This work has been published in Nature Cell Biology, Aug 15, 2010 [Epub ahead of print].
DOI: 10.1038/ncb2092

Live imaging RNAi screen identifies PP2A-B55α and Importin β1 as key mitotic exit regulators in human cells

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When vertebrate cells exit mitosis, they reorganize various cellular structures to build functional interphase cells[1]. This depends on Cdk1 inactivation and subsequent dephosphorylation of its substrates[2-4]. Members of PP1 and PP2A phosphatase families can dephosphorylate Cdk1 substrates in biochemical extracts during mitotic exit[5, 6], but how this relates to postmitotic reassembly of interphase structures in intact cells is not known. Here, we used a live imaging assay to screen by RNAi a genome-wide library of protein phosphatases for mitotic exit functions in human cells. We identified a trimeric PP2A-B55α complex as a key factor for postmitotic reassembly of the nuclear envelope, the Golgi apparatus, and decondensed chromatin, as well as for mitotic spindle breakdown. Using a chemically-induced mitotic exit assay, we found that PP2A-B55α functions downstream of Cdk1 inactivation. PP2A-B55α isolated from mitotic cells had reduced phosphatase activity towards the Cdk1 substrate histone H1 and it was hyper-phosphorylated on all subunits. Mitotic PP2A complexes co-purified with the nuclear transport factor Importin β1, and RNAi depletion of Importin β1 delayed mitotic exit synergistically with PP2A-B55α. This demonstrates that PP2A-B55α and Importin β1 cooperate in the regulation of postmitotic assembly mechanisms in human cells.

In budding yeast, Cdk1 substrate dephosphorylation and mitotic exit depend on the Cdc14 phosphatase[7], but this function does not seem to be conserved in Cdc14 homologues of other species[2, 3, 8-11]. Studies in cycling *Xenopus* embryonic extracts suggest that phosphatases of both PP1[5] and PP2A[6] families can contribute to Cdk1 substrate dephosphorylation during vertebrate mitotic exit, whereas Ca^{2+}-triggered mitotic exit from cytostatic factor-arrested egg extracts depends on calcineurin[12, 13]. Early genetic studies in *Drosophila melanogaster*[14, 15] and *Aspergillus nidulans*[16] reported late mitotic defects for PP1 and PP2A mutants. However, the assays used in these studies were not specific for mitotic exit, because they scored prometaphase arrest or anaphase chromosome bridges, which can result from earlier mitotic defects.

Intracellular targeting of serine/threonine phosphatase complexes to specific substrates is mediated by association of a small group of common catalytic subunits with a diverse spectrum of regulatory/targeting subunits[3, 4, 17]. It is possible that mitotic exit in intact cells requires phosphatases that have not been detected with previous assays using *in vitro* extracts. In practice, the short duration of mitotic exit makes it difficult to assay this process, which explains why previous RNAi screening on cell division regulators[18] did not annotate mitotic exit phenotypes.

To assay mitotic exit in live human cells, we measured the timing from anaphase onset until nuclear reformation. We generated a HeLa cell line stably expressing a chromatin marker (histone 2B fused to a red fluorescent protein; H2B-mCherry[19]) to visualize the metaphase - anaphase transition (Fig. 1a-c). To probe for postmitotic nuclear reassembly, we stably co-expressed a nuclear import substrate (importin β-binding domain of importin α fused to monomeric EGFP; IBB-mEGFP[20]), which is cytoplasmic in mitosis, and co-localizes with chromatin regions after reassembly of a functional nuclear envelope (Fig. 1a, b).

To annotate mitotic exit timing automatically in time-lapse movies, we used in house-developed computational methods (*CellCognition*[21]). Individual cells were detected and tracked over time, and the mitotic stage of each cell was assigned based on classification of chromatin morphology (Fig. 1c). Nuclear breakdown and reassembly was determined based on the ratio of mean IBB-mEGFP fluorescence on chromatin regions versus surrounding cytoplasmic regions (Fig. 1d). Automated annotation of mitotic exit timing (4.70±0.89 min; mean±s.d.) closely matched manual annotation (4.88±0.84 min; mean±s.d.; n = 270 cells, see Supplementary Information, Fig. S1).

We next imaged cells over ~24 h with time-intervals of ~3.8 min after transfection of 675 different siRNAs targeting a genome-wide set of 225 annotated human protein phosphatases, including catalytic and associated regulatory and scaffolding subunits (3 different siRNAs per gene, two technical replicas; full list of siRNAs see Supplementary Information, Table 1). On average, this yielded ~87 automatically annotated mitotic events per movie (total: 113,236 mitotic events). We determined the mean mitotic exit timing for all data sets that contained more than 10 mitotic events (n = 1,278 out of the 1,350 movies). Five siRNAs reproducibly scored as hits above a significance cut-off at three standard deviations above the mean of all data points (z-score = 3; Fig. 2a). These five siRNAs

targeted three distinct genes, encoding each of the three subunits of a heterotrimeric PP2A complex, PPP2CA (catalytic subunit alpha, subsequently labelled as "CA"), PPP2R1A (scaffold subunit alpha, subsequently labelled as "R1A"), and PPP2R2A (regulatory B-type subunit, also termed PR55α or B55α, subsequently labelled as "B55α"). The remaining four siRNAs targeting the same PP2A genes also prolonged mitotic exit, albeit below the cut-off level (Fig. 2a).

To validate the hits, we tested an extended set of 6 siRNAs per gene, which all significantly ($p < 0.001$; t-test) prolonged mitotic exit (Supplementary Information, Fig. S2a-c). The mRNA depletion levels correlated with phenotypic penetrance (Supplementary Information, Fig. S2a-f), indicating specificity of the phenotype. The RNAi depletion was also efficient at the protein level (Supplementary Information, Fig. S2g). We next depleted endogenous B55α in a HeLa cell line stably expressing EGFP-tagged mouse B55α. Transfection of a siRNA targeting a non-conserved sequence on the human B55α mRNA efficiently depleted endogenous B55α, but not the exogenous mouse B55α (Fig. 2b), and these cells showed normal mitotic exit timing (Fig. 2c). In contrast, transfection of a siRNA targeting both human and mouse B55α mRNA, or R1A, in these cells efficiently delayed mitotic exit (Fig. 2c). This validates that the observed phenotype was caused by on-target depletion of B55α mRNA.

The family of PP2A protein phosphatases is involved in many cellular processes, including earlier mitotic stages[3]. It is generally believed that the regulatory B-type subunit confers substrate specificity and thereby regulates diverse functions of PP2A[3, 17]. Depletion of CA or R1A significantly ($p < 0.001$; t-test) prolonged mitotic progression from nuclear envelope breakdown until anaphase (Fig. 2d; same cells shown in Fig. 2e), as expected from the known functions of PP2A complexes involving other B-type subunits in spindle assembly and chromosome cohesion[3]. In contrast, early mitotic progression was unaffected in B55α-depleted cells. These data indicate that PP2A function is required at all stages of mitosis, whereas the B55α subunit is rate-limiting only for post-anaphase progression.

Cells depleted for PP2A-B55α subunits were delayed but not arrested during mitotic exit (Fig. 2e). This may be explained by incomplete RNAi depletion or involvement of other unknown factors with redundant function. To investigate if additional phosphatases become limiting in the absence of B55α, we screened the phosphatase-targeting siRNA library in a background of synthetic B55α RNAi depletion. Increased mitotic exit delay occurred upon co-depletion of R1A or CA subunits with B55α (2/3 oligos scoring above a z-score threshold of 3; Fig. 2f). However, none of the other 222 phosphatases showed consistent additive phenotype increase (5 other siRNA oligos delayed slightly above the z-score threshold, but could not be confirmed by different siRNAs targeting the same genes). Co-transfection of siRNAs targeting all three PP2A-B55α subunits (labelled as siPP2A-B55α throughout the manuscript) caused the most pronounced prolongation of mitotic exit (14.76±6.50 min versus 4.86±1.07 min in control; mean±s.d.; $n \geq 205$; Fig. 2g; Supplementary Information, Fig. S2g). The additive effect of combinatorial PP2A-B55α subunit depletions suggests that residual levels of this phosphatase may account for a slow and gradual mitotic exit. That no other RNAi conditions further delayed mitotic exit in combination with B55α depletion underlines the particular importance of PP2A-B55α for mitotic exit.

To address if PP2A-B55α controls postmitotic reassembly of cellular structures other than the nucleus, we generated a HeLa cell line stably expressing a fluorescent Golgi marker (galactosyl transferase, GalT-mEGFP[22]) and H2B-mCherry (Fig. 3a). Confocal time-lapse microscopy showed that depletion of the PP2A-B55α complex significantly ($p < 0.001$; t-test) delayed postmitotic clustering of Golgi fragments (Fig. 3a, b, e; 25.5±5.86 min versus 11.17±2.73 min in control; mean±s.d.; $n \geq 30$; for single depletion of B55α see Supplementary Information, Fig. S3b, c). In another mitotic exit assay, we imaged a HeLa cell line stably expressing H2B-mCherry and mEGFP-α-tubulin[19] (Fig. 3c). PP2A-B55α-depleted cells showed significantly delayed disassembly of spindle pole-associated microtubules (Fig. 3c, d, f). Postmitotic chromosome decondensation was also significantly ($p < 0.001$; t-test) delayed in PP2A-B55α-depleted cells (18.29±2.29 min versus 8.94±5.89 min in control; mean±s.d.; $n \geq 97$; see also Supplementary Information Fig. S3d). These data show that PP2A-B55α contributes to postmitotic reassembly of various interphase cell structures.

We next investigated how PP2A-B55α depletion affected progression through interphase, using a monoclonal cell line expressing H2B-mCherry and a DNA replication marker (EGFP-PCNA[23];

Supplementary Information, Fig. S4a-d). PP2A-B55α-depleted cells were prolonged in G1 (8.00±2.09 h versus 5.77±1.11 h in control; mean±s.d.; n ≥ 39; Supplementary Information, Fig. S4b), as expected after perturbed mitotic exit. On the other hand, PP2A-B55α-depleted cells had a significantly ($p < 0.001$; t-test) shorter G2 phase (2.91±0.39 h versus 3.95±0.78 h in control; mean±s.d.; n ≥ 38; Supplementary Information, Fig. S4d). This is consistent with previous observations in *Xenopus* embryonic extracts[6, 24].

The mitotic exit phenotypes observed after PP2A-B55α depletion could be due either to a failure in Cdk1 inactivation, or to misregulated Cdk1 substrate dephosphorylation, or both. To discriminate between these possibilities, we established a mitotic exit assay using chemical inactivation of Cdk1. Cells were first arrested in metaphase by the proteasome inhibitor MG132 and then forced to exit from mitosis by adding the Cdk inhibitor flavopiridol to 20 μM final concentration, still in the presence of MG132[25] (Fig. 4a). This efficiently promoted most hallmarks of physiological mitotic exit, including nuclear reassembly (>95% of all metaphase cells; n = 99), Golgi clustering (>90%; n = 103), chromosome decondensation, and re-attachment of the cells to the substratum (Fig. 4b, d). Only chromosome segregation did not occur, presumably due to the suppression of securin degradation by MG132. Higher concentrations of flavopiridol did not further accelerate nuclear reassembly (9.4±1.1 min at 160 μM compared to 9.3±1.3 min at 20 μM; mean±s.d.; n ≥ 30), indicating that Cdk1 inhibition was complete. PP2A-B55α depletion significantly ($p < 0.001$; t-test) delayed nuclear reassembly in this assay (20.67±3.30 min versus 9.86±0.95 min in control; mean±s.d.; n ≥ 29; Fig. 4b, c, f; for single depletion of B55α, see Supplementary Information, Fig. S5a-c). Golgi reformation was also delayed (36.01±9.38 min versus 16.91±2.27 min in control; n ≥ 35; Fig. 4d, e, g). We conclude that a main function of PP2A-B55α in promoting mitotic exit must be downstream of Cdk1 inactivation.

To test if PP2A-B55α depletion affected Cdk1 substrate dephosphorylation, we prepared extracts from HeLa cells synchronized to different time points after chemical induction of mitotic exit. Cdk1 substrate phosphorylation, detected on quantitative Western Blots by an anti-phospho-serine antibody that specifically recognizes the Cdk target sequence (K/R) pS PX (K/R) (pS = phospho-serine), dropped to ~23% within 18 min in negative controls, whereas it remained at ~66% in PP2A-B55α-depleted cells (Fig. 4h; for single depletion of B55α see Supplementary Information, Fig. S5e). This substantiates the conclusion that PP2A-B55α functions downstream of Cdk inactivation during mitotic exit and shows that PP2A-B55α is required for timely Cdk1 substrate dephosphorylation.

Previous studies in *Xenopus* embryonic extracts[5, 13] and HeLa cells[26] indicated reduced phosphatase activity towards Cdk1 targets during early mitosis. Human PP2A-B55α isolated from mitotic cells had significantly reduced activity towards Cdk1-phosphorylated histone H1 (Fig. 5a; 71±15% versus 100±11% in interphase, mean±s.d.; n = 15; $p < 0.001$; t-test). However, we did not detect any cell cycle-dependent differences in the phosphatase activity towards another well-characterized model substrate, phosphorylase *a* (Fig. 5b). This suggests cell cycle-regulated changes of PP2A-B55α substrate specificity.

All three PP2A-B55α subunits were expressed at similar levels in interphase and mitosis (Supplementary Information, Fig. S6a), suggesting that mitotic PP2A-B55α is unlikely to be regulated at the protein level. We addressed potential changes in PP2A complex composition at different cell cycle stages by purification of Localization and Affinity Purification (LAP)-tagged R1A or B55α stably expressed from endogenous promoters[27]. R1A co-purified with several mitosis-specific binding partners (Fig. 5c), two of which were identified by mass spectrometry as the nuclear transport factors Importin α1 and Importin β1. Besides the function in nuclear transport during interphase, Importin β1 is part of a mitotic regulatory system involving the small GTPase Ran, which is known to control mitotic spindle and nuclear envelope assembly[28]. After validation of the mitosis-specific interaction between Importin β1 and R1A by Western Blotting (Fig. 5d), we investigated if Importin β1 contributes to mitotic exit progression. Because the specificity of the nuclear reassembly assay may be compromised after depletion of a nuclear import factor, we assayed mitotic exit by Golgi reformation. Importin β1 depletion (Supplementary Information, Fig. S2h, i) significantly delayed postmitotic Golgi reassembly (Fig. 5e; 14.7±5.0 min versus 10.1±1.4 min in control; mean±s.d.; n ≥ 30; $p \leq 0.001$), which was further increased after co-transfection of siRNAs targeting R1A or B55α (25.9±6.3 min, and 22.5±8.1 min, respectively). Importin β1 depletion also prolonged earlier mitotic

stages (Supplementary Information, Fig. S7), as expected from its known function in spindle assembly. These data demonstrate that PP2A-B55α and Importin β1 jointly promote mitotic exit.

By mass spectrometry, we detected five phosphorylation sites on the PP2A complex purified from mitotic cells (Fig. 5f). We estimated the relative quantities of phosphopeptides by a semi-quantitative approach, using the extracted ion chromatogram for peak area quantitation of the peptide elution profiles (Supplementary Information, Fig. S8). S167 phosphorylation on B55α was estimated highly abundant at 55% (mean; n = 2 independent experiments), whereas the other sites were phosphorylated on <1% of the eluted peptides (quantifications provided in Fig. 5f; the phosphorylation levels of S8 on R1A could not be determined because no unmodified peptides containing this site were detected). PP2A is known to auto-dephosphorylate[29], therefore the absolute phosphorylation levels in cells may be higher. All of the four quantified phosphorylations were enriched more than 5-fold on PP2A purified from mitotic cells (Fig. 5f; Supplementary Information, Fig. S8). To test if the most abundant mitotic phosphorylation, S167 on B55α, contributes to the regulation of PP2A complex assembly, we expressed GST-tagged phospho-mimicking S167E mutant of B55α for isolation of PP2A complexes from interphase and mitotic HeLa cells. Indeed, the S167E mutant bound less efficiently to the CA and R1A subunits, as compared to wildtype B55α, or a non-phosphorylatable S167A mutant (Fig. 5g; Supplementary Information, Fig. S9h).

To the best of our knowledge, this study provides the first comprehensive screen for mitotic exit phosphatases in human cells. B55α has been previously shown to increase PP2A activity towards Cdk1 phosphorylation sites[30], consistent with the possibility that PP2A-B55α promotes mitotic exit by direct dephosphorylation of Cdk1 substrates. The *in vitro* phosphatase activity of mitotic PP2A-B55α towards Cdk1-phyosphorylated H1 was downregulated. However, it is not known which of the many putative PP2A substrates may be affected by this regulation, and we therefore cannot precisely estimate the extent by which PP2A regulation shapes the kinetics of Cdk1 substrate dephosphorylation.

Our data raise interesting possibilities for PP2A regulatory mechanisms (Fig. 5h). Phospho-mimicking S167E mutation on B55α impaired the binding of R1A and CA subunits, consistent with the possibility that phosphorylation contributes to a cell cycle-dependent regulation of PP2A-B55α complex assembly. This may further involve mitotic CA-T304 hyper-phosphorylation, as a previous study showed that a phospho-mimicking CA-T304D mutation also suppresses assembly of B55α into PP2A complexes[31]. Importin β1 may regulate PP2A by direct binding, by a nuclear-cytoplasmic targeting mechanism, or as a molecular chaperone[28]. In this context, it is interesting to note that Importin β1 is structurally related to the R1A subunit and members of the B' family of regulatory PP2A subunits[32]. Even though it is possible that Importin β1 functions in a mitotic exit pathway independently of PP2A, the here observed physical and functional interaction suggests a link between the Importin/Ran and Cdk1-phosphorylation regulatory systems.

In contrast to the *Xenopus* embryonic extract system[6], depletion of B55δ in HeLa cells (down to 20% mRNA level; Supplementary Information, Fig. S2j) did not delay mitotic exit. This may reflect different relative expression levels of the B55-subfamily isoforms in the two systems or technical limitations of the depletion methods. A previous study proposed that PP1 dominates as a Cdk1-counteracting phosphatase in cycling *Xenopus* embryonic extracts[5]. That we did not detect mitotic exit delays after RNAi depletion of any of the PP1 catalytic or regulatory subunits may be due to the cellular context of our phenotypic assays instead of homogenized extracts, or to differences between embryonic and somatic mitosis. However, potential functional redundancy between different PP1 catalytic isoforms that were targeted only individually in our screen may have masked phenotypes and we therefore cannot rule out that PP1 also contributes to mitotic exit in human somatic cells.

In conclusion, our study reveals PP2A-B55α and Importin β1 as key regulators of cellular reassembly mechanisms during mitotic exit. Mitotic exit has been recently recognized as a target for improved, next-generation cancer therapeutics[33]. B55α and Importin β1 are therefore good target protein candidates for the development of mitotic exit-specific inhibitors.

Acknowledgments

The authors thank F. Uhlmann and B. Novak for critical comments on the manuscript. We thank S. Maar, the ETHZ Light Microscopy Centre (LMC) and the ETHZ RNAi Screening Centre (RISC), M. Augsburg (MPI-CBG), M. Leuschner (MPI-CBG), and A. Ssykor (MPI-CBG) for excellent technical assistance. We thank U. Kutay (ETHZ) for anti-Importin β1 and anti-nucleolin antibodies, J. Rohrer (University Zurich) for providing GalT-EGFP plasmid, J. Ellenberg (EMBL Heidelberg) for IBB-EGFP, M.C. Cardoso (Technical University Darmstadt) for EGFP-PCNA plasmid, and Sanofi Aventis and the National Cancer Institute for providing Flavopiridol. This work was supported by SNF research grant 3100A0-114120, SNF ProDoc grant PDFMP3_124904, a European Young Investigator (EURYI) award of the European Science Foundation to DWG, and a MBL Summer Research Fellowship by the Evelyn and Melvin Spiegel Fund to DWG, a Roche Ph.D. fellowship to MHAS, and a Mueller fellowship of the Molecular Life Sciences Ph.D. program Zurich to MH. MH and MHAS are fellows of the Zurich Ph.D. Program in Molecular Life Sciences. VJ and JG were supported by grants of the 'Geconcerteerde OnderzoeksActies' of the Flemish government, the 'Interuniversitary Attraction Poles' of the Belgian Science Policy P6/28 and the 'Fonds voor Wetenschappelijk Onderzoek-Vlaanderen'. AIL is a Wellcome Trust Principal Research Fellow. AAH acknowledges funding by the Max Planck Society, the EU-FP6 integrated project MitoCheck, and the BMBF grant DiGtoP [01GS0859]. Work in the groups of KM and JMP was supported by the EU-FP6 integrated project MitoCheck, Boehringer Ingelheim and by the GEN-AU programme of the Austrian Federal Ministry of Science and Research (Austrian Proteomics Platform III), by MeioSys within the Seventh Framework Programme of the European Commission, and by Chromosome Dynamics, which is funded by the Austrian Science Foundation (FWF).

Author contributions

MHAS performed all experiments except of the mass spectrometry and *in vitro* phosphatase assays, and wrote part of the paper. MH implemented software for automated imaging and data analysis. VJ, EI, and JG performed *in vitro* phosphatase assays and B55α phospho-mutant analysis. JH and JMP designed and performed PP2A purification. KM and OH performed mass spectrometry. LTM and AIL compiled the phosphatase screening library. IP and AAH generated the cell lines stably expressing LAP-tagged PP2A subunits. DWG conceived the project, designed the screening strategy, and wrote the paper.

Figure legends

Figure 1. Live imaging assay for mitotic exit timing. (a) Automated time-lapse imaging of HeLa cell line stably expressing a chromatin marker (H2B-mCherry; red) and a nuclear import substrate IBB-EGFP (green). The selected images show about 13% of the movie field-of-view. See Supplementary Information, Movie S1. **(b)** Single cell progressing through mitosis. **(c)** Automated detection of chromatin regions, tracking of cells over time, and annotation of mitotic stages by supervised machine learning and classification of chromatin morphologies. See Supplementary Information, Movie S2. **(d)** Automated detection of nuclear breakdown and reassembly. Chromatin regions (red) were defined by automated segmentation of the chromatin fluorescence (see Fig. 1c). Cytoplasmic regions (green indicates outer boundary, red is inner boundary) were derived by dilation of the chromatin regions. The ratio of mean IBB-EGFP fluorescence in chromatin / cytoplasm regions served to automatically determine nuclear envelope breakdown (orange bar) and reformation after anaphase (IBB onset, blue bar). Anaphase onset was defined by the classification of chromatin morphology (violet bar, see (c)). Scale bars: 10 μm.

Figure 2. RNAi screen for mitotic exit regulators. (a) RNAi screen of a genome-wide library of annotated protein phosphatases using the mitotic exit assay shown in Fig. 1. Individual data points correspond to the z-score based on the mean mitotic exit timing in individual movies, determined in two technical replicas. Negative controls are black. SiRNA oligos causing phenotypes reproducibly scoring above a z-score threshold of > 3 (dashed lines) were considered as hits (highlighted by colours as indicated in legend; siRNAs targeting the same genes as the hits but with z-scores below threshold are also highlighted). **(b)** RNAi depletion of B55α in a HeLa cell line stably expressing localization-and-affinity (LAP)-tagged mouse-B55α from a bacterial artificial chromosome (BAC; for localization see Supplementary Information, Fig. S6b). Cells were transfected with siRNA targeting either human B55α alone (h), or both human- and mouse-B55α (m/h). Quantitative Western Blot probing with anti-B55α antibody that recognizes both mouse and human B55α. **(c)** Rescue of mitotic exit delay phenotype by exogenous B55α. Mouse-B55α-LAP cells were RNAi-depleted for human (h) or both human/mouse (m/h) B55α, as validated in (b). **(d)** Cumulative histograms for early mitotic progression. Nuclear envelope breakdown (NEBD) until anaphase onset was measured in control and RNAi-depleted cells ($n \geq 64$ in all conditions). **(e)** Cumulative histograms of mitotic exit. Anaphase onset until nuclear import of IBB-EGFP was measured for the same cells shown in (d). **(f)** Synthetic depletion RNAi screen for mitotic exit phosphatases. Assay, sample preparation, and siRNA library was identical to the screen shown in (a), except that siRNA targeting B55α was co-transfected in each experimental condition. Negative controls (black) were only transfected by non-targeting siRNA. The plot shows the ranked z-scores of a single replica, calculated as in (a). Dashed line indicates z-score threshold. **(g)** Time-lapse images of a cell depleted of all three PP2A-B55α subunits progressing through mitotic exit, full movie shown in Supplementary Information, Movie S4. For negative control, see Supplementary Information, Movie S3. Scale bars: 10 μm.

Figure 3. PP2A-B55α controls postmitotic Golgi assembly, spindle breakdown and chromatin decondensation. (a) Confocal time-lapse movie of a control cell expressing H2B-mCherry and the Golgi marker GalT-EGFP, see Supplementary Information, Movie S5. Golgi reassembly was scored based on clustering into two distinct patches per cell (t = 9 min). **(b)** Golgi reassembly in a PP2A-B55α-depleted cell, see Supplementary Information, Movie S6. **(c)** Confocal time-lapse images of mitotic spindle disassembly and chromosome decondensation in a control cell, see also Supplementary Information, Movie S7. Spindle disassembly was scored based on the first apparent detachment of spindle pole-associated microtubules from chromatin masses (t = 9 min). **(d)** Mitotic spindle disassembly in a PP2A-B55α-depleted cell, see Supplementary Information, Movie S8. **(e, f)** Cumulative histograms of postmitotic Golgi clustering **(e)**, or spindle disassembly **(f)** relative to anaphase onset (t = 0 min). Scale bars: 10 μm.

Figure 4. PP2A-B55α functions downstream of Cdk1 inactivation. **(a)** Experimental protocol for mitotic exit induced by chemical inactivation of Cdks in absence of proteasome-mediated degradation. **(b)** Time-lapse images of a control cell expressing H2B-mCherry and IBB-EGFP, see Supplementary Information, Movie S9. Dashed red line indicates addition of flavopiridol, green bar indicates onset of nuclear IBB-EGFP import. **(c)** Time-lapse images of a cell transfected with siRNAs targeting PP2A-B55α, see Supplementary Information, Movie S10. **(d, e)** Golgi reassembly after chemically-induced mitotic exit. **(d)** Control cell. **(e)** Cell transfected with siRNAs targeting PP2A-B55α. **(f, g)** Cumulative histograms of nuclear reassembly **(f)** and Golgi reassembly **(g)** timing based on the data shown in (b-e). **(h)** Detection of Cdk1 substrate phosphorylation by an anti-phospho-serine antibody that specifically recognizes the Cdk target sequence (K/R) pS PX (K/R) (pS = phospho-serine) on Western Blot. Samples were prepared after chemical induction of mitotic exit in synchronized cells in presence of proteasome inhibitor as in (a). In control cells, Cdk substrates dephosphorylate rapidly (siControl, lanes 1-7). Cells depleted for PP2A-B55α show delayed dephosphorylation (lanes 8-14). Scale bars: 10 μm.

Figure 5. Cell cycle-dependent regulation of PP2A-B55α. **(a)** PP2A-B55α isolated from nocodazol-treated mitotic (M) or unsynchronized interphase cells (I) by pulldown of GST-B55α was assayed for phosphatase activity towards Cdk1/cyclin B-phosphorylated histone H1 (n = 15, bars indicate mean; error bars indicate s.d.; ** depicts significance by t-test; $p < 0.001$). **(b)** PP2A-B55α activity towards substrate phosphorylase a (n = 3). **(c)** Purification of PP2A complexes from interphase (I) or mitotic (M) HeLa cells stably expressing LAP-tagged R1A or B55α baits. Two mitosis-specific bands were identified by mass spectrometry: Importin β1 (1), and Importin α1 (2). Expected positions of the bands from endogenous PP2A subunits are indicated on the right, migration positions of mouse baits are marked with asterisks. **(d)** PP2A complexes were purified with R1A-LAP and probed by anti-R1A and anti-Importin β1 antibodies on a Western Blot. **(e)** Importin β1 function in mitotic exit. Cells expressing H2B-mCherry and GalT-EGFP were transfected with siRNAs as indicated. Timing from anaphase (t = 0 min) until Golgi reassembly was assayed as in Fig. 3 ($n \geq 30$ for each condition). **(f)** Phosphorylation sites on PP2A-B55α identified by mass spectrometry highlighted in red on the 3D structure of PP2A-B55α[34] and in the primary sequence context. The abundance of phosphorylated peptide in the mitotic sample was estimated by peak area quantification of the elution profiles, indicated as percentage of total peptide based on elution profile peak area normalization. Mitotic phosphorylation increase (indicated in brackets) was estimated by comparing the normalized peak area quantifications of phosphorylated peptides in interphase (I) and mitotic (M) samples. **(g)** B55α-S167 phosphorylation affects PP2A complex assembly. GST-tagged wildtype-B55α, non-phosphorylatable S167A, or phospho-mimicking S167E mutants of B55α were isolated from unsynchronized (I), or mitotic (M) cells by GST-pulldown. PP2A subunits were detected on Western Blots by anti-GST, anti-R1A, and anti-CA antibodies. **(h)** Model for mitotic exit control. Dephosphorylation of a broad range of mitotic Cdk1 substrates promotes reassembly of interphase cells during mitotic exit. A balance of kinase (Cdk1-Cyclin B) and phosphatase (PP2A-B55α) activities determines the substrate dephosphorylation kinetics during mitotic exit. Green indicates activated state, red indicates lower activity, P indicates phosphorylation.

Online Methods

Cell lines and plasmids

The HeLa Kyoto cell line was obtained from S. Narumiya, Kyoto University and cultured in DMEM (GIBCO) supplemented with 10% foetal bovine serum (PAA Laboratories) and 1% Penicillin/Streptomycin (Invitrogen). All live imaging experiments were performed using monoclonal reporter cell lines that were generated as described in [35]. For a complete list of plasmids and cell lines see Supplementary Information, Tables 3 and 4. Cells were grown either in 96 well microtiter plates (Greiner), or on LabTek chambered coverslips (Nunc) for live microscopy. Live cell imaging was performed in DMEM containing 10% foetal calf serum and 1% Penicillin/Streptomycin, but without phenolred and riboflavin to reduce autofluorescence of the medium[35].

The BAC RP24-103C16, harboring mouse PP2A-B55α (PPP2R2A) as well as BAC RP24-255O20 harboring mouse PPP2CA, were obtained from the BACPAC Resources Center (http://bacpac.chori.org). The LAP (EGFP-IRES-Neo)-cassette was PCR amplified using primers that carry 50 nucleotides of homology to the C-terminus of each of the target genes. Recombineering and stable transfection of the modified BAC was performed as described[27].

Live cell imaging

Automated microscopy with reflection-based laser autofocus was performed on a Molecular Devices ImageXpressMicro screening microscope equipped with 10x 0.5 N.A. S Fluor dry objective (Nikon), controlled by in-house developed Metamorph macros[21]. Cells were maintained in a microscope stage incubator at 37ºC in humidified atmosphere of 5% CO_2 throughout the entire experiment. Illumination was adjusted that cell death rate was below 5% in untreated control cells. Confocal microscopy was performed on a customized Zeiss LSM 510 Axiovert microscope using a 20x 0.8 N.A. Plan-

Apochromat dry, a 40x 1.3 N.A. Oil DIC EC Plan-Neofluar, or 63x 1.4 N.A. Oil Plan-Apochromat objective (Zeiss). The microscope was equipped with piezo focus drives (piezosystemjena), custom-designed filters (Chroma), and EMBL incubation chamber (European Molecular Biology Laboratory), providing a humidified atmosphere at 37°C with 5% CO_2.

For imaging chemically-induced mitotic exit, cells were seeded in chambered LabTek coverslips overnight and transfected with the respective siRNAs as described above. 52 h post transfection, the medium was replaced with imaging medium containing 30 μM of the proteasome inhibitor MG132 (Sigma). The chambered coverslips were placed to the microscope stage incubator at 37ºC in humidified atmosphere of 5% CO_2 for around 45 minutes, during which imaging locations with metaphase arrested cells were selected. These cells were imaged for 10-15 minutes, before mitotic exit was induced with 20 μM of the CDK inhibitor Flavopiridol[25].

Image analysis and statistical analysis

Automated image analysis was performed by in house-developed *CellCognition* software[21] (http://www.cellcognition.org). Cell nuclei and mitotic chromosome masses were detected by local adaptive thresholding. Cytoplasmic regions were derived by region growing of the chromatin segmentation to a fixed size. Next, texture and shape features were calculated for each object and samples for mitotic classes were manually annotated for supervised classification. Support vector machine classification was by radial-based kernel and probability estimates. Tracking cells over time was by a constrained nearest-neighbour, with an algorithm that supported trajectory splitting and merging. Mitotic events were detected in the graph structure based on the transition from prophase to prometaphase. Increase of the nuclear/cytoplasmic ratio of mean IBB-mEGFP fluorescence >1.5-fold above the ratio at the time point of chromosome segregation defined the state with nuclear envelope assembled. In the RNAi screen, mean mitotic exit timing was normalized per 96-well plate to compensate slight differences in the temporal sampling rate. Z-scores were calculated based on the mean and standard deviation of all data points. All statistical testing was by two-tailed Student's t-test.

RNAi

The human siRNA phosphatase library was based on version V3.0 from Qiagen and complemented with custom siRNAs targeting missing phosphatases. For a complete list of siRNA oligos see Supplementary Information, Tables 1 and 2. RNAi duplexes were transfected in liquid phase with either Oligofectamine (Invitrogen) or HiPerfect (Qiagen) according to the manufacturer's protocols. Final siRNA concentrations were 50 nM for Oligofectamine or 10 nM for HiPerfect. Cells were reversely transfected in 96 well microtiter plates and incubated for about 40 h before imaging.

Quantitative real time PCR

mRNA was extracted from cells 40 h after transfection of siRNAs, using the TurboCapture 8 mRNA Kit (Qiagen), cDNA was prepared using random hexamer primers (Microsynth) and Ready-to-go you-prime first-strand beads (GE Healthcare). Real time PCR was performed using LightCycler 480 SYBR Green I Master (Roche Diagnostics). Primers were designed using AutoPrime (www.autoprime.de) or Clone Manager. Primer pairs were: *CA* (5'-GGAGCTGGTTACACCTTTG-3', 5'-CCAGTTATATCCCTCCATCAC-3'), *R1A* (5'-CTTCAATGTGGCCAAGTCTC-3', 5'-TCTAGGATGGGCTTGACTTC-3') *B55α* (5'-ATTCGGCTATGTGACATGAG-3', 5'-GACCTGTTACTGGGATCTTC-3'), *B55δ* (5'-CTG AAAGACGAAGATGGAAG-3', 5'-AATATTGGGACCCGTAGC-3', *Importin β1* (5'- CAGATACG AGGGTACGAGTG-3', 5'-TTTCATTGCTTCGATTGTG-3', *GAPDH* (5'-CGTGTCAGTGGTGGACCTGACC-3', 5'-CTGCTTCACCACCTTCTTGATGTCA-3').

Protein blotting

Pelleted cells were washed with PBS and total protein lysates prepared in lysis buffer (50 mM Tris, pH 7.5, 150 mM NaCl, 1% Nonidet P-40, 10% glycerol, 2 mM EDTA), supplemented with Mini-Complete protease inhibitor tablet (Roche), and 20 mM beta-glycerophosphate. Protein concentrations were determined using a BCA kit (Pierce). The following primary antibodies were used: polyclonal rabbit-anti-PPP2CA (1:2,000 dilution, Cell Signaling), polyclonal rabbit-anti-PPP2R1A (1:2,000 dilution, Cell Signaling), monoclonal mouse-anti-PP2A-B55-alpha (1:500 dilution, Santa Cruz), polyclonal rabbit-anti-phospho-(Ser) CDKs substrate (1:1,000 dilution, Cell Signaling), monoclonal mouse-anti-CyclinB1 (1:5,000 dilution, Santa Cruz), monoclonal mouse-anti-Actin (1:50,000 dilution, Millipore).

For the chemically-induced mitotic exit assay, nocodazole arrested cells (100 ng/ml for 17 h; Sigma) were incubated for 30 min in 30 μM of MG132 (Sigma), collected by shake-off, washed in PBS containing MG132, resuspended in 800 μl of PBS (+MG132), and 100 μl of this suspension was aliquoted in 1.5 ml centrifugation tubes and kept at 37°C. Mitotic exit was induced by adding flavopiridol to 20 μM (provided by the National Cancer Institute with permission by Sanofi Aventis). Cell aliquots were lysed at 3 minute intervals over a time period of 18 minutes, by adding 5x concentrated SDS cracking buffer to the respective aliquot, and boiling it for 5 minutes at 95°C. Quantitative Western blotting was performed using the LICOR Odyssey system or with the FluorChem system from Alpha Innotec.

Immunoprecipitation and GST pull downs

Immunoprecipitations of HA-CA-transfected HeLa Kyoto cells were performed as described[31]. HA-CA complexes were subjected to Western blotting with monoclonal mouse anti-C and anti-A (1:2,000, Dr. S. Dilworth), and polyclonal rabbit anti-B55α antibodies (1:500, Calbiochem).

