.50514741	0.382882832	1.319326352	0.149608255	1.319326352	0.042804608	p<0.05
: A_23_P164702	MRPL4	2.085039837	1.58011777	1.31954711	0.132931894	1.31954711	0.017544835	p<0.05
: A_23_P16953	HTR2B	2.338643329	1.772146116	1.319667328	0.039560696	1.319667328	0.011193325	p<0.05
: A_23_P50872	NDUFB7	0.985229759	0.746220109	1.320293767	0.192672212	1.320293767	0.044889533	p<0.05
: A_23_P9582	TUFM	1.931446034	1.461868358	1.321217484	0.116770082	1.321217484	0.01463881	p<0.05
: A_23_P110099	NIT2	1.89467589	1.433057345	1.322121475	0.095744409	1.322121475	0.031557248	p<0.05
: A_23_P51646	PLK3	2.77544564	2.097350004	1.323310671	0.155624556	1.323310671	0.038461158	p<0.05
: A_23_P168965	FLJ11267	0.926789788	0.699990692	1.324003016	0.016830569	1.324003016	0.030913189	p<0.05
: A_23_P168470	LOC55971	0.889221314	0.671471778	1.324286952	0.182047001	1.324286952	0.017856953	p<0.05
: A_23_P204039	CPSF6	2.412330803	1.820045656	1.325423236	0.105580504	1.325423236	0.025998213	p<0.05
: A_23_P66213	PAQR4	1.478857767	1.115702762	1.325494404	0.083614837	1.325494404	0.012598234	p<0.05
: A_23_P132358	MT	1.116922188	0.841575528	1.327179975	0.083148548	1.327179975	0.022991551	p<0.05
: A_23_P142774	EIF3S5	1.056465852	0.795901841	1.327382093	0.260731958	1.327382093	0.048761564	p<0.05
: A_23_P17219	CRIP1	1.672025971	1.259477823	1.327554913	0.222110262	1.327554913	0.049799453	p<0.05
: A_23_P369966	APOBEC3B	0.701843328	0.527792363	1.329771663	0.280597163	1.329771663	0.047366343	p<0.05
: A_23_P40677	CBX6	1.077692635	0.810083341	1.330347855	0.145572156	1.330347855	0.022207384	p<0.05
: A_23_P36738	ANKRD13	1.588481093	1.193670522	1.330753389	0.23758874	1.330753389	0.038988102	p<0.05
: A_23_P252521	KIAA1900	1.262422174	0.948471325	1.331007212	0.057212968	1.331007212	0.010207449	p<0.05
: A_23_P130182	AURKB	1.185572191	0.890367178	1.33155424	0.12865853	1.33155424	0.033694725	p<0.05
: A_23_P36439		3.674260516	2.758771963	1.331846403	0.292759325	1.331846403	0.049088454	p<0.05
: A_23_P46365	RAB13	0.964435105	0.723275176	1.333427632	0.162437709	1.333427632	0.018809276	p<0.05
: A_23_P111635	DUSP24	1.052127757	0.789022848	1.333456642	0.029663913	1.333456642	0.019435001	p<0.05
: A_23_P55196	FLJ40137	1.075748689	0.805944041	1.334768464	0.062320636	1.334768464	0.014741115	p<0.05
: A_23_P126790	SARS	2.055971643	1.540303973	1.334783055	0.140045812	1.334783055	0.042779417	p<0.05
: A_23_P430788	FLJ32830	2.086787198	1.562869461	1.335228085	0.06605996	1.335228085	0.047024291	p<0.05
: A_23_P396785	N-PAC	1.301378956	0.974463923	1.335481925	0.069180719	1.335481925	0.031690531	p<0.05
: A_23_P342165	FLJ35700	1.429589788	1.070380208	1.335590641	0.147537558	1.335590641	0.043869864	p<0.05
: A_23_P379746	MGC24039	1.964189753	1.470109823	1.336083687	0.255512434	1.336083687	0.049566555	p<0.05
: A_23_P39684	TLK1	2.5439555	1.903019965	1.336799165	0.059726379	1.336799165	0.042586556	p<0.05
: A_23_P305723	MI-ER1	3.606589921	2.697546235	1.336989103	0.226998497	1.336989103	0.02607686	p<0.05
: A_23_P167276	PAQR3	2.878046185	2.152374089	1.337149615	0.294220073	1.337149615	0.04574336	p<0.05