Subconfluent HeLa Kyoto cells expressing GST-B55α were untreated (I) or mitotically arrested with nocodazole (100 ng/ml for 16 h) (M). Following collection by scraping (I) or shake off (M), cells were washed in PBS, pooled and lysed in 1 ml NET buffer (50 mM Tris, pH 7.4, 150 mM NaCl, 1% Nonidet P-40, 15 mM EDTA), supplemented with Mini-Complete protease inhibitors (Roche) and, when appropriate, with phosphatase inhibitor tablet (Roche). Equal amounts of the cleared lysates (as measured by BCA (Pierce)) were added to 25 μl Glutathione-Sepharose (GE Healthcare) and allowed to bind for 1h at 4°C. As previously shown[31], this method allows isolation of catalytically competent PP2A-B55α trimers. After 4 washes inNENT-100[31] and 1 wash in PP2A assay buffer (20 mM Tris pH 7.4, 5 mM DTT), assay buffer was added to the beads for phosphatase assays on two different substrates (histone H1, phosphorylase *a*) for at least two time points and with three replicas for each measurement (final volume 100-120 μl). A small aliquot was used for Western blotting with anti-C and anti-A (monoclonals Dr. S. Dilworth, 1:2,000) and anti-GST antibodies (Sigma, 1:10,000) to double-check for equal input.

Phosphatase assays

6 μg of histone H1 (Roche) were phosphorylated with Cdk1/cyclin B1 (Biaffin) or Cdk2/cyclin A[36] in the presence of [^{32}P]-ATP (GE Healthcare) to a level of 5-7 moles/mole. [^{32}P]radiolabelled histone H1 was precipitated in 25% trichloroacetic acid (TCA), washed twice in 25% TCA, once in acetone/HCl (200:1) and once inacetone. This pellet was solubilised in PP2A assay buffer and used at 0.3 μM. Following different incubation times with PP2A-B55α at 30°C (2, 5, 10 or 20 minutes), release of inorganic [^{32}P]-phosphate was measured through extraction of a phospho-molybdate complex andscintillation counting[37]. Under these conditions phosphate release was <10% of the phosphorylated substrate and thus remained in the linear range. Phosphorylase *a* phosphatase assays were performed as described[38], by measuring the liberated TCA soluble [^{32}P]-phosphate following a 10-or 20-minute incubation with PP2A-B55α. Each measurement of phosphatase activity was in triplicate. PP2A-B55α activities from mitotic cells were normalized to PP2A-B55α activities from interphase cells.

Affinity purification of protein complexes

HeLa cell pools expressing LAP-tagged mouse PP2A subunits in bacterial artificial chromosomes (BACs) were cultured in ten 25-cm square tissue culture trays. Cells were harvested from two culture conditions: prometaphase arrest induced by incubation in 0.1 μg ml^{-1} nocodazole for 18 hr; and during exponential ('log-phase') growth, yielding cells typically >90% in interphase. PP2A complexes were isolated from concentrated extracts of these cells, using the two-step purification procedure previously described[27], except that okadaic acid was included the extract buffer and all subsequent solutions, to restrain auto-dephosphorylation. 20% of the purified protein complex was analysed by SDS-PAGE and silver staining; the remaining sample was processed as described[39], then divided into two aliquots for parallel in-solution digestion by trypsin and subtilisin, then analysis by liquid chromatography - mass spectrometry (MS) for protein identification and phosphorylation site mapping.

Trypsin digestion of SDS-PAGE gel slices

Selected silver-stained protein bands were excised from an SDS-PAGE gel, cut into smaller piecesand washed by incubating in a shaking incubator once with 200 µl of 50 mM triethyl ammonium bicarbonate (TEAB), then once with 100 µl acetonitrile (ACN) plus 100 µl of 50 mM TEAB. Each wash step was performed in a shaking incubator at room temperature. This two-step wash procedure was repeated once, and then excess liquid removed. To shrink the gel pieces, 100 µl ACN was added to them.

Proteins were reduced by incubating the gel pieces in 100 µl of 1 mg ml^{-1} dithiothreitol in 50 mM TEAB at 57°C for 30 min, then excess liquid was removed. Proteins were alkylated by incubating the gel pieces with 100 µl of 5 mg ml^{-1} iodacetamide in 50 mM TEAB at room temperature, in the dark, for 35 min. Gel pieces were subjected to the two-step wash and shrinking procedures as previously described, and were then centrifuged in a vacuum concentrator (SpeedVac, Thermo Scientific) until dry (5-7 min).

Trypsin Gold (Promega) was first dissolved in 100 ng $µl^{-1}$ in 50 mM acetic acid, then diluted in 50 mM TEAB to a concentration of 12 ng $µl^{-1}$. Gel pieces were incubated with 20 µl trypsin/TEAB solution at 4°C for 5 min. Excess liquid was removed, and 20 µl of 50 mM TEAB was added, followed by incubation at 37°C overnight. After centrifugation, the supernatant was transferred into a fresh tube and stored at 5°C. 20 µl of 5% formic acid was added to the gel pieces, followed by sonication for 10 min in a cooled ultrasonic waterbath. The sample was spun and the supernatant transferred to the tube as mentioned previously. This formic acid / sonication step was repeated once, and the supernatant pooled with the first, generating a sample of volume 60 µl, ready for analysis by MS.

NanoLC-MS

The nano HPLC system used in all experiments was an UltiMate 3000 Dual Gradient HPLC system (Dionex, Amsterdam, The Netherlands), equipped with a Proxeon nanospray source (Proxeon, Odense, Denmark), coupled to an LTQ-FT mass spectrometer (Thermo Fisher Scientific, Bremen, Germany) in the first analysis and coupled to an LTQ Velos Orbitrap mass spectrometer (Thermo Fisher Scientific) in the second analysis. The LTQ FT was operated in data-dependent mode using a full scan in the ICR cell followed by MS/ MS scans of the five most abundant ions in the linear ion trap. MS/MS spectra were acquired in the multistage activation mode, where subsequent activation was performed on fragment ions resulting from the neutral loss of -98, -49, or -32.6 m/z. Precursor ions selected for fragmentation were put on a dynamic exclusion list for 180 s. Monoisotopic precursor selection was enabled. Phosphopeptides identified by database search and validated by manual inspection were put onto an inclusion list and replicate analyses were carried out on an LTQ Velos Orbitrap mass spectrometer.

Analysis of MS data

For peptide identification, all MS/MS spectra were searched using Mascot 2.2.0 (Matrix Science, London, UK) against a customised protein sequence database comprising the complete human

sequences from Swiss-Prot, TrEMBL, PIR, GenBank, EMBL, DDBJ, RefSeq and Celera (hKBMS), plus the Swiss-Prot entries corresponding to the mouse 'bait' proteins. The following search parameters were used: carbamidomethylation on cysteine was set as a fixed modification, oxidation on methionine, phosphorylation on serine, threonine and tyrosine was set as variable modifications. Monoisotopic masses were searched within unrestricted protein masses for tryptic peptides. The peptide mass tolerance was set to ±5 ppm and the fragment mass tolerance to ±0.5 Da. The maximal number of missed cleavages was set to 2. Each MS/MS spectrum corresponding to a predicted phosphopeptide was validated by visual inspection. A label-free quantification approach was used to determine abundance change from interphase (log) to mitosis (noc) of the different peptides by peak area integration. For peak area quantification we extracted the ion chromatograms of the peptides with a mass tolerance of 3 ppm using the Qual Browser application from the Xcalibur software package. The mass traces of peak area integration for the phosphopeptides shown in Fig. 5f were extracted from the base peak chromatogram with ±3ppm mass tolerance, manually reviewed and are shown in Supplementary Information, Fig. S8.

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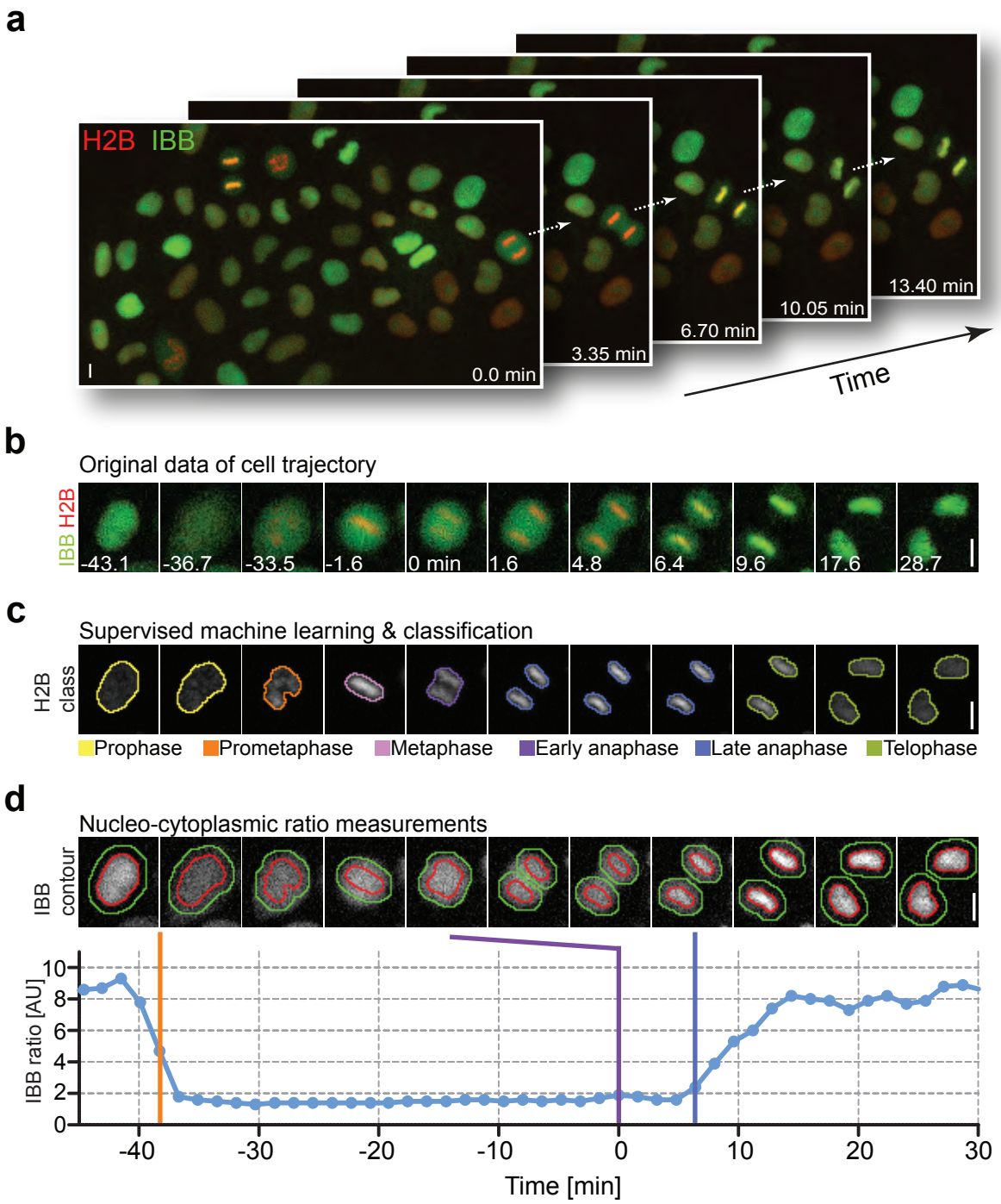
Figure 1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H2B IBB
0.0 min
3.35 min
6.70 min
10.05 min
13.40 min
Time
b
Original data of cell trajectory
IBB H2B
-43.1
-36.7
-33.5
-1.6
0 min
1.6
4.8
6.4
9.6
17.6
28.7
c
Supervised machine learning & classification
H2B class
Prophase
Prometaphase
Metaphase
Early anaphase
Late anaphase
Telophase
d
Nucleo-cytoplasmic ratio measurements
IBB contour
IBB ratio [AU]
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2
4
6
8
10
-40
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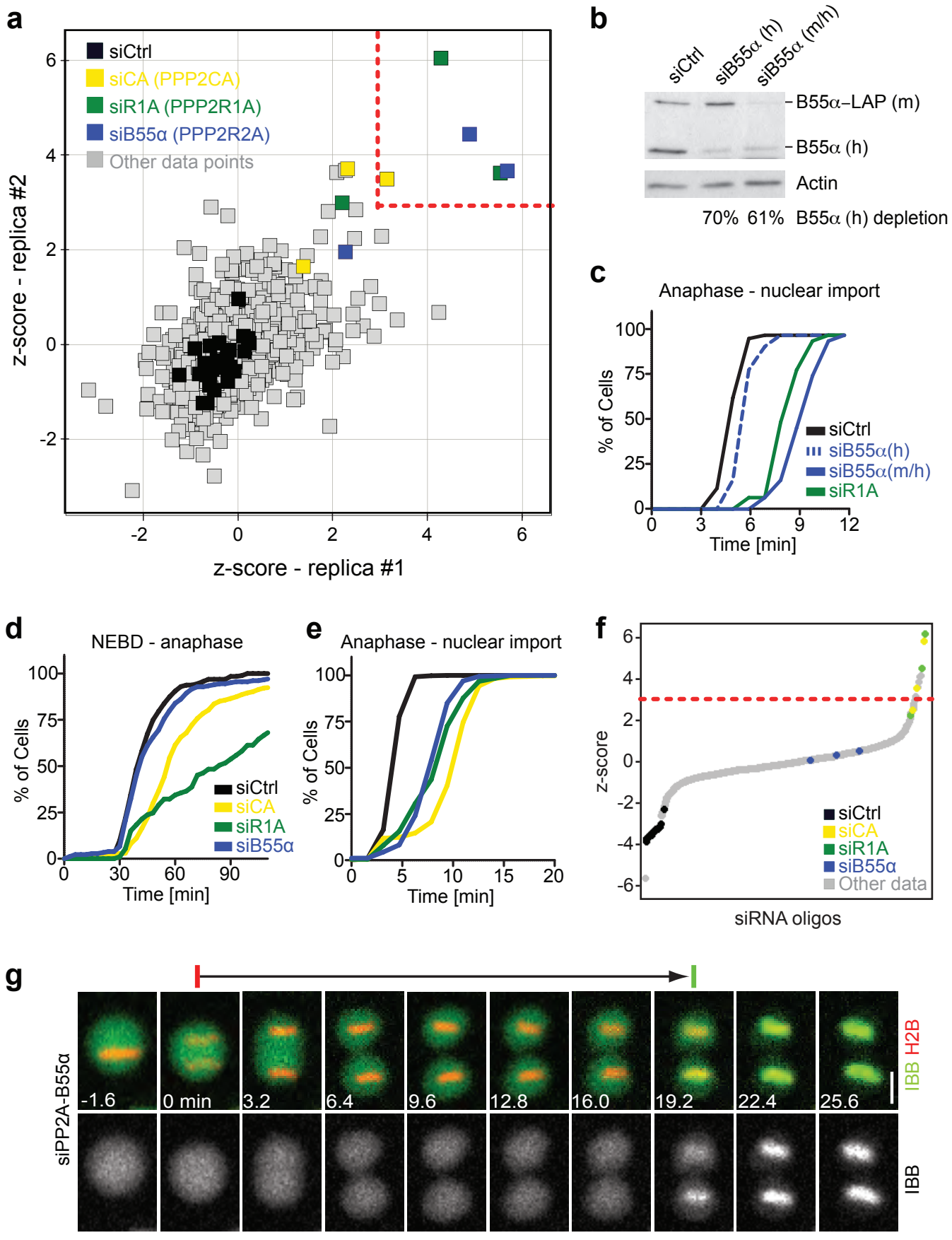
-20
-10
0
10
20
30
Time [min]

Figure 2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siCA (PPP2CA)
siR1A (PPP2R1A)
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Other data points
z-score - replica #2
z-score - replica #1
b
siCtrl
siB55α (h)
siB55α (m/h)
B55α–LAP (m)
B55α (h)
Actin
70% 61% B55α (h) depletion
c
Anaphase - nuclear import
% of Cells
Time [min]
siCtrl
siB55α(h)
siB55α(m/h)
siR1A
d
NEBD - anaphase
% of Cells
Time [min]
siCtrl
siCA
siR1A
siB55α
e
Anaphase - nuclear import
% of Cells
Time [min]
f
z-score
siRNA oligos
siCtrl
siCA
siR1A
siB55α
Other data
g
siPP2A-B55α
-1.6
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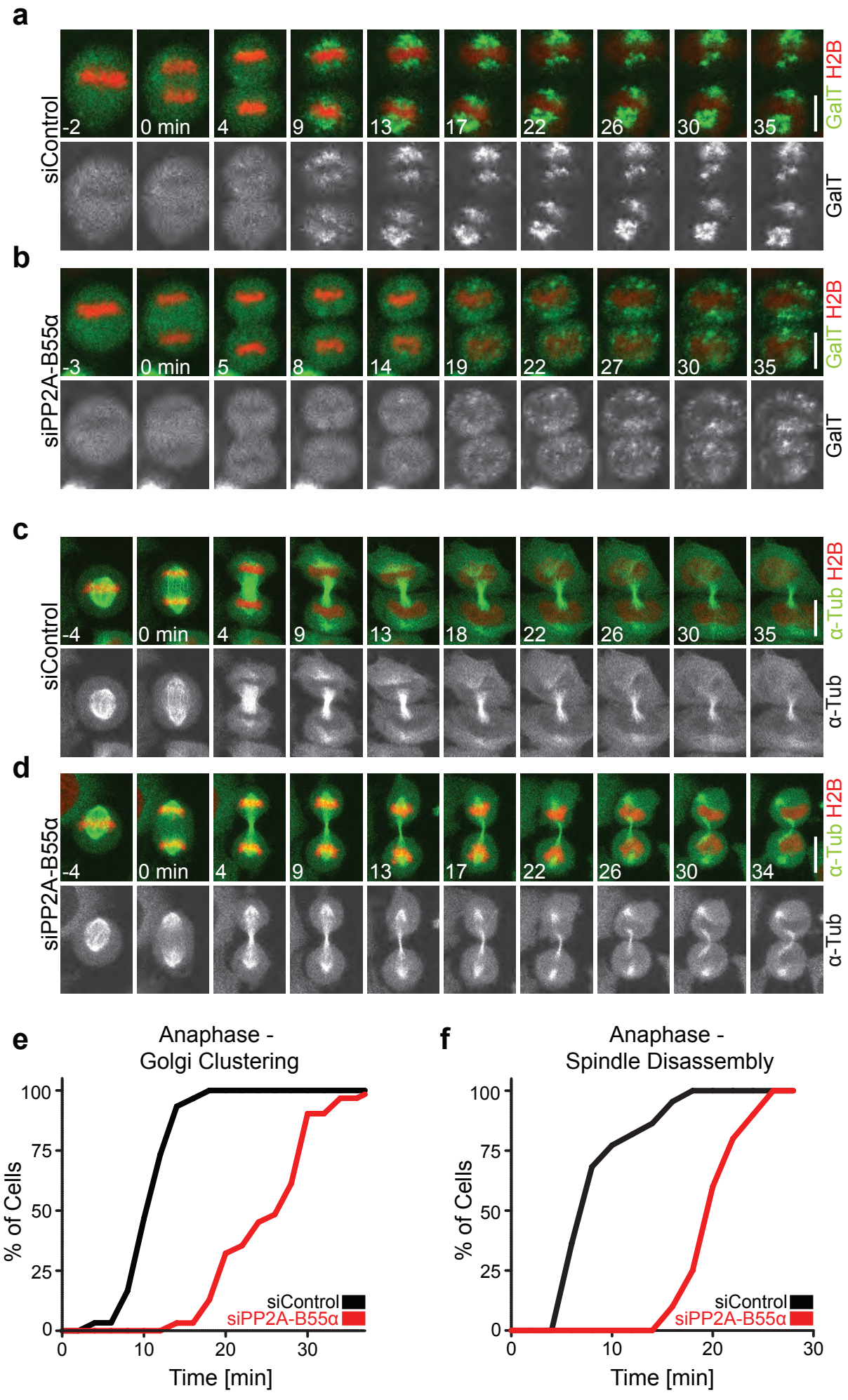
22.4
25.6
IBB H2B
IBB

Figure 3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13
17
22
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GalT
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-3
0 min
5
8
14
19
22
27
30
35
GalT H2B
GalT
c
siControl
-4
0 min
4
9
13
18
22
26
30
35
α-Tub H2B
α-Tub
d
siPP2A-B55α
-4
0 min
4
9
13
17
22
26
30
34
α-Tub H2B
α-Tub
e
Anaphase -
Golgi Clustering
% of Cells
100
75
50
25
0
0
10
20
30
Time [min]
siControl
siPP2A-B55α
f
Anaphase -
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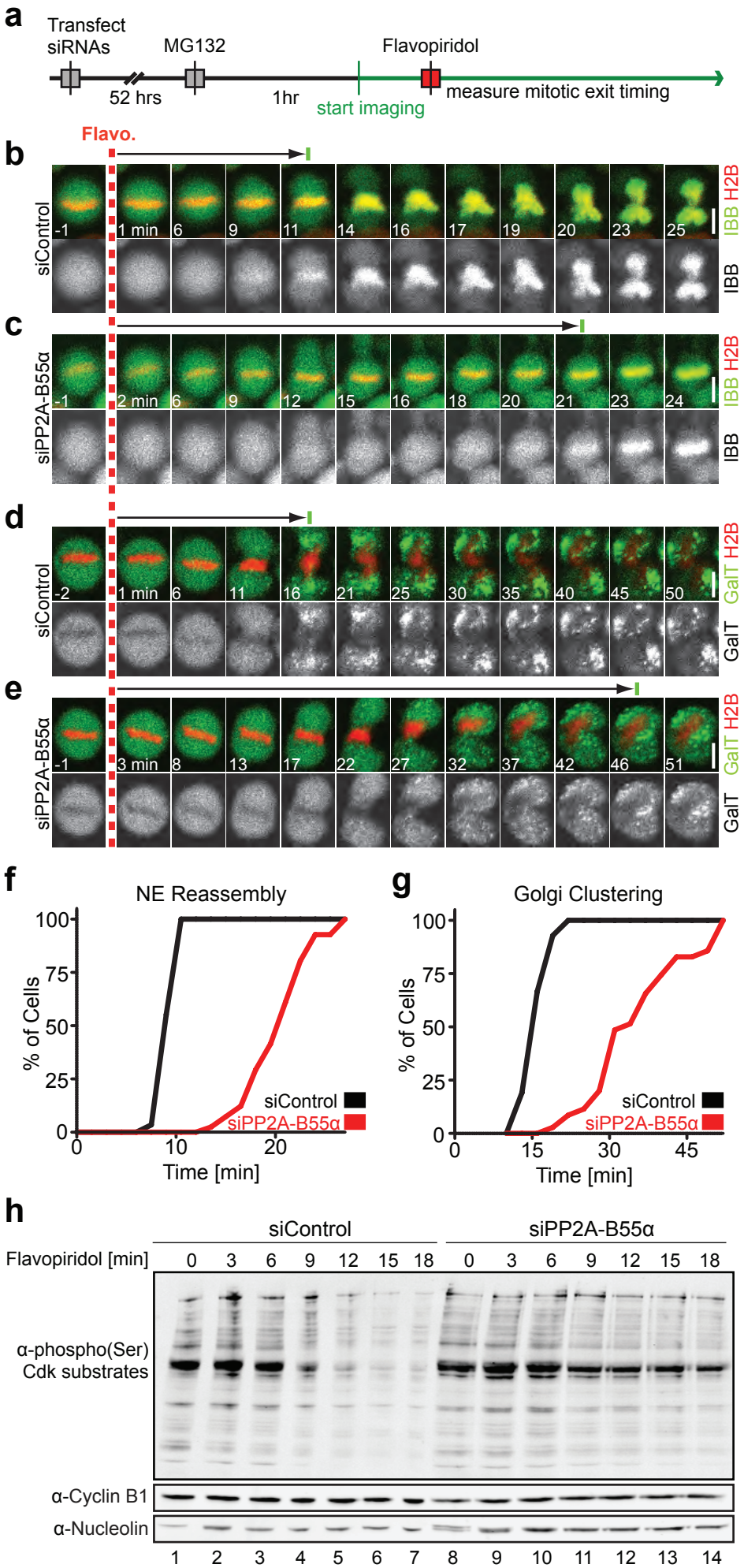
Figure 4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start imaging
measure mitotic exit timing
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IBB H2B
IBB
c
siPP2A-B55α
d
GalT H2B
GalT
e
f
NE Reassembly
% of Cells
Time [min]
siControl
siPP2A-B55α
g
Golgi Clustering
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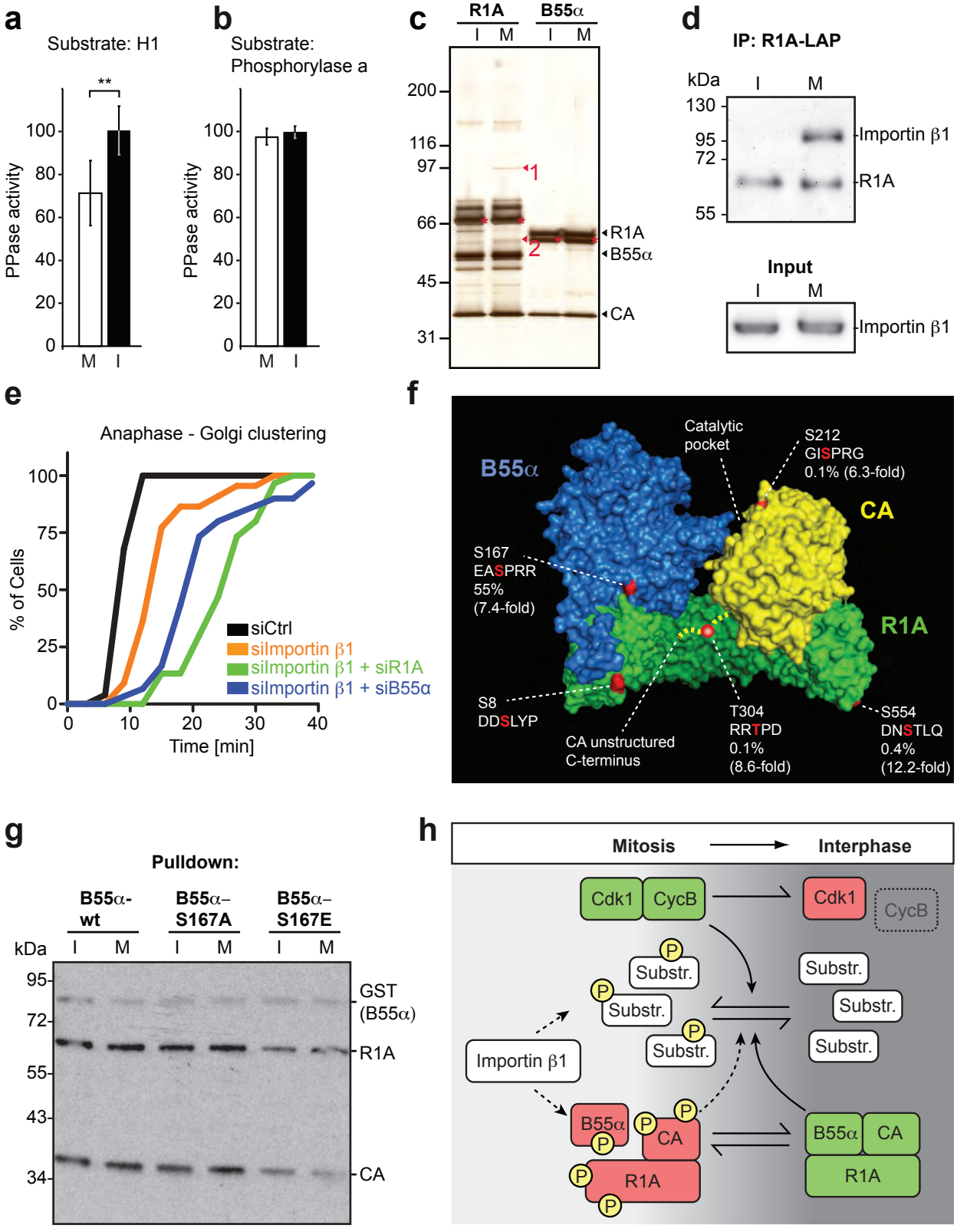
α-Cyclin B1
α-Nucleolin

Figure 5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Substrate: H1
PPase activity
b
Substrate:
Phosphorylase a
PPase activity
c
R1A
B55α
I M I M
200
116
97
66
45
31
1
2
R1A
B55α
CA
d
IP: R1A-LAP
kDa
I M
130
95
72
55
Importin β1
R1A
Input
I M
Importin β1
e
Anaphase - Golgi clustering
% of Cells
Time [min]
siCtrl
siImportin β1
siImportin β1 + siR1A
siImportin β1 + siB55α
f
B55α
Catalytic pocket
S212
GISPRG
0.1% (6.3-fold)
CA
S167
EASPRR
55%
(7.4-fold)
R1A
S8
DDSLYP
CA unstructured
C-terminus
T304
RRTPD
0.1%
(8.6-fold)
S554
DNSTLQ
0.4%
(12.2-fold)
g
Pulldown:
B55α-wt
B55α–S167A
B55α–S167E
kDa
I M I M I M
95
72
55
43
34
GST (B55α)
R1A
CA
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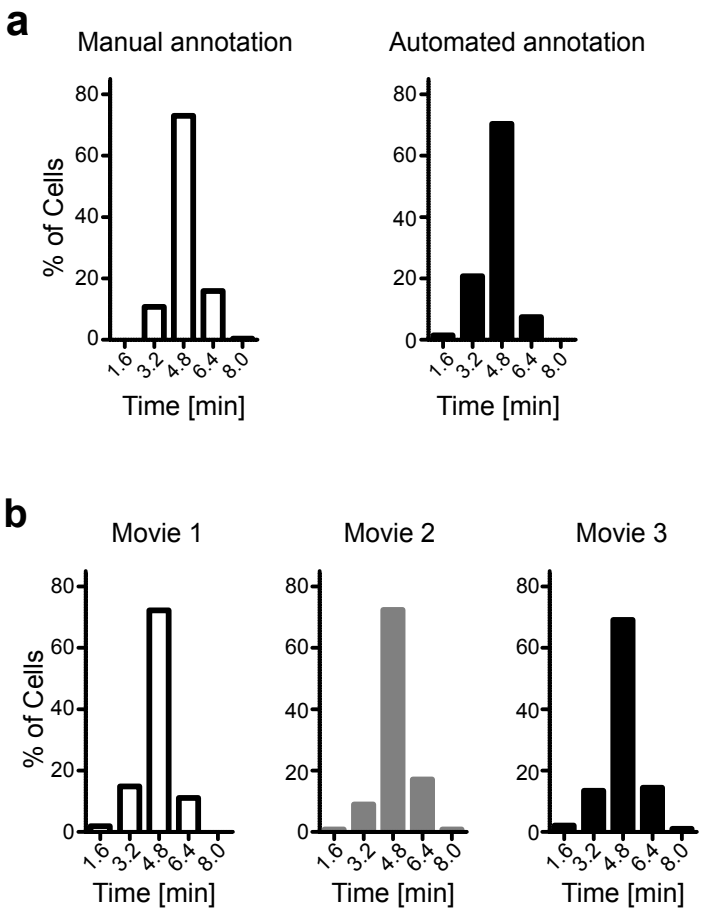
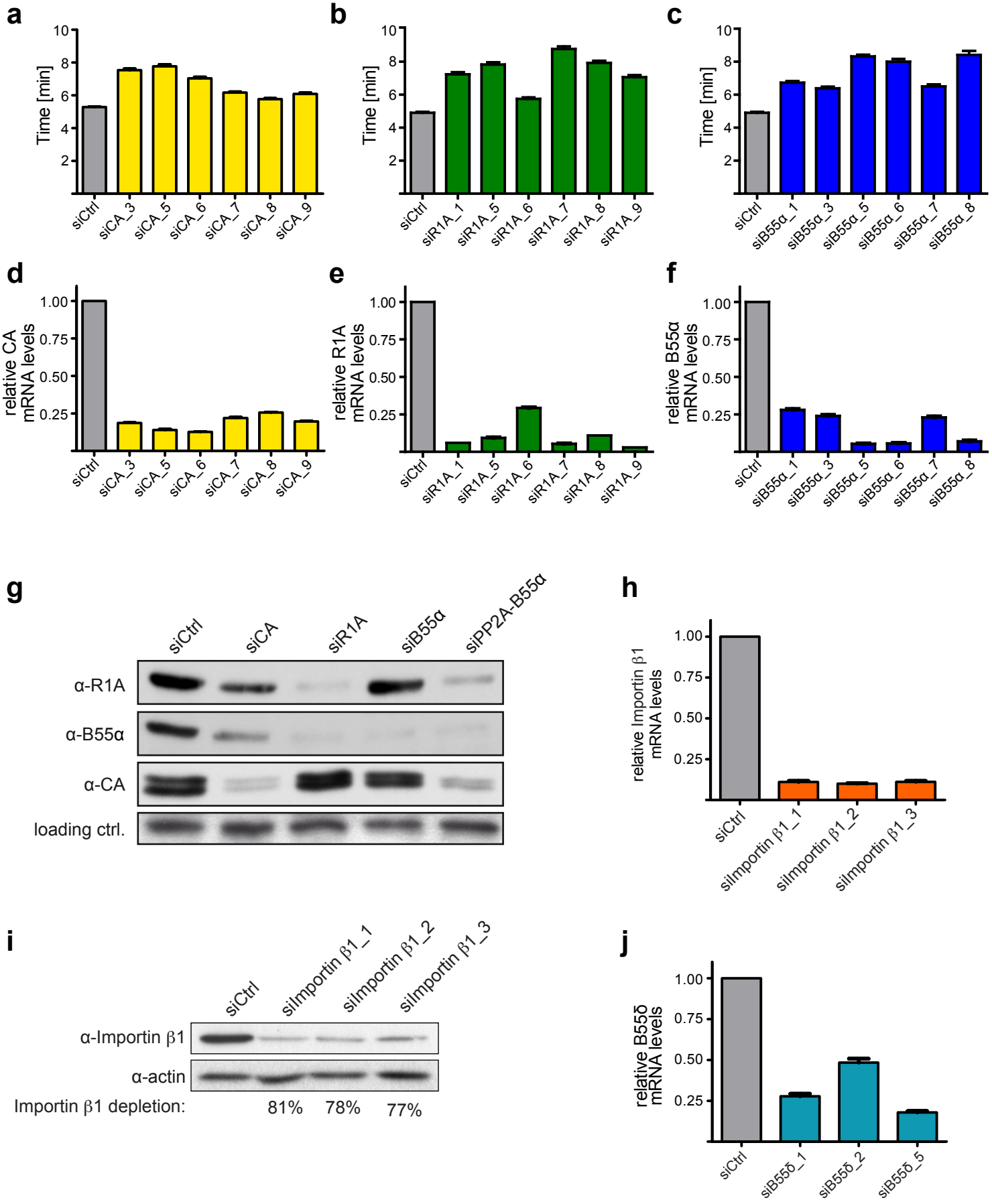
Mitosis
Interphase
Cdk1
CycB
Substr.
Importin β1
B55α
CA
R1A

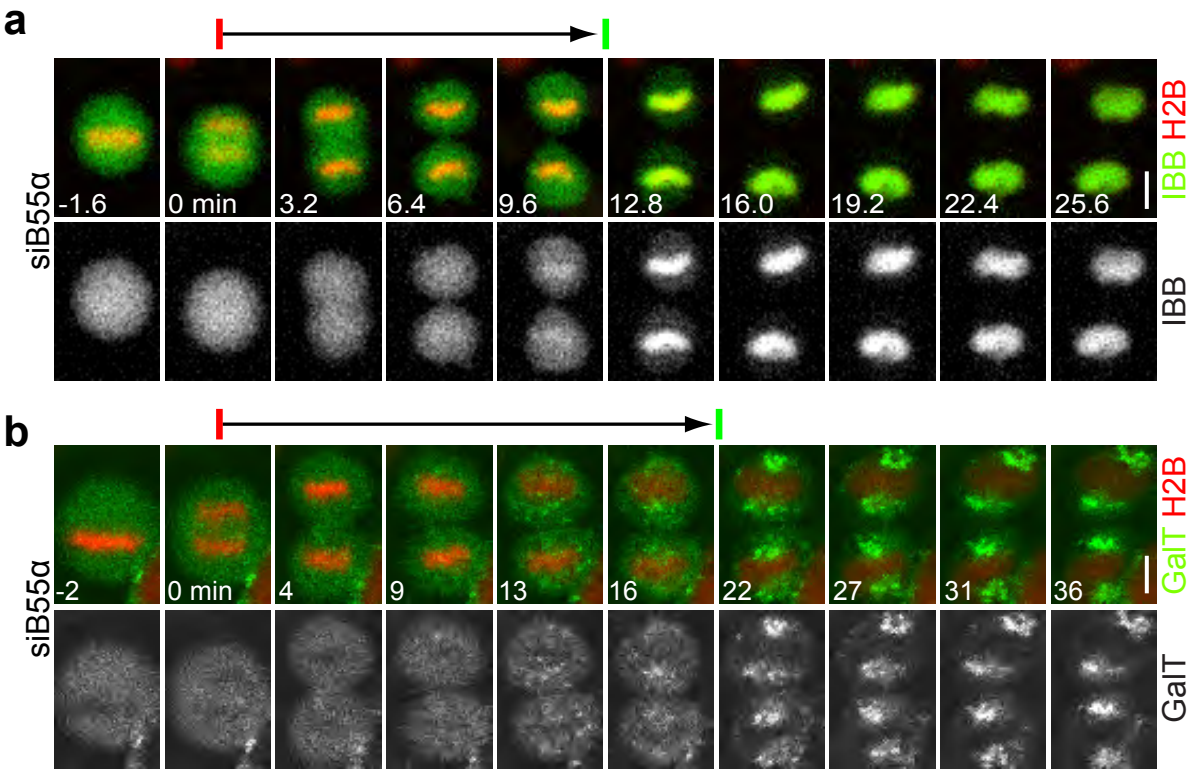
Supplementary Information, Figure S1

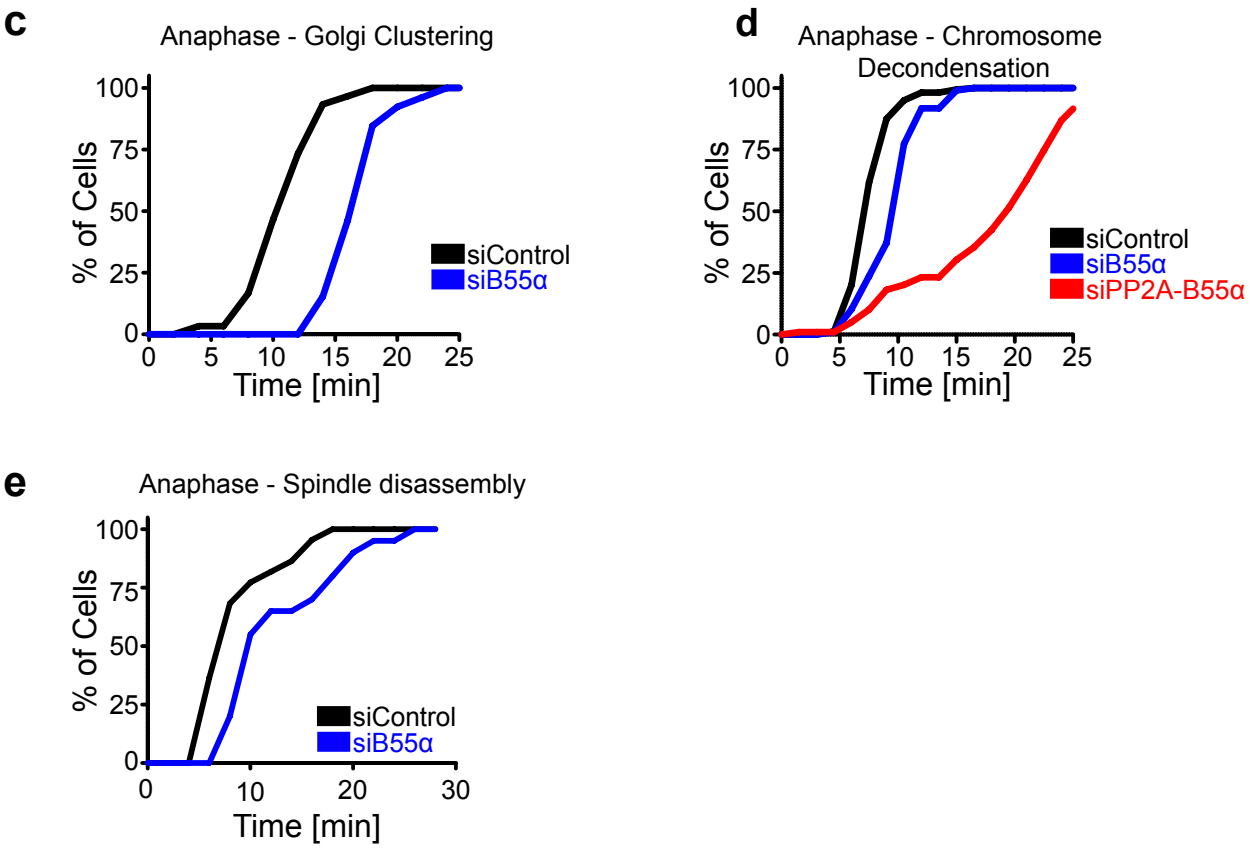


Supplementary Information, Figure S2

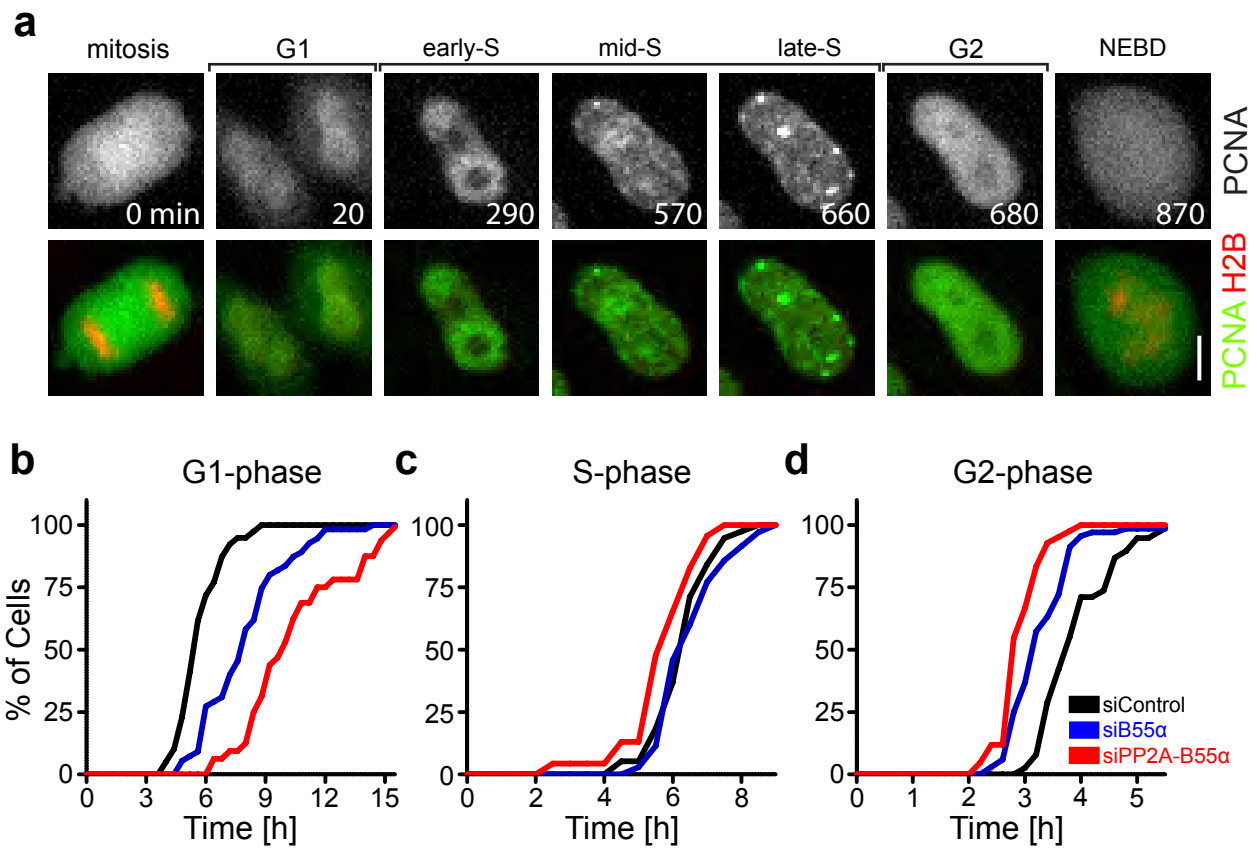


Supplementary Information, Figure S3

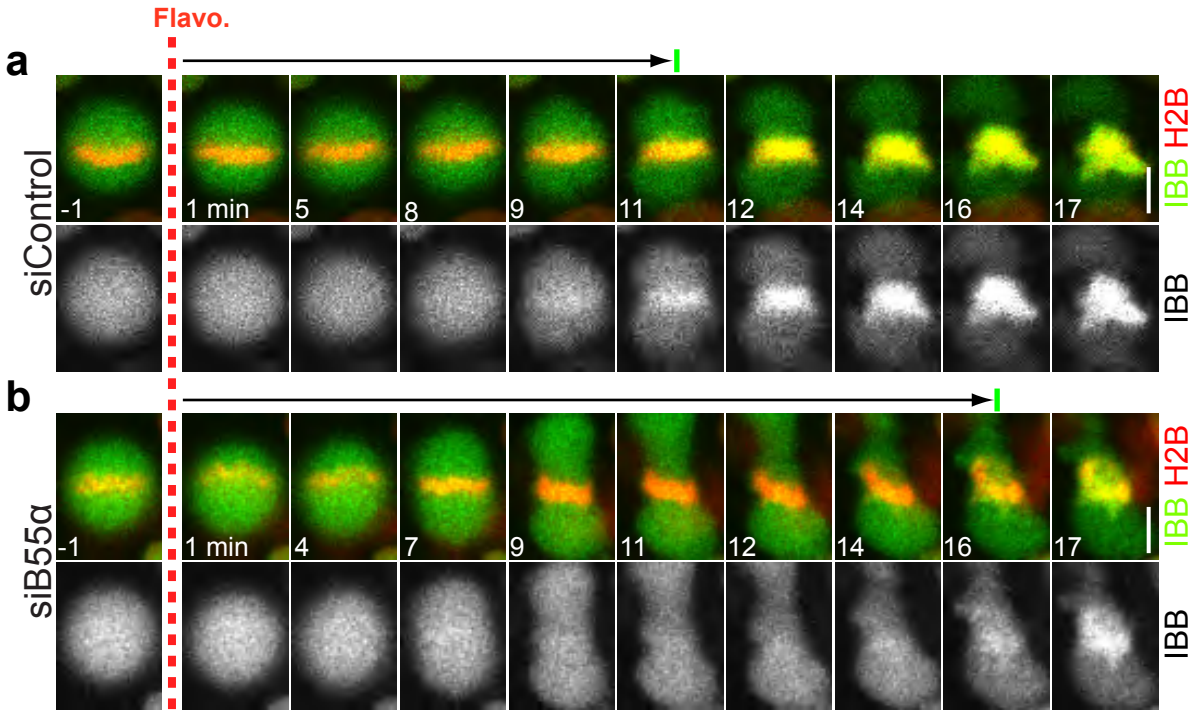


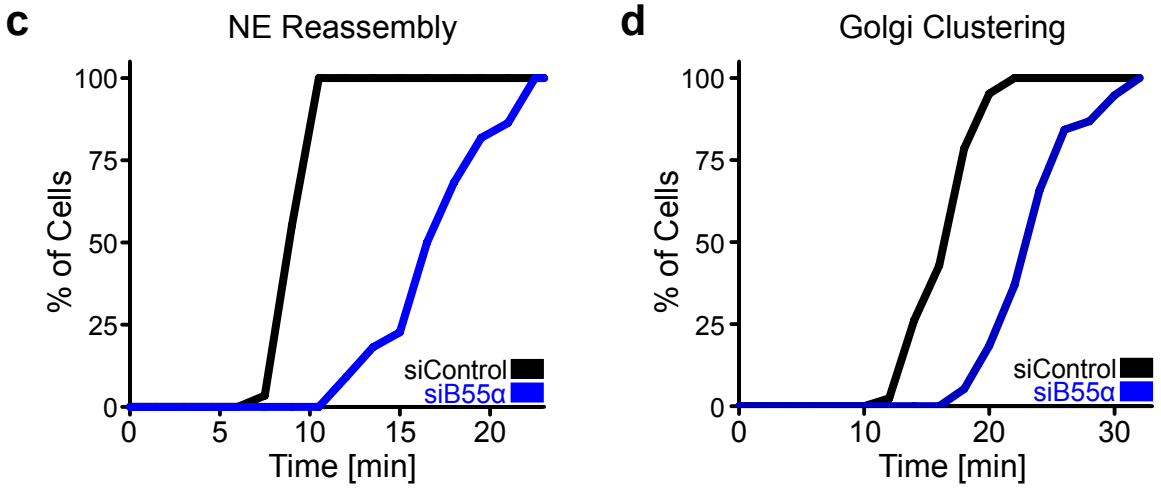


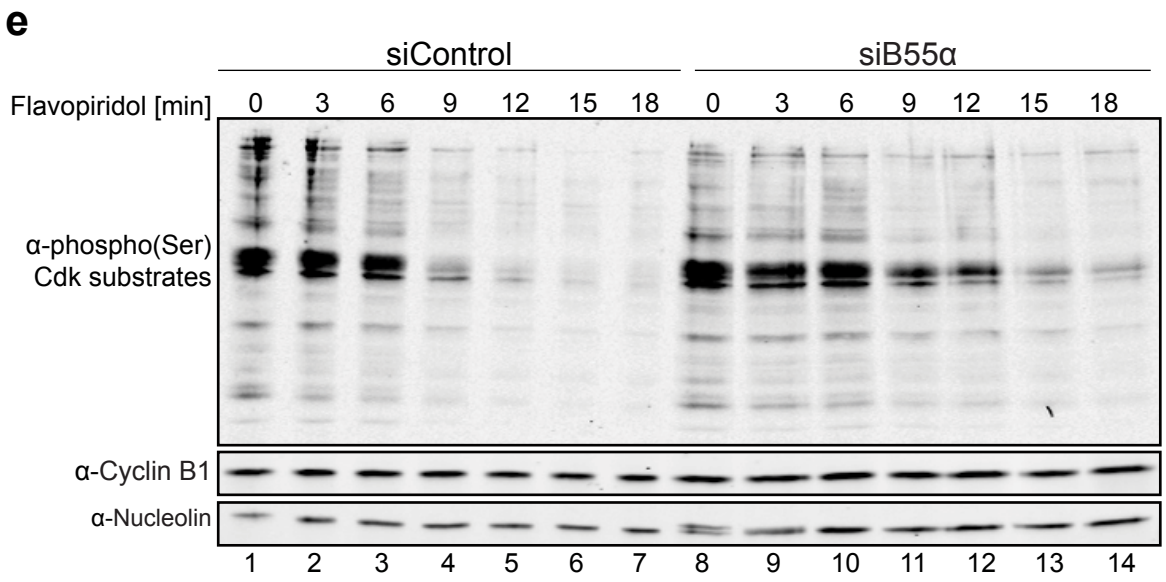
Supplementary Information, Figure S4



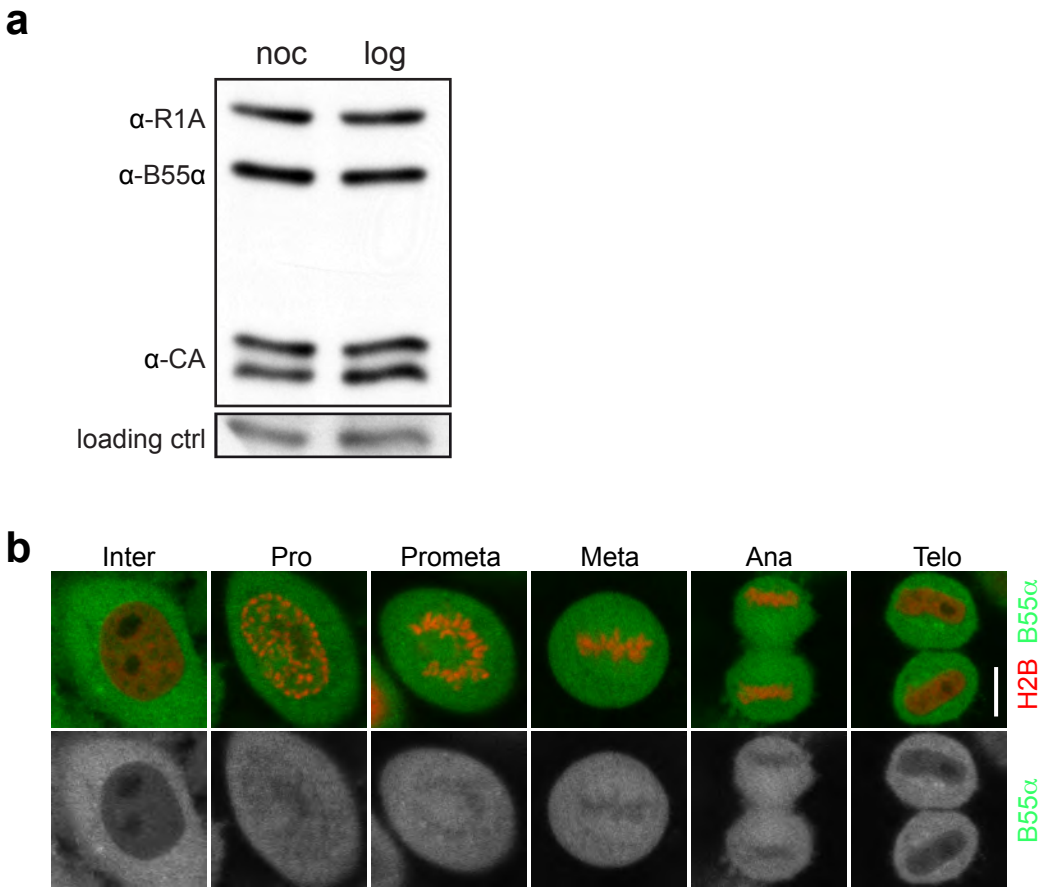
Supplementary Information, Figure S5



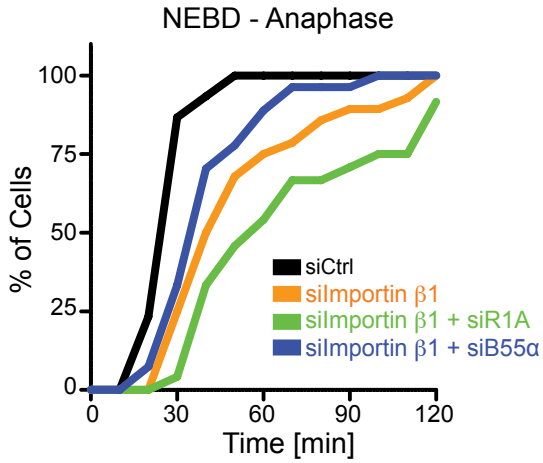




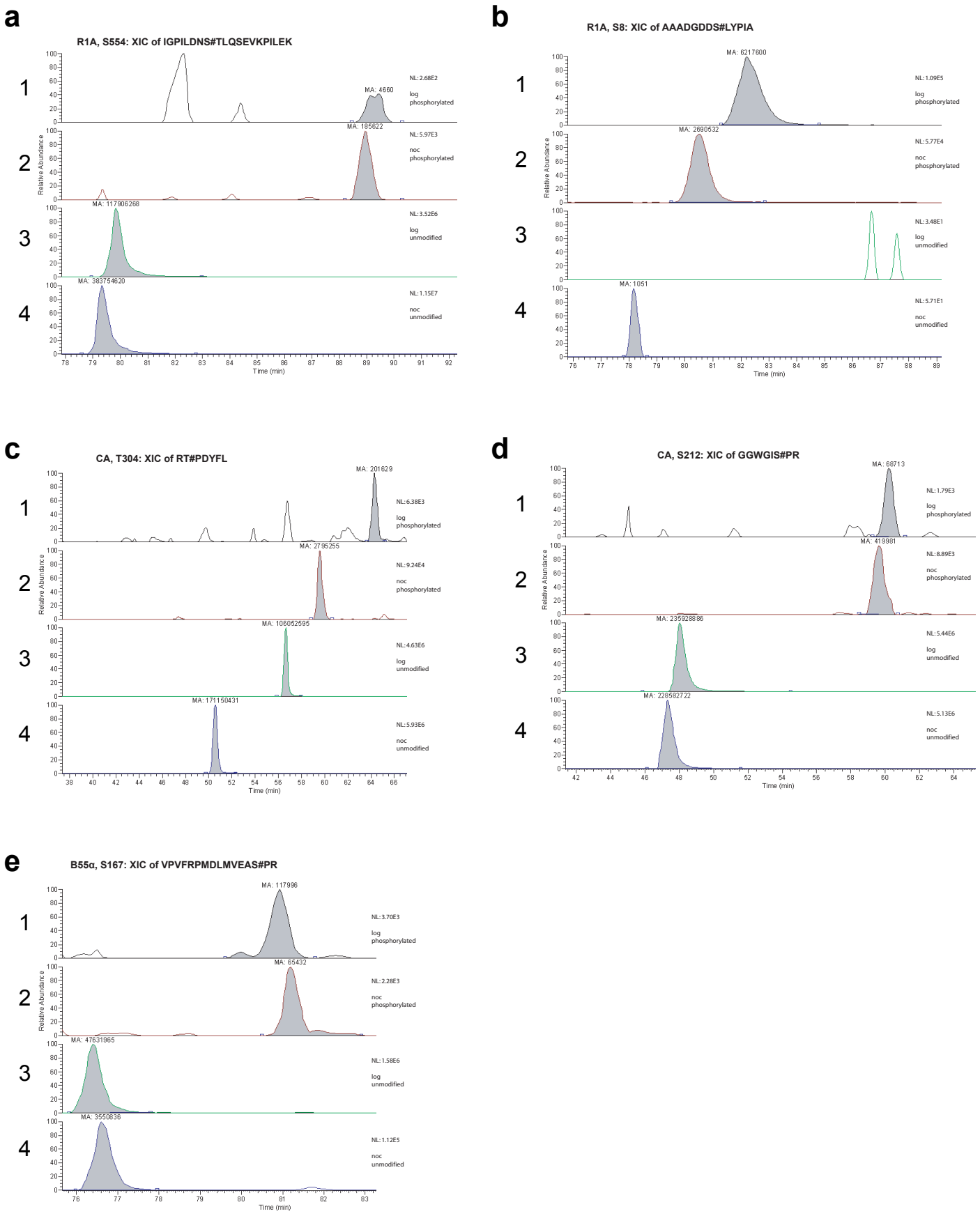
Supplementary Figure S6



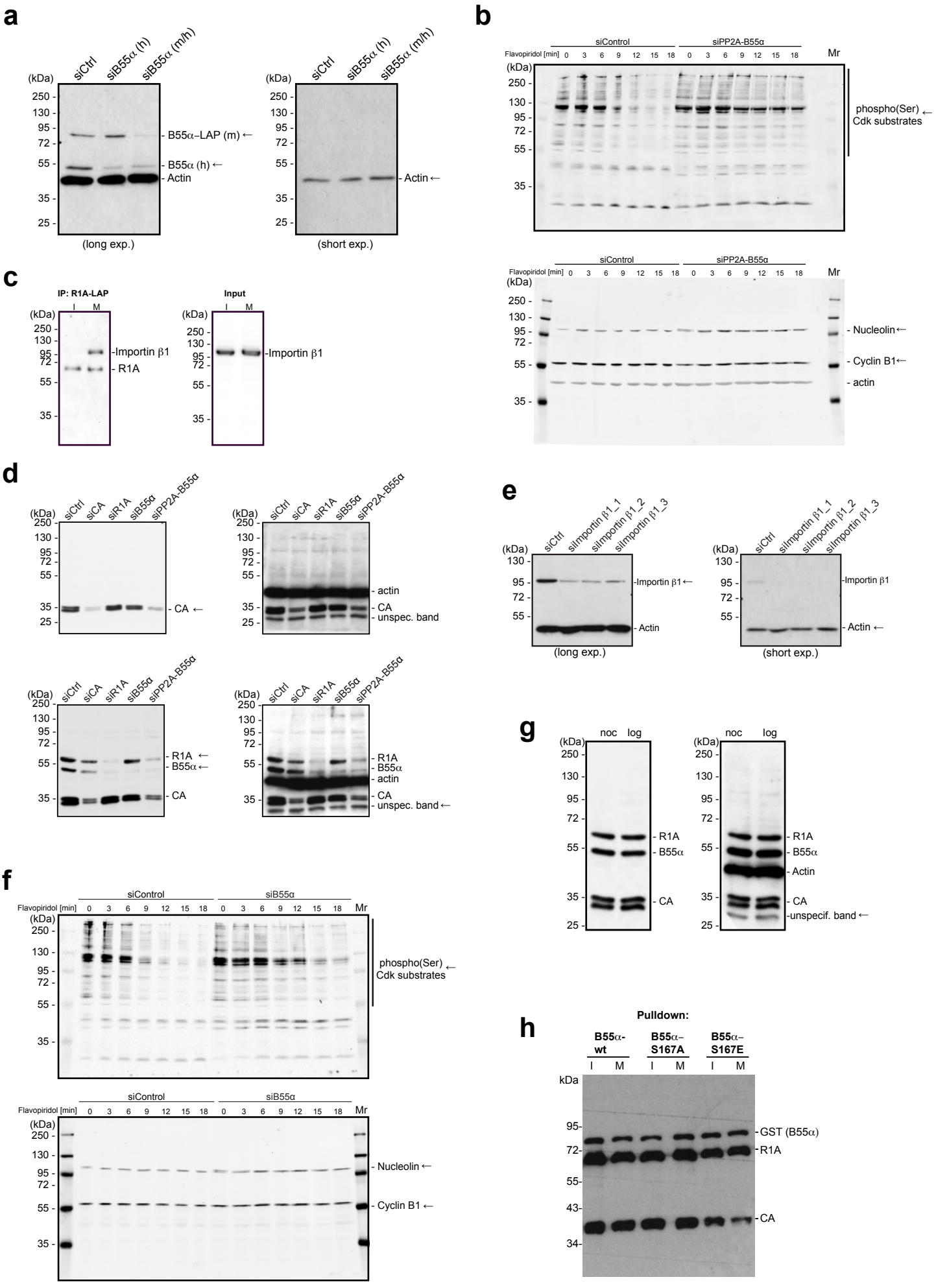
Supplementary Information, Figure S7



Supplementary Information, Figure S8



Supplemental Figure S9



Supplementary figure legends

Figure S1. Validation of automated image analysis. (a) Histograms of mitotic exit timing based on IBB-import after anaphase onset (t = 0) of the same dataset analysed manually (left, white bars), or automatically (right, black bars). **(b)** Automated annotation is highly reproducibly between movies (three independent movies shown).

Figure S2. Validation of RNAi efficiency. (a-c) Mitotic exit timing measured as in Figure 1, for six different siRNAs targeting CA ($n \geq 382$ for each siRNA condition; mean±s.d) **(a)**, R1A ($n \geq 175$ for each siRNA condition) **(b)**, or B55α ($n \geq 108$ for each siRNA condition) **(c)**. **(d-f)** Quantification of mRNA knockdown 40 h post transfection by real-time PCR for the same siRNAs as in (a-c), targeting CA **(d)**, R1A **(e)**, or B55α **(f)**, normalized against GAPDH (n = 3 for each condition; mean±s.d). See Supplementary Information, Table 2 for siRNA sequences. **(g)** Protein depletion levels of CA, R1A, and B55α, detected by Western blotting in cells depleted for the indicated siRNAs 60 h post-transfection. Note that depletion of CA or R1A co-depletes other subunits of the PP2A-B55α complex, consistent with previous reports[39, 40]. **(h)** Quantification of Importin β1 mRNA knockdown 48 h post transfection. **(i)** Importin β1 protein levels, detected by Western blotting 64 h after siRNA transfection. **(j)** Quantification of B55δ mRNA knockdown 48 h post transfection.

Figure S3. Phenotypes of B55α single depletions. (a) Nuclear reassembly timing in a B55α-depleted cell, see also Supplementary Information, Movie S11. **(b)** Golgi reassembly timing in a B55α-depleted cell, see also Supplementary Information, Movie S12. **(c-e)** Cumulative histograms of postmitotic Golgi clustering **(c)**, chromosome decondensation **(d)**, and spindle disassembly **(e)** relative to anaphase onset (0 min). Scale bars: 10 μm.

Figure S4. Effect of PP2A-B55α-depletion on cell cycle progression. (a) Cell cycle staging by DNA replication factor pattern of EGFP-PCNA. **(b, c, d)** Cumulative histograms of G1-phase **(b)**, S-phase **(c)**, and G2-phase **(d)** duration. Scale bars: 10 μm.

Figure S5. B55α functions downstream of Cdk1-cyclin B inactivation. **(a)** Movie of a cell transfected with non-silencing control siRNA, following the protocol indicated in Figure 4a. Arrowhead indicates onset of nuclear import of IBB-EGFP. **(b)** Time-lapse images of a cell transfected with siRNA targeting B55α, see also Supplementary Information, Movie S13. **(c, d)** Cumulative histograms of nuclear envelope assembly **(c)** and Golgi clustering **(d)** timing based on the data shown in (a-b, and data not shown). **(e)** Chemical induction of mitotic exit in presence of proteasome inhibitor in nocodazole arrested mitotic cells results in rapid dephosphorylation of Cdk substrates (siControl, lanes 1-7). Cells depleted for B55α show delayed dephosphorylation (siB55α, lanes 8-14).Scale bars: 10 μm.

Figure S6. Expression levels and localization of PP2A-B55α. (a) PP2A-B55α subunits are expressed at constant levels during the cell cycle. Whole cell lysates were probed by Western Blotting using the antibodies against CA, R1A, and B55α. Left lane: 17 h nocodazole arrested cells (noc), right lane: unsynchronized interphase cells (log). Note that CA migrates as a doublet band (see also Supplementary Information, Figure S2g). **(b)** Localization of B55α. Confocal live images of cells expressing EGFP-mouse-B55α from endogenous promotor (see Fig. 2b). Scale bar: 10 μm.

Figure S7. Early mitotic progression in Importin β1-depleted cells. Timing from prometaphase until anaphase was measured for the same cells shown in Fig. 5e.

Figure S8. Quantification of phosphorylation levels by extracted ion chromatograms. Extracted ion chromatograms (XICs) of phosphopeptides identified (hash indicates the phosphorylated amino acid), and their unmodified counterparts, from purified PP2A complexes. Peak-area values for the phosphopeptides were used for quantification of the mitotic increase in phosphorylation abundance, whereas those of the unmodified peptides were used for normalization, as described in the legend for Fig. 5f. The panels show: 1. XIC featuring the phosphorylated peptide identified from the PP2A complex purified from interphase (log) cells. 2. XIC featuring the same phosphorylated peptide identified from the mitotic (noc) cell state. 3. XIC featuring the unmodified counterpart peptide from interphase. 4. XIC featuring the unmodified counterpart peptide from the mitotic (noc) cell state. **(a)** Quantitation of S554 phosphorylation on R1A. **(b)** S8 phosphorylation on R1A. **(c)** T304 phosphorylation on CA. **(d)** S212 phosphorylation on CA. **(e)** S167 phosphorylation on B55α.

Figure S9. Full scans of blots. (a) Full scan for B55α and Actin immunoblot of Figure 2b. **(b)** Full scan for phospho(Ser)Cdk substrates (upper) and Cyclin B1, Nucleolin, and Actin (lower) immunoblot of Figure 4f. **(c)** Full scan for Importin ß1 and R1A IP-blot (left) and Importin ß1 Input-blot (right) of Figure 5d. **(d)** Full scan for CA (upper left), R1A and B55α (lower left), and loading control blots (right panels) of Figure S2g. **(e)** Full scan for Importin ß1 and Actin immunoblot of Figure S2i. **(f)** Full scan for phospho(Ser)Cdk substrates (upper) and Cyclin B1, and Nucleolin (lower) immunoblot of Figure S5e. **(g)** Full scan for CA, R1A, and B55α (right) and Actin (left) immunoblot of Figure S6a. (Sliced bands are indicated with arrows). **(h)** Relevance of B55α-S167 phosphorylation for PP2A complex assembly. Independent replica of the experiment shown in Fig. 5g.

Supplementary movie legends

Movie S1 Monoclonal fluorescent HeLa cell line expressing chromatin marker H2B-mCherry and the nuclear import substrate IBB-EGFP. The movie shows 13% of the total image size and represent a typical overnight screening movie. Time-lapse covers a period of ~21 hours.

Movie S2 H2B-mCherry / IBB-EGFP reporter cell that has been automatically detected, tracked, and segmented over time. Movie shows original images (left); mitotic stage classification with color label as in Fig. 1c (middle), and regions of IBB measurements (right). Time-lapse covers a period of 216 minutes.

Movie S3 H2B-mCherry / IBB-EGFP cell treated with siControl. This movie shows mitotic progression and nuclear envelope reassembly in a control cell. Time-lapse covers a period of 192 minutes.

Movie S4 H2B-mCherry / IBB-EGFP cell treated with siPP2A-B55α. This movie shows mitotic progression and delayed nuclear envelope reassembly in a cell depleted for PP2A-B55α. Time-lapse covers a period of 192 minutes.

Movie S5 H2B-mCherry / GalT-EGFP cell treated with siControl. This movie shows mitotic progression and Golgi reassembly in a control cell. Time-lapse covers a period of 132 minutes.

Movie S6 H2B-mCherry / GalT-EGFP cell treated with siPP2A-B55α. This movie shows mitotic progression and delayed Golgi reassembly in a cell depleted for PP2A-B55α. Time-lapse covers a period of 161 minutes.

Movie S7 H2B-mCherry / mEGFP-α-tubulin cell treated with siControl. This movie shows mitotic progression and mitotic spindle dynamics in a control cell. Time-lapse covers a period of 108 minutes.

Movie S8 H2B-mCherry / mEGFP-α-tubulin cell treated with siPP2A-B55α. This movie shows mitotic progression and delayed mitotic spindle disassembly in a cell depleted for PP2A-B55α. Time-lapse covers a period of 108 minutes.

Movie S9 H2B-mCherry / IBB-EGFP cell treated with siControl. This movie shows forced mitotic exit in presence of MG132 by addition of the Cdk inhibitor flavopiridol in a control cell. Time-lapse covers a period of 47 minutes.

Movie S10 H2B-mCherry / IBB-EGFP cell treated with siPP2A-B55α. This movie shows delayed mitotic exit in presence of MG132 by addition of the Cdk inhibitor flavopiridol in a cell depleted for PP2A-B55α. Time-lapse covers a period of 47 minutes.