: A_23_P377376	ACTR2	1.974967458	1.476876139	1.337260049	0.158572525	1.337260049	0.011603852	p<0.05
: A_23_P205997	PSFL	1.883596709	1.408377466	1.337423208	0.159332471	1.337423208	0.024205748	p<0.05
: A_23_P259189	CLIC4	0.68069194	0.508872994	1.33764603	0.103418127	1.33764603	0.012754331	p<0.05
: A_23_P144338	CCRN4L	0.65854533	0.492129641	1.338154165	0.010147973	1.338154165	0.042713979	p<0.05
: A_23_P168818	IMPA1	1.191641469	0.890223114	1.338587428	0.287266379	1.338587428	0.046552008	p<0.05
: A_23_P33113	FLJ20989	1.267212601	0.946336141	1.339072392	0.220806559	1.339072392	0.046704018	p<0.05
: A_23_P77562	LOC124446	0.670563156	0.500629448	1.339440095	0.273100079	1.339440095	0.037257861	p<0.05
: A_23_P208356	RPL28	1.591233347	1.187895658	1.339539661	0.098196021	1.339539661	0.025286772	p<0.05
: A_23_P47210	BANF1	1.468993536	1.096480612	1.339735076	0.076693923	1.339735076	0.019848366	p<0.05
: A_23_P163972	RAB37	1.626886262	1.213429153	1.340734445	0.082844832	1.340734445	0.031732001	p<0.05
: A_23_P22639		1.320193472	0.98466891	1.340748609	0.080562024	1.340748609	0.022455029	p<0.05
: A_23_P316501	TCBA1	1.996730924	1.488294325	1.34162369	0.064591859	1.34162369	0.026050088	p<0.05
: A_23_P159510	HADHA	1.069047001	0.796755071	1.34175111	0.132540168	1.34175111	0.018150578	p<0.05

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: A_23_P32558	WDR5	1.558587958	1.160331118	1.343226888	0.166211646	1.343226888	0.037955063	p<0.05
: A_23_P44836	FLJ12442	0.833155822	0.619745238	1.344352117	0.103303909	1.344352117	0.036644052	p<0.05
: A_23_P433791	DKFZP547N043	2.20364552	1.637792907	1.345497047	0.068639196	1.345497047	0.028479275	p<0.05
: A_23_P143084	MPV17	0.982864225	0.730248638	1.345930925	0.12331718	1.345930925	0.013063141	p<0.05
: A_23_P37416	KIAA0256	0.849173914	0.630787024	1.346213351	0.172699814	1.346213351	0.017367981	p<0.05
: A_23_P158837		1.235430469	0.916644584	1.347774798	0.198379908	1.347774798	0.011175684	p<0.05
: A_23_P40415	ADAMTS5	1.60167036	1.187298725	1.349003689	0.037831801	1.349003689	0.033031359	p<0.05
: A_23_P218486	PTD008	1.436733378	1.064623231	1.349522851	0.124113626	1.349522851	0.015739442	p<0.05
: A_23_P64243	UPK2	1.228242919	0.909746334	1.350093838	0.149047888	1.350093838	0.043225779	p<0.05
: A_23_P216149	TERF1	2.119254792	1.568965225	1.350734074	0.271892157	1.350734074	0.037919721	p<0.05
: A_23_P124470	STIP1	1.093897354	0.809640692	1.35108989	0.134650123	1.35108989	0.039746628	p<0.05
: A_23_P76515	LASS5	0.9402622	0.69534744	1.352219259	0.158420975	1.352219259	0.013863961	p<0.05
: A_23_P75710	OR5T3	1.229843139	0.90906515	1.352865787	0.022514298	1.352865787	0.043087841	p<0.05
: A_23_P86002	TMED5	1.644853757	1.215047106	1.353736615	0.279748084	1.353736615	0.047592733	p<0.05
: A_23_P72989	CCR4	2.506969518	1.85047282	1.354772408	0.024433873	1.354772408	0.012747549	p<0.05
: A_23_P131887		1.204762068	0.888756223	1.355559643	0.038026561	1.355559643	0.010177957	p<0.05
: A_23_P158605		1.201079933	0.884222515	1.358345792	0.216188056	1.358345792	0.039636602	p<0.05