Supplementary Information Table 1. Library of siRNA oligos

geneId	symbol	Qiagen productName	mrnaAccessions	Qiagen productId	description	sirna	antisense	sense
52	ACP1	Hs_ACP1_5	NM_004300 NM_007099 NM_177554	SI02665614	acid phosphatase 1, soluble	CCCATAGTGCACACTTGTATA	UAUACAAGUGUGCACUAUGgg	CAUAGUGCACACUUGUAUAtt
52	ACP1	Hs_ACP1_6	NM_004300 NM_007099 NM_177554	SI02776851	acid phosphatase 1, soluble	ATGGATGAAAGCAATCTGAGA	UCUCAGAUUGCUUUCAUCCat	GGAUGAAAGCAAUCUGAGAtt
52	ACP1	Hs_ACP1_7	NM_001040649 NM_004300 NM_007099 N	SI03068772	acid phosphatase 1, soluble	CAGGAAACTTGTAACCGATCA	UGAUCGGUUACAAGUUUCCtg	GGAAACUUGUAACCGAUCAtt
53	ACP2	Hs_ACP2_5	NM_001610	SI02658628	acid phosphatase 2, lysosomal	CTGGATGTCTACAATGGTGAA	UUCACCAUUGUAGACAUCCag	GGAUGUCUACAAUGGUGAAtt
53	ACP2	Hs_ACP2_6	NM_001610	SI02658635	acid phosphatase 2, lysosomal	CAGCCTGAAGTCTTCGGCAAA	UUUGCCGAAGACUUCAGGCtg	GCCUGAAGUCUUCGGCAAAtt
53	ACP2	Hs_ACP2_7	NM_001610	SI03063319	acid phosphatase 2, lysosomal	CAGAATGAGAGTTCTCGGAAT	AUUCCGAGAACUCUCAUUCtg	GAAUGAGAGUUCUCGGAAUtt
54	ACP5	Hs_ACP5_1	NM_001611	SI00291095	acid phosphatase 5, tartrate resistant	CTCGGGCAAGTCCCTCTTTAA	UUAAAGAGGGACUUGCCCGag	CGGGCAAGUCCCUCUUUAAtt
54	ACP5	Hs_ACP5_3	NM_001611	SI00291109	acid phosphatase 5, tartrate resistant	ACGGCGCTGCTCATCCTGCAA	UUGCAGGAUGAGCAGCGCCgt	GGCGCUGCUCAUCCUGCAAtt
54	ACP5	Hs_ACP5_4	NM_001611	SI00291116	acid phosphatase 5, tartrate resistant	CACTGGTGTGCAAGACATCAA	UUGAUGUCUUGCACACCAGtg	CUGGUGUGCAAGACAUCAAtt
55	ACPP	Hs_ACPP_1	NM_001099	SI00021882	acid phosphatase, prostate	CTCTATTACCATTATGGATAA	UUAUCCAUAAUGGUAAUAGag	CUAUUACCAUUAUGGAUAAtt
55	ACPP	Hs_ACPP_2	NM_001099	SI00021889	acid phosphatase, prostate	ACAGATGGCGCTAGATGTTTA	UAAACAUCUAGCGCCAUCUgt	AGAUGGCGCUAGAUGUUUAtt
55	ACPP	Hs_ACPP_3	NM_001099	SI00021896	acid phosphatase, prostate	CCGGACTTTGATGAGTGCTAT	AUAGCACUCAUCAAAGUCCgg	GGACUUUGAUGAGUGCUAUtt
248	ALPI	Hs_ALPI_5	NM_001631	SI02665579	alkaline phosphatase, intestinal	CACGTCCATCCTGTACGGCAA	UUGCCGUACAGGAUGGACGtg	CGUCCAUCCUGUACGGCAAtt
248	ALPI	Hs_ALPI_6	NM_001631	SI03083157	alkaline phosphatase, intestinal	CCGTTGGACCTTCACCTCCTA	UAGGAGGUGAAGGUCCAACgg	GUUGGACCUUCACCUCCUAtt
248	ALPI	Hs_ALPI_3	NM_001631	SI00026607	alkaline phosphatase, intestinal	CCAGACAATAAAGGGACCAAA	UUUGGUCCCUUUAUUGUCUgg	AGACAAUAAAGGGACCAAAtt
249	ALPL	Hs_ALPL_5	NM_000478	SI02658600	alkaline phosphatase, liver/bone/kidney	CCGGGACTGGTACTCAGACAA	UUGUCUGAGUACCAGUCCCgg	GGGACUGGUACUCAGACAAtt
249	ALPL	Hs_ALPL_6	NM_000478	SI02658607	alkaline phosphatase, liver/bone/kidney	CAGGATTGGAACATCAGTTAA	UUAACUGAUGUUCCAAUCCtg	GGAUUGGAACAUCAGUUAAtt
249	ALPL	Hs_ALPL_3	NM_000478	SI00010283	alkaline phosphatase, liver/bone/kidney	CACCATGATTTCACCATTCTT	AAGAAUGGUGAAAUCAUGGtg	CCAUGAUUUCACCAUUCUUtt
251	ALPPL2	Hs_ALPPL2_5	NM_031313	SI02759414	alkaline phosphatase, placental-like 2	CACGGTCCTCCTATACGGAAA	UUUCCGUAUAGGAGGACCGtg	CGGUCCUCCUAUACGGAAAtt
251	ALPPL2	Hs_ALPPL2_1	NM_031313	SI00294763	alkaline phosphatase, placental-like 2	TGGGTGCAGGATAGCAGTCCA	UGGACUGCUAUCCUGCACCca	GGUGCAGGAUAGCAGUCCAtt
251	ALPPL2	Hs_ALPPL2_2	NM_031313	SI00294770	alkaline phosphatase, placental-like 2	CTCAGCAAGGAAGACTCATTA	UAAUGAGUCUUCCUUGCUGag	CAGCAAGGAAGACUCAUUAtt
993	CDC25A	Hs_CDC25A_6	NM_001789 NM_201567	SI02225545	cell division cycle 25 homolog A (S. pombe)	CTGGCCAAATAGCAAAGACAA	UUGUCUUUGCUAUUUGGCCag	GGCCAAAUAGCAAAGACAAtt
993	CDC25A	Hs_CDC25A_9	NM_001789 NM_201567	SI02653273	cell division cycle 25 homolog A (S. pombe)	AAGGGTTATCTCTTTCATACA	UGUAUGAAAGAGAUAACCCtt	GGGUUAUCUCUUUCAUACAtt
993	CDC25A	Hs_CDC25A_5	NM_001789 NM_201567	1024687	cell division cycle 25 homolog A (S. pombe)	AAGGCGCTATTTGGCGCTTCA	UGAAGCGCCAAAUAGCGCCtt	GGCGCUAUUUGGCGCUUCAtt
994	CDC25B	Hs_CDC25B_10	NM_004358 NM_021872 NM_021873 NM_	SI02659272	cell division cycle 25 homolog B (S. pombe)	CCCAGTCTGTTGAGTTAGTTA	UAACUAACUCAACAGACUGgg	CAGUCUGUUGAGUUAGUUAtt
994	CDC25B	Hs_CDC25B_11	NM_004358 NM_021872 NM_021873 NM_	SI02659279	cell division cycle 25 homolog B (S. pombe)	CGCCGAGAGCTTCCTACTGAA	UUCAGUAGGAAGCUCUCGGcg	CCGAGAGCUUCCUACUGAAtt
994	CDC25B	Hs_CDC25B_8	NM_004358 NM_021872 NM_021873 NM_	SI02652916	cell division cycle 25 homolog B (S. pombe)	CAGGAGGCTGAGGAACCTAAA	UUUAGGUUCCUCAGCCUCCtg	GGAGGCUGAGGAACCUAAAtt
995	CDC25C	Hs_CDC25C_8	NM_001790 NM_022809	SI02658642	cell division cycle 25 homolog C (S. pombe)	CCAGGGAGCCTTAAACTTATA	UAUAAGUUUAAGGCUCCCUgg	AGGGAGCCUUAAACUUAUAtt
995	CDC25C	Hs_CDC25C_9	NM_001790 NM_022809	SI02658649	cell division cycle 25 homolog C (S. pombe)	GAGCTGCAATCTAGTTAACTA	UAGUUAACUAGAUUGCAGCtc	GCUGCAAUCUAGUUAACUAtt
995	CDC25C	Hs_CDC25C_5	NM_001790 NM_022809	SI02627079	cell division cycle 25 homolog C (S. pombe)	CAGGAAGGGCTTATGTTTAAA	UUUAAACAUAAGCCCUUCCtg	GGAAGGGCUUAUGUUUAAAtt
1033	CDKN3	Hs_CDKN3_6	NM_005192	SI02665621	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	TCGGGACAAATTAGCTGCACA	UGUGCAGCUAAUUUGUCCCga	GGGACAAAUUAGCUGCACAtt
1033	CDKN3	Hs_CDKN3_7	NM_005192	SI02665628	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CACAATCAAGATCTGTATCAA	UUGAUACAGAUCUUGAUUGtg	CAAUCAAGAUCUGUAUCAAtt
1033	CDKN3	Hs_CDKN3_1	NM_005192	SI00073563	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CTAGCATAATTTGTATTGAAA	UUUCAAUACAAAUUAUGCUag	AGCAUAAUUUGUAUUGAAAtt
1843	DUSP1	Hs_DUSP1_1	NM_004417	SI00374801	dual specificity phosphatase 1	TAGCGTCAAGACATTTGCTGA	UCAGCAAAUGUCUUGACGCta	GCGUCAAGACAUUUGCUGAtt
1843	DUSP1	Hs_DUSP1_3	NM_004417	SI00374815	dual specificity phosphatase 1	CACGAACAGTGCGCTGAGCTA	UAGCUCAGCGCACUGUUCGtg	CGAACAGUGCGCUGAGCUAtt
1843	DUSP1	Hs_DUSP1_4	NM_004417	SI00374822	dual specificity phosphatase 1	CAGTTGTATGTTTGCTGATTA	UAAUCAGCAAACAUACAACtg	GUUGUAUGUUUGCUGAUUAtt
1844	DUSP2	Hs_DUSP2_5	NM_004418	SI03024469	dual specificity phosphatase 2	TTGGAAACTTAGCACTTTATA	UAUAAAGUGCUAAGUUUCCaa	GGAAACUUAGCACUUUAUAtt
1844	DUSP2	Hs_DUSP2_6	NM_004418	SI03025848	dual specificity phosphatase 2	TTGTGCTCAGCTGACATTTAA	UUAAAUGUCAGCUGAGCACaa	GUGCUCAGCUGACAUUUAAtt
1844	DUSP2	Hs_DUSP2_7	NM_004418	SI03028095	dual specificity phosphatase 2	AACATTCAGGATTTGTCAATA	UAUUGACAAAUCCUGAAUGtt	CAUUCAGGAUUUGUCAAUAtt
1845	DUSP3	Hs_DUSP3_5	NM_004090	SI02665600	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	CCGTATTTACTTAACAAGATT	AAUCUUGUUAAGUAAAUACgg	GUAUUUACUUAACAAGAUUtt
1845	DUSP3	Hs_DUSP3_6	NM_004090	SI02665607	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	CCCGCGGATCTACGTGGGCAA	UUGCCCACGUAGAUCCGCGgg	CGCGGAUCUACGUGGGCAAtt
1845	DUSP3	Hs_DUSP3_1	NM_004090	SI00059612	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	TACGTTATTGTTATTATGGAA	UUCCAUAAUAACAAUAACGta	CGUUAUUGUUAUUAUGGAAtt
1846	DUSP4	Hs_DUSP4_2	NM_001394 NM_057158	SI00374920	dual specificity phosphatase 4	CACCAACAGATGAATAATTAT	AUAAUUAUUCAUCUGUUGGtg	CCAACAGAUGAAUAAUUAUtt
1846	DUSP4	Hs_DUSP4_3	NM_001394 NM_057158	SI00374927	dual specificity phosphatase 4	TACAGTGGATTTAGAATATAT	AUAUAUUCUAAAUCCACUGta	CAGUGGAUUUAGAAUAUAUtt
1846	DUSP4	Hs_DUSP4_4	NM_001394 NM_057158	SI00374934	dual specificity phosphatase 4	TACCCAGAATTCTGTTCTAAA	UUUAGAACAGAAUUCUGGGta	CCCAGAAUUCUGUUCUAAAtt
1847	DUSP5	Hs_DUSP5_10	NM_004419	SI03206903	dual specificity phosphatase 5	CTGAGTGTTGCGTGGATGTAA	UUACAUCCACGCAACACUCag	GAGUGUUGCGUGGAUGUAAtt
1847	DUSP5	Hs_DUSP5_6	NM_004419	SI02655828	dual specificity phosphatase 5	ACCCGTGTGAATGTGAAGAAA	UUUCUUCACAUUCACACGGgt	CCGUGUGAAUGUGAAGAAAtt
1847	DUSP5	Hs_DUSP5_8	NM_004419	SI03128272	dual specificity phosphatase 5	AAGACTCATGGACATTTCATA	UAUGAAAUGUCCAUGAGUCtt	GACUCAUGGACAUUUCAUAtt
1848	DUSP6	Hs_DUSP6_1	NM_001946 NM_022652	SI00030324	dual specificity phosphatase 6	TGCGGAATTGGTTAATACTAA	UUAGUAUUAACCAAUUCCGca	CGGAAUUGGUUAAUACUAAtt
1848	DUSP6	Hs_DUSP6_4	NM_001946 NM_022652	SI00030345	dual specificity phosphatase 6	TAGCACGGAGTCCGAATTAAT	AUUAAUUCGGACUCCGUGCta	GCACGGAGUCCGAAUUAAUtt
1848	DUSP6	Hs_DUSP6_5	NM_001946 NM_022652	SI02627338	dual specificity phosphatase 6	TACGGACACTATTATCACTAA	UUAGUGAUAAUAGUGUCCGta	CGGACACUAUUAUCACUAAtt
1849	DUSP7	Hs_DUSP7_6	NM_001947	SI02658656	dual specificity phosphatase 7	TACGACTTTGTCAAGAGGAAA	UUUCCUCUUGACAAAGUCGta	CGACUUUGUCAAGAGGAAAtt
1849	DUSP7	Hs_DUSP7_7	NM_001947	SI02658663	dual specificity phosphatase 7	CAAGGTGGTTTCAACAAGTTT	AAACUUGUUGAAACCACCUtg	AGGUGGUUUCAACAAGUUUtt
1849	DUSP7	Hs_DUSP7_8	NM_001947	SI03096835	dual specificity phosphatase 7	CTGGACGTGCTCGGCAAGTAT	AUACUUGCCGAGCACGUCCag	GGACGUGCUCGGCAAGUAUtt
1850	DUSP8	Hs_DUSP8_5	NM_004420	SI02658887	dual specificity phosphatase 8	TCCATCGAGTTCATCGATAAA	UUUAUCGAUGAACUCGAUGga	CAUCGAGUUCAUCGAUAAAtt
1850	DUSP8	Hs_DUSP8_6	NM_004420	SI03027885	dual specificity phosphatase 8	AACATACGTTTCTAAGCAATA	UAUUGCUUAGAAACGUAUGtt	CAUACGUUUCUAAGCAAUAtt
1850	DUSP8	Hs_DUSP8_7	NM_004420	SI03045126	dual specificity phosphatase 8	AGGCCCGTTATAAATGTATAT	AUAUACAUUUAUAACGGGCct	GCCCGUUAUAAAUGUAUAUtt
1852	DUSP9	Hs_DUSP9_5	NM_001395	SI02665572	dual specificity phosphatase 9	CTGAATAAACAGTTTATTTAA	UUAAAUAAACUGUUUAUUCag	GAAUAAACAGUUUAUUUAAtt
1852	DUSP9	Hs_DUSP9_6	NM_001395	SI03191349	dual specificity phosphatase 9	CCGGGATTCCGCCAATTTGGA	UCCAAAUUGGCGGAAUCCCgg	GGGAUUCCGCCAAUUUGGAtt
1852	DUSP9	Hs_DUSP9_2	NM_001395	SI00375004	dual specificity phosphatase 9	CCCAAACTTCTTCGAGAAGAA	UUCUUCUCGAAGAAGUUUGgg	CAAACUUCUUCGAGAAGAAtt
1854	DUT	Hs_DUT_1	NM_001025248 NM_001025249 NM_0019	SI00030380	dUTP pyrophosphatase	AAGCCTGTATTTAACTCATAT	AUAUGAGUUAAAUACAGGCtt	GCCUGUAUUUAACUCAUAUtt
1854	DUT	Hs_DUT_2	NM_001025248 NM_001025249 NM_0019	SI00030387	dUTP pyrophosphatase	ACCCGCCATTTCACCCAGTAA	UUACUGGGUGAAAUGGCGGgt	CCGCCAUUUCACCCAGUAAtt
1854	DUT	Hs_DUT_3	NM_001025248 NM_001025249 NM_0019	SI00030394	dUTP pyrophosphatase	TCCCTTCTCTTCACTAGTCTA	UAGACUAGUGAAGAGAAGGga	CCUUCUCUUCACUAGUCUAtt
2203	FBP1	Hs_FBP1_5	NM_000507	SI02659468	fructose-1,6-bisphosphatase 1	TTCCTAGAGAGCAGAAATAAA	UUUAUUUCUGCUCUCUAGGaa	CCUAGAGAGCAGAAAUAAAtt
2203	FBP1	Hs_FBP1_6	NM_000507	SI02659475	fructose-1,6-bisphosphatase 1	CTCGCTCTGCACAGCAGTCAA	UUGACUGCUGUGCAGAGCGag	CGCUCUGCACAGCAGUCAAtt
2203	FBP1	Hs_FBP1_7	NM_000507	SI03084340	fructose-1,6-bisphosphatase 1	CGCCATCATAGTGGAACCGGA	UCCGGUUCCACUAUGAUGGcg	CCAUCAUAGUGGAACCGGAtt
2538	G6PC	Hs_G6PC_2	NM_000151	SI00003136	glucose-6-phosphatase, catalytic subunit	CAGCAGGTGTATACTACGTGA	UCACGUAGUAUACACCUGCtg	GCAGGUGUAUACUACGUGAtt
2538	G6PC	Hs_G6PC_5	NM_000151	SI03045847	glucose-6-phosphatase, catalytic subunit	AGGGATTGAGGAGGACTACTA	UAGUAGUCCUCCUCAAUCCct	GGAUUGAGGAGGACUACUAtt
2538	G6PC	Hs_G6PC_6	NM_000151	SI03074330	glucose-6-phosphatase, catalytic subunit	CCAAGTCGAGCTGGTCTTCTA	UAGAAGACCAGCUCGACUUgg	AAGUCGAGCUGGUCUUCUAtt
3612	IMPA1	Hs_IMPA1_5	NM_005536	SI02779609	inositol(myo)-1(or 4)-monophosphatase 1	TAGAAAGTTAACTGTTTGGAA	UUCCAAACAGUUAACUUUCta	GAAAGUUAACUGUUUGGAAtt
3612	IMPA1	Hs_IMPA1_6	NM_005536	SI03053078	inositol(myo)-1(or 4)-monophosphatase 1	CAACGAGACGACGAAGATTAA	UUAAUCUUCGUCGUCUCGUtg	ACGAGACGACGAAGAUUAAtt
3612	IMPA1	Hs_IMPA1_7	NM_005536	SI03072433	inositol(myo)-1(or 4)-monophosphatase 1	CAGGTTATACCTTTGCAACGA	UCGUUGCAAAGGUAUAACCtg	GGUUAUACCUUUGCAACGAtt
3628	INPP1	Hs_INPP1_5	NM_002194	SI02658670	inositol polyphosphate-1-phosphatase	TAGATTCAACTTATCAGTATA	UAUACUGAUAAGUUGAAUCta	GAUUCAACUUAUCAGUAUAtt
3628	INPP1	Hs_INPP1_6	NM_002194	SI02759176	inositol polyphosphate-1-phosphatase	CTGATGGGAGTCATCAATCAA	UUGAUUGAUGACUCCCAUCag	GAUGGGAGUCAUCAAUCAAtt
3628	INPP1	Hs_INPP1_7	NM_002194	SI02759183	inositol polyphosphate-1-phosphatase	CACCAGCAGCTGCAACTGAAA	UUUCAGUUGCAGCUGCUGGtg	CCAGCAGCUGCAACUGAAAtt
3632	INPP5A	Hs_INPP5A_1	NM_005539 XM_001133189	SI00078547	inositol polyphosphate-5-phosphatase, 40kDa	CGGAAGGTTATGCTCCAGTTA	UAACUGGAGCAUAACCUUCcg	GAAGGUUAUGCUCCAGUUAtt
3632	INPP5A	Hs_INPP5A_2	NM_005539 XM_001133189	SI00078554	inositol polyphosphate-5-phosphatase, 40kDa	AACAATAATATCATGGGAGAA	UUCUCCCAUGAUAUUAUUGtt	CAAUAAUAUCAUGGGAGAAtt
3632	INPP5A	Hs_INPP5A_3	NM_005539 XM_001133189	SI00078561	inositol polyphosphate-5-phosphatase, 40kDa	CGAGTGCAAATGGTCAAGAAA	UUUCUUGACCAUUUGCACUcg	AGUGCAAAUGGUCAAGAAAtt
3633	INPP5B	Hs_INPP5B_5	NM_005540	SI02658579	inositol polyphosphate-5-phosphatase, 75kDa	TTGCGGGAACATACAATGTAA	UUACAUUGUAUGUUCCCGCaa	GCGGGAACAUACAAUGUAAtt
3633	INPP5B	Hs_INPP5B_6	NM_005540	SI02658586	inositol polyphosphate-5-phosphatase, 75kDa	CTGCGAGATACAATTGTGAAA	UUUCACAAUUGUAUCUCGCag	GCGAGAUACAAUUGUGAAAtt
3633	INPP5B	Hs_INPP5B_2	NM_005540	SI00447783	inositol polyphosphate-5-phosphatase, 75kDa	AAGAAGAGGATTACACCTATA	UAUAGGUGUAAUCCUCUUCtt	GAAGAGGAUUACACCUAUAtt
3635	INPP5D	Hs_INPP5D_1	NM_001017915 NM_005541	SI00078575	inositol polyphosphate-5-phosphatase, 145kDa	CAGGTGCTATGCCACATTGAA	UUCAAUGUGGCAUAGCACCtg	GGUGCUAUGCCACAUUGAAtt
3635	INPP5D	Hs_INPP5D_2	NM_001017915 NM_005541	SI00078582	inositol polyphosphate-5-phosphatase, 145kDa	TCCCATCAACATGGTGTCCAA	UUGGACACCAUGUUGAUGGga	CCAUCAACAUGGUGUCCAAtt
3635	INPP5D	Hs_INPP5D_3	NM_001017915 NM_005541	SI00078589	inositol polyphosphate-5-phosphatase, 145kDa	CCCGGGACTGTTGACAGCCAA	UUGGCUGUCAACAGUCCCGgg	CGGGACUGUUGACAGCCAAtt
3704	ITPA	Hs_ITPA_5	NM_033453 NM_181493	SI02659335	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	CTGGATGAGACTTGTTTCCAA	UUGGAAACAAGUCUCAUCCag	GGAUGAGACUUGUUUCCAAtt
3704	ITPA	Hs_ITPA_6	NM_033453 NM_181493	SI03025407	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	TTGGGTGGTAAAGCTGTACTT	AAGUACAGCUUUACCACCCaa	GGGUGGUAAAGCUGUACUUtt
3704	ITPA	Hs_ITPA_7	NM_033453 NM_181493	SI03065020	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	CAGATTCTAGGAGATAAGTTT	AAACUUAUCUCCUAGAAUCtg	GAUUCUAGGAGAUAAGUUUtt
3936	LCP1	Hs_LCP1_1	NM_002298	SI00469252	lymphocyte cytosolic protein 1 (L-plastin)	TAGGTTTCTATTCTTGATTTA	UAAAUCAAGAAUAGAAACCta	GGUUUCUAUUCUUGAUUUAtt
3936	LCP1	Hs_LCP1_2	NM_002298	SI00469259	lymphocyte cytosolic protein 1 (L-plastin)	CAGGCATGGAGCTATAACTAA	UUAGUUAUAGCUCCAUGCCtg	GGCAUGGAGCUAUAACUAAtt
3936	LCP1	Hs_LCP1_3	NM_002298	SI00469266	lymphocyte cytosolic protein 1 (L-plastin)	CTGCAAGATCTGTTACCTAAA	UUUAGGUAACAGAUCUUGCag	GCAAGAUCUGUUACCUAAAtt
4534	MTM1	Hs_MTM1_5	NM_000252	SI02665558	myotubularin 1	TCGGTATGAGTGGGAAACGAA	UUCGUUUCCCACUCAUACCga	GGUAUGAGUGGGAAACGAAtt
4534	MTM1	Hs_MTM1_6	NM_000252	SI02665565	myotubularin 1	CGAATAGGTCATGGTGATAAA	UUUAUCACCAUGACCUAUUcg	AAUAGGUCAUGGUGAUAAAtt
4659	PPP1R12A	Hs_PPP1R12A_3	NM_002480	SI00038437	protein phosphatase 1, regulatory (inhibitor) subunit 12A	ATAGTACTCAACCATAATTAA	UUAAUUAUGGUUGAGUACUat	AGUACUCAACCAUAAUUAAtt
4659	PPP1R12A	Hs_PPP1R12A_4	NM_002480	SI00038444	protein phosphatase 1, regulatory (inhibitor) subunit 12A	AACGAAGAGCTCTAGAAAGAA	UUCUUUCUAGAGCUCUUCGtt	CGAAGAGCUCUAGAAAGAAtt
4659	PPP1R12A	Hs_PPP1R12A_5	NM_002480	SI02628682	protein phosphatase 1, regulatory (inhibitor) subunit 12A	CAGGCAGGCTATGATGTTAAT	AUUAACAUCAUAGCCUGCCtg	GGCAGGCUAUGAUGUUAAUtt
4660	PPP1R12B	Hs_PPP1R12B_4	NM_002481 NM_032103 NM_032104 NM_	SI00038472	protein phosphatase 1, regulatory (inhibitor) subunit 12B	CGGGAGGTAGTAATCCTACAA	UUGUAGGAUUACUACCUCCcg	GGAGGUAGUAAUCCUACAAtt
4660	PPP1R12B	Hs_PPP1R12B_6	NM_002481 NM_032103 NM_032104 NM_	SI03063403	protein phosphatase 1, regulatory (inhibitor) subunit 12B	CAGACACGAAGGTCTACTCAA	UUGAGUAGACCUUCGUGUCtg	GACACGAAGGUCUACUCAAtt
4660	PPP1R12B	Hs_PPP1R12B_7	NM_002481 NM_032103 NM_032104 NM_	SI03074078	protein phosphatase 1, regulatory (inhibitor) subunit 12B	CATGTAAGACTTCTACCCTAA	UUAGGGUAGAAGUCUUACAtg	UGUAAGACUUCUACCCUAAtt
5167	ENPP1	Hs_ENPP1_6	NM_006208	SI02659006	ectonucleotide pyrophosphatase/phosphodiesterase 1	CACCGGCTCCTAATAACGGAA	UUCCGUUAUUAGGAGCCGGtg	CCGGCUCCUAAUAACGGAAtt
5167	ENPP1	Hs_ENPP1_7	NM_006208	SI02659013	ectonucleotide pyrophosphatase/phosphodiesterase 1	CAGATAAATACTATTCATTTA	UAAAUGAAUAGUAUUUAUCtg	GAUAAAUACUAUUCAUUUAtt
5167	ENPP1	Hs_ENPP1_2	NM_006208	SI00085617	ectonucleotide pyrophosphatase/phosphodiesterase 1	TGGGCAAACAGTAGACTTATA	UAUAAGUCUACUGUUUGCCca	GGCAAACAGUAGACUUAUAtt
5168	ENPP2	Hs_ENPP2_5	NM_001040092 NM_006209	SI02759337	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	CAGATATATTTAAGCCTTATA	UAUAAGGCUUAAAUAUAUCtg	GAUAUAUUUAAGCCUUAUAtt
5168	ENPP2	Hs_ENPP2_6	NM_001040092 NM_006209	SI03045133	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	AGGCCGGTGTACCCAACTAAA	UUUAGUUGGGUACACCGGCct	GCCGGUGUACCCAACUAAAtt
5168	ENPP2	Hs_ENPP2_7	NM_001040092 NM_006209	SI03111752	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	TAGGATTCACTGCACATCGAA	UUCGAUGUGCAGUGAAUCCta	GGAUUCACUGCACAUCGAAtt
5169	ENPP3	Hs_ENPP3_2	NM_005021	SI00071400	ectonucleotide pyrophosphatase/phosphodiesterase 3	TAGCAATTTGGTACCTATGTA	UACAUAGGUACCAAAUUGCta	GCAAUUUGGUACCUAUGUAtt
5169	ENPP3	Hs_ENPP3_3	NM_005021	SI00071407	ectonucleotide pyrophosphatase/phosphodiesterase 3	ATGGTTATAACAATGAGTTTA	UAAACUCAUUGUUAUAACCat	GGUUAUAACAAUGAGUUUAtt
5169	ENPP3	Hs_ENPP3_4	NM_005021	SI00071414	ectonucleotide pyrophosphatase/phosphodiesterase 3	CGCATCCGAGCTCATAATATA	UAUAUUAUGAGCUCGGAUGcg	CAUCCGAGCUCAUAAUAUAtt
5470	PPEF2	Hs_PPEF2_1	NM_006239 NM_152933 NM_152934	SI00086072	protein phosphatase, EF-hand calcium binding domain 2	CTGCAGGAGCATTGCGCTTAA	UUAAGCGCAAUGCUCCUGCag	GCAGGAGCAUUGCGCUUAAtt
5470	PPEF2	Hs_PPEF2_2	NM_006239 NM_152933 NM_152934	SI00086079	protein phosphatase, EF-hand calcium binding domain 2	CACATGAATATCGACATTACA	UGUAAUGUCGAUAUUCAUGtg	CAUGAAUAUCGACAUUACAtt
5470	PPEF2	Hs_PPEF2_3	NM_006239 NM_152933 NM_152934	SI00086086	protein phosphatase, EF-hand calcium binding domain 2	CGGAGCATTGATTTCAACAAA	UUUGUUGAAAUCAAUGCUCcg	GAGCAUUGAUUUCAACAAAtt
5475	PPEF1	Hs_PPEF1_1	NM_006240 NM_152223 NM_152224 NM_	SI00086100	protein phosphatase, EF-hand calcium binding domain 1	CCCAATCGGTACAATCGTTGA	UCAACGAUUGUACCGAUUGgg	CAAUCGGUACAAUCGUUGAtt
5475	PPEF1	Hs_PPEF1_2	NM_006240 NM_152223 NM_152224 NM_	SI00086107	protein phosphatase, EF-hand calcium binding domain 1	ATCGAATATGCTGATGAACAA	UUGUUCAUCAGCAUAUUCGat	CGAAUAUGCUGAUGAACAAtt
5475	PPEF1	Hs_PPEF1_5	NM_006240 NM_152223 NM_152224 NM_	SI03073448	protein phosphatase, EF-hand calcium binding domain 1	CAGTTCGAATCTGGTAAACAT	AUGUUUACCAGAUUCGAACtg	GUUCGAAUCUGGUAAACAUtt
5494	PPM1A	Hs_PPM1A_5	NM_021003 NM_177952	SI02659258	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	AAGCGTGATTTCAAACCATAA	UUAUGGUUUGAAAUCACGCtt	GCGUGAUUUCAAACCAUAAtt
5494	PPM1A	Hs_PPM1A_6	NM_021003 NM_177952	SI02659265	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	TTCCATGAGTATTGCAGGTAA	UUACCUGCAAUACUCAUGGaa	CCAUGAGUAUUGCAGGUAAtt
5494	PPM1A	Hs_PPM1A_7	NM_021003 NM_177951 NM_177952	SI03040625	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	ACCTAGAGGATCAAGACATAA	UUAUGUCUUGAUCCUCUAGgt	CUAGAGGAUCAAGACAUAAtt
5495	PPM1B	Hs_PPM1B_6	NM_001033556 NM_001033557 NM_0027	SI02658677	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	CGAGATAACATGAGTATTGTA	UACAAUACUCAUGUUAUCUcg	AGAUAACAUGAGUAUUGUAtt
5495	PPM1B	Hs_PPM1B_7	NM_001033557 NM_002706 NM_177969	SI02759190	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	CAACCAAGTGTTTAGAATGAA	UUCAUUCUAAACACUUGGUtg	ACCAAGUGUUUAGAAUGAAtt
5495	PPM1B	Hs_PPM1B_8	NM_001033557 NM_002706 NM_177969	SI02759197	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	TAGCCTAACTACACACATCAA	UUGAUGUGUGUAGUUAGGCta	GCCUAACUACACACAUCAAtt
5496	PPM1G	Hs_PPM1G_6	NM_002707 NM_177983	SI02658684	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	CAGGACCTGAGGACTCAACTA	UAGUUGAGUCCUCAGGUCCtg	GGACCUGAGGACUCAACUAtt
5496	PPM1G	Hs_PPM1G_7	NM_002707 NM_177983	SI02658691	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	CCAGAGGATGAAGTAGAACTA	UAGUUCUACUUCAUCCUCUgg	AGAGGAUGAAGUAGAACUAtt
5496	PPM1G	Hs_PPM1G_2	NM_002707 NM_177983	SI00041622	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	TACTCTGTGAACTTTATTTAA	UUAAAUAAAGUUCACAGAGta	CUCUGUGAACUUUAUUUAAtt
5499	PPP1CA	Hs_PPP1CA_10	NM_001008709 NM_002708 NM_206873	SI02225755	protein phosphatase 1, catalytic subunit, alpha isoform	AAGAGACGCTACAACATCAAA	UUUGAUGUUGUAGCGUCUCtt	GAGACGCUACAACAUCAAAtt
5499	PPP1CA	Hs_PPP1CA_9	NM_001008709 NM_002708 NM_206873	SI02225748	protein phosphatase 1, catalytic subunit, alpha isoform	CCGCAATTCCGCCAAAGCCAA	UUGGCUUUGGCGGAAUUGCgg	GCAAUUCCGCCAAAGCCAAtt
5499	PPP1CA	Hs_PPP1CA_3	NM_001008709 NM_002708 NM_206873	SI00041657	protein phosphatase 1, catalytic subunit, alpha isoform	CTGCCTGCTGCTGGCCTATAA	UUAUAGGCCAGCAGCAGGCag	GCCUGCUGCUGGCCUAUAAtt
5500	PPP1CB	Hs_PPP1CB_5	NM_002709 NM_206876	SI02225762	protein phosphatase 1, catalytic subunit, beta isoform	TACGAGGATGTCGTCCAGGAA	UUCCUGGACGACAUCCUCGta	CGAGGAUGUCGUCCAGGAAtt
5500	PPP1CB	Hs_PPP1CB_6	NM_002709 NM_206876 NM_206877	SI02759204	protein phosphatase 1, catalytic subunit, beta isoform	CACTATTGGATGTGATTCTAA	UUAGAAUCACAUCCAAUAGtg	CUAUUGGAUGUGAUUCUAAtt
5500	PPP1CB	Hs_PPP1CB_7	NM_002709 NM_206876 NM_206877	SI03027724	protein phosphatase 1, catalytic subunit, beta isoform	AACAGCTAATCCGCCGAAGAA	UUCUUCGGCGGAUUAGCUGtt	CAGCUAAUCCGCCGAAGAAtt
5501	PPP1CC	Hs_PPP1CC_5	NM_002710	SI02225769	protein phosphatase 1, catalytic subunit, gamma isoform	CTGGTTATAACAGCAAATGAA	UUCAUUUGCUGUUAUAACCag	GGUUAUAACAGCAAAUGAAtt
5501	PPP1CC	Hs_PPP1CC_6	NM_002710	SI02225776	protein phosphatase 1, catalytic subunit, gamma isoform	AACATCGACAGCATTATCCAA	UUGGAUAAUGCUGUCGAUGtt	CAUCGACAGCAUUAUCCAAtt
5501	PPP1CC	Hs_PPP1CC_8	NM_002710	SI02759211	protein phosphatase 1, catalytic subunit, gamma isoform	GAGGAGTAAGTGTACAATTGA	UCAAUUGUACACUUACUCCtc	GGAGUAAGUGUACAAUUGAtt
5502	PPP1R1A	Hs_PPP1R1A_5	NM_006741	SI02759344	protein phosphatase 1, regulatory (inhibitor) subunit 1A	GAGGAGGTATCTTGGGATCAA	UUGAUCCCAAGAUACCUCCtc	GGAGGUAUCUUGGGAUCAAtt
5502	PPP1R1A	Hs_PPP1R1A_6	NM_006741	SI03039400	protein phosphatase 1, regulatory (inhibitor) subunit 1A	ACCCGTTAGCAACAATGGATA	UAUCCAUUGUUGCUAACGGgt	CCGUUAGCAACAAUGGAUAtt
5502	PPP1R1A	Hs_PPP1R1A_7	NM_006741	SI03096443	protein phosphatase 1, regulatory (inhibitor) subunit 1A	CTGGAAGACTCGGCGCTCTAA	UUAGAGCGCCGAGUCUUCCag	GGAAGACUCGGCGCUCUAAtt
5504	PPP1R2	Hs_PPP1R2_6	NM_006241	SI03026842	protein phosphatase 1, regulatory (inhibitor) subunit 2	AAAGGTATGTTCAAGTCATAA	UUAUGACUUGAACAUACCUtt	AGGUAUGUUCAAGUCAUAAtt
5504	PPP1R2	Hs_PPP1R2_7	NM_006241	SI03064152	protein phosphatase 1, regulatory (inhibitor) subunit 2	CAGAGGAGTAAGGCATGCCAA	UUGGCAUGCCUUACUCCUCtg	GAGGAGUAAGGCAUGCCAAtt
5504	PPP1R2	Hs_PPP1R2_8	NM_006241	SI03108042	protein phosphatase 1, regulatory (inhibitor) subunit 2	TACACTACACGTACTGTAATA	UAUUACAGUACGUGUAGUGta	CACUACACGUACUGUAAUAtt
5506	PPP1R3A	Hs_PPP1R3A_2	NM_002711	SI00041734	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	TAGGCCATCAATATCACAATA	UAUUGUGAUAUUGAUGGCCta	GGCCAUCAAUAUCACAAUAtt
5506	PPP1R3A	Hs_PPP1R3A_3	NM_002711	SI00041741	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	CAGAGGAAACTACTTCAAATA	UAUUUGAAGUAGUUUCCUCtg	GAGGAAACUACUUCAAAUAtt
5506	PPP1R3A	Hs_PPP1R3A_6	NM_002711	SI02629270	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)	TCAGGTGGGATTAATTCTGAA	UUCAGAAUUAAUCCCACCUga	AGGUGGGAUUAAUUCUGAAtt
5507	PPP1R3C	Hs_PPP1R3C_7	NM_005398	SI02658978	protein phosphatase 1, regulatory (inhibitor) subunit 3C	TACGATGAATTTCAACGACGA	UCGUCGUUGAAAUUCAUCGta	CGAUGAAUUUCAACGACGAtt
5507	PPP1R3C	Hs_PPP1R3C_8	NM_005398	SI02658985	protein phosphatase 1, regulatory (inhibitor) subunit 3C	TCCGGAGAATCAAGATCTTAA	UUAAGAUCUUGAUUCUCCGga	CGGAGAAUCAAGAUCUUAAtt
5507	PPP1R3C	Hs_PPP1R3C_3	NM_005398	SI00076496	protein phosphatase 1, regulatory (inhibitor) subunit 3C	TGGCCTCTTATCGATGAATTA	UAAUUCAUCGAUAAGAGGCca	GCCUCUUAUCGAUGAAUUAtt
5509	PPP1R3D	Hs_PPP1R3D_5	NM_006242	SI02659020	protein phosphatase 1, regulatory (inhibitor) subunit 3D	CTGAGTTAGGCAATCACTTAA	UUAAGUGAUUGCCUAACUCag	GAGUUAGGCAAUCACUUAAtt
5509	PPP1R3D	Hs_PPP1R3D_6	NM_006242	SI02659027	protein phosphatase 1, regulatory (inhibitor) subunit 3D	CAGGTACCCACCAACTTTATA	UAUAAAGUUGGUGGGUACCtg	GGUACCCACCAACUUUAUAtt
5509	PPP1R3D	Hs_PPP1R3D_2	NM_006242	SI00086163	protein phosphatase 1, regulatory (inhibitor) subunit 3D	AAGGATAGCTTTCTTCGGTAT	AUACCGAAGAAAGCUAUCCtt	GGAUAGCUUUCUUCGGUAUtt
5510	PPP1R7	Hs_PPP1R7_5	NM_002712	SI02759218	protein phosphatase 1, regulatory (inhibitor) subunit 7	CCAGATCAAGAAGATTGAGAA	UUCUCAAUCUUCUUGAUCUgg	AGAUCAAGAAGAUUGAGAAtt
5510	PPP1R7	Hs_PPP1R7_6	NM_002712	SI03032540	protein phosphatase 1, regulatory (inhibitor) subunit 7	AAGATTGAAGGATTTGAGGTA	UACCUCAAAUCCUUCAAUCtt	GAUUGAAGGAUUUGAGGUAtt
5510	PPP1R7	Hs_PPP1R7_7	NM_002712	SI03042424	protein phosphatase 1, regulatory (inhibitor) subunit 7	AGAGTTCTGGATGAACGACAA	UUGUCGUUCAUCCAGAACUct	AGUUCUGGAUGAACGACAAtt
5511	PPP1R8	Hs_PPP1R8_7	NM_002713 NM_014110 NM_138558	SI02759225	protein phosphatase 1, regulatory (inhibitor) subunit 8	CTGCTGAAGTTTCTTATTTAA	UUAAAUAAGAAACUUCAGCag	GCUGAAGUUUCUUAUUUAAtt
5511	PPP1R8	Hs_PPP1R8_8	NM_002713 NM_014110 NM_138558	SI02759232	protein phosphatase 1, regulatory (inhibitor) subunit 8	AACCCTGAAGCTGTAAATGAA	UUCAUUUACAGCUUCAGGGtt	CCCUGAAGCUGUAAAUGAAtt
5511	PPP1R8	Hs_PPP1R8_9	NM_002713 NM_014110 NM_138558	SI03098249	protein phosphatase 1, regulatory (inhibitor) subunit 8	CTGGCTAACAAACATAGGAGA	UCUCCUAUGUUUGUUAGCCag	GGCUAACAAACAUAGGAGAtt
5514	PPP1R10	Hs_PPP1R10_1	NM_002714	SI00041811	protein phosphatase 1, regulatory (inhibitor) subunit 10	CACAGGATCAGCTGCACTTAA	UUAAGUGCAGCUGAUCCUGtg	CAGGAUCAGCUGCACUUAAtt
5514	PPP1R10	Hs_PPP1R10_4	NM_002714	SI00041832	protein phosphatase 1, regulatory (inhibitor) subunit 10	CAGCAACATCTAAGCCCTTGA	UCAAGGGCUUAGAUGUUGCtg	GCAACAUCUAAGCCCUUGAtt
5514	PPP1R10	Hs_PPP1R10_5	NM_002714	SI03032666	protein phosphatase 1, regulatory (inhibitor) subunit 10	AAGCAATAGTCAGGAGCGATA	UAUCGCUCCUGACUAUUGCtt	GCAAUAGUCAGGAGCGAUAtt
5515	PPP2CA	Hs_PPP2CA_5	NM_002715	SI02225783	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	ATGGAACTTGACGATACTCTA	UAGAGUAUCGUCAAGUUCCat	GGAACUUGACGAUACUCUAtt
5515	PPP2CA	Hs_PPP2CA_6	NM_002715	SI02225790	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	CAAACAATCATTGGAGCTTAA	UUAAGCUCCAAUGAUUGUUtg	AACAAUCAUUGGAGCUUAAtt
5515	PPP2CA	Hs_PPP2CA_3	NM_002715	SI00041853	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	ACACCTCGTGAATACAATTTA	UAAAUUGUAUUCACGAGGUgt	ACCUCGUGAAUACAAUUUAtt
5516	PPP2CB	Hs_PPP2CB_12	NM_001009552 NM_004156	SI02225797	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	CCGACAAATTACCCAAGTATA	UAUACUUGGGUAAUUUGUCgg	GACAAAUUACCCAAGUAUAtt
5516	PPP2CB	Hs_PPP2CB_13	NM_001009552 NM_004156	SI02225804	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	TGGGATCTGTCTTGGCATTAA	UUAAUGCCAAGACAGAUCCca	GGAUCUGUCUUGGCAUUAAtt
5516	PPP2CB	Hs_PPP2CB_14	NM_001009552 NM_004156	SI02777397	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	ATGGAATTAGATGACACTTTA	UAAAGUGUCAUCUAAUUCCat	GGAAUUAGAUGACACUUUAtt
5518	PPP2R1A	Hs_PPP2R1A_5	NM_014225	SI02225811	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	CTGGTGTCCGATGCCAACCAA	UUGGUUGGCAUCGGACACCag	GGUGUCCGAUGCCAACCAAtt

5518	PPP2R1A	Hs_PPP2R1A_6	NM_014225	SI02225818	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	ACGGCTGAACATCATCTCTAA	UUAGAGAUGAUGUUCAGCCgt	GGCUGAACAUCAUCUCUAAtt
5518	PPP2R1A	Hs_PPP2R1A_1	NM_014225	SI00103733	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	TCCCATCTTGGGCAAAGACAA	UUGUCUUUGCCCAAGAUGGga	CCAUCUUGGGCAAAGACAAtt
5519	PPP2R1B	Hs_PPP2R1B_10	NM_002716 NM_181699	SI02653364	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	CAGGAAATAACTACTAAGCAA	UUGCUUAGUAGUUAUUUCCtg	GGAAAUAACUACUAAGCAAtt
5519	PPP2R1B	Hs_PPP2R1B_11	NM_002716 NM_181699	SI02653763	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	CAGAAGTTAGGTCAAGATGAA	UUCAUCUUGACCUAACUUCtg	GAAGUUAGGUCAAGAUGAAtt
5519	PPP2R1B	Hs_PPP2R1B_12	NM_002716 NM_181699	SI02659433	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	CTGACGTTCGTTTGAATATCA	UGAUAUUCAAACGAACGUCag	GACGUUCGUUUGAAUAUCAtt
5520	PPP2R2A	Hs_PPP2R2A_5	NM_002717	SI02225825	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	CTGCAGATGATTTGCGGATTA	UAAUCCGCAAAUCAUCUGCag	GCAGAUGAUUUGCGGAUUAtt
5520	PPP2R2A	Hs_PPP2R2A_6	NM_002717	SI02225832	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	ATGGAAGGTATAGAGATCCTA	UAGGAUCUCUAUACCUUCCat	GGAAGGUAUAGAGAUCCUAtt
5520	PPP2R2A	Hs_PPP2R2A_1	NM_002717	SI00041895	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	CTCGCCGTGTCTGGCACTGAA	UUCAGUGCCAGACACGGCGag	CGCCGUGUCUGGCACUGAAtt
5521	PPP2R2B	Hs_PPP2R2B_7	NM_004576 NM_181674 NM_181675 NM_	SI02658894	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	CGGCTACAAATAACCTATATA	UAUAUAGGUUAUUUGUAGCcg	GCUACAAAUAACCUAUAUAtt
5521	PPP2R2B	Hs_PPP2R2B_8	NM_004576 NM_181674 NM_181675 NM_	SI02658901	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	CCGGAAGATCCAAGCAACAGA	UCUGUUGCUUGGAUCUUCCgg	GGAAGAUCCAAGCAACAGAtt
5521	PPP2R2B	Hs_PPP2R2B_5	NM_004576 NM_181674 NM_181675 NM_	SI02633575	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	CAGGAAATGATTGGAATAGAA	UUCUAUUCCAAUCAUUUCCtg	GGAAAUGAUUGGAAUAGAAtt
5522	PPP2R2C	Hs_PPP2R2C_6	NM_020416 NM_181876	SI02659237	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	ACCGCTCATTCTTCTCGGAAA	UUUCCGAGAAGAAUGAGCGgt	CGCUCAUUCUUCUCGGAAAtt
5522	PPP2R2C	Hs_PPP2R2C_7	NM_020416 NM_181876	SI03032498	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	AAGATTACCGAACGAGATAAA	UUUAUCUCGUUCGGUAAUCtt	GAUUACCGAACGAGAUAAAtt
5522	PPP2R2C	Hs_PPP2R2C_4	NM_020416 NM_181876	SI00126434	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	TACTGTCACATCATAGATTTA	UAAAUCUAUGAUGUGACAGta	CUGUCACAUCAUAGAUUUAtt
5523	PPP2R3A	Hs_PPP2R3A_6	NM_002718 NM_181897	SI02649717	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	CAGGAGGATTTCATCCCTCTA	UAGAGGGAUGAAAUCCUCCtg	GGAGGAUUUCAUCCCUCUAtt
5523	PPP2R3A	Hs_PPP2R3A_7	NM_002718 NM_181897	SI03038469	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	ACCACGGTTATTCAGAGAATA	UAUUCUCUGAAUAACCGUGgt	CACGGUUAUUCAGAGAAUAtt
5523	PPP2R3A	Hs_PPP2R3A_8	NM_002718 NM_181897	SI03082961	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	CCGGTTTGCCGCTGAGGAGTA	UACUCCUCAGCGGCAAACCgg	GGUUUGCCGCUGAGGAGUAtt
5524	PPP2R4	Hs_PPP2R4_5	NM_021131 NM_178000 NM_178001 NM_	SI02659419	protein phosphatase 2A activator, regulatory subunit 4	CTCCGGGTGGATGACCAAATA	UAUUUGGUCAUCCACCCGGag	CCGGGUGGAUGACCAAAUAtt
5524	PPP2R4	Hs_PPP2R4_6	NM_021131 NM_178000 NM_178001 NM_	SI02659426	protein phosphatase 2A activator, regulatory subunit 4	CTGAGGTGGCTGTTTACCTAA	UUAGGUAAACAGCCACCUCag	GAGGUGGCUGUUUACCUAAtt
5524	PPP2R4	Hs_PPP2R4_7	NM_021131 NM_178000 NM_178001 NM_	SI03097353	protein phosphatase 2A activator, regulatory subunit 4	CTGGAGTCGATGCCTTTCTAA	UUAGAAAGGCAUCGACUCCag	GGAGUCGAUGCCUUUCUAAtt
5525	PPP2R5A	Hs_PPP2R5A_5	NM_006243	SI02225839	protein phosphatase 2, regulatory subunit B', alpha isoform	CTGTATCATGGCCATAGTATA	UAUACUAUGGCCAUGAUACag	GUAUCAUGGCCAUAGUAUAtt
5525	PPP2R5A	Hs_PPP2R5A_6	NM_006243	SI02225846	protein phosphatase 2, regulatory subunit B', alpha isoform	CAGCGTATTCTGATATAGTAA	UUACUAUAUCAGAAUACGCtg	GCGUAUUCUGAUAUAGUAAtt
5525	PPP2R5A	Hs_PPP2R5A_7	NM_006243	SI03022782	protein phosphatase 2, regulatory subunit B', alpha isoform	TTCGATGACCTTACTAGCTCA	UGAGCUAGUAAGGUCAUCGaa	CGAUGACCUUACUAGCUCAtt
5526	PPP2R5B	Hs_PPP2R5B_5	NM_006244	SI02659034	protein phosphatase 2, regulatory subunit B', beta isoform	CCGCATGATCTCAGTGAATAT	AUAUUCACUGAGAUCAUGCgg	GCAUGAUCUCAGUGAAUAUtt
5526	PPP2R5B	Hs_PPP2R5B_6	NM_006244	SI03073770	protein phosphatase 2, regulatory subunit B', beta isoform	CATCGTATCACTGATCTACAA	UUGUAGAUCAGUGAUACGAtg	UCGUAUCACUGAUCUACAAtt
5526	PPP2R5B	Hs_PPP2R5B_7	NM_006244	SI03078642	protein phosphatase 2, regulatory subunit B', beta isoform	CCCGGGAGCGTGAGTACCTCA	UGAGGUACUCACGCUCCCGgg	CGGGAGCGUGAGUACCUCAtt
5527	PPP2R5C	Hs_PPP2R5C_12	NM_002719 NM_178586 NM_178587 NM_	SI02663626	protein phosphatase 2, regulatory subunit B', gamma isoform	CTGGAAATATTGGGAAGTATA	UAUACUUCCCAAUAUUUCCag	GGAAAUAUUGGGAAGUAUAtt
5527	PPP2R5C	Hs_PPP2R5C_13	NM_002719 NM_178586 NM_178587 NM_	SI02757573	protein phosphatase 2, regulatory subunit B', gamma isoform	AACGAGCTGCTTTAAGTGAAA	UUUCACUUAAAGCAGCUCGtt	CGAGCUGCUUUAAGUGAAAtt
5527	PPP2R5C	Hs_PPP2R5C_14	NM_002719 NM_178586 NM_178587 NM_	SI03051986	protein phosphatase 2, regulatory subunit B', gamma isoform	ATGGTAGAATATATCACCCAT	AUGGGUGAUAUAUUCUACCat	GGUAGAAUAUAUCACCCAUtt
5528	PPP2R5D	Hs_PPP2R5D_5	NM_006245 NM_180976 NM_180977	SI02653350	protein phosphatase 2, regulatory subunit B', delta isoform	CAGGAGATTATTCTCACCAAA	UUUGGUGAGAAUAAUCUCCtg	GGAGAUUAUUCUCACCAAAtt
5528	PPP2R5D	Hs_PPP2R5D_6	NM_006245 NM_180976 NM_180977	SI02653812	protein phosphatase 2, regulatory subunit B', delta isoform	GAAGTTGTTTATGGAAATGAA	UUCAUUUCCAUAAACAACUtc	AGUUGUUUAUGGAAAUGAAtt
5528	PPP2R5D	Hs_PPP2R5D_7	NM_006245 NM_180976 NM_180977	SI02661456	protein phosphatase 2, regulatory subunit B', delta isoform	CAAGGAGGTGATGTTCTTGAA	UUCAAGAACAUCACCUCCUtg	AGGAGGUGAUGUUCUUGAAtt
5529	PPP2R5E	Hs_PPP2R5E_6	NM_006246	SI02659041	protein phosphatase 2, regulatory subunit B', epsilon isoform	CACCGGGATTGCAAATCTAAT	AUUAGAUUUGCAAUCCCGGtg	CCGGGAUUGCAAAUCUAAUtt
5529	PPP2R5E	Hs_PPP2R5E_7	NM_006246	SI02659048	protein phosphatase 2, regulatory subunit B', epsilon isoform	CCGGTGATATTGACAATAGGA	UCCUAUUGUCAAUAUCACCgg	GGUGAUAUUGACAAUAGGAtt
5529	PPP2R5E	Hs_PPP2R5E_3	NM_006246	SI00086282	protein phosphatase 2, regulatory subunit B', epsilon isoform	AAGGACTTCAATCCAAAGTTT	AAACUUUGGAUUGAAGUCCtt	GGACUUCAAUCCAAAGUUUtt
5530	PPP3CA	Hs_PPP3CA_6	NM_000944	SI02658614	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	TCGGCCTGTATGGGACTGTAA	UUACAGUCCCAUACAGGCCga	GGCCUGUAUGGGACUGUAAtt
5530	PPP3CA	Hs_PPP3CA_7	NM_000944	SI02759155	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	CTGACATATACTGGAAATGTA	UACAUUUCCAGUAUAUGUCag	GACAUAUACUGGAAAUGUAtt
5530	PPP3CA	Hs_PPP3CA_2	NM_000944	SI00018942	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	CACGCTTCAGCTACTATCTAA	UUAGAUAGUAGCUGAAGCGtg	CGCUUCAGCUACUAUCUAAtt
5531	PPP4C	Hs_PPP4C_8	NM_002720	SI02658698	protein phosphatase 4 (formerly X), catalytic subunit	CGGACAATCGACCGAAAGCAA	UUGCUUUCGGUCGAUUGUCcg	GACAAUCGACCGAAAGCAAtt
5531	PPP4C	Hs_PPP4C_9	NM_002720	SI02658705	protein phosphatase 4 (formerly X), catalytic subunit	TCGCCAGATCACGCAGGTCTA	UAGACCUGCGUGAUCUGGCga	GCCAGAUCACGCAGGUCUAtt
5531	PPP4C	Hs_PPP4C_5	NM_002720	1024897	protein phosphatase 4 (formerly X), catalytic subunit	AAGGCCAGAGAGATCTTGGTA	UACCAAGAUCUCUCUGGCCtt	GGCCAGAGAGAUCUUGGUAtt
5532	PPP3CB	Hs_PPP3CB_1	NM_021132	SI00129458	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	CAGGGTTCCCTTCATTAATAA	UUAUUAAUGAAGGGAACCCtg	GGGUUCCCUUCAUUAAUAAtt
5532	PPP3CB	Hs_PPP3CB_5	NM_021132	SI02644572	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	AAGGGTTTGGATAGGATCAAT	AUUGAUCCUAUCCAAACCCtt	GGGUUUGGAUAGGAUCAAUtt
5532	PPP3CB	Hs_PPP3CB_6	NM_021132	SI03048290	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	ATCGATTATTAGAGCTCATGA	UCAUGAGCUCUAAUAAUCGat	CGAUUAUUAGAGCUCAUGAtt
5533	PPP3CC	Hs_PPP3CC_5	NM_005605	SI03037230	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	AAGTTGGAGGATCACCTAGTA	UACUAGGUGAUCCUCCAACtt	GUUGGAGGAUCACCUAGUAtt
5533	PPP3CC	Hs_PPP3CC_6	NM_005605	SI03044384	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	AGGAAGCACTACAGTTCGTAA	UUACGAACUGUAGUGCUUCct	GAAGCACUACAGUUCGUAAtt
5533	PPP3CC	Hs_PPP3CC_7	NM_005605	SI03076052	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	CCCAAGATGCTGGGTATCGAA	UUCGAUACCCAGCAUCUUGgg	CAAGAUGCUGGGUAUCGAAtt
5534	PPP3R1	Hs_PPP3R1_5	NM_000945	SI02759162	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	TCCCTTTATAGTTTCTCTATA	UAUAGAGAAACUAUAAAGGga	CCUUUAUAGUUUCUCUAUAtt
5534	PPP3R1	Hs_PPP3R1_6	NM_000945	SI02759169	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	GAGCCTCATGAAGCCAACTAA	UUAGUUGGCUUCAUGAGGCtc	GCCUCAUGAAGCCAACUAAtt
5534	PPP3R1	Hs_PPP3R1_7	NM_000945	SI03059826	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	CACGAGGGATAGAGCATGCAT	AUGCAUGCUCUAUCCCUCGtg	CGAGGGAUAGAGCAUGCAUtt
5536	PPP5C	Hs_PPP5C_5	NM_006247	SI02225853	protein phosphatase 5, catalytic subunit	CTCGTGGAAACCACACTCAAA	UUUGAGUGUGGUUUCCACGag	CGUGGAAACCACACUCAAAtt
5536	PPP5C	Hs_PPP5C_6	NM_006247	SI03065041	protein phosphatase 5, catalytic subunit	CAGATTCTGGTACAGGTCAAA	UUUGACCUGUACCAGAAUCtg	GAUUCUGGUACAGGUCAAAtt
5536	PPP5C	Hs_PPP5C_7	NM_006247	SI03076626	protein phosphatase 5, catalytic subunit	CCCAGATGTACGAGCTCTTTA	UAAAGAGCUCGUACAUCUGgg	CAGAUGUACGAGCUCUUUAtt
5537	PPP6C	Hs_PPP6C_5	NM_002721	SI02225860	protein phosphatase 6, catalytic subunit	CACAAATGAGTTTGTTCATAT	AUAUGAACAAACUCAUUUGtg	CAAAUGAGUUUGUUCAUAUtt
5537	PPP6C	Hs_PPP6C_6	NM_002721	SI02225867	protein phosphatase 6, catalytic subunit	CAGCAGCAAAGTTGTTATTCA	UGAAUAACAACUUUGCUGCtg	GCAGCAAAGUUGUUAUUCAtt
5537	PPP6C	Hs_PPP6C_3	NM_002721	SI00041993	protein phosphatase 6, catalytic subunit	CTGGTTTGGTCAGATCCTGAA	UUCAGGAUCUGACCAAACCag	GGUUUGGUCAGAUCCUGAAtt
5723	PSPH	Hs_PSPH_5	NM_004577	SI02658908	phosphoserine phosphatase	TGCCAATAGGCTGAAATTCTA	UAGAAUUUCAGCCUAUUGGca	CCAAUAGGCUGAAAUUCUAtt
5723	PSPH	Hs_PSPH_6	NM_004577	SI02658915	phosphoserine phosphatase	CCGGCATAAGGGAGCTGGTAA	UUACCAGCUCCCUUAUGCCgg	GGCAUAAGGGAGCUGGUAAtt
5723	PSPH	Hs_PSPH_7	NM_004577	SI03091438	phosphoserine phosphatase	CTCGCGGTTTGTTCCGTTTCA	UGAAACGGAACAAACCGCGag	CGCGGUUUGUUCCGUUUCAtt
5728	PTEN	Hs_PTEN_6	NM_000314	SI00301504	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	AAGGCGTATACAGGAACAATA	UAUUGUUCCUGUAUACGCCtt	GGCGUAUACAGGAACAAUAtt
5728	PTEN	Hs_PTEN_8	NM_000314	SI03048178	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	ATCGATAGCATTTGCAGTATA	UAUACUGCAAAUGCUAUCGat	CGAUAGCAUUUGCAGUAUAtt
5728	PTEN	Hs_PTEN_9	NM_000314	SI03116092	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	TCGACTTAGACTTGACCTATA	UAUAGGUCAAGUCUAAGUCga	GACUUAGACUUGACCUAUAtt
5770	PTPN1	Hs_PTPN1_1	NM_002827	SI00043806	protein tyrosine phosphatase, non-receptor type 1	CACGTGGGTATTTAATAAGAA	UUCUUAUUAAAUACCCACGtg	CGUGGGUAUUUAAUAAGAAtt
5770	PTPN1	Hs_PTPN1_2	NM_002827	SI00043813	protein tyrosine phosphatase, non-receptor type 1	CAGGCATGCCGCGGTAGGTAA	UUACCUACCGCGGCAUGCCtg	GGCAUGCCGCGGUAGGUAAtt
5770	PTPN1	Hs_PTPN1_3	NM_002827	SI00043820	protein tyrosine phosphatase, non-receptor type 1	CAGGAATAGGCATTTGCCTAA	UUAGGCAAAUGCCUAUUCCtg	GGAAUAGGCAUUUGCCUAAtt
5771	PTPN2	Hs_PTPN2_10	NM_002828 NM_080422 NM_080423	SI02759239	protein tyrosine phosphatase, non-receptor type 2	CACAAAGGAGTTACATCTTAA	UUAAGAUGUAACUCCUUUGtg	CAAAGGAGUUACAUCUUAAtt
5771	PTPN2	Hs_PTPN2_9	NM_002828 NM_080422 NM_080423	SI02225895	protein tyrosine phosphatase, non-receptor type 2	CCGCTGTACTTGGAAATTCGA	UCGAAUUUCCAAGUACAGCgg	GCUGUACUUGGAAAUUCGAtt
5771	PTPN2	Hs_PTPN2_11	NM_002828 NM_080422 NM_080423	SI03046414	protein tyrosine phosphatase, non-receptor type 2	ATAAAGGGAGATTCTAGTATA	UAUACUAGAAUCUCCCUUUat	AAAGGGAGAUUCUAGUAUAtt
5774	PTPN3	Hs_PTPN3_5	NM_002829	SI02658712	protein tyrosine phosphatase, non-receptor type 3	CCGGGTATTATTGCAGGGAAA	UUUCCCUGCAAUAAUACCCgg	GGGUAUUAUUGCAGGGAAAtt
5774	PTPN3	Hs_PTPN3_6	NM_002829	SI02658719	protein tyrosine phosphatase, non-receptor type 3	CAGGTTATTCAGCGATAGTTA	UAACUAUCGCUGAAUAACCtg	GGUUAUUCAGCGAUAGUUAtt
5774	PTPN3	Hs_PTPN3_7	NM_002829	SI03043894	protein tyrosine phosphatase, non-receptor type 3	AGCGCGGACCCTCGACTTCTA	UAGAAGUCGAGGGUCCGCGct	CGCGGACCCUCGACUUCUAtt
5775	PTPN4	Hs_PTPN4_6	NM_002830	SI03052168	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	ATGGTGGTATTCCACATGATA	UAUCAUGUGGAAUACCACCat	GGUGGUAUUCCACAUGAUAtt
5775	PTPN4	Hs_PTPN4_7	NM_002830	SI03063900	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	CAGAGATATTTCGCCTTATGA	UCAUAAGGCGAAAUAUCUCtg	GAGAUAUUUCGCCUUAUGAtt
5775	PTPN4	Hs_PTPN4_8	NM_002830	SI03071474	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	CAGGGTACGAATGAATACCTT	AAGGUAUUCAUUCGUACCCtg	GGGUACGAAUGAAUACCUUtt
5777	PTPN6	Hs_PTPN6_5	NM_002831 NM_080548 NM_080549	SI02658726	protein tyrosine phosphatase, non-receptor type 6	CCGGAACAAATGCGTCCCATA	UAUGGGACGCAUUUGUUCCgg	GGAACAAAUGCGUCCCAUAtt
5777	PTPN6	Hs_PTPN6_6	NM_002831 NM_080548 NM_080549	SI02658733	protein tyrosine phosphatase, non-receptor type 6	TAGGCCCTGATGAGAACGCTA	UAGCGUUCUCAUCAGGGCCta	GGCCCUGAUGAGAACGCUAtt
5777	PTPN6	Hs_PTPN6_7	NM_002831 NM_080548 NM_080549	SI03096898	protein tyrosine phosphatase, non-receptor type 6	CTGGACGTTTCTTGTGCGTGA	UCACGCACAAGAAACGUCCag	GGACGUUUCUUGUGCGUGAtt
5778	PTPN7	Hs_PTPN7_6	NM_002832 NM_080588 NM_080589	SI02658740	protein tyrosine phosphatase, non-receptor type 7	CTGGCATTTATGACAGACAAA	UUUGUCUGUCAUAAAUGCCag	GGCAUUUAUGACAGACAAAtt
5778	PTPN7	Hs_PTPN7_7	NM_002832 NM_080588 NM_080589	SI02658747	protein tyrosine phosphatase, non-receptor type 7	CAGGTCTACCTCAGGACTGAA	UUCAGUCCUGAGGUAGACCtg	GGUCUACCUCAGGACUGAAtt
5778	PTPN7	Hs_PTPN7_8	NM_002832 NM_080588 NM_080589	SI03099138	protein tyrosine phosphatase, non-receptor type 7	CTGGGTATGCAGGACCCACTA	UAGUGGGUCCUGCAUACCCag	GGGUAUGCAGGACCCACUAtt
5780	PTPN9	Hs_PTPN9_5	NM_002833 XM_001128975	SI02658754	protein tyrosine phosphatase, non-receptor type 9	ACCAAACTAGAGTGAAGCTAA	UUAGCUUCACUCUAGUUUGgt	CAAACUAGAGUGAAGCUAAtt
5780	PTPN9	Hs_PTPN9_6	NM_002833 XM_001128975	SI02759246	protein tyrosine phosphatase, non-receptor type 9	CCAGTAGCAATGTGTTCTTAA	UUAAGAACACAUUGCUACUgg	AGUAGCAAUGUGUUCUUAAtt
5780	PTPN9	Hs_PTPN9_7	NM_002833 XM_001128975	SI02759253	protein tyrosine phosphatase, non-receptor type 9	CAAGTGGACAGTTCAGTACAA	UUGUACUGAACUGUCCACUtg	AGUGGACAGUUCAGUACAAtt
5781	PTPN11	Hs_PTPN11_5	NM_002834	SI00301539	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	AAGGTGGTTTCATGGACATCT	AGAUGUCCAUGAAACCACCtt	GGUGGUUUCAUGGACAUCUtt
5781	PTPN11	Hs_PTPN11_6	NM_002834	SI02225902	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	CAGAAGCACAGTACCGATTTA	UAAAUCGGUACUGUGCUUCtg	GAAGCACAGUACCGAUUUAtt
5781	PTPN11	Hs_PTPN11_7	NM_002834	SI02225909	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	CCGCTCATGACTATACGCTAA	UUAGCGUAUAGUCAUGAGCgg	GCUCAUGACUAUACGCUAAtt
5782	PTPN12	Hs_PTPN12_7	NM_002835	SI02658761	protein tyrosine phosphatase, non-receptor type 12	TTGCAGGTTATCAGAGATCAA	UUGAUCUCUGAUAACCUGCaa	GCAGGUUAUCAGAGAUCAAtt
5782	PTPN12	Hs_PTPN12_8	NM_002835	SI02658768	protein tyrosine phosphatase, non-receptor type 12	AAGCTTAATGAGGAAATATCA	UGAUAUUUCCUCAUUAAGCtt	GCUUAAUGAGGAAAUAUCAtt
5782	PTPN12	Hs_PTPN12_1	NM_002835	SI00044030	protein tyrosine phosphatase, non-receptor type 12	GTGGATCATGATAACACTTCA	UGAAGUGUUAUCAUGAUCCac	GGAUCAUGAUAACACUUCAtt
5783	PTPN13	Hs_PTPN13_6	NM_006264 NM_080683 NM_080684 NM_	SI02659342	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	CGGTCTATTCTTACTAAGAAA	UUUCUUAGUAAGAAUAGACcg	GUCUAUUCUUACUAAGAAAtt
5783	PTPN13	Hs_PTPN13_7	NM_006264 NM_080683 NM_080684 NM_	SI02659349	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	TCGATGGATAAGTATCATATA	UAUAUGAUACUUAUCCAUCga	GAUGGAUAAGUAUCAUAUAtt
5783	PTPN13	Hs_PTPN13_4	NM_006264 NM_080683 NM_080684 NM_	SI00086660	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	AACCTTTGGATCAGTGTCTAA	UUAGACACUGAUCCAAAGGtt	CCUUUGGAUCAGUGUCUAAtt
5784	PTPN14	Hs_PTPN14_5	NM_005401	SI02225916	protein tyrosine phosphatase, non-receptor type 14	CGGTGTGGCATTTACAATATA	UAUAUUGUAAAUGCCACACcg	GUGUGGCAUUUACAAUAUAtt
5784	PTPN14	Hs_PTPN14_6	NM_005401	SI02225923	protein tyrosine phosphatase, non-receptor type 14	AAGGGCGATTACGATGTACAT	AUGUACAUCGUAAUCGCCCtt	GGGCGAUUACGAUGUACAUtt
5784	PTPN14	Hs_PTPN14_7	NM_005401	SI02759323	protein tyrosine phosphatase, non-receptor type 14	CTGGCCCAAACTAGGTTCAAA	UUUGAACCUAGUUUGGGCCag	GGCCCAAACUAGGUUCAAAtt
5786	PTPRA	Hs_PTPRA_5	NM_002836 NM_080840 NM_080841	SI02658775	protein tyrosine phosphatase, receptor type, A	CAGAGTGATCATTCCAGTTAA	UUAACUGGAAUGAUCACUCtg	GAGUGAUCAUUCCAGUUAAtt
5786	PTPRA	Hs_PTPRA_6	NM_002836 NM_080840 NM_080841	SI02658782	protein tyrosine phosphatase, receptor type, A	CCGGAGAATGGCAGACGACAA	UUGUCGUCUGCCAUUCUCCgg	GGAGAAUGGCAGACGACAAtt
5786	PTPRA	Hs_PTPRA_3	NM_002836 NM_080840 NM_080841	SI00044072	protein tyrosine phosphatase, receptor type, A	AGGCATTACAATTTCACCAAA	UUUGGUGAAAUUGUAAUGCct	GCAUUACAAUUUCACCAAAtt
5787	PTPRB	Hs_PTPRB_5	NM_002837	SI02225937	protein tyrosine phosphatase, receptor type, B	CCGGTCGACTTTATCAAGTTA	UAACUUGAUAAAGUCGACCgg	GGUCGACUUUAUCAAGUUAtt
5787	PTPRB	Hs_PTPRB_6	NM_002837	SI02225944	protein tyrosine phosphatase, receptor type, B	CCCGGAGATGTGGATAACTAT	AUAGUUAUCCACAUCUCCGgg	CGGAGAUGUGGAUAACUAUtt
5787	PTPRB	Hs_PTPRB_3	NM_002837	SI00044100	protein tyrosine phosphatase, receptor type, B	TCGGGTGTATCAGACTAATTA	UAAUUAGUCUGAUACACCCga	GGGUGUAUCAGACUAAUUAtt
5788	PTPRC	Hs_PTPRC_5	NM_002838 NM_080921 NM_080922	SI02629690	protein tyrosine phosphatase, receptor type, C	AAGAATTGCGATTTCCGTGTA	UACACGGAAAUCGCAAUUCtt	GAAUUGCGAUUUCCGUGUAtt
5788	PTPRC	Hs_PTPRC_6	NM_002838 NM_080921 NM_080922 NM_	SI03034500	protein tyrosine phosphatase, receptor type, C	AAGGACGCATGCTGTTTCTTA	UAAGAAACAGCAUGCGUCCtt	GGACGCAUGCUGUUUCUUAtt
5788	PTPRC	Hs_PTPRC_7	NM_002838 NM_080921 NM_080922 NM_	SI03041640	protein tyrosine phosphatase, receptor type, C	ACGGCTGACTTCCAGATATGA	UCAUAUCUGGAAGUCAGCCgt	GGCUGACUUCCAGAUAUGAtt
5789	PTPRD	Hs_PTPRD_6	NM_001040712 NM_002839 NM_130391 N	SI02665586	protein tyrosine phosphatase, receptor type, D	CTGGGTGTCATTGAAGCAATA	UAUUGCUUCAAUGACACCCag	GGGUGUCAUUGAAGCAAUAtt
5789	PTPRD	Hs_PTPRD_7	NM_001040712 NM_002839 NM_130391 N	SI02665593	protein tyrosine phosphatase, receptor type, D	ACGGCCAGTCCCGAACAGTAA	UUACUGUUCGGGACUGGCCgt	GGCCAGUCCCGAACAGUAAtt
5789	PTPRD	Hs_PTPRD_8	NM_001040712 NM_002839 NM_130391 N	SI03046512	protein tyrosine phosphatase, receptor type, D	ATACGCGAATGTAATCGCATA	UAUGCGAUUACAUUCGCGUat	ACGCGAAUGUAAUCGCAUAtt
5790	PTPRCAP	Hs_PTPRCAP_1	NM_005608	SI00079464	protein tyrosine phosphatase, receptor type, C-associated protein	CAGGCAACCATTTGAAATAAA	UUUAUUUCAAAUGGUUGCCtg	GGCAACCAUUUGAAAUAAAtt
5790	PTPRCAP	Hs_PTPRCAP_2	NM_005608	SI02656367	protein tyrosine phosphatase, receptor type, C-associated protein	CAGGGCCTCCATGTCACCGCA	UGCGGUGACAUGGAGGCCCtg	GGGCCUCCAUGUCACCGCAtt
5790	PTPRCAP	Hs_PTPRCAP_3	NM_005608	SI02656374	protein tyrosine phosphatase, receptor type, C-associated protein	CACGCCTTTGCTGGCAGCGCA	UGCGCUGCCAGCAAAGGCGtg	CGCCUUUGCUGGCAGCGCAtt
5791	PTPRE	Hs_PTPRE_5	NM_006504 NM_130435	SI02665635	protein tyrosine phosphatase, receptor type, E	CCGAGTGATCCTTTCCATGAA	UUCAUGGAAAGGAUCACUCgg	GAGUGAUCCUUUCCAUGAAtt
5791	PTPRE	Hs_PTPRE_2	NM_006504 NM_130435	SI00089068	protein tyrosine phosphatase, receptor type, E	ACCACGGGCAATTAAACTTTA	UAAAGUUUAAUUGCCCGUGgt	CACGGGCAAUUAAACUUUAtt
5791	PTPRE	Hs_PTPRE_3	NM_006504 NM_130435	SI00089075	protein tyrosine phosphatase, receptor type, E	GACCATCGTCATGTTAACAAA	UUUGUUAACAUGACGAUGGtc	CCAUCGUCAUGUUAACAAAtt
5792	PTPRF	Hs_PTPRF_5	NM_002840 NM_130440	SI02658789	protein tyrosine phosphatase, receptor type, F	CAGCGCTATCTAGATAGGTAA	UUACCUAUCUAGAUAGCGCtg	GCGCUAUCUAGAUAGGUAAtt
5792	PTPRF	Hs_PTPRF_6	NM_002840 NM_130440	SI02658796	protein tyrosine phosphatase, receptor type, F	CATCGTGTTTGCAAAGGTTAA	UUAACCUUUGCAAACACGAtg	UCGUGUUUGCAAAGGUUAAtt
5792	PTPRF	Hs_PTPRF_7	NM_002840 NM_130440	SI03091557	protein tyrosine phosphatase, receptor type, F	CTCGCTTGTCAGGTGGTTCTA	UAGAACCACCUGACAAGCGag	CGCUUGUCAGGUGGUUCUAtt
5793	PTPRG	Hs_PTPRG_7	NM_002841	SI02658803	protein tyrosine phosphatase, receptor type, G	TCGGTGAGCTCTATTCTAATA	UAUUAGAAUAGAGCUCACCga	GGUGAGCUCUAUUCUAAUAtt
5793	PTPRG	Hs_PTPRG_8	NM_002841	SI02759260	protein tyrosine phosphatase, receptor type, G	TAGGCACTGTTCAATACTGTA	UACAGUAUUGAACAGUGCCta	GGCACUGUUCAAUACUGUAtt
5793	PTPRG	Hs_PTPRG_9	NM_002841	SI02759267	protein tyrosine phosphatase, receptor type, G	CAGACTCTAGGTTATACAATA	UAUUGUAUAACCUAGAGUCtg	GACUCUAGGUUAUACAAUAtt
5794	PTPRH	Hs_PTPRH_1	NM_002842	SI00044226	protein tyrosine phosphatase, receptor type, H	CCGGGACGTTGTACAATTTCA	UGAAAUUGUACAACGUCCCgg	GGGACGUUGUACAAUUUCAtt
5794	PTPRH	Hs_PTPRH_2	NM_002842	SI00044233	protein tyrosine phosphatase, receptor type, H	CCGGGTCATTGTATACGTGTT	AACACGUAUACAAUGACCCgg	GGGUCAUUGUAUACGUGUUtt
5794	PTPRH	Hs_PTPRH_5	NM_002842	SI03046904	protein tyrosine phosphatase, receptor type, H	ATCACCGTGGATAGACTTGAA	UUCAAGUCUAUCCACGGUGat	CACCGUGGAUAGACUUGAAtt
5795	PTPRJ	Hs_PTPRJ_5	NM_001098503 NM_002843	SI02658810	protein tyrosine phosphatase, receptor type, J	TCGGGTAGAAATAACCACCAA	UUGGUGGUUAUUUCUACCCga	GGGUAGAAAUAACCACCAAtt
5795	PTPRJ	Hs_PTPRJ_6	NM_002843	SI02658817	protein tyrosine phosphatase, receptor type, J	TCCGAGTATGTCTACCATTTA	UAAAUGGUAGACAUACUCGga	CGAGUAUGUCUACCAUUUAtt
5795	PTPRJ	Hs_PTPRJ_3	NM_001098503 NM_002843	SI00044268	protein tyrosine phosphatase, receptor type, J	ACCCGTATCTTCTACAATCAA	UUGAUUGUAGAAGAUACGGgt	CCGUAUCUUCUACAAUCAAtt
5796	PTPRK	Hs_PTPRK_5	NM_002844	SI02759274	protein tyrosine phosphatase, receptor type, K	CCGGCGAGTCAAGTTATCAAA	UUUGAUAACUUGACUCGCCgg	GGCGAGUCAAGUUAUCAAAtt
5796	PTPRK	Hs_PTPRK_6	NM_002844	SI02759281	protein tyrosine phosphatase, receptor type, K	CAGGATTTGTATCGCTGTGTA	UACACAGCGAUACAAAUCCtg	GGAUUUGUAUCGCUGUGUAtt
5796	PTPRK	Hs_PTPRK_7	NM_002844	SI03033352	protein tyrosine phosphatase, receptor type, K	AAGCCTTAAGATCTCGGCGTA	UACGCCGAGAUCUUAAGGCtt	GCCUUAAGAUCUCGGCGUAtt
5797	PTPRM	Hs_PTPRM_2	NM_002845	SI00044317	protein tyrosine phosphatase, receptor type, M	CACATCCGTAGTTATGCTAAA	UUUAGCAUAACUACGGAUGtg	CAUCCGUAGUUAUGCUAAAtt
5797	PTPRM	Hs_PTPRM_5	NM_002845	SI02629718	protein tyrosine phosphatase, receptor type, M	AAGGGTCAAATGCTGCAAATA	UAUUUGCAGCAUUUGACCCtt	GGGUCAAAUGCUGCAAAUAtt
5797	PTPRM	Hs_PTPRM_6	NM_002845	SI03030958	protein tyrosine phosphatase, receptor type, M	AAGAACGTCCTCGAAGAACTA	UAGUUCUUCGAGGACGUUCtt	GAACGUCCUCGAAGAACUAtt
5798	PTPRN	Hs_PTPRN_3	NM_002846	SI00044352	protein tyrosine phosphatase, receptor type, N	CTGGTGAAGTCTGAACTGGAA	UUCCAGUUCAGACUUCACCag	GGUGAAGUCUGAACUGGAAtt
5798	PTPRN	Hs_PTPRN_4	NM_002846	SI00044359	protein tyrosine phosphatase, receptor type, N	CAGGAAGGTGAACAAGTGCTA	UAGCACUUGUUCACCUUCCtg	GGAAGGUGAACAAGUGCUAtt
5798	PTPRN	Hs_PTPRN_5	NM_002846	SI03059938	protein tyrosine phosphatase, receptor type, N	CACGATGACCTCACCCAGTAT	AUACUGGGUGAGGUCAUCGtg	CGAUGACCUCACCCAGUAUtt
5799	PTPRN2	Hs_PTPRN2_6	NM_002847 NM_130842 NM_130843	SI02658824	protein tyrosine phosphatase, receptor type, N polypeptide 2	CAGCGCAGTTTAGCAGTTAAA	UUUAACUGCUAAACUGCGCtg	GCGCAGUUUAGCAGUUAAAtt
5799	PTPRN2	Hs_PTPRN2_7	NM_002847 NM_130842 NM_130843	SI02658831	protein tyrosine phosphatase, receptor type, N polypeptide 2	AAGGTGCTAAAGAGATTGATA	UAUCAAUCUCUUUAGCACCtt	GGUGCUAAAGAGAUUGAUAtt
5799	PTPRN2	Hs_PTPRN2_2	NM_002847 NM_130842 NM_130843	SI00044373	protein tyrosine phosphatase, receptor type, N polypeptide 2	ACGGATGTTGTCAGGAATCAT	AUGAUUCCUGACAACAUCCgt	GGAUGUUGUCAGGAAUCAUtt
5801	PTPRR	Hs_PTPRR_6	NM_002849 NM_130846	SI03038896	protein tyrosine phosphatase, receptor type, R	ACCATTCGAAACCTTGTCTTA	UAAGACAAGGUUUCGAAUGgt	CAUUCGAAACCUUGUCUUAtt
5801	PTPRR	Hs_PTPRR_7	NM_002849 NM_130846	SI03049697	protein tyrosine phosphatase, receptor type, R	ATGATTGTCATTGGGTATATA	UAUAUACCCAAUGACAAUCat	GAUUGUCAUUGGGUAUAUAtt
5801	PTPRR	Hs_PTPRR_8	NM_002849 NM_130846	SI03059042	protein tyrosine phosphatase, receptor type, R	CACCTCATGGCCTGATCACAA	UUGUGAUCAGGCCAUGAGGtg	CCUCAUGGCCUGAUCACAAtt
5802	PTPRS	Hs_PTPRS_5	NM_002850 NM_130853 NM_130854 NM_	SI02759288	protein tyrosine phosphatase, receptor type, S	CAGGACATTCTCTCTGCACAA	UUGUGCAGAGAGAAUGUCCtg	GGACAUUCUCUCUGCACAAtt
5802	PTPRS	Hs_PTPRS_6	NM_002850 NM_130853 NM_130854 NM_	SI03051475	protein tyrosine phosphatase, receptor type, S	ATGGCGTGCCCGAATACCCAA	UUGGGUAUUCGGGCACGCCat	GGCGUGCCCGAAUACCCAAtt
5802	PTPRS	Hs_PTPRS_7	NM_002850 NM_130853 NM_130854 NM_	SI03056284	protein tyrosine phosphatase, receptor type, S	CACAGGCTGCTTTATCGTCAT	AUGACGAUAAAGCAGCCUGtg	CAGGCUGCUUUAUCGUCAUtt
5803	PTPRZ1	Hs_PTPRZ1_1	NM_002851	SI00044450	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	CCGCCAAATTTATATCATTAA	UUAAUGAUAUAAAUUUGGCgg	GCCAAAUUUAUAUCAUUAAtt
5803	PTPRZ1	Hs_PTPRZ1_2	NM_002851	SI00044457	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	ACGCTGGAATTTGGTAGTGAA	UUCACUACCAAAUUCCAGCgt	GCUGGAAUUUGGUAGUGAAtt
5803	PTPRZ1	Hs_PTPRZ1_3	NM_002851	SI00044464	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	TAGCCATATACCAATACCTAA	UUAGGUAUUGGUAUAUGGCta	GCCAUAUACCAAUACCUAAtt
6305	SBF1	Hs_SBF1_5	NM_002972	SI02658838	SET binding factor 1	CAGCGCCGAGCTCTTCCGTAA	UUACGGAAGAGCUCGGCGCtg	GCGCCGAGCUCUUCCGUAAtt
6305	SBF1	Hs_SBF1_6	NM_002972	SI02759295	SET binding factor 1	GACGCCTGTGTTCCACAATTA	UAAUUGUGGAACACAGGCGtc	CGCCUGUGUUCCACAAUUAtt
6305	SBF1	Hs_SBF1_1	NM_002972	SI00046326	SET binding factor 1	CCGCGTGGTGTGGCCCTGTTA	UAACAGGGCCACACCACGCgg	GCGUGGUGUGGCCCUGUUAtt
6992	PPP1R11	Hs_PPP1R11_5	NM_021959 NM_170781	SI02759379	protein phosphatase 1, regulatory (inhibitor) subunit 11	CAGAGATCAGTCAAATCCATA	UAUGGAUUUGACUGAUCUCtg	GAGAUCAGUCAAAUCCAUAtt
6992	PPP1R11	Hs_PPP1R11_6	NM_021959 NM_170781	SI02759386	protein phosphatase 1, regulatory (inhibitor) subunit 11	TGGCTTGAGATTGGTCACTTA	UAAGUGACCAAUCUCAAGCca	GCUUGAGAUUGGUCACUUAtt
6992	PPP1R11	Hs_PPP1R11_2	NM_021959 NM_170781	SI00131740	protein phosphatase 1, regulatory (inhibitor) subunit 11	CGCCCTAACTTTGCTTGCTAA	UUAGCAAGCAAAGUUAGGGcg	CCCUAACUUUGCUUGCUAAtt
7179	TPTE	Hs_TPTE_3	NM_013315 NM_199259 NM_199260 NM_	SI00101500	transmembrane phosphatase with tensin homology	CTGAAATATGTTCAACTGCAA	UUGCAGUUGAACAUAUUUCag	GAAAUAUGUUCAACUGCAAtt
7179	TPTE	Hs_TPTE_5	NM_013315 NM_199259 NM_199260 NM_	SI03073595	transmembrane phosphatase with tensin homology	CAGTTTCTGACCCAACAGTTA	UAACUGUUGGGUCAGAAACtg	GUUUCUGACCCAACAGUUAtt
7179	TPTE	Hs_TPTE_6	NM_013315 NM_199259 NM_199260 NM_	SI03092222	transmembrane phosphatase with tensin homology	CTCGTTATGTACGTGATCTAA	UUAGAUCACGUACAUAACGag	CGUUAUGUACGUGAUCUAAtt
7803	PTP4A1	Hs_PTP4A1_5	NM_003463	SI02225874	protein tyrosine phosphatase type IVA, member 1	CCCTTTGATCACGTTAATCTA	UAGAUUAACGUGAUCAAAGgg	CUUUGAUCACGUUAAUCUAtt
7803	PTP4A1	Hs_PTP4A1_6	NM_003463	SI03024630	protein tyrosine phosphatase type IVA, member 1	TTGGAGAAGTATCGTCCTAAA	UUUAGGACGAUACUUCUCCaa	GGAGAAGUAUCGUCCUAAAtt
7803	PTP4A1	Hs_PTP4A1_7	NM_003463	SI03065118	protein tyrosine phosphatase type IVA, member 1	CAGATTGTTGATGACTGGTTA	UAACCAGUCAUCAACAAUCtg	GAUUGUUGAUGACUGGUUAtt
8073	PTP4A2	Hs_PTP4A2_5	NM_003479 XM_001132357 XM_00113236	SI02225881	protein tyrosine phosphatase type IVA, member 2	CAGAGAATGCTGGTAGCTTAA	UUAAGCUACCAGCAUUCUCtg	GAGAAUGCUGGUAGCUUAAtt
8073	PTP4A2	Hs_PTP4A2_6	NM_003479 XM_001132357 XM_00113236	SI02225888	protein tyrosine phosphatase type IVA, member 2	AACAGCATACCTGCTAAGCTA	UAGCUUAGCAGGUAUGCUGtt	CAGCAUACCUGCUAAGCUAtt
8073	PTP4A2	Hs_PTP4A2_8	NM_003479 NM_080391 NM_080392 XM_	SI03022124	protein tyrosine phosphatase type IVA, member 2	TTCCATTATGCTTGGCACATA	UAUGUGCCAAGCAUAAUGGaa	CCAUUAUGCUUGGCACAUAtt
8446	DUSP11	Hs_DUSP11_5	NM_003584	SI02658845	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	CCCTTATGTATTCAAGCTTAA	UUAAGCUUGAAUACAUAAGgg	CUUAUGUAUUCAAGCUUAAtt
8446	DUSP11	Hs_DUSP11_6	NM_003584	SI02658852	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	CAGAAACTGTTCCTTACTTAA	UUAAGUAAGGAACAGUUUCtg	GAAACUGUUCCUUACUUAAtt
8446	DUSP11	Hs_DUSP11_7	NM_003584	SI03036523	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	AAGGTGGTATCCTTATAATTA	UAAUUAUAAGGAUACCACCtt	GGUGGUAUCCUUAUAAUUAtt
8493	PPM1D	Hs_PPM1D_5	NM_003620	SI02658859	protein phosphatase 1D magnesium-dependent, delta isoform	ACGGGTCTTCCTAGCACATCA	UGAUGUGCUAGGAAGACCCgt	GGGUCUUCCUAGCACAUCAtt
8493	PPM1D	Hs_PPM1D_6	NM_003620	SI02759302	protein phosphatase 1D magnesium-dependent, delta isoform	ATGGCCAAGGGTGAATTCTAA	UUAGAAUUCACCCUUGGCCat	GGCCAAGGGUGAAUUCUAAtt
8493	PPM1D	Hs_PPM1D_7	NM_003620	SI03032463	protein phosphatase 1D magnesium-dependent, delta isoform	AAGATGTATGTAGCTCACGTA	UACGUGAGCUACAUACAUCtt	GAUGUAUGUAGCUCACGUAtt