: A_23_P89460	AATF	2.446951169	1.799345179	1.359912038	0.078597471	1.359912038	0.020832403	p<0.05
: A_23_P64567	PME-1	1.395476604	1.026121066	1.359953178	0.197152546	1.359953178	0.049567497	p<0.05
: A_23_P57626		2.69097586	1.976810176	1.361271757	0.046816897	1.361271757	0.029328346	p<0.05
: A_23_P104116	RBM8A	1.609701718	1.181623635	1.362279554	0.125887617	1.362279554	0.02388495	p<0.05
: A_23_P9903	APG4B	1.434906747	1.053046024	1.362624914	0.093996459	1.362624914	0.014896774	p<0.05
: A_23_P91870	CHCHD6	0.710213343	0.521175324	1.36271483	0.148399959	1.36271483	0.012972807	p<0.05
: A_23_P62907	ATF6	1.272993828	0.933753707	1.363307924	0.130702802	1.363307924	0.016380748	p<0.05
: A_23_P64474	OR52N5	1.468297209	1.075655228	1.365025866	0.034046266	1.365025866	0.03449757	p<0.05
: A_23_P154442		1.191800076	0.872721345	1.36561353	0.066682322	1.36561353	0.032893152	p<0.05
: A_23_P251118	LPP	1.208531077	0.88460586	1.366180274	0.047853097	1.366180274	0.046548308	p<0.05
: A_23_P434289	GPR62	0.563358441	0.412316647	1.366324754	0.128569063	1.366324754	0.026622978	p<0.05
: A_23_P170848	PFKM	2.405276515	1.759465418	1.367049611	0.245551903	1.367049611	0.031378076	p<0.05
: A_23_P203389	MGC13379	1.413635726	1.033632904	1.367638085	0.029274235	1.367638085	0.028523769	p<0.05
: A_23_P136874	ATRX	1.344961581	0.983125822	1.368046237	0.011100452	1.368046237	0.01126254	p<0.05
: A_23_P115392	KIAA1324	0.770756029	0.563382347	1.368086936	0.219815029	1.368086936	0.043586895	p<0.05
: A_23_P12523	TP53BP2	2.456868917	1.794579539	1.369049888	0.181246399	1.369049888	0.018112023	p<0.05
: A_23_P161407	ARL8	2.202387279	1.607880195	1.369745884	0.060227954	1.369745884	0.012771532	p<0.05
: A_23_P418537	GRB2	1.483483935	1.082702782	1.370167289	0.02323103	1.370167289	0.026119793	p<0.05
: A_23_P145146	PDCD2	2.048224098	1.493360946	1.371553277	0.170854589	1.371553277	0.028039202	p<0.05
: A_23_P74368		2.785582904	2.030705585	1.371731542	0.209333721	1.371731542	0.018733139	p<0.05
: A_23_P22286	ZNF224	0.757732653	0.552328638	1.371887318	0.138194673	1.371887318	0.010032195	p<0.05
: A_23_P206032		2.017599666	1.468377081	1.374033749	0.020742616	1.374033749	0.019196113	p<0.05
: A_23_P115106	DKFZp566C0424	2.444297756	1.777589458	1.375063148	0.068304929	1.375063148	0.010208357	p<0.05
: A_23_P252796		1.282859598	0.932802981	1.375273904	0.201589915	1.375273904	0.049496387	p<0.05
: A_23_P81780		1.143829021	0.830340881	1.377541498	0.130285842	1.377541498	0.025113103	p<0.05
: A_23_P41992	GFRA3	0.863097337	0.626355784	1.377966579	0.080803876	1.377966579	0.012087974	p<0.05
: A_23_P95441	KIF13B	2.057046824	1.4926258	1.378139668	0.110374348	1.378139668	0.018515988	p<0.05
: A_23_P330486	MGC40214	1.784098494	1.294379287	1.378342895	0.02187247	1.378342895	0.023289851	p<0.05
: A_23_P84388	ITLN1	0.783352507	0.567833855	1.379545266	0.027594907	1.379545266	0.017709558	p<0.05
: A_23_P161769	FXYD2	0.798870564	0.578979235	1.379791392	0.229314311	1.379791392	0.029395337	p<0.05
: A_23_P5566	MGC5391	1.857845179	1.346285123	1.379978986	0.275815643	1.379978986	0.030168461	p<0.05
: A_23_P48314	PABPC3	2.932146655	2.124456704	1.38018659	0.084412529	1.38018659	0.019047406	p<0.05
: A_23_P15326	TRIM25	1.004547806	0.727289231	1.38122189	0.01431854	1.38122189	0.027617212	p<0.05
: A_23_P45851	HIAT1	1.979425786	1.430301693	1.383921865	0.191600548	1.383921865	0.039742656	p<0.05
: A_23_P169307	IFNA17	1.353888233	0.977895964	1.384491074	0.059303394	1.384491074	0.019269982	p<0.05
: A_23_P40063	PMS1	1.589015098	1.147081505	1.385267823	0.201322641	1.385267823	0.029625194	p<0.05

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: A_23_P159071	MGC4645	0.844125921	0.60903643	1.386002345	0.077915415	1.386002345	0.028511393	p<0.05
: A_23_P86072	LOC65121	1.037074863	0.746896947	1.388511315	0.147285579	1.388511315	0.03540994	p<0.05
: A_23_P374129	DRD5	1.104161647	0.795069226	1.388761646	0.144607344	1.388761646	0.01869421	p<0.05
: A_23_P12392	PTPRC	5.101292836	3.673059081	1.388840398	0.115047048	1.388840398	0.010811456	p<0.05
: A_23_P105957	ACTN1	1.191157163	0.857412368	1.389246536	0.208960383	1.389246536	0.03048886	p<0.05
: A_23_P151368	LOC221143	1.204791898	0.866737029	1.390031646	0.162649748	1.390031646	0.021299374	p<0.05
: A_23_P130293	ANKRD12	1.61518076	1.161481209	1.390621516	0.088306511	1.390621516	0.033657016	p<0.05
: A_23_P43630		2.372795736	1.705691254	1.391105061	0.068693324	1.391105061	0.019500767	p<0.05
: A_23_P27613	MAN2B1	0.84543925	0.607545206	1.391565996	0.186747972	1.391565996	0.022510824	p<0.05
: A_23_P31713	E2F5	3.316060843	2.382386468	1.391907185	0.078338049	1.391907185	0.011173325	p<0.05
: A_23_P344421	ROBO4	1.978109767	1.420683415	1.392364933	0.038069521	1.392364933	0.020682229	p<0.05
: A_23_P154981	ZNF70	1.132048278	0.812870199	1.392655653	0.037526732	1.392655653	0.035598679	p<0.05
: A_23_P133842	HIST1H1T	3.783784562	2.71627675	1.393004067	0.054237575	1.393004067	0.019428103	p<0.05
: A_23_P35021	B3GALT6	2.939257969	2.108457956	1.394032051	0.155693212	1.394032051	0.02491462	p<0.05
: A_23_P17015	SCRN3	2.382143661	1.708777692	1.394062945	0.070625661	1.394062945	0.015462633	p<0.05
: A_23_P487	UCK2	3.278665411	2.350226696	1.395042196	0.07307595	1.395042196	0.012950314	p<0.05
: A_23_P371254	TAS2R43	1.954744061	1.40110158	1.395147996	0.009751812	1.395147996	0.020566643	p<0.05
: A_23_P158239	SHMT2	2.097534438	1.502537794	1.395994461	0.250131357	1.395994461	0.042993761	p<0.05
: A_23_P66392	OR4D1	1.133081971	0.811416287	1.396424977	0.248533657	1.396424977	0.038034356	p<0.05
: A_23_P41159	PPP4R2	1.993364359	1.426824912	1.397063047	0.129349335	1.397063047	0.032289027	p<0.05
: A_23_P120773	SLC25A1	0.847992167	0.606114148	1.399063475	0.090731957	1.399063475	0.040611082	p<0.05
: A_23_P43248	TAF2	3.435722986	2.455134789	1.399402999	0.188382337	1.399402999	0.025813928	p<0.05
: A_23_P145323	LY6G5C	1.716656213	1.226155958	1.400030886	0.014620834	1.400030886	0.014432933	p<0.05
: A_23_P251836	NPY5R	0.890457289	0.636010935	1.400066006	0.227530863	1.400066006	0.045539324	p<0.05
: A_23_P5115	WDR18	2.739140841	1.955894464	1.400454315	0.154479913	1.400454315	0.029497272	p<0.05
: A_23_P329399	NOD3	1.003058659	0.716231083	1.400467925	0.180834696	1.400467925	0.020691099	p<0.05