8497	PPFIA4	Hs_PPFIA4_5	NM_015053	SI02759141	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	TCCCTGGGTAATGGATGGTAA	UUACCAUCCAUUACCCAGGga	CCUGGGUAAUGGAUGGUAAtt
8497	PPFIA4	Hs_PPFIA4_7	NM_015053	SI04023439	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	CAGGGACTCAGTCCAGATTAT	AUAAUCUGGACUGAGUCCCtg	GGGACUCAGUCCAGAUUAUtt
8497	PPFIA4	Hs_PPFIA4_8	NM_015053	SI04023446	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	TGGGTGTGTACGTACCAATAA	UUAUUGGUACGUACACACCca	GGUGUGUACGUACCAAUAAtt
8499	PPFIA2	Hs_PPFIA2_1	NM_003625	SI00053865	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	TCCAATGAACGCCTACAACTA	UAGUUGUAGGCGUUCAUUGga	CAAUGAACGCCUACAACUAtt
8499	PPFIA2	Hs_PPFIA2_2	NM_003625	SI00053872	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	ACCGATGAAACTAGTCAAATA	UAUUUGACUAGUUUCAUCGgt	CGAUGAAACUAGUCAAAUAtt
8499	PPFIA2	Hs_PPFIA2_5	NM_003625	SI03069801	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	CAGGATATCGAATCCCTAACA	UGUUAGGGAUUCGAUAUCCtg	GGAUAUCGAAUCCCUAACAtt
8500	PPFIA1	Hs_PPFIA1_5	NM_003626 NM_177423	SI02759407	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	TTCCAAGGTACAAACTCTTAA	UUAAGAGUUUGUACCUUGGaa	CCAAGGUACAAACUCUUAAtt
8500	PPFIA1	Hs_PPFIA1_6	NM_003626 NM_177423	SI03117233	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	TCGGTTAGACCGGCTGCACAA	UUGUGCAGCCGGUCUAACCga	GGUUAGACCGGCUGCACAAtt
8500	PPFIA1	Hs_PPFIA1_2	NM_003626 NM_177423	SI00160090	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	CACGAGGTTGGTCATGAAAGA	UCUUUCAUGACCAACCUCGtg	CGAGGUUGGUCAUGAAAGAtt
8541	PPFIA3	Hs_PPFIA3_6	NM_003660	SI02658866	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	CACGGGTAAAGAGAACTGTTT	AAACAGUUCUCUUUACCCGtg	CGGGUAAAGAGAACUGUUUtt
8541	PPFIA3	Hs_PPFIA3_8	NM_003660	SI03054569	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	CAAGGCTAATCATGTCCCTAA	UUAGGGACAUGAUUAGCCUtg	AGGCUAAUCAUGUCCCUAAtt
8541	PPFIA3	Hs_PPFIA3_9	NM_003660	SI03056305	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	CACAGGGTGAGTCTACATTAT	AUAAUGUAGACUCACCCUGtg	CAGGGUGAGUCUACAUUAUtt
8555	CDC14B	Hs_CDC14B_2	NM_001077181 NM_003671 NM_033331	SI00054432	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	CCAAATAATGTCGGCTTACAA	UUGUAAGCCGACAUUAUUUgg	AAAUAAUGUCGGCUUACAAtt
8555	CDC14B	Hs_CDC14B_4	NM_001077181 NM_003671 NM_033331	SI00054446	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	AAGGAAGACTCTAGGACTGAA	UUCAGUCCUAGAGUCUUCCtt	GGAAGACUCUAGGACUGAAtt
8555	CDC14B	Hs_CDC14B_7	NM_003671 NM_033331 NM_033332	SI03085334	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	CGCGGTGGGCACGCACGGTTA	UAACCGUGCGUGCCCACCGcg	CGGUGGGCACGCACGGUUAtt
8556	CDC14A	Hs_CDC14A_5	NM_003672 NM_033312 NM_033313	SI02631552	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	ACAGATATTGCTGCAAACTAA	UUAGUUUGCAGCAAUAUCUgt	AGAUAUUGCUGCAAACUAAtt
8556	CDC14A	Hs_CDC14A_7	NM_003672 NM_033312 NM_033313	SI03026744	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	AAAGCTGGTCTTGGAAGAACA	UGUUCUUCCAAGACCAGCUtt	AGCUGGUCUUGGAAGAACAtt
8556	CDC14A	Hs_CDC14A_8	NM_003672 NM_033312 NM_033313	SI03046281	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	AGGTGCCTATGCAGTAATCTA	UAGAUUACUGCAUAGGCACct	GUGCCUAUGCAGUAAUCUAtt
8611	PPAP2A	Hs_PPAP2A_5	NM_003711 NM_176895	SI02659391	phosphatidic acid phosphatase type 2A	AACCCTGTCTGTTTACTGTAA	UUACAGUAAACAGACAGGGtt	CCCUGUCUGUUUACUGUAAtt
8611	PPAP2A	Hs_PPAP2A_6	NM_003711 NM_176895	SI02659398	phosphatidic acid phosphatase type 2A	CTGACATTGCCAAGTATTCAA	UUGAAUACUUGGCAAUGUCag	GACAUUGCCAAGUAUUCAAtt
8611	PPAP2A	Hs_PPAP2A_3	NM_003711 NM_176895	SI00160027	phosphatidic acid phosphatase type 2A	CATGCTGTTTGTGGCACTTTA	UAAAGUGCCACAAACAGCAtg	UGCUGUUUGUGGCACUUUAtt
8612	PPAP2C	Hs_PPAP2C_5	NM_003712 NM_177526 NM_177543	SI02659405	phosphatidic acid phosphatase type 2C	CCGGGTCAACTGCTCGGTCTA	UAGACCGAGCAGUUGACCCgg	GGGUCAACUGCUCGGUCUAtt
8612	PPAP2C	Hs_PPAP2C_6	NM_003712 NM_177526 NM_177543	SI02659412	phosphatidic acid phosphatase type 2C	TCGCTCGGACTTCAACAACTA	UAGUUGUUGAAGUCCGAGCga	GCUCGGACUUCAACAACUAtt
8612	PPAP2C	Hs_PPAP2C_7	NM_003712 NM_177526 NM_177543	SI03087840	phosphatidic acid phosphatase type 2C	CTACGTGGCTGCTGTATACAA	UUGUAUACAGCAGCCACGUag	ACGUGGCUGCUGUAUACAAtt
8613	PPAP2B	Hs_PPAP2B_10	NM_003713 NM_177414	SI04023131	phosphatidic acid phosphatase type 2B	CAGCACAATTTCAGAAGAAAT	AUUUCUUCUGAAAUUGUGCtg	GCACAAUUUCAGAAGAAAUtt
8613	PPAP2B	Hs_PPAP2B_4	NM_003713 NM_177414	SI00055006	phosphatidic acid phosphatase type 2B	CAGCGCAGCTCCCATTCATTA	UAAUGAAUGGGAGCUGCGCtg	GCGCAGCUCCCAUUCAUUAtt
8613	PPAP2B	Hs_PPAP2B_7	NM_003713 NM_177414	SI03043761	phosphatidic acid phosphatase type 2B	AGCGATCGTCCCGGAGAGCAA	UUGCUCUCCGGGACGAUCGct	CGAUCGUCCCGGAGAGCAAtt
8732	RNGTT	Hs_RNGTT_1	NM_003800	SI00055972	RNA guanylyltransferase and 5'-phosphatase	CAGGGTTGTTAAGTTGTACTA	UAGUACAACUUAACAACCCtg	GGGUUGUUAAGUUGUACUAtt
8732	RNGTT	Hs_RNGTT_3	NM_003800	SI00055986	RNA guanylyltransferase and 5'-phosphatase	ATGGATTTAAAGGGCGGCTAA	UUAGCCGCCCUUUAAAUCCat	GGAUUUAAAGGGCGGCUAAtt
8732	RNGTT	Hs_RNGTT_4	NM_003800	SI00055993	RNA guanylyltransferase and 5'-phosphatase	CGGGATTTCTATATGGACATA	UAUGUCCAUAUAGAAAUCCcg	GGAUUUCUAUAUGGACAUAtt
8773	SNAP23	Hs_SNAP23_1	NM_003825 NM_130798	SI00056448	synaptosomal-associated protein, 23kDa	CAGGCCTATTAACATCATACA	UGUAUGAUGUUAAUAGGCCtg	GGCCUAUUAACAUCAUACAtt
8773	SNAP23	Hs_SNAP23_2	NM_003825 NM_130798	SI00056455	synaptosomal-associated protein, 23kDa	TACCACATGAATTCAGATTTA	UAAAUCUGAAUUCAUGUGGta	CCACAUGAAUUCAGAUUUAtt
8773	SNAP23	Hs_SNAP23_3	NM_003825 NM_130798	SI00056462	synaptosomal-associated protein, 23kDa	AAGAGGTTGTTACCTCAGTAA	UUACUGAGGUAACAACCUCtt	GAGGUUGUUACCUCAGUAAtt
8789	FBP2	Hs_FBP2_1	NM_003837	SI00056588	fructose-1,6-bisphosphatase 2	AGGACCCTAAATGAACGATAA	UUAUCGUUCAUUUAGGGUCct	GACCCUAAAUGAACGAUAAtt
8789	FBP2	Hs_FBP2_2	NM_003837	SI00056595	fructose-1,6-bisphosphatase 2	CAGGTTATGCGCTGTACGGTA	UACCGUACAGCGCAUAACCtg	GGUUAUGCGCUGUACGGUAtt
8789	FBP2	Hs_FBP2_3	NM_003837	SI00056602	fructose-1,6-bisphosphatase 2	CTCAATGCTGACGGCCATCAA	UUGAUGGCCGUCAGCAUUGag	CAAUGCUGACGGCCAUCAAtt
8821	INPP4B	Hs_INPP4B_5	NM_003866	SI02759309	inositol polyphosphate-4-phosphatase, type II, 105kDa	ATCGATGTCAGTGACACTTGA	UCAAGUGUCACUGACAUCGat	CGAUGUCAGUGACACUUGAtt
8821	INPP4B	Hs_INPP4B_6	NM_003866	SI02759316	inositol polyphosphate-4-phosphatase, type II, 105kDa	CTCCATAGATTTGAAACAGAA	UUCUGUUUCAAAUCUAUGGag	CCAUAGAUUUGAAACAGAAtt
8821	INPP4B	Hs_INPP4B_7	NM_003866	SI03040562	inositol polyphosphate-4-phosphatase, type II, 105kDa	ACCGTTCGAACCAGTGTCCTA	UAGGACACUGGUUCGAACGgt	CGUUCGAACCAGUGUCCUAtt
8897	MTMR3	Hs_LOC400924_1	NM_001013676 NM_021090 NM_153050 N	SI00548632	myotubularin related protein 3	AAACAATCTCTGGCTATTAAA	UUUAAUAGCCAGAGAUUGUtt	ACAAUCUCUGGCUAUUAAAtt
8897	MTMR3	Hs_LOC400924_2	NM_001013676 NM_021090 NM_153050 N	SI00548639	myotubularin related protein 3	AAACATCAAGATGAGAATTAA	UUAAUUCUCAUCUUGAUGUtt	ACAUCAAGAUGAGAAUUAAtt
8897	MTMR3	Hs_LOC400924_3	NM_001013676 NM_021090 NM_153050 N	SI00548646	myotubularin related protein 3	AAGAATATTCTATGAATTAGA	UCUAAUUCAUAGAAUAUUCtt	GAAUAUUCUAUGAAUUAGAtt
8898	MTMR2	Hs_MTMR2_1	NM_016156 NM_201278 NM_201281	SI00113918	myotubularin related protein 2	TAGGATGAGTTTAGAACTGTA	UACAGUUCUAAACUCAUCCta	GGAUGAGUUUAGAACUGUAtt
8898	MTMR2	Hs_MTMR2_2	NM_016156 NM_201278 NM_201281	SI00113925	myotubularin related protein 2	ACCACTGCAATTCACATTATA	UAUAAUGUGAAUUGCAGUGgt	CACUGCAAUUCACAUUAUAtt
9050	PSTPIP2	Hs_PSTPIP2_5	NM_024430	SI02665649	proline-serine-threonine phosphatase interacting protein 2	CCACGTTATGTCAGCAATGAA	UUCAUUGCUGACAUAACGUgg	ACGUUAUGUCAGCAAUGAAtt
9050	PSTPIP2	Hs_PSTPIP2_6	NM_024430	SI02665656	proline-serine-threonine phosphatase interacting protein 2	CCGGCTAGTGCTTCTGTGATA	UAUCACAGAAGCACUAGCCgg	GGCUAGUGCUUCUGUGAUAtt
9050	PSTPIP2	Hs_PSTPIP2_7	NM_024430	SI03045329	proline-serine-threonine phosphatase interacting protein 2	AGGCTCAAGAATGTGAACGAA	UUCGUUCACAUUCUUGAGCct	GCUCAAGAAUGUGAACGAAtt
9051	PSTPIP1	Hs_PSTPIP1_1	NM_003978	SI00058569	proline-serine-threonine phosphatase interacting protein 1	CCGGCTGACCATTCTCCGCAA	UUGCGGAGAAUGGUCAGCCgg	GGCUGACCAUUCUCCGCAAtt
9051	PSTPIP1	Hs_PSTPIP1_2	NM_003978	SI00058576	proline-serine-threonine phosphatase interacting protein 1	ACCGGGCGCTCTACGATTATA	UAUAAUCGUAGAGCGCCCGgt	CGGGCGCUCUACGAUUAUAtt
9051	PSTPIP1	Hs_PSTPIP1_3	NM_003978	SI00058583	proline-serine-threonine phosphatase interacting protein 1	CAGCATAGACGCCGACATCGA	UCGAUGUCGGCGUCUAUGCtg	GCAUAGACGCCGACAUCGAtt
9107	MTMR6	Hs_MTMR6_6	NM_004685	SI02658922	myotubularin related protein 6	CCCGGATAGCAAGCAAACCAA	UUGGUUUGCUUGCUAUCCGgg	CGGAUAGCAAGCAAACCAAtt
9107	MTMR6	Hs_MTMR6_7	NM_004685	SI02658929	myotubularin related protein 6	CCCGTAAATGATGCTCTTCGA	UCGAAGAGCAUCAUUUACGgg	CGUAAAUGAUGCUCUUCGAtt
9107	MTMR6	Hs_MTMR6_2	NM_004685	SI00067053	myotubularin related protein 6	AAGGGAAGTACAGATAGTTTA	UAAACUAUCUGUACUUCCCtt	GGGAAGUACAGAUAGUUUAtt
9110	MTMR4	Hs_MTMR4_5	NM_004687	SI03030419	myotubularin related protein 4	AACTACCGGCTGCATATCAAA	UUUGAUAUGCAGCCGGUAGtt	CUACCGGCUGCAUAUCAAAtt
9110	MTMR4	Hs_MTMR4_6	NM_004687	SI03041549	myotubularin related protein 4	ACGGCAAATCGAAGCAGGGTA	UACCCUGCUUCGAUUUGCCgt	GGCAAAUCGAAGCAGGGUAtt
9110	MTMR4	Hs_MTMR4_7	NM_004687	SI03100909	myotubularin related protein 4	CTTGCCATAGATGTAACCTAA	UUAGGUUACAUCUAUGGCAag	UGCCAUAGAUGUAACCUAAtt
9150	CTDP1	Hs_CTDP1_6	NM_004715 NM_048368	SI02658943	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	CCGGCTGTACGCACACACCAT	AUGGUGUGUGCGUACAGCCgg	GGCUGUACGCACACACCAUtt
9150	CTDP1	Hs_CTDP1_7	NM_004715 NM_048368	SI03071264	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	CAGGGCACGGGTGATATGAAT	AUUCAUAUCACCCGUGCCCtg	GGGCACGGGUGAUAUGAAUtt
9150	CTDP1	Hs_CTDP1_1	NM_004715 NM_048368	SI00067354	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	CCCGACAAACTTCCCGATAGA	UCUAUCGGGAAGUUUGUCGgg	CGACAAACUUCCCGAUAGAtt
9200	PTPLA	Hs_PTPLA_7	NM_014241	SI02659111	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	ACCACTTGCCATACTTCATTA	UAAUGAAGUAUGGCAAGUGgt	CACUUGCCAUACUUCAUUAtt
9200	PTPLA	Hs_PTPLA_8	NM_014241	SI02659118	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	CACTGTTTAATTGGAATTGTA	UACAAUUCCAAUUAAACAGtg	CUGUUUAAUUGGAAUUGUAtt
9200	PTPLA	Hs_PTPLA_3	NM_014241	SI00103957	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	AAGTGAGTTCAAGAATCTTTA	UAAAGAUUCUUGAACUCACtt	GUGAGUUCAAGAAUCUUUAtt
9562	MINPP1	Hs_MINPP1_6	NM_004897	SI02658950	multiple inositol polyphosphate histidine phosphatase, 1	CCGAGTGCAGATGTTATTAAA	UUUAAUAACAUCUGCACUCgg	GAGUGCAGAUGUUAUUAAAtt
9562	MINPP1	Hs_MINPP1_7	NM_004897	SI02658957	multiple inositol polyphosphate histidine phosphatase, 1	CACGGTCAAACAGATCCGCAA	UUGCGGAUCUGUUUGACCGtg	CGGUCAAACAGAUCCGCAAtt
9562	MINPP1	Hs_MINPP1_2	NM_004897	SI00069748	multiple inositol polyphosphate histidine phosphatase, 1	AAGTCGGAAAGTACAATGAAA	UUUCAUUGUACUUUCCGACtt	GUCGGAAAGUACAAUGAAAtt
9647	PPM1F	Hs_PPM1F_5	NM_014634	SI03042585	protein phosphatase 1F (PP2C domain containing)	AGCACCGTATATGGAATACAA	UUGUAUUCCAUAUACGGUGct	CACCGUAUAUGGAAUACAAtt
9647	PPM1F	Hs_PPM1F_6	NM_014634	SI03064460	protein phosphatase 1F (PP2C domain containing)	CAGAGTTTCTTTAACCGCCTT	AAGGCGGUUAAAGAAACUCtg	GAGUUUCUUUAACCGCCUUtt
9647	PPM1F	Hs_PPM1F_7	NM_014634	SI03092026	protein phosphatase 1F (PP2C domain containing)	CTCGTCCCAAGCTAAATGTAA	UUACAUUUAGCUUGGGACGag	CGUCCCAAGCUAAAUGUAAtt
9701	SAPS2	Hs_KIAA0685_1	NM_014678 XM_001129019	SI00454916	SAPS domain family, member 2	CACGATGTTCTGGAAGTTTGA	UCAAACUUCCAGAACAUCGtg	CGAUGUUCUGGAAGUUUGAtt
9701	SAPS2	Hs_KIAA0685_2	NM_014678	SI00454923	SAPS domain family, member 2	TTGCCTGAATACATGATTTAA	UUAAAUCAUGUAUUCAGGCaa	GCCUGAAUACAUGAUUUAAtt
9701	SAPS2	Hs_KIAA0685_3	NM_014678	SI00454930	SAPS domain family, member 2	CAGGATGAAGATAGGCAGTCA	UGACUGCCUAUCUUCAUCCtg	GGAUGAAGAUAGGCAGUCAtt
9989	PPP4R1	Hs_PPP4R1_3	NM_001042388 NM_005134	SI00072835	protein phosphatase 4, regulatory subunit 1	CAGGAGCTCATTGAACGATTT	AAAUCGUUCAAUGAGCUCCtg	GGAGCUCAUUGAACGAUUUtt
9989	PPP4R1	Hs_PPP4R1_6	NM_001042388 NM_005134	SI03030328	protein phosphatase 4, regulatory subunit 1	AACGTTCGGAGTGGACCTCAT	AUGAGGUCCACUCCGAACGtt	CGUUCGGAGUGGACCUCAUtt
9989	PPP4R1	Hs_PPP4R1_7	NM_001042388 NM_005134	SI03050005	protein phosphatase 4, regulatory subunit 1	ATGCCGCATCTGCTAACCTTA	UAAGGUUAGCAGAUGCGGCat	GCCGCAUCUGCUAACCUUAtt
10106	CTDSP2	Hs_CTDSP2_5	NM_005730	SI02658992	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	CCCGGAAACAGCGGGAAGTAA	UUACUUCCCGCUGUUUCCGgg	CGGAAACAGCGGGAAGUAAtt
10106	CTDSP2	Hs_CTDSP2_6	NM_005730	SI02658999	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	TACGATCAGCGTGACAGAGTA	UACUCUGUCACGCUGAUCGta	CGAUCAGCGUGACAGAGUAtt
10106	CTDSP2	Hs_CTDSP2_7	NM_005730	SI03033870	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	AAGCTCGGGATCATTTCCATA	UAUGGAAAUGAUCCCGAGCtt	GCUCGGGAUCAUUUCCAUAtt
10199	MPHOSPH10	Hs_MPHOSPH10_1	NM_005791	SI00647675	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	CAGGATATTTCTGTTCATAAA	UUUAUGAACAGAAAUAUCCtg	GGAUAUUUCUGUUCAUAAAtt
10199	MPHOSPH10	Hs_MPHOSPH10_4	NM_005791	SI00647696	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	GAGGATGCATATGAATATAAA	UUUAUAUUCAUAUGCAUCCtc	GGAUGCAUAUGAAUAUAAAtt
10199	MPHOSPH10	Hs_MPHOSPH10_5	NM_005791	SI03139143	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	ACCGCCTGTACCAGAGATTAA	UUAAUCUCUGGUACAGGCGgt	CGCCUGUACCAGAGAUUAAtt
10217	CTDSPL	Hs_CTDSPL_5	NM_001008392 NM_005808	SI02759330	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	TTCGTTTAAGCCTATTAGTAA	UUACUAAUAGGCUUAAACGaa	CGUUUAAGCCUAUUAGUAAtt
10217	CTDSPL	Hs_CTDSPL_7	NM_001008392 NM_005808	SI03082933	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CCGGTTGAAATCGATGGAACT	AGUUCCAUCGAUUUCAACCgg	GGUUGAAAUCGAUGGAACUtt
10217	CTDSPL	Hs_CTDSPL_8	NM_001008392 NM_005808	SI03093685	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	CTGAGTGTTCCAAACCAGTAA	UUACUGGUUUGGAACACUCag	GAGUGUUCCAAACCAGUAAtt
11072	DUSP14	Hs_DUSP14_7	NM_007026	SI02659055	dual specificity phosphatase 14	ACCCTTATTATTTAGCTGTTA	UAACAGCUAAAUAAUAAGGgt	CCUUAUUAUUUAGCUGUUAtt
11072	DUSP14	Hs_DUSP14_8	NM_007026	SI02659062	dual specificity phosphatase 14	AAGGGAATGCATACATTGCTA	UAGCAAUGUAUGCAUUCCCtt	GGGAAUGCAUACAUUGCUAtt
11072	DUSP14	Hs_DUSP14_9	NM_007026	SI03085369	dual specificity phosphatase 14	CGCGTACCTGATGAAATTCCA	UGGAAUUUCAUCAGGUACGcg	CGUACCUGAUGAAAUUCCAtt
11099	PTPN21	Hs_PTPN21_6	NM_007039	SI02659069	protein tyrosine phosphatase, non-receptor type 21	GTGCATAGATTTCTATCTTAA	UUAAGAUAGAAAUCUAUGCac	GCAUAGAUUUCUAUCUUAAtt
11099	PTPN21	Hs_PTPN21_7	NM_007039	SI02659076	protein tyrosine phosphatase, non-receptor type 21	GAGGAGACCATTCAATTTCAA	UUGAAAUUGAAUGGUCUCCtc	GGAGACCAUUCAAUUUCAAtt
11099	PTPN21	Hs_PTPN21_2	NM_007039	SI00093975	protein tyrosine phosphatase, non-receptor type 21	CCCACCGCAGTTGCACTATAA	UUAUAGUGCAACUGCGGUGgg	CACCGCAGUUGCACUAUAAtt
11156	PTP4A3	Hs_PTP4A3_2	NM_007079 NM_032611 XM_001126214 X	SI00094437	protein tyrosine phosphatase type IVA, member 3	CCGCGGAGCCATCAACAGCAA	UUGCUGUUGAUGGCUCCGCgg	GCGGAGCCAUCAACAGCAAtt
11156	PTP4A3	Hs_PTP4A3_5	NM_007079 NM_032611	SI03072202	protein tyrosine phosphatase type IVA, member 3	CAGGTGCTCCGGACACCCGAA	UUCGGGUGUCCGGAGCACCtg	GGUGCUCCGGACACCCGAAtt
11156	PTP4A3	Hs_PTP4A3_6	NM_007079 NM_032611	SI03092285	protein tyrosine phosphatase type IVA, member 3	CTCGTTTCTCTTGGACAAGCA	UGCUUGUCCAAGAGAAACGag	CGUUUCUCUUGGACAAGCAtt
11221	DUSP10	Hs_DUSP10_5	NM_007207 NM_144728 NM_144729	SI03038791	dual specificity phosphatase 10	ACCATGACTGATGCTTATAAA	UUUAUAAGCAUCAGUCAUGgt	CAUGACUGAUGCUUAUAAAtt
11221	DUSP10	Hs_DUSP10_6	NM_007207 NM_144728 NM_144729	SI03058223	dual specificity phosphatase 10	CACCGAGAATCCTTACACCAA	UUGGUGUAAGGAUUCUCGGtg	CCGAGAAUCCUUACACCAAtt
11221	DUSP10	Hs_DUSP10_7	NM_007207 NM_144728 NM_144729	SI03118178	dual specificity phosphatase 10	TGCCATAAACCTTGTTACATA	UAUGUAACAAGGUUUAUGGca	CCAUAAACCUUGUUACAUAtt
11266	DUSP12	Hs_DUSP12_5	NM_007240	SI02659083	dual specificity phosphatase 12	TACCGTTTCACAAGGATTGAA	UUCAAUCCUUGUGAAACGGta	CCGUUUCACAAGGAUUGAAtt
11266	DUSP12	Hs_DUSP12_6	NM_007240	SI02659090	dual specificity phosphatase 12	ATGCTTTACATGGCAATCAAA	UUUGAUUGCCAUGUAAAGCat	GCUUUACAUGGCAAUCAAAtt
11266	DUSP12	Hs_DUSP12_7	NM_007240	SI03036978	dual specificity phosphatase 12	AAGTGGATACCTCTAGTGCAA	UUGCACUAGAGGUAUCCACtt	GUGGAUACCUCUAGUGCAAtt
11284	PNKP	Hs_PNKP_1	NM_007254	SI00095886	polynucleotide kinase 3'-phosphatase	CACGTGTGAGACAGCCCTGAA	UUCAGGGCUGUCUCACACGtg	CGUGUGAGACAGCCCUGAAtt
11284	PNKP	Hs_PNKP_2	NM_007254	SI00095893	polynucleotide kinase 3'-phosphatase	CACGTGAACAGGGACACGCTA	UAGCGUGUCCCUGUUCACGtg	CGUGAACAGGGACACGCUAtt
11284	PNKP	Hs_PNKP_3	NM_007254	SI00095900	polynucleotide kinase 3'-phosphatase	CAAGCTGGTGATCTTCACCAA	UUGGUGAAGAUCACCAGCUtg	AGCUGGUGAUCUUCACCAAtt
22843	PPM1E	Hs_PPM1E_7	NM_014906	SI02659139	protein phosphatase 1E (PP2C domain containing)	CCCATTTAGGTCTGTACTAAA	UUUAGUACAGACCUAAAUGgg	CAUUUAGGUCUGUACUAAAtt
22843	PPM1E	Hs_PPM1E_8	NM_014906	SI02659146	protein phosphatase 1E (PP2C domain containing)	GAGGCGGTTTATAGTCAGAAA	UUUCUGACUAUAAACCGCCtc	GGCGGUUUAUAGUCAGAAAtt
22843	PPM1E	Hs_PPM1E_9	NM_014906	SI03061345	protein phosphatase 1E (PP2C domain containing)	CACGGTTATTGTGGTATTCCT	AGGAAUACCACAAUAACCGtg	CGGUUAUUGUGGUAUUCCUtt
22870	SAPS1	Hs_KIAA1115_3	NM_014931	SI00456946	SAPS domain family, member 1	CCGTCGAAGGATGAGAATCAA	UUGAUUCUCAUCCUUCGACgg	GUCGAAGGAUGAGAAUCAAtt
22870	SAPS1	Hs_SAPS1_2	NM_014931	SI03163853	SAPS domain family, member 1	CACGCCTCCTCCGATACCCAA	UUGGGUAUCGGAGGAGGCGtg	CGCCUCCUCCGAUACCCAAtt
22870	SAPS1	Hs_SAPS1_3	NM_014931	SI03244689	SAPS domain family, member 1	TTGGAGCGTTGCCTCCTAGAA	UUCUAGGAGGCAACGCUCCaa	GGAGCGUUGCCUCCUAGAAtt
22876	INPP5F	Hs_INPP5F_5	NM_014937 NM_198331 NR_003251	SI02659440	inositol polyphosphate-5-phosphatase F	AAGACCTTTACGCATATTAAA	UUUAAUAUGCGUAAAGGUCtt	GACCUUUACGCAUAUUAAAtt
22876	INPP5F	Hs_INPP5F_6	NM_014937 NM_198331 NR_003251	SI02659447	inositol polyphosphate-5-phosphatase F	CAGATCTTCCATGGTGGCTTA	UAAGCCACCAUGGAAGAUCtg	GAUCUUCCAUGGUGGCUUAtt
22876	INPP5F	Hs_INPP5F_7	NM_014937 NM_198330 NR_003252	SI03072531	inositol polyphosphate-5-phosphatase F	CAGGTTGCTAGTATTACCCAA	UUGGGUAAUACUAGCAACCtg	GGUUGCUAGUAUUACCCAAtt
23076	RRP1B	Hs_KIAA0179_1	NM_015056	SI00452424	ribosomal RNA processing 1 homolog B (S. cerevisiae)	CACGTTGATCTGAACTTTAAA	UUUAAAGUUCAGAUCAACGtg	CGUUGAUCUGAACUUUAAAtt
23076	RRP1B	Hs_KIAA0179_2	NM_015056	SI00452431	ribosomal RNA processing 1 homolog B (S. cerevisiae)	AAGGACTTTGTTTACGATCAA	UUGAUCGUAAACAAAGUCCtt	GGACUUUGUUUACGAUCAAtt
23076	RRP1B	Hs_KIAA0179_3	NM_015056	SI00452438	ribosomal RNA processing 1 homolog B (S. cerevisiae)	CACAAGAATATGTCACATAAA	UUUAUGUGACAUAUUCUUGtg	CAAGAAUAUGUCACAUAAAtt
23164	M-RIP	Hs_M-RIP_3	NM_015134 NM_201274	SI00109725	myosin phosphatase-Rho interacting protein	CCGGACCAACAAGCAGAATCA	UGAUUCUGCUUGUUGGUCCgg	GGACCAACAAGCAGAAUCAtt
23164	M-RIP	Hs_M-RIP_4	NM_015134 NM_201274	SI00109732	myosin phosphatase-Rho interacting protein	CGGGAGCTAGAGAAACTTCGA	UCGAAGUUUCUCUAGCUCCcg	GGAGCUAGAGAAACUUCGAtt
23164	M-RIP	Hs_M-RIP_5	NM_015134 NM_201274	SI03042368	myosin phosphatase-Rho interacting protein	AGAGGTCTTATTGCGGGTAAA	UUUACCCGCAAUAAGACCUct	AGGUCUUAUUGCGGGUAAAtt
23368	PPP1R13B	Hs_PPP1R13B_5	NM_015316	SI02659153	protein phosphatase 1, regulatory (inhibitor) subunit 13B	CGCGATGATGCCGATGATATT	AAUAUCAUCGGCAUCAUCGcg	CGAUGAUGCCGAUGAUAUUtt
23368	PPP1R13B	Hs_PPP1R13B_6	NM_015316	SI03028907	protein phosphatase 1, regulatory (inhibitor) subunit 13B	AACCGTGTGAATGGCACGTCA	UGACGUGCCAUUCACACGGtt	CCGUGUGAAUGGCACGUCAtt
23368	PPP1R13B	Hs_PPP1R13B_7	NM_015316	SI03038210	protein phosphatase 1, regulatory (inhibitor) subunit 13B	ACCAAGAACTACAGATTCGTA	UACGAAUCUGUAGUUCUUGgt	CAAGAACUACAGAUUCGUAtt
23371	TENC1	Hs_TENC1_5	NM_015319 NM_170754 NM_198316	SI02665684	tensin like C1 domain containing phosphatase (tensin 2)	ACAGCACGTGGTCGTACTATA	UAUAGUACGACCACGUGCUgt	AGCACGUGGUCGUACUAUAtt
23371	TENC1	Hs_TENC1_6	NM_015319 NM_170754 NM_198316	SI02665691	tensin like C1 domain containing phosphatase (tensin 2)	CAAGGTGGCGACGCACAGAAA	UUUCUGUGCGUCGCCACCUtg	AGGUGGCGACGCACAGAAAtt
23371	TENC1	Hs_TENC1_2	NM_015319 NM_170754 NM_198316	SI00164087	tensin like C1 domain containing phosphatase (tensin 2)	CTCGGTCTCTGTCGACTACAA	UUGUAGUCGACAGAGACCGag	CGGUCUCUGUCGACUACAAtt
23645	PPP1R15A	Hs_PPP1R15A_5	NM_014330	SI02659125	protein phosphatase 1, regulatory (inhibitor) subunit 15A	CCAGTTGTTGATCTTATGCAA	UUGCAUAAGAUCAACAACUgg	AGUUGUUGAUCUUAUGCAAtt
23645	PPP1R15A	Hs_PPP1R15A_6	NM_014330	SI02659132	protein phosphatase 1, regulatory (inhibitor) subunit 15A	TGGGTTTATATAAGGAATAAA	UUUAUUCCUUAUAUAAACCca	GGUUUAUAUAAGGAAUAAAtt
23645	PPP1R15A	Hs_PPP1R15A_7	NM_014330	SI03106936	protein phosphatase 1, regulatory (inhibitor) subunit 15A	GTGGATAGTGAGGATAAGGAA	UUCCUUAUCCUCACUAUCCac	GGAUAGUGAGGAUAAGGAAtt
25930	PTPN23	Hs_PTPN23_5	NM_015466	SI02225930	protein tyrosine phosphatase, non-receptor type 23	AACCTTGTACAGTCCATGCAA	UUGCAUGGACUGUACAAGGtt	CCUUGUACAGUCCAUGCAAtt
25930	PTPN23	Hs_PTPN23_6	NM_015466	SI02659160	protein tyrosine phosphatase, non-receptor type 23	CCGCCAGATCCTTACGCTCAA	UUGAGCGUAAGGAUCUGGCgg	GCCAGAUCCUUACGCUCAAtt
25930	PTPN23	Hs_PTPN23_7	NM_015466	SI03037818	protein tyrosine phosphatase, non-receptor type 23	ACAGCGGATGAGCAAGCATAA	UUAUGCUUGCUCAUCCGCUgt	AGCGGAUGAGCAAGCAUAAtt
26051	PPP1R16B	Hs_PPP1R16B_1	NM_015568	SI00111447	protein phosphatase 1, regulatory (inhibitor) subunit 16B	ACGGGCGAGAGTAGCAGTGAA	UUCACUGCUACUCUCGCCCgt	GGGCGAGAGUAGCAGUGAAtt
26051	PPP1R16B	Hs_PPP1R16B_3	NM_015568	SI00111461	protein phosphatase 1, regulatory (inhibitor) subunit 16B	ATGGAGCTAGTCTCAGTGCAA	UUGCACUGAGACUAGCUCCat	GGAGCUAGUCUCAGUGCAAtt
26051	PPP1R16B	Hs_PPP1R16B_4	NM_015568	SI00111468	protein phosphatase 1, regulatory (inhibitor) subunit 16B	CAGGCAATTTCGTTCCTGGAA	UUCCAGGAACGAAAUUGCCtg	GGCAAUUUCGUUCCUGGAAtt
26095	PTPN20B	Hs_DKFZP566K0524_1	NM_001042357 NM_001042358 NM_0010	SI00111559	protein tyrosine phosphatase, non-receptor type 20B	TTGAATTGGTTGAATAATTAA	UUAAUUAUUCAACCAAUUCaa	GAAUUGGUUGAAUAAUUAAtt
26095	PTPN20B	Hs_DKFZP566K0524_4	NM_001042357 NM_001042358 NM_0010	SI00111580	protein tyrosine phosphatase, non-receptor type 20B	TCACCTCTGTTGAAACATTTA	UAAAUGUUUCAACAGAGGUga	ACCUCUGUUGAAACAUUUAtt
26095	PTPN20B	Hs_PTPN20B_1	NM_001042357 NM_001042358 NM_0010	SI03024112	protein tyrosine phosphatase, non-receptor type 20B	TTGCCCTTTAGCTAACTAATA	UAUUAGUUAGCUAAAGGGCaa	GCCCUUUAGCUAACUAAUAtt
26191	PTPN22	Hs_PTPN22_1	NM_012411 NM_015967	SI00112763	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	CCGGGTAGAACTATCCCTGAT	AUCAGGGAUAGUUCUACCCgg	GGGUAGAACUAUCCCUGAUtt
26191	PTPN22	Hs_PTPN22_2	NM_012411 NM_015967	SI00112770	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	CCCAGGGTCCTTTATCTACAA	UUGUAGAUAAAGGACCCUGgg	CAGGGUCCUUUAUCUACAAtt
26191	PTPN22	Hs_PTPN22_3	NM_012411 NM_015967	SI00112777	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	TACGTAATGCCTCTAATGTAA	UUACAUUAGAGGCAUUACGta	CGUAAUGCCUCUAAUGUAAtt
26469	PTPN18	Hs_PTPN18_5	NM_014369	SI02759351	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	GTGGGCCTGGATCAAAGTTAA	UUAACUUUGAUCCAGGCCCac	GGGCCUGGAUCAAAGUUAAtt
26469	PTPN18	Hs_PTPN18_6	NM_014369	SI02759358	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	CCGGGTGTAAGTCTAACGCCA	UGGCGUUAGACUUACACCCgg	GGGUGUAAGUCUAACGCCAtt
26469	PTPN18	Hs_PTPN18_7	NM_014369	SI03064964	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	CAGATTACTAGACAGATATAA	UUAUAUCUGUCUAGUAAUCtg	GAUUACUAGACAGAUAUAAtt
27124	PIB5PA	Hs_PIB5PA_5	NM_001002837 NM_014422	SI02759365	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	CTGGAGGTCATCCATTAGGAA	UUCCUAAUGGAUGACCUCCag	GGAGGUCAUCCAUUAGGAAtt
27124	PIB5PA	Hs_PIB5PA_6	NM_001002837 NM_014422	SI03040380	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	ACCGTATCCTATGGAAGGTCA	UGACCUUCCAUAGGAUACGgt	CGUAUCCUAUGGAAGGUCAtt
27124	PIB5PA	Hs_PIB5PA_7	NM_001002837 NM_014422	SI03108686	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	TACCAGTGCCAAGAAACGGAA	UUCCGUUUCUUGGCACUGGta	CCAGUGCCAAGAAACGGAAtt
28227	PPP2R3B	Hs_PR48_5	NM_199326	SI02665698	protein phosphatase 2 (formerly 2A), regulatory subunit B'', beta	CACGTGTCTCTGTCACGTGAA	UUCACGUGACAGAGACACGtg	CGUGUCUCUGUCACGUGAAtt
28227	PPP2R3B	Hs_PR48_6	NM_199326	SI02665705	protein phosphatase 2 (formerly 2A), regulatory subunit B'', beta	CTGGGCCTGAGTGAGCAGTAA	UUACUGCUCACUCAGGCCCag	GGGCCUGAGUGAGCAGUAAtt
28227	PPP2R3B	Hs_PPP2R3B_1	NM_013239 NM_199326	SI03099502	protein phosphatase 2 (formerly 2A), regulatory subunit B'', beta	CTGGTCAAGCCGAGGACTGAA	UUCAGUCCUCGGCUUGACCag	GGUCAAGCCGAGGACUGAAtt
29085	PHPT1	Hs_PHPT1_5	NM_014172	SI02659097	phosphohistidine phosphatase 1	TCGGGCGACATGCAGAAGCAA	UUGCUUCUGCAUGUCGCCCga	GGGCGACAUGCAGAAGCAAtt
29085	PHPT1	Hs_PHPT1_6	NM_014172	SI02659104	phosphohistidine phosphatase 1	CACGCCATTTCAACTGAGAAA	UUUCUCAGUUGAAAUGGCGtg	CGCCAUUUCAACUGAGAAAtt
29085	PHPT1	Hs_PHPT1_1	NM_014172	SI00103432	phosphohistidine phosphatase 1	CCGATTCCACGTTTCCTTTAA	UUAAAGGAAACGUGGAAUCgg	GAUUCCACGUUUCCUUUAAtt
51205	ACP6	Hs_ACP6_5	NM_016361	SI02659195	acid phosphatase 6, lysophosphatidic	CCATGTCAGTTTATACCTTAA	UUAAGGUAUAAACUGACAUgg	AUGUCAGUUUAUACCUUAAtt
51205	ACP6	Hs_ACP6_6	NM_016361	SI02659202	acid phosphatase 6, lysophosphatidic	CCCGCTGGACATGTTCTTGAA	UUCAAGAACAUGUCCAGCGgg	CGCUGGACAUGUUCUUGAAtt
51205	ACP6	Hs_ACP6_2	NM_016361	SI00115640	acid phosphatase 6, lysophosphatidic	GTGCCTTTATACAATGCCAAA	UUUGGCAUUGUAUAAAGGCac	GCCUUUAUACAAUGCCAAAtt
51207	DUSP13	Hs_DUSP13_1	NM_001007271 NM_001007272 NM_0010	SI00115717	dual specificity phosphatase 13	TCAGTCCATCTCTATAATAAA	UUUAUUAUAGAGAUGGACUga	AGUCCAUCUCUAUAAUAAAtt
51207	DUSP13	Hs_DUSP13_2	NM_001007271 NM_001007272 NM_0010	SI00115724	dual specificity phosphatase 13	ACCCTGAGATGTAAACAGCAA	UUGCUGUUUACAUCUCAGGgt	CCUGAGAUGUAAACAGCAAtt
51207	DUSP13	Hs_DUSP13_4	NM_001007271 NM_001007272 NM_0010	SI00115738	dual specificity phosphatase 13	ACCCAATTCAGAGATTCTTTA	UAAAGAAUCUCUGAAUUGGgt	CCAAUUCAGAGAUUCUUUAtt
51400	PPME1	Hs_PME-1_5	NM_016147	SI02659174	protein phosphatase methylesterase 1	AGGCGATACATCTGAGTTCAA	UUGAACUCAGAUGUAUCGCct	GCGAUACAUCUGAGUUCAAtt
51400	PPME1	Hs_PME-1_6	NM_016147	SI02659181	protein phosphatase methylesterase 1	AACATCGAGCTCTGTTGTAAA	UUUACAACAGAGCUCGAUGtt	CAUCGAGCUCUGUUGUAAAtt
51400	PPME1	Hs_PME-1_3	NM_016147	SI00113820	protein phosphatase methylesterase 1	ACGGCAGCGATTATTAGTAGA	UCUACUAAUAAUCGCUGCCgt	GGCAGCGAUUAUUAGUAGAtt
51657	STYXL1	Hs_DUSP24_5	NM_016086	SI02224691	serine/threonine/tyrosine interacting-like 1	CAAGATTCAGAAGGACTTGAA	UUCAAGUCCUUCUGAAUCUtg	AGAUUCAGAAGGACUUGAAtt
51657	STYXL1	Hs_DUSP24_7	NM_016086	SI02659167	serine/threonine/tyrosine interacting-like 1	CACCCTGGAGATACTCTTAAA	UUUAAGAGUAUCUCCAGGGtg	CCCUGGAGAUACUCUUAAAtt
51657	STYXL1	Hs_DUSP24_8	NM_016086	SI02660175	serine/threonine/tyrosine interacting-like 1	CAGGCTTGTCTGGAAGGAGAA	UUCUCCUUCCAGACAAGCCtg	GGCUUGUCUGGAAGGAGAAtt
51763	SKIP	Hs_SKIP_9	NM_016532 NM_130766	SI02659209	skeletal muscle and kidney enriched inositol phosphatase	CTGGAATTAGCCGCTTAAATA	UAUUUAAGCGGCUAAUUCCag	GGAAUUAGCCGCUUAAAUAtt
51763	SKIP	Hs_SKIP_10	NM_016532 NM_130766	SI02659216	skeletal muscle and kidney enriched inositol phosphatase	CAGCCAAGTGTCGTCCACATA	UAUGUGGACGACACUUGGCtg	GCCAAGUGUCGUCCACAUAtt
51763	SKIP	Hs_SKIP_4	NM_016532 NM_130766	SI00116529	skeletal muscle and kidney enriched inositol phosphatase	ACGGTCGGAGTCCGGAAGAAA	UUUCUUCCGGACUCCGACCgt	GGUCGGAGUCCGGAAGAAAtt
54545	MTMR12	Hs_MTMR12_1	NM_001040446 NM_019061	SI03064544	myotubularin related protein 12	CAGATAGCCTGTATATACCTA	UAGGUAUAUACAGGCUAUCtg	GAUAGCCUGUAUAUACCUAtt
54545	MTMR12	Hs_MTMR12_2	NM_001040446 NM_019061	SI03078467	myotubularin related protein 12	CCCGGCATTTGAATTCACAGA	UCUGUGAAUUCAAAUGCCGgg	CGGCAUUUGAAUUCACAGAtt
54545	MTMR12	Hs_MTMR12_3	NM_001040446 NM_019061	SI03100538	myotubularin related protein 12	CTGTGAGAGATTGCCAGCATA	UAUGCUGGCAAUCUCUCACag	GUGAGAGAUUGCCAGCAUAtt