: A_23_P147984	TRIP12	1.819722093	1.298605152	1.401289753	0.181308003	1.401289753	0.034571991	p<0.05
: A_23_P130527	CDC37	1.665849545	1.188713172	1.401388984	0.077519133	1.401388984	0.042358128	p<0.05
: A_23_P141309	GLP2R	1.861448678	1.328067569	1.401621967	0.068020235	1.401621967	0.029596562	p<0.05
: A_23_P74766	HTR6	2.958026045	2.106029226	1.40455128	0.0721466	1.40455128	0.035710968	p<0.05
: A_23_P143992	APG7L	1.236247332	0.879512231	1.405605618	0.180961867	1.405605618	0.0444547	p<0.05
: A_23_P62136	PQBP1	1.169763779	0.831779528	1.406338748	0.15891381	1.406338748	0.01686087	p<0.05
: A_23_P213728	CAMLG	3.097256732	2.202038226	1.406540856	0.124220598	1.406540856	0.029225211	p<0.05
: A_23_P108657	WDSAM1	2.097807352	1.488381614	1.409455299	0.154641163	1.409455299	0.029152811	p<0.05
: A_23_P145463	SLC35B3	1.884980595	1.33720318	1.409644116	0.070995847	1.409644116	0.024444177	p<0.05
: A_23_P216564	FLJ20457	1.400479965	0.992072873	1.411670455	0.074480591	1.411670455	0.026732223	p<0.05
: A_23_P340953	DOC2A	4.543821496	3.217546488	1.412200729	0.138549722	1.412200729	0.014583274	p<0.05
: A_23_P3784	KIAA1972	1.904939244	1.348633862	1.412495487	0.243628234	1.412495487	0.028185171	p<0.05
: A_23_P52517		1.80779374	1.279829479	1.412527036	0.179403191	1.412527036	0.018344209	p<0.05
: A_23_P36305	FLJ00012	1.210993527	0.855744851	1.415133875	0.16391201	1.415133875	0.022053327	p<0.05
: A_23_P258992	LOC51252	1.390896186	0.981017346	1.417809983	0.196811187	1.417809983	0.023382642	p<0.05
: A_23_P70077		1.690324024	1.190944909	1.419313363	0.115363406	1.419313363	0.012713147	p<0.05
: A_23_P93531	TRAR1	3.233749323	2.276281087	1.420628297	0.183893629	1.420628297	0.013569052	p<0.05
: A_23_P345692	IL17D	1.963686217	1.381441596	1.421476103	0.138439129	1.421476103	0.041599928	p<0.05
: A_23_P341938	NOG	1.183753276	0.832453834	1.422004715	0.044236722	1.422004715	0.025230546	p<0.05
: A_23_P387624	FLJ36749	3.292482835	2.314947938	1.422270791	0.105902106	1.422270791	0.038084466	p<0.05
: A_23_P111088	OR2B2	1.138314171	0.800126991	1.422666882	0.180418589	1.422666882	0.021767218	p<0.05
: A_23_P27515	PLD3	2.673177635	1.877349666	1.423910358	0.094014915	1.423910358	0.01462087	p<0.05
: A_23_P43940	ADAMTSL3	0.761967564	0.534632226	1.425218172	0.00546977	1.425218172	0.02135752	p<0.05
: A_23_P423208	TPCN1	3.231392779	2.261870518	1.428637384	0.072244644	1.428637384	0.014890475	p<0.05
: A_23_P70290	TMEM30A	1.664392406	1.164666533	1.429072064	0.267902951	1.429072064	0.047945538	p<0.05
: A_23_P50121	MC4R	2.767065621	1.935445617	1.429678828	0.091210972	1.429678828	0.030042501	p<0.05
: A_23_P300080	FKSG83	1.446909571	1.0115111	1.430443593	0.13125928	1.430443593	0.026645537	p<0.05

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: A_23_P38603	KRTAP4-4	1.592216858	1.11192127	1.431951076	0.033192196	1.431951076	0.012642017	p<0.05
: A_23_P99536	MPP5	1.735197756	1.211093793	1.432752579	0.21228661	1.432752579	0.035309695	p<0.05
: A_23_P85874		1.150460327	0.80291228	1.4328593	0.291138382	1.4328593	0.039753464	p<0.05