54704	PPM2C	Hs_PPM2C_5	NM_018444	SI02759372	protein phosphatase 2C, magnesium-dependent, catalytic subunit	ATCGTACTTCTTATTTAGTAA	UUACUAAAUAAGAAGUACGat	CGUACUUCUUAUUUAGUAAtt
54704	PPM2C	Hs_PPM2C_6	NM_018444	SI03046232	protein phosphatase 2C, magnesium-dependent, catalytic subunit	AGGTAACTTACCACCGATTAA	UUAAUCGGUGGUAAGUUACct	GUAACUUACCACCGAUUAAtt
54704	PPM2C	Hs_PPM2C_7	NM_018444	SI03060484	protein phosphatase 2C, magnesium-dependent, catalytic subunit	CACGCTGTCTAATGACCACAA	UUGUGGUCAUUAGACAGCGtg	CGCUGUCUAAUGACCACAAtt
54776	PPP1R12C	Hs_PPP1R12C_5	NM_017607	SI02779602	protein phosphatase 1, regulatory (inhibitor) subunit 12C	CAGGAGGACCTTCGGAACCAA	UUGGUUCCGAAGGUCCUCCtg	GGAGGACCUUCGGAACCAAtt
54776	PPP1R12C	Hs_PPP1R12C_6	NM_017607	SI03039750	protein phosphatase 1, regulatory (inhibitor) subunit 12C	ACCGACGGAGGTCCTACCAGA	UCUGGUAGGACCUCCGUCGgt	CGACGGAGGUCCUACCAGAtt
54776	PPP1R12C	Hs_PPP1R12C_7	NM_017607	SI03085796	protein phosphatase 1, regulatory (inhibitor) subunit 12C	CGGAGGCTTTAGGACGCTGTA	UACAGCGUCCUAAAGCCUCcg	GAGGCUUUAGGACGCUGUAtt
54866	PPP1R14D	Hs_PPP1R14D_1	NM_017726	SI00119434	protein phosphatase 1, regulatory (inhibitor) subunit 14D	CCGCCTGACAGTGAAGTATGA	UCAUACUUCACUGUCAGGCgg	GCCUGACAGUGAAGUAUGAtt
54866	PPP1R14D	Hs_PPP1R14D_2	NM_017726	SI00119441	protein phosphatase 1, regulatory (inhibitor) subunit 14D	CAGGAGCTCTTCCAGGATCAA	UUGAUCCUGGAAGAGCUCCtg	GGAGCUCUUCCAGGAUCAAtt
54866	PPP1R14D	Hs_PPP1R14D_5	NM_017726	SI03045546	protein phosphatase 1, regulatory (inhibitor) subunit 14D	AGGGACATTTGCATACTCCTA	UAGGAGUAUGCAAAUGUCCct	GGACAUUUGCAUACUCCUAtt
54935	DUSP23	Hs_DUSP23_1	NM_017823	SI00374885	dual specificity phosphatase 23	CAGTTCTACCAGCGAACGAAA	UUUCGUUCGCUGGUAGAACtg	GUUCUACCAGCGAACGAAAtt
54935	DUSP23	Hs_DUSP23_2	NM_017823	SI00374892	dual specificity phosphatase 23	GAAGTGGACTAAAGTATTAAA	UUUAAUACUUUAGUCCACUtc	AGUGGACUAAAGUAUUAAAtt
54935	DUSP23	Hs_DUSP23_5	NM_017823	SI03025750	dual specificity phosphatase 23	TTGTACTGCTTTGTTGAATAA	UUAUUCAACAAAGCAGUACaa	GUACUGCUUUGUUGAAUAAtt
55066	PDPR	Hs_PDPR_5	NM_017990 XM_001134215	SI02642983	pyruvate dehydrogenase phosphatase regulatory subunit	ATCTCTTATCTCCTTGATATA	UAUAUCAAGGAGAUAAGAGat	CUCUUAUCUCCUUGAUAUAtt
55066	PDPR	Hs_PDPR_6	NM_017990 XM_001134215	SI03052651	pyruvate dehydrogenase phosphatase regulatory subunit	CAAAGGGTGTACGTTGCATAA	UUAUGCAACGUACACCCUUtg	AAGGGUGUACGUUGCAUAAtt
55066	PDPR	Hs_PDPR_7	NM_017990	SI03065846	pyruvate dehydrogenase phosphatase regulatory subunit	CAGCATAGCACGACTGAACAA	UUGUUCAGUCGUGCUAUGCtg	GCAUAGCACGACUGAACAAtt
55183	RIF1	Hs_RIF1_1	NM_018151	SI00703227	RAP1 interacting factor homolog (yeast)	CTCATGGAAATTACAATTAAA	UUUAAUUGUAAUUUCCAUGag	CAUGGAAAUUACAAUUAAAtt
55183	RIF1	Hs_RIF1_2	NM_018151	SI00703234	RAP1 interacting factor homolog (yeast)	AAGGAAATGCATGTAAAGTAA	UUACUUUACAUGCAUUUCCtt	GGAAAUGCAUGUAAAGUAAtt
55183	RIF1	Hs_RIF1_3	NM_018151	SI00703241	RAP1 interacting factor homolog (yeast)	CAGGAGAATTTAATTGAGAAA	UUUCUCAAUUAAAUUCUCCtg	GGAGAAUUUAAUUGAGAAAtt
55291	SAPS3	Hs_C11orf23_1	NM_018312	SI00317317	SAPS domain family, member 3	CAGAGCAATCTGCATATTTAA	UUAAAUAUGCAGAUUGCUCtg	GAGCAAUCUGCAUAUUUAAtt
55291	SAPS3	Hs_C11orf23_2	NM_018312	SI00317324	SAPS domain family, member 3	CCGAAGCATGCTAATTGTTTA	UAAACAAUUAGCAUGCUUCgg	GAAGCAUGCUAAUUGUUUAtt
55291	SAPS3	Hs_C11orf23_3	NM_018312	SI00317331	SAPS domain family, member 3	AAGAAGAAGATCGACATTCAA	UUGAAUGUCGAUCUUCUUCtt	GAAGAAGAUCGACAUUCAAtt
55370	PPP4R1L	Hs_PPP4R1L_1	NM_018498 NR_003505	SI00691579	protein phosphatase 4, regulatory subunit 1-like	CGGGACTTCGGTAACAATGAA	UUCAUUGUUACCGAAGUCCcg	GGACUUCGGUAACAAUGAAtt
55370	PPP4R1L	Hs_PPP4R1L_2	NM_018498	SI00691586	protein phosphatase 4, regulatory subunit 1-like	AGGCAATTTATTTGAACCAAA	UUUGGUUCAAAUAAAUUGCct	GCAAUUUAUUUGAACCAAAtt
55370	PPP4R1L	Hs_PPP4R1L_3	NM_018498	SI00691593	protein phosphatase 4, regulatory subunit 1-like	AAGGTATAAACAGAATTCCAA	UUGGAAUUCUGUUUAUACCtt	GGUAUAAACAGAAUUCCAAtt
55607	PPP1R9A	Hs_PPP1R9A_2	NM_017650 XM_371933 XM_374491	SI00691474	protein phosphatase 1, regulatory (inhibitor) subunit 9A	GAGGGTAATATTTATCCTCTA	UAGAGGAUAAAUAUUACCCtc	GGGUAAUAUUUAUCCUCUAtt
55607	PPP1R9A	Hs_PPP1R9A_5	NM_017650 XM_371933 XM_374491	SI03077620	protein phosphatase 1, regulatory (inhibitor) subunit 9A	CCCGAGGACTCCACATCTAAT	AUUAGAUGUGGAGUCCUCGgg	CGAGGACUCCACAUCUAAUtt
55607	PPP1R9A	Hs_PPP1R9A_6	NM_017650 XM_371933 XM_374491	SI03093776	protein phosphatase 1, regulatory (inhibitor) subunit 9A	CTGATATGGAGTACTCGGAAA	UUUCCGAGUACUCCAUAUCag	GAUAUGGAGUACUCGGAAAtt
55613	MTMR8	Hs_MTMR8_5	NM_017677	SI02659223	myotubularin related protein 8	CAGCCCAAGCAGAGTATGCTA	UAGCAUACUCUGCUUGGGCtg	GCCCAAGCAGAGUAUGCUAtt
55613	MTMR8	Hs_MTMR8_6	NM_017677	SI02659230	myotubularin related protein 8	CGGGAAGATCTAAGAGTCTAT	AUAGACUCUUAGAUCUUCCcg	GGAAGAUCUAAGAGUCUAUtt
55613	MTMR8	Hs_MTMR8_1	NM_017677	SI00119210	myotubularin related protein 8	GGGAATTACTTTACTGATTAA	UUAAUCAGUAAAGUAAUUCcc	GAAUUACUUUACUGAUUAAtt
55671	SMEK1	Hs_KIAA2010_1	NM_017936 NM_032560	SI00462140	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	AAGAAAGATTATTGGATTAAA	UUUAAUCCAAUAAUCUUUCtt	GAAAGAUUAUUGGAUUAAAtt
55671	SMEK1	Hs_KIAA2010_2	NM_017936 NM_032560	SI00462147	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	CAGATTTGTTTGCACAACTAA	UUAGUUGUGCAAACAAAUCtg	GAUUUGUUUGCACAACUAAtt
55671	SMEK1	Hs_KIAA2010_4	NM_017936 NM_032560	SI00462161	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	CAGCCAGTCATCTACAACAAA	UUUGUUGUAGAUGACUGGCtg	GCCAGUCAUCUACAACAAAtt
55844	PPP2R2D	Hs_PPP2R2D_5	NM_001003656 NM_018461	SI02759148	protein phosphatase 2, regulatory subunit B, delta isoform	TTCATCCATATCCGATGTAAA	UUUACAUCGGAUAUGGAUGaa	CAUCCAUAUCCGAUGUAAAtt
55844	PPP2R2D	Hs_LOC440009_1	XM_495852	SI00564788	protein phosphatase 2, regulatory subunit B, delta isoform	CTGCTAATAAGTGGAACTCGA	UCGAGUUCCACUUAUUAGCag	GCUAAUAAGUGGAACUCGAtt
55844	PPP2R2D	Hs_LOC440009_2	XM_495852	SI00564795	protein phosphatase 2, regulatory subunit B, delta isoform	TCGGCAGACCTGCTCCAGAAA	UUUCUGGAGCAGGUCUGCCga	GGCAGACCUGCUCCAGAAAtt
56252	YLPM1	Hs_YLPM1_1	NM_019589 XM_085151 XM_930487 XM_	SI00764491	YLP motif containing 1	AGGACTGAATTCAGAATTTAA	UUAAAUUCUGAAUUCAGUCct	GACUGAAUUCAGAAUUUAAtt
56252	YLPM1	Hs_YLPM1_2	NM_019589 XM_085151 XM_930487 XM_	SI00764498	YLP motif containing 1	CAGTAGCAACATCATCATTAA	UUAAUGAUGAUGUUGCUACtg	GUAGCAACAUCAUCAUUAAtt
56252	YLPM1	Hs_YLPM1_3	NM_019589 XM_085151 XM_930487 XM_	SI00764505	YLP motif containing 1	CCGAGATATATCCACTAATAA	UUAUUAGUGGAUAUAUCUCgg	GAGAUAUAUCCACUAAUAAtt
56623	INPP5E	Hs_INPP5E_2	NM_019892	SI00124684	inositol polyphosphate-5-phosphatase, 72 kDa	CAGAAATGTGCCCGACACCAA	UUGGUGUCGGGCACAUUUCtg	GAAAUGUGCCCGACACCAAtt
56623	INPP5E	Hs_INPP5E_3	NM_019892	SI00124691	inositol polyphosphate-5-phosphatase, 72 kDa	CACGTACGACAGCACCTCCAA	UUGGAGGUGCUGUCGUACGtg	CGUACGACAGCACCUCCAAtt
56623	INPP5E	Hs_INPP5E_4	NM_019892	SI00124698	inositol polyphosphate-5-phosphatase, 72 kDa	CTGGACTACACCAGGACTGTA	UACAGUCCUGGUGUAGUCCag	GGACUACACCAGGACUGUAtt
56940	DUSP22	Hs_DUSP22_1	NM_020185 XM_001132925	SI00125272	dual specificity phosphatase 22	AAGCAACATAGAGTTTAAGTA	UACUUAAACUCUAUGUUGCtt	GCAACAUAGAGUUUAAGUAtt
56940	DUSP22	Hs_DUSP22_2	NM_020185	SI00125279	dual specificity phosphatase 22	GGGCAACTTAGCCAAGTTTAA	UUAAACUUGGCUAAGUUGCcc	GCAACUUAGCCAAGUUUAAtt
56940	DUSP22	Hs_DUSP22_3	NM_020185 XM_001132925	SI00125286	dual specificity phosphatase 22	CATGTTTATGTTGAGAACTAA	UUAGUUCUCAACAUAAACAtg	UGUUUAUGUUGAGAACUAAtt
57171	DOLPP1	Hs_DOLPP1_5	NM_020438	SI02659244	dolichyl pyrophosphate phosphatase 1	AAGAATGCACCAAACAAACAA	UUGUUUGUUUGGUGCAUUCtt	GAAUGCACCAAACAAACAAtt
57171	DOLPP1	Hs_DOLPP1_6	NM_020438	SI02659251	dolichyl pyrophosphate phosphatase 1	CAGGGTCTACCTGCTGTACCA	UGGUACAGCAGGUAGACCCtg	GGGUCUACCUGCUGUACCAtt
57171	DOLPP1	Hs_DOLPP1_7	NM_020438	SI03087504	dolichyl pyrophosphate phosphatase 1	CGTGACCCTCATCATATTTAA	UUAAAUAUGAUGAGGGUCAcg	UGACCCUCAUCAUAUUUAAtt
57546	PDP2	Hs_PDP2_6	NM_020786	SI02665642	pyruvate dehydrogenase phosphatase isoenzyme 2	CAGGACGATCATCATGGAGGA	UCCUCCAUGAUGAUCGUCCtg	GGACGAUCAUCAUGGAGGAtt
57546	PDP2	Hs_PDP2_7	NM_020786	SI03110499	pyruvate dehydrogenase phosphatase isoenzyme 2	TAGACCATATTTAGTATAGGA	UCCUAUACUAAAUAUGGUCta	GACCAUAUUUAGUAUAGGAtt
57546	PDP2	Hs_PDP2_4	NM_020786	SI00127806	pyruvate dehydrogenase phosphatase isoenzyme 2	CCCATCCTATTGTCAAGGTTA	UAACCUUGACAAUAGGAUGgg	CAUCCUAUUGUCAAGGUUAtt
57818	G6PC2	Hs_G6PC2_1	NM_001081686 NM_021176	SI00129969	glucose-6-phosphatase, catalytic, 2	TTGGTTAAATCTTATATTTAA	UUAAAUAUAAGAUUUAACCaa	GGUUAAAUCUUAUAUUUAAtt
57818	G6PC2	Hs_G6PC2_3	NM_001081686 NM_021176	SI00129983	glucose-6-phosphatase, catalytic, 2	CAGGAATGGAGTGCTCATAAT	AUUAUGAGCACUCCAUUCCtg	GGAAUGGAGUGCUCAUAAUtt
57818	G6PC2	Hs_G6PC2_5	NM_001081686 NM_021176	SI02644635	glucose-6-phosphatase, catalytic, 2	CTGGTGGGTCCAAGAAACTCA	UGAGUUUCUUGGACCCACCag	GGUGGGUCCAAGAAACUCAtt
63904	DUSP21	Hs_DUSP21_1	NM_022076	SI00132405	dual specificity phosphatase 21	ACGTACGATGATATCAATGTA	UACAUUGAUAUCAUCGUACgt	GUACGAUGAUAUCAAUGUAtt
63904	DUSP21	Hs_DUSP21_2	NM_022076	SI00132412	dual specificity phosphatase 21	AACGTAGTAAGCCTTACCTTA	UAAGGUAAGGCUUACUACGtt	CGUAGUAAGCCUUACCUUAtt
63904	DUSP21	Hs_DUSP21_3	NM_022076	SI00132419	dual specificity phosphatase 21	ACCGGATGGTGCCTTGTTAAA	UUUAACAAGGCACCAUCCGgt	CGGAUGGUGCCUUGUUAAAtt
64077	LHPP	Hs_LHPP_5	NM_022126	SI02778587	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	ACCACTCACCATGGGCCTTTA	UAAAGGCCCAUGGUGAGUGgt	CACUCACCAUGGGCCUUUAtt
64077	LHPP	Hs_LHPP_6	NM_022126	SI03063389	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	CAGAATTTGATCAGATCGACA	UGUCGAUCUGAUCAAAUUCtg	GAAUUUGAUCAGAUCGACAtt
64077	LHPP	Hs_LHPP_7	NM_022126	SI03094322	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	CTGCAGCACGCCGACAAGTGA	UCACUUGUCGGCGUGCUGCag	GCAGCACGCCGACAAGUGAtt
64748	LPPR2	Hs_LPPR2_5	NM_022737	SI02659286	lipid phosphate phosphatase-related protein type 2	CCGGGACAACTTCAGCCCTTA	UAAGGGCUGAAGUUGUCCCgg	GGGACAACUUCAGCCCUUAtt
64748	LPPR2	Hs_LPPR2_6	NM_022737	SI02659293	lipid phosphate phosphatase-related protein type 2	CCCGTGTCTAAGCATGTGCAA	UUGCACAUGCUUAGACACGgg	CGUGUCUAAGCAUGUGCAAtt
64748	LPPR2	Hs_LPPR2_2	NM_022737	SI00134267	lipid phosphate phosphatase-related protein type 2	CCGCGTGGCCGAGTACCGAAA	UUUCGGUACUCGGCCACGCgg	GCGUGGCCGAGUACCGAAAtt
66036	MTMR9	Hs_MTMR9_5	NM_015458	SI03022600	myotubularin related protein 9	TTCGAATTATTCAGTTGGATA	UAUCCAACUGAAUAAUUCGaa	CGAAUUAUUCAGUUGGAUAtt
66036	MTMR9	Hs_MTMR9_6	NM_015458	SI03072713	myotubularin related protein 9	CAGTACTAAGCTATTACCACA	UGUGGUAAUAGCUUAGUACtg	GUACUAAGCUAUUACCACAtt
66036	MTMR9	Hs_MTMR9_7	NM_015458	SI03103849	myotubularin related protein 9	GAGGCTAAGCTATGTCAATAA	UUAUUGACAUAGCUUAGCCtc	GGCUAAGCUAUGUCAAUAAtt
79368	FCRL2	Hs_FCRL2_1	NM_030764 NM_138738	SI03048031	Fc receptor-like 2	ATCGACTTGAGTGTAAACATA	UAUGUUUACACUCAAGUCGat	CGACUUGAGUGUAAACAUAtt
79368	FCRL2	Hs_FCRL2_2	NM_030764 NM_138738	SI03095750	Fc receptor-like 2	CTGCTACCTTCTCTTAAGCAA	UUGCUUAAGAGAAGGUAGCag	GCUACCUUCUCUUAAGCAAtt
79368	FCRL2	Hs_FCRL2_3	NM_030764 NM_138738	SI03105284	Fc receptor-like 2	GCGCTTGATATTGGTCTAGGA	UCCUAGACCAAUAUCAAGCgc	GCUUGAUAUUGGUCUAGGAtt
79660	PPP1R3B	Hs_PPP1R3B_6	NM_024607	SI02665663	protein phosphatase 1, regulatory (inhibitor) subunit 3B	CACCCAAGTTCTTATACGTTA	UAACGUAUAAGAACUUGGGtg	CCCAAGUUCUUAUACGUUAtt
79660	PPP1R3B	Hs_PPP1R3B_7	NM_024607	SI03052714	protein phosphatase 1, regulatory (inhibitor) subunit 3B	CAAAGTGTTCTCGGAATTCGA	UCGAAUUCCGAGAACACUUtg	AAGUGUUCUCGGAAUUCGAtt
79660	PPP1R3B	Hs_PPP1R3B_8	NM_024607	SI03110331	protein phosphatase 1, regulatory (inhibitor) subunit 3B	TACTTAGACTTTAGAAATCGA	UCGAUUUCUAAAGUCUAAGta	CUUAGACUUUAGAAAUCGAtt
80316	PPP1R2P9	Hs_PPP1R2P9_1	NR_002191	SI03651809	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	AACGAAGAATTGAACATCAAA	UUUGAUGUUCAAUUCUUCGtt	CGAAGAAUUGAACAUCAAAtt
80316	PPP1R2P9	Hs_PPP1R2P9_2	NR_002191	SI03651816	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	ACGTACAGAGATTACGATTTA	UAAAUCGUAAUCUCUGUACgt	GUACAGAGAUUACGAUUUAtt
80316	PPP1R2P9	Hs_PPP1R2P9_3	NR_002191	SI03651823	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9	AGCGGCAGTTCGAAATGAGAA	UUCUCAUUUCGAACUGCCGct	CGGCAGUUCGAAAUGAGAAtt
80824	DUSP16	Hs_DUSP16_5	NM_030640	SI02759421	dual specificity phosphatase 16	AACCCAGTTGTTACTCTCTTA	UAAGAGAGUAACAACUGGGtt	CCCAGUUGUUACUCUCUUAtt
80824	DUSP16	Hs_DUSP16_6	NM_030640	SI03120964	dual specificity phosphatase 16	TGGGAGCGTGGAGGACAATTA	UAAUUGUCCUCCACGCUCCca	GGAGCGUGGAGGACAAUUAtt
80824	DUSP16	Hs_DUSP16_2	NM_030640	SI00374836	dual specificity phosphatase 16	CCGGCCATTTGTGGAATACAA	UUGUAUUCCACAAAUGGCCgg	GGCCAUUUGUGGAAUACAAtt
80895	ILKAP	Hs_ILKAP_5	NM_030768 NM_176799	SI00287994	integrin-linked kinase-associated serine/threonine phosphatase 2C	TTCGGTGATCTTTGGTCTGAA	UUCAGACCAAAGAUCACCGaa	CGGUGAUCUUUGGUCUGAAtt
80895	ILKAP	Hs_ILKAP_8	NM_030768 NM_176799	SI02659902	integrin-linked kinase-associated serine/threonine phosphatase 2C	ATGGAGGAATTCGAGCCTCAA	UUGAGGCUCGAAUUCCUCCat	GGAGGAAUUCGAGCCUCAAtt
80895	ILKAP	Hs_ILKAP_9	NM_030768 NM_176799	SI03042599	integrin-linked kinase-associated serine/threonine phosphatase 2C	AGCACGCATGGTATTGACTTA	UAAGUCAAUACCAUGCGUGct	CACGCAUGGUAUUGACUUAtt
81537	SGPP1	Hs_SGPP1_5	NM_030791	SI02659300	sphingosine-1-phosphate phosphatase 1	AGAGATTAACTTTCCATATAA	UUAUAUGGAAAGUUAAUCUct	AGAUUAACUUUCCAUAUAAtt
81537	SGPP1	Hs_SGPP1_6	NM_030791	SI02659307	sphingosine-1-phosphate phosphatase 1	ATCGGTATATTACCTATGGAA	UUCCAUAGGUAAUAUACCGat	CGGUAUAUUACCUAUGGAAtt
81537	SGPP1	Hs_SGPP1_3	NM_030791	SI00139454	sphingosine-1-phosphate phosphatase 1	CTGCCATTACCTTTCATGTTA	UAACAUGAAAGGUAAUGGCag	GCCAUUACCUUUCAUGUUAtt
81706	PPP1R14C	Hs_PPP1R14C_2	NM_030949	SI00139930	protein phosphatase 1, regulatory (inhibitor) subunit 14C	CCGCAGAAGAAGAGTGTATGA	UCAUACACUCUUCUUCUGCgg	GCAGAAGAAGAGUGUAUGAtt
81706	PPP1R14C	Hs_PPP1R14C_3	NM_030949	SI00139937	protein phosphatase 1, regulatory (inhibitor) subunit 14C	GACAGTGAAATACGATCGTAA	UUACGAUCGUAUUUCACUGtc	CAGUGAAAUACGAUCGUAAtt
81706	PPP1R14C	Hs_PPP1R14C_6	NM_030949	SI03030321	protein phosphatase 1, regulatory (inhibitor) subunit 14C	AACGTTCACTTTATGCACCAA	UUGGUGCAUAAAGUGAACGtt	CGUUCACUUUAUGCACCAAtt
84152	PPP1R1B	Hs_PPP1R1B_1	NM_032192 NM_181505	SI00161861	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	CTGAGTCTCACCTGCAGTCTA	UAGACUGCAGGUGAGACUCag	GAGUCUCACCUGCAGUCUAtt
84152	PPP1R1B	Hs_PPP1R1B_3	NM_032192 NM_181505	SI00161875	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	CAGGGATTTGCCCTTCACAAT	AUUGUGAAGGGCAAAUCCCtg	GGGAUUUGCCCUUCACAAUtt
84152	PPP1R1B	Hs_PPP1R1B_6	NM_032192 NM_181505	SI03023041	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	TTCGGGAGCTGGGTTATCCAA	UUGGAUAACCCAGCUCCCGaa	CGGGAGCUGGGUUAUCCAAtt
84687	PPP1R9B	Hs_PPP1R9B_5	NM_032595	SI02659314	protein phosphatase 1, regulatory (inhibitor) subunit 9B	CAACTCGAAGCTGGTCAGCAA	UUGCUGACCAGCUUCGAGUtg	ACUCGAAGCUGGUCAGCAAtt
84687	PPP1R9B	Hs_PPP1R9B_6	NM_032595	SI02759393	protein phosphatase 1, regulatory (inhibitor) subunit 9B	CACTGAGGAATTCCAATTCTA	UAGAAUUGGAAUUCCUCAGtg	CUGAGGAAUUCCAAUUCUAtt
84687	PPP1R9B	Hs_PPP1R9B_7	NM_032595	SI02779140	protein phosphatase 1, regulatory (inhibitor) subunit 9B	CCGGGAGGTGCGCAAGATTAA	UUAAUCUUGCGCACCUCCCgg	GGGAGGUGCGCAAGAUUAAtt
84867	PTPN5	Hs_PTPN5_1	NM_001039970 NM_006906 NM_032781	SI00144277	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	CAGCTGAGGGAGAGTTCTCTA	UAGAGAACUCUCCCUCAGCtg	GCUGAGGGAGAGUUCUCUAtt
84867	PTPN5	Hs_PTPN5_3	NM_001039970 NM_006906 NM_032781	SI00144291	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	ATCGAGGAGATGAACGAGAAA	UUUCUCGUUCAUCUCCUCGat	CGAGGAGAUGAACGAGAAAtt
84867	PTPN5	Hs_PTPN5_4	NM_001039970 NM_006906 NM_032781	SI00144298	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	CCCTCTGAGTTCCTACATCAA	UUGAUGUAGGAACUCAGAGgg	CUCUGAGUUCCUACAUCAAtt
84919	PPP1R15B	Hs_PPP1R15B_5	NM_032833	SI03045462	protein phosphatase 1, regulatory (inhibitor) subunit 15B	AGGCTTTGTACAGACAGGTAA	UUACCUGUCUGUACAAAGCct	GCUUUGUACAGACAGGUAAtt
84919	PPP1R15B	Hs_PPP1R15B_6	NM_032833	SI03050257	protein phosphatase 1, regulatory (inhibitor) subunit 15B	ATGCTATTGGATATTGCTTGA	UCAAGCAAUAUCCAAUAGCat	GCUAUUGGAUAUUGCUUGAtt
84919	PPP1R15B	Hs_PPP1R15B_7	NM_032833	SI03079923	protein phosphatase 1, regulatory (inhibitor) subunit 15B	CCGAATAAGTGTAGTTGATTA	UAAUCAACUACACUUAUUCgg	GAAUAAGUGUAGUUGAUUAtt
84988	PPP1R16A	Hs_PPP1R16A_1	NM_032902	SI00144921	protein phosphatase 1, regulatory (inhibitor) subunit 16A	CCCGAGCAGCCCTGTGGGCAA	UUGCCCACAGGGCUGCUCGgg	CGAGCAGCCCUGUGGGCAAtt
84988	PPP1R16A	Hs_PPP1R16A_2	NM_032902	SI02658187	protein phosphatase 1, regulatory (inhibitor) subunit 16A	CCGAGCCAGCCTGAGCGCTAA	UUAGCGCUCAGGCUGGCUCgg	GAGCCAGCCUGAGCGCUAAtt
84988	PPP1R16A	Hs_PPP1R16A_3	NM_032902	SI02658194	protein phosphatase 1, regulatory (inhibitor) subunit 16A	CCGGAAGCTGGAACCTTGTTA	UAACAAGGUUCCAGCUUCCgg	GGAAGCUGGAACCUUGUUAtt
89801	PPP1R3F	Hs_PPP1R3F_5	NM_033215 XM_372210	SI02759428	protein phosphatase 1, regulatory (inhibitor) subunit 3F	CGGGTTGGTACGCGTGCTGAA	UUCAGCACGCGUACCAACCcg	GGUUGGUACGCGUGCUGAAtt
89801	PPP1R3F	Hs_PPP1R3F_6	NM_033215 XM_372210	SI02759435	protein phosphatase 1, regulatory (inhibitor) subunit 3F	CACAATAGAGCTCTATGAGAA	UUCUCAUAGAGCUCUAUUGtg	CAAUAGAGCUCUAUGAGAAtt
89801	PPP1R3F	Hs_PPP1R3F_1	NM_033215 XM_372210	SI00691439	protein phosphatase 1, regulatory (inhibitor) subunit 3F	AACATGGATGATAACACCTTT	AAAGGUGUUAUCAUCCAUGtt	CAUGGAUGAUAACACCUUUtt
90673	PPP1R3E	Hs_PPP1R3E_1	XM_927029	SI04380887	protein phosphatase 1, regulatory (inhibitor) subunit 3E	TCACGAGTTCTGGGACAACAA	UUGUUGUCCCAGAACUCGUga	ACGAGUUCUGGGACAACAAtt
90673	PPP1R3E	Hs_PPP1R3E_2	XM_927029	SI04380894	protein phosphatase 1, regulatory (inhibitor) subunit 3E	CAGAACTATGACTCGATCATA	UAUGAUCGAGUCAUAGUUCtg	GAACUAUGACUCGAUCAUAtt
90673	PPP1R3E	Hs_PPP1R3E_3	XM_927029	SI04380901	protein phosphatase 1, regulatory (inhibitor) subunit 3E	CAGGGCTTCGGTAAGCTGTTA	UAACAGCUUACCGAAGCCCtg	GGGCUUCGGUAAGCUGUUAtt
92579	G6PC3	Hs_G6PC3_5	NM_138387	SI02659363	glucose 6 phosphatase, catalytic, 3	CAGGTGCTGGCTGGCCTAATA	UAUUAGGCCAGCCAGCACCtg	GGUGCUGGCUGGCCUAAUAtt
92579	G6PC3	Hs_G6PC3_6	NM_138387	SI02659370	glucose 6 phosphatase, catalytic, 3	GTGGCTCAACCTCATCTTCAA	UUGAAGAUGAGGUUGAGCCac	GGCUCAACCUCAUCUUCAAtt
92579	G6PC3	Hs_G6PC3_7	NM_138387	SI03085278	glucose 6 phosphatase, catalytic, 3	CGCGGGCATCGTGATAGCCGA	UCGGCUAUCACGAUGCCCGcg	CGGGCAUCGUGAUAGCCGAtt
93492	TPTE2	Hs_TPTE2_2	NM_130785 NM_199254 NM_199255	SI00149751	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	ACCTGGAGAACTGATAATAAA	UUUAUUAUCAGUUCUCCAGgt	CUGGAGAACUGAUAAUAAAtt
93492	TPTE2	Hs_TPTE2_3	NM_130785 NM_199254 NM_199255	SI00149758	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	AATGATTGAAATAGAGCTATA	UAUAGCUCUAUUUCAAUCAtt	UGAUUGAAAUAGAGCUAUAtt
93492	TPTE2	Hs_TPTE2_5	NM_130785 NM_199254 NM_199255	SI03087567	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	CGTGGTGATGTATGTGATCTA	UAGAUCACAUACAUCACCAcg	UGGUGAUGUAUGUGAUCUAtt
93650	ACPT	Hs_ACPT_1	NM_033068 NM_080789 NM_080790 NM_	SI00145278	acid phosphatase, testicular	CCCGCCAAAGATGGAGGGAAT	AUUCCCUCCAUCUUUGGCGgg	CGCCAAAGAUGGAGGGAAUtt
93650	ACPT	Hs_ACPT_3	NM_033068 NM_080789 NM_080790 NM_	SI02647134	acid phosphatase, testicular	CTGCTGAATGCTATCCTTGCA	UGCAAGGAUAGCAUUCAGCag	GCUGAAUGCUAUCCUUGCAtt
93650	ACPT	Hs_ACPT_5	NM_033068 NM_080789 NM_080790 NM_	SI03052014	acid phosphatase, testicular	ATGGTCATGTACTCAGCTCAT	AUGAGCUGAGUACAUGACCat	GGUCAUGUACUCAGCUCAUtt
94274	PPP1R14A	Hs_PPP1R14A_5	NM_033256	SI02659321	protein phosphatase 1, regulatory (inhibitor) subunit 14A	CCCGATGAGATCAACATTGAT	AUCAAUGUUGAUCUCAUCGgg	CGAUGAGAUCAACAUUGAUtt
94274	PPP1R14A	Hs_PPP1R14A_6	NM_033256	SI02659328	protein phosphatase 1, regulatory (inhibitor) subunit 14A	TTGTATTTAATGGTTCTGTAA	UUACAGAACCAUUAAAUACaa	GUAUUUAAUGGUUCUGUAAtt
94274	PPP1R14A	Hs_PPP1R14A_7	NM_033256	SI03065671	protein phosphatase 1, regulatory (inhibitor) subunit 14A	CAGCAGCGCGATGGCAGCTCA	UGAGCUGCCAUCGCGCUGCtg	GCAGCGCGAUGGCAGCUCAtt
114971	PTPMT1	Hs_PLIP_1	NM_175732 XM_374879	SI00687183	protein tyrosine phosphatase, mitochondrial 1	CAGCTGCGGCTCAGCACAGTA	UACUGUGCUGAGCCGCAGCtg	GCUGCGGCUCAGCACAGUAtt
114971	PTPMT1	Hs_PLIP_2	NM_175732 XM_374879	SI00687190	protein tyrosine phosphatase, mitochondrial 1	CACCTTGGACAACCTCCAGAA	UUCUGGAGGUUGUCCAAGGtg	CCUUGGACAACCUCCAGAAtt
114971	PTPMT1	Hs_PLIP_3	NM_175732 XM_374879	SI00687197	protein tyrosine phosphatase, mitochondrial 1	AACCTCCAGAAGGGAGTCCAA	UUGGACUCCCUUCUGGAGGtt	CCUCCAGAAGGGAGUCCAAtt
128646	SIRPD	Hs_PTPNS1L2_1	NM_178460	SI00161112	signal-regulatory protein delta	CAGGGCCAAACCGGAAATTAA	UUAAUUUCCGGUUUGGCCCtg	GGGCCAAACCGGAAAUUAAtt
128646	SIRPD	Hs_PTPNS1L2_3	NM_178460	SI00161126	signal-regulatory protein delta	AAGGTAACTTTCCCAGAGTAA	UUACUCUGGGAAAGUUACCtt	GGUAACUUUCCCAGAGUAAtt
128646	SIRPD	Hs_PTPNS1L2_4	NM_178460	SI00161133	signal-regulatory protein delta	AAGCTCCAGGTTTCACCACAA	UUGUGGUGAAACCUGGAGCtt	GCUCCAGGUUUCACCACAAtt
128853	DUSP15	Hs_DUSP15_1	NM_001012644 NM_080611 NM_177991	SI00160461	dual specificity phosphatase 15	CACCACGATTGTGACAGCGTA	UACGCUGUCACAAUCGUGGtg	CCACGAUUGUGACAGCGUAtt
128853	DUSP15	Hs_DUSP15_2	NM_001012644 NM_080611 NM_177991	SI00160468	dual specificity phosphatase 15	ACGGGCCTGGAGGGTATTAAA	UUUAAUACCCUCCAGGCCCgt	GGGCCUGGAGGGUAUUAAAtt
128853	DUSP15	Hs_DUSP15_5	NM_001012644 NM_080611 NM_177991	SI03094392	dual specificity phosphatase 15	CTGCAGGATATCACCTACCTT	AAGGUAGGUGAUAUCCUGCag	GCAGGAUAUCACCUACCUUtt
132160	PPM1M	Hs_FLJ32332_5	NM_144641	SI02659377	protein phosphatase 1M (PP2C domain containing)	CCCAGAGACTCGGATTATCAA	UUGAUAAUCCGAGUCUCUGgg	CAGAGACUCGGAUUAUCAAtt
132160	PPM1M	Hs_FLJ32332_6	NM_144641	SI02659384	protein phosphatase 1M (PP2C domain containing)	CAGAGTGACTTTACAACTTAA	UUAAGUUGUAAAGUCACUCtg	GAGUGACUUUACAACUUAAtt
132160	PPM1M	Hs_PPM1M_1	NM_144641	SI03025561	protein phosphatase 1M (PP2C domain containing)	TTGGTGCGGAGAGATGAGATA	UAUCUCAUCUCUCCGCACCaa	GGUGCGGAGAGAUGAGAUAtt
138639	PTPDC1	Hs_PTPDC1_5	NM_152422 NM_177995	SI02665670	protein tyrosine phosphatase domain containing 1	CGGAATGTTGAGTGCCTTCAA	UUGAAGGCACUCAACAUUCcg	GAAUGUUGAGUGCCUUCAAtt
138639	PTPDC1	Hs_PTPDC1_6	NM_152422 NM_177995	SI02665677	protein tyrosine phosphatase domain containing 1	TACGTAGATACCAGAGGCCAA	UUGGCCUCUGGUAUCUACGta	CGUAGAUACCAGAGGCCAAtt
138639	PTPDC1	Hs_PTPDC1_2	NM_152422 NM_177995	SI00154567	protein tyrosine phosphatase domain containing 1	AACAGAGGGTTTCAAAGCATA	UAUGCUUUGAAACCCUCUGtt	CAGAGGGUUUCAAAGCAUAtt
140885	SIRPA	Hs_PTPNS1_2	NM_001040022 NM_001040023 NM_0807	SI00148995	signal-regulatory protein alpha	CCCGAGAAGAATGCCAGAGAA	UUCUCUGGCAUUCUUCUCGgg	CGAGAAGAAUGCCAGAGAAtt
140885	SIRPA	Hs_PTPNS1_4	NM_001040022 NM_001040023 NM_0807	SI00149009	signal-regulatory protein alpha	CTCGCTGTGGACGCCTGTAAA	UUUACAGGCGUCCACAGCGag	CGCUGUGGACGCCUGUAAAtt
140885	SIRPA	Hs_SIRPA_1	NM_001040022 NM_001040023 NM_0807	SI03062647	signal-regulatory protein alpha	CAGAAACGGCCTCAACCGTTA	UAACGGUUGAGGCCGUUUCtg	GAAACGGCCUCAACCGUUAtt
142679	DUSP19	Hs_DUSP19_6	NM_080876	SI02659356	dual specificity phosphatase 19	CAGAGTTAACCTAATGAGTCA	UGACUCAUUAGGUUAACUCtg	GAGUUAACCUAAUGAGUCAtt
142679	DUSP19	Hs_DUSP19_1	NM_080876	SI00149401	dual specificity phosphatase 19	AAGGTCATATATACTATACAA	UUGUAUAGUAUAUAUGACCtt	GGUCAUAUAUACUAUACAAtt
142679	DUSP19	Hs_DUSP19_2	NM_080876	SI00149408	dual specificity phosphatase 19	ATGGTCAGTATCACTGGATAA	UUAUCCAGUGAUACUGACCat	GGUCAGUAUCACUGGAUAAtt
148713	PTPRV	Hs_PTPRV_1	NR_002930 XM_086287 XM_941020	SI00695863	protein tyrosine phosphatase, receptor type, V (pseudogene)	AACGCTGAAGCAGTATATCTA	UAGAUAUACUGCUUCAGCGtt	CGCUGAAGCAGUAUAUCUAtt
148713	PTPRV	Hs_PTPRV_4	NR_002930 XM_086287 XM_941020	SI00695884	protein tyrosine phosphatase, receptor type, V (pseudogene)	ATGCCACAGAGTGGACCTATA	UAUAGGUCCACUCUGUGGCat	GCCACAGAGUGGACCUAUAtt
148713	PTPRV	Hs_PTPRV_5	NR_002930	SI02812502	protein tyrosine phosphatase, receptor type, V (pseudogene)	CAGGGAGCGCTTGCTATCTGA	UCAGAUAGCAAGCGCUCCCtg	GGGAGCGCUUGCUAUCUGAtt
150290	DUSP18	Hs_DUSP18_1	NM_152511	SI00154784	dual specificity phosphatase 18	CAAGCTCATGCTGTCTAGCAA	UUGCUAGACAGCAUGAGCUtg	AGCUCAUGCUGUCUAGCAAtt
150290	DUSP18	Hs_DUSP18_2	NM_152511	SI00154791	dual specificity phosphatase 18	CAGGAATGAATCTGCTACAAT	AUUGUAGCAGAUUCAUUCCtg	GGAAUGAAUCUGCUACAAUtt
150290	DUSP18	Hs_DUSP18_3	NM_152511	SI00154798	dual specificity phosphatase 18	ACGGGTCTCTCTCCCGAAGAA	UUCUUCGGGAGAGAGACCCgt	GGGUCUCUCUCCCGAAGAAtt
151242	PPP1R1C	Hs_PPP1R1C_1	NM_001080545 XM_087137 XM_929092 X	SI00691411	protein phosphatase 1, regulatory (inhibitor) subunit 1C	CTCGATCTGGAATTACAGCTA	UAGCUGUAAUUCCAGAUCGag	CGAUCUGGAAUUACAGCUAtt
151242	PPP1R1C	Hs_PPP1R1C_5	NM_001080545 XM_087137 XM_929092 X	SI03046911	protein phosphatase 1, regulatory (inhibitor) subunit 1C	ATCACCGTGGATGTTGAAGAA	UUCUUCAACAUCCACGGUGat	CACCGUGGAUGUUGAAGAAtt
151242	PPP1R1C	Hs_PPP1R1C_6	NM_001080545 XM_087137 XM_929092 X	SI03064313	protein phosphatase 1, regulatory (inhibitor) subunit 1C	CAGAGTCAGATTGCACCTGAA	UUCAGGUGCAAUCUGACUCtg	GAGUCAGAUUGCACCUGAAtt
151742	PPM1L	Hs_PPM1L_3	NM_139245	SI00152047	protein phosphatase 1 (formerly 2C)-like	CTGTAGAGTCACATATATGAA	UUCAUAUAUGUGACUCUACag	GUAGAGUCACAUAUAUGAAtt
151742	PPM1L	Hs_PPM1L_6	NM_139245	SI03044146	protein phosphatase 1 (formerly 2C)-like	AGCGTGAACCCATATTGATAA	UUAUCAAUAUGGGUUCACGct	CGUGAACCCAUAUUGAUAAtt
151742	PPM1L	Hs_PPM1L_7	NM_139245	SI03046274	protein phosphatase 1 (formerly 2C)-like	AGGTCTATAATCAGTGACGAA	UUCGUCACUGAUUAUAGACct	GUCUAUAAUCAGUGACGAAtt
151987	PPP4R2	Hs_PPP4R2_1	NM_174907	SI00691607	protein phosphatase 4, regulatory subunit 2	CTGGAAATTCACCAAGCTATA	UAUAGCUUGGUGAAUUUCCag	GGAAAUUCACCAAGCUAUAtt
151987	PPP4R2	Hs_PPP4R2_2	NM_174907	SI00691614	protein phosphatase 4, regulatory subunit 2	CAGCGACTATGTGAATTGTTA	UAACAAUUCACAUAGUCGCtg	GCGACUAUGUGAAUUGUUAtt
151987	PPP4R2	Hs_PPP4R2_3	NM_174907	SI00691621	protein phosphatase 4, regulatory subunit 2	AAGAGGCAAATTTGCAGCAAA	UUUGCUGCAAAUUUGCCUCtt	GAGGCAAAUUUGCAGCAAAtt
157313	CDCA2	Hs_CDCA2_1	NM_152562	SI00341313	cell division cycle associated 2	TACAAATATAATGAACATTAA	UUAAUGUUCAUUAUAUUUGta	CAAAUAUAAUGAACAUUAAtt
157313	CDCA2	Hs_CDCA2_2	NM_152562	SI00341320	cell division cycle associated 2	CCGGAGAAGATCCTCTCTTAA	UUAAGAGAGGAUCUUCUCCgg	GGAGAAGAUCCUCUCUUAAtt
157313	CDCA2	Hs_CDCA2_3	NM_152562	SI00341327	cell division cycle associated 2	CTGCACTGTATCGAAATGTTA	UAACAUUUCGAUACAGUGCag	GCACUGUAUCGAAAUGUUAtt
160760	PPTC7	Hs_TA-PP2C_5	NM_139283	SI02759400	PTC7 protein phosphatase homolog (S. cerevisiae)	CTCAATTCTCAGGGACTTTAA	UUAAAGUCCCUGAGAAUUGag	CAAUUCUCAGGGACUUUAAtt
160760	PPTC7	Hs_PPTC7_1	NM_139283	SI03044573	PTC7 protein phosphatase homolog (S. cerevisiae)	AGGACGGTTCGTACCTAGTAA	UUACUAGGUACGAACCGUCct	GACGGUUCGUACCUAGUAAtt
160760	PPTC7	Hs_TA-PP2C_1	NM_139283	SI00152131	PTC7 protein phosphatase homolog (S. cerevisiae)	CACAAATTGTACGTAATGATA	UAUCAUUACGUACAAUUUGtg	CAAAUUGUACGUAAUGAUAtt
162466	PHOSPHO1	Hs_PHOSPHO1_1	NM_178500	SI00161168	phosphatase, orphan 1	TACAACTATAAAGGAGGTGAA	UUCACCUCCUUUAUAGUUGta	CAACUAUAAAGGAGGUGAAtt
162466	PHOSPHO1	Hs_PHOSPHO1_2	NM_178500	SI00161175	phosphatase, orphan 1	CGCCAACATGTGCAAGCACAA	UUGUGCUUGCACAUGUUGGcg	CCAACAUGUGCAAGCACAAtt
162466	PHOSPHO1	Hs_PHOSPHO1_3	NM_178500	SI00161182	phosphatase, orphan 1	CCGTCCCTATCTATTCAGTTA	UAACUGAAUAGAUAGGGACgg	GUCCCUAUCUAUUCAGUUAtt
170954	KIAA1949	Hs_KIAA1949_1	NM_133471 XM_929867 XM_934039 XM_	SI02824402	KIAA1949	CAGGTTTACAAGCCACGCTTA	UAAGCGUGGCUUGUAAACCtg	GGUUUACAAGCCACGCUUAtt
170954	KIAA1949	Hs_KIAA1949_3	NM_133471 XM_929867 XM_934035 XM_	SI02824416	KIAA1949	CTCCTAGTGGTTCACAATTGA	UCAAUUGUGAACCACUAGGag	CCUAGUGGUUCACAAUUGAtt