: A_23_P412526	BCAP29	2.142621299	1.494661039	1.433516525	0.295250461	1.433516525	0.045712265	p<0.05
: A_23_P82693	PABPC1	2.889384888	2.01543032	1.433631746	0.091555436	1.433631746	0.018006418	p<0.05
: A_23_P213237	CBR4	3.322847442	2.317266124	1.43395159	0.278248494	1.43395159	0.039457342	p<0.05
: A_23_P20876	PTPDC1	0.67832093	0.472916638	1.434335093	0.229504611	1.434335093	0.023192444	p<0.05
: A_23_P365844	CRJ2	2.894642078	2.018031663	1.43438883	0.19005004	1.43438883	0.019963194	p<0.05
: A_23_P43079	FLJ20530	2.272551714	1.584179448	1.434529223	0.242039511	1.434529223	0.029462262	p<0.05
: A_23_P13554	ALG8	1.679518802	1.169451305	1.436159672	0.219894136	1.436159672	0.030316322	p<0.05
: A_23_P110304	CNOT6L	1.794772399	1.24930233	1.436619748	0.03438576	1.436619748	0.032355788	p<0.05
: A_23_P86403	KIF5B	2.059735506	1.431820791	1.438542811	0.083927694	1.438542811	0.010229997	p<0.05
: A_23_P216200	AGPAT5	1.686029563	1.171652046	1.439019006	0.052667398	1.439019006	0.013401578	p<0.05
: A_23_P251421	CDCA7	2.365134016	1.641593037	1.44075539	0.19089013	1.44075539	0.010786468	p<0.05
: A_23_P121	FLJ14100	0.612309561	0.424894588	1.441085807	0.202796984	1.441085807	0.021424787	p<0.05
: A_23_P162970	IPO4	2.209985772	1.531894545	1.442648764	0.024875604	1.442648764	0.011627017	p<0.05
: A_23_P217546	TMLHE	1.936564879	1.340667889	1.444477707	0.118490953	1.444477707	0.018102334	p<0.05
: A_23_P101932	ZNF527	0.764417665	0.528816557	1.445525209	0.272958909	1.445525209	0.0337302	p<0.05
: A_23_P2998	OXA1L	1.229688966	0.850596753	1.445677945	0.167312252	1.445677945	0.039457682	p<0.05
: A_23_P118530		1.295259597	0.895185414	1.446917675	0.050165149	1.446917675	0.011092001	p<0.05
: A_23_P41693	SIAT8D	1.197926482	0.826786726	1.448894188	0.057352327	1.448894188	0.011378336	p<0.05
: A_23_P323774	PTER	4.512341457	3.113419078	1.449320295	0.221081789	1.449320295	0.038215387	p<0.05
: A_23_P201227	T3JAM	0.961659144	0.663255174	1.449908242	0.053055667	1.449908242	0.017385369	p<0.05
: A_23_P98699	OR4A5	2.454978974	1.692304245	1.450672349	0.082943666	1.450672349	0.017795417	p<0.05
: A_23_P216869	ZNF189	1.144696309	0.788830177	1.451131489	0.276119105	1.451131489	0.048413871	p<0.05
: A_23_P43779	COPS4	3.19234531	2.199274665	1.451544621	0.25219049	1.451544621	0.03977588	p<0.05
: A_23_P98561	NYD-SP21	0.508251522	0.349971998	1.452263398	0.305843287	1.452263398	0.047427153	p<0.05
: A_23_P91168	Sep-10	2.051152026	1.411755632	1.45290869	0.169970867	1.45290869	0.021049962	p<0.05
: A_23_P151294	IFNG	2.365229929	1.626994804	1.453741538	0.02719774	1.453741538	0.04673704	p<0.05
: A_23_P5686	TBR1	1.822743726	1.253780681	1.453797903	0.02839311	1.453797903	0.03475128	p<0.05
: A_23_P143417	C20orf52	1.002687565	0.688133743	1.457111464	0.175447633	1.457111464	0.017178734	p<0.05
: A_23_P55641	P15RS	1.28347868	0.880786128	1.457196746	0.192736309	1.457196746	0.037576839	p<0.05
: A_23_P42331	HMGAI	2.681604368	1.836082341	1.460503327	0.108604054	1.460503327	0.013251997	p<0.05
: A_23_P14204	NARG1L	1.510123762	1.033956115	1.460529843	0.072273909	1.460529843	0.011467447	p<0.05
: A_23_P211227	POFUT2	1.137646214	0.778107562	1.462068059	0.245921317	1.462068059	0.041709923	p<0.05
: A_23_P30509		1.921987581	1.313796252	1.462926673	0.098857214	1.462926673	0.022097661	p<0.05
: A_23_P204669	CLEC1	2.060374096	1.407638097	1.463710097	0.153365496	1.463710097	0.021937495	p<0.05
: A_23_P209251		0.799907588	0.54629058	1.464252942	0.095330844	1.464252942	0.025350389	p<0.05
: A_23_P90172	PPP1R15A	1.505538065	1.025102949	1.468670114	0.225386987	1.468670114	0.028817586	p<0.05
: A_23_P66664	TADA2L	2.035512407	1.385314891	1.469349979	0.028390347	1.469349979	0.022994454	p<0.05
: A_23_P54918	LDHD	0.931857826	0.633504598	1.470956689	0.168680415	1.470956689	0.014300037	p<0.05
: A_23_P122134	NMUR2	2.164281108	1.471143191	1.471155984	0.142335149	1.471155984	0.047940526	p<0.05
: A_23_P98605	LOC51035	1.884845213	1.279621181	1.472971252	0.191962146	1.472971252	0.019030299	p<0.05
: A_23_P144872	GM2A	2.651555926	1.797573845	1.475074826	0.086542358	1.475074826	0.048440521	p<0.05
: A_23_P69931		2.23320537	1.511699092	1.477281677	0.059855288	1.477281677	0.023687846	p<0.05
: A_23_P205256	WDR20	0.420859661	0.28479131	1.477782668	0.064005454	1.477782668	0.04366136	p<0.05
: A_23_P32463	EXOSC4	0.844995843	0.570959214	1.479958326	0.110010948	1.479958326	0.027220225	p<0.05
: A_23_P105845	ARHGEF7	2.569936335	1.73435979	1.481778088	0.089585007	1.481778088	0.035514983	p<0.05
: A_23_P500000	SCEL	0.596007807	0.401635108	1.483953457	0.132227561	1.483953457	0.023342121	p<0.05
: A_23_P95619		1.613891058	1.086309792	1.485663731	0.068161003	1.485663731	0.028211185	p<0.05
: A_23_P255363	BAG2	2.64158878	1.776123279	1.487277832	0.230663762	1.487277832	0.038631265	p<0.05
: A_23_P211047	BACH1	1.425078998	0.95812848	1.487356892	0.269252694	1.487356892	0.033588364	p<0.05
: A_23_P36050	OR8K3	2.817084036	1.89306261	1.488109279	0.158198573	1.488109279	0.03496918	p<0.05

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: A_23_P65401	CFL2	1.794623384	1.205461963	1.488743269	0.237323058	1.488743269	0.026579659	p<0.05
: A_23_P21519	STK32B	1.890040528	1.267879773	1.490709583	0.222793804	1.490709583	0.042084509	p<0.05
: A_23_P300728	C7orf2	3.374243802	2.263012369	1.491040813	0.222204939	1.491040813	0.018696373	p<0.05
: A_23_P205098	APRIN	2.645412651	1.77314141	1.49193552	0.069494565	1.49193552	0.015717284	p<0.05
: A_23_P8279	SLC2A12	1.959168599	1.31290041	1.49224464	0.13687091	1.49224464	0.021358778	p<0.05
: A_23_P27256	TWSG1	2.17282637	1.455608936	1.492726732	0.060615803	1.492726732	0.020088354	p<0.05
: A_23_P41005	TEX264	1.922952658	1.287841426	1.493159498	0.20312692	1.493159498	0.015784593	p<0.05
: A_23_P254974	TATDN1	2.142367265	1.433231563	1.494780969	0.200957113	1.494780969	0.042190843	p<0.05
: A_23_P131176	FAM11B	1.68385961	1.125334395	1.496319331	0.10545254	1.496319331	0.011586102	p<0.05
: A_23_P106441	PAK2	1.079588547	0.719991128	1.499447014	0.223628222	1.499447014	0.023014158	p<0.05
: A_23_P105833	BIVM	0.909318425	0.60625008	1.499906483	0.264025195	1.499906483	0.0299319	p<0.05

FIG. 8
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