170954	KIAA1949	Hs_KIAA1949_4	NM_133471 XM_929867 XM_934035 XM	SI02824423	KIAA1949	TCCGTTCGAGGCCGAGAGAAA	UUUCUCUCGGCCUCGAACGga	CGUUCGAGGCCGAGAGAAAtt
201562	PTPLB	Hs_PTPLB_5	NM_198402	SI02659454	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	CACGGCGTACCTGGTCATCTA	UAGAUGACCAGGUACGCCGtg	CGGCGUACCUGGUCAUCUAtt
201562	PTPLB	Hs_PTPLB_6	NM_198402	SI02659461	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	CAGCCAAGAAATAGTTTGGTA	UACCAAACUAUUUCUUGGCtg	GCCAAGAAAUAGUUUGGUAtt
201562	PTPLB	Hs_PTPLB_3	NM_198402	SI00164171	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	TACGCTTAACTTTCTATGCAT	AUGCAUAGAAAGUUAAGCGta	CGCUUAACUUUCUAUGCAUtt
286262	C9orf75	Hs_C9orf75_1	NM_173691	SI00335965	chromosome 9 open reading frame 75	CTCCTCAAGAAAGAAGATGAA	UUCAUCUUCUUUCUUGAGGag	CCUCAAGAAAGAAGAUGAAtt
286262	C9orf75	Hs_C9orf75_2	NM_173691	SI00335972	chromosome 9 open reading frame 75	CACAGTGGTGCCCAAGAGGAA	UUCCUCUUGGGCACCACUGtg	CAGUGGUGCCCAAGAGGAAtt
286262	C9orf75	Hs_C9orf75_3	NM_173691	SI00335979	chromosome 9 open reading frame 75	TCGAAATTCTTTCATGGTCAT	AUGACCAUGAAAGAAUUUCga	GAAAUUCUUUCAUGGUCAUtt
391025	LOC391025	Hs_LOC391025_5	XM_001131226 XM_372775	SI04380859	similar to protein tyrosine phosphatase, receptor type, U isoform 2 precursor	CCGCAGGAAGCCGATGAACGA	UCGUUCAUCGGCUUCCUGCgg	GCAGGAAGCCGAUGAACGAtt
391025	LOC391025	Hs_LOC391025_6	XM_001131226 XM_372775	SI04380866	similar to protein tyrosine phosphatase, receptor type, U isoform 2 precursor	CCACATGATGAGCACCATGGA	UCCAUGGUGCUCAUCAUGUgg	ACAUGAUGAGCACCAUGGAtt
391025	LOC391025	Hs_LOC391025_7	XM_001131226 XM_372775	SI04380873	similar to protein tyrosine phosphatase, receptor type, U isoform 2 precursor	CCTGTCCTTCATAGACACTCA	UGAGUGUCUAUGAAGGACAgg	UGUCCUUCAUAGACACUCAtt
400927	LOC400927	Hs_LOC400927_1	XM_376010	SI00548660	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	TCCAGGTGATCTGAACCTGAA	UUCAGGUUCAGAUCACCUGga	CAGGUGAUCUGAACCUGAAtt
400927	LOC400927	Hs_LOC400927_2	NM_001034843 NR_002821 XM_376010	SI00548667	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	ATGGATGTTCTTCTTCGAGTA	UACUCGAAGAAGAACAUCCat	GGAUGUUCUUCUUCGAGUAtt
400927	LOC400927	Hs_LOC400927_3	NM_001034843 NR_002821 XM_376010	SI00548674	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	TCCACAGACAAACGAATTTAA	UUAAAUUCGUUUGUCUGUGga	CACAGACAAACGAAUUUAAtt

Supplementary Information Table 2. SiRNA oligos targeting PP2A-B55α, B55δ, and Importin ß1.

Entrez Gene ID	NCBI gene symbol	Symbol used this study	Gene Description	mRNA Accessions	siRNA Target Sequence	Qiagen Product ID	Product Name	mRNA knockdown this study
5515	PPP2CA	CA_3	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	ACACCTCGTGAATACAATTTA	SI00041853	HS_PPP2CA_3	81%
5515	PPP2CA	CA_5	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	ATGGAACTTGACGATACTCTA	SI02225783	HS_PPP2CA_5	86%
5515	PPP2CA	CA_6	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	CAAACAATCATTGGAGCTTAA	SI02225790	HS_PPP2CA_6	87%
5515	PPP2CA	CA_7	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	TAAGACGATGTGACTGCACAA	SI04436453	HS_PPP2CA_7	78%
5515	PPP2CA	CA_8	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	ATGGTGGTCTCTCGCCATCTA	SI04436460	HS_PPP2CA_8	74%
5515	PPP2CA	CA_9	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	NM_002715	TACAAAGCCTCTTGTCATCAA	SI04436467	HS_PPP2CA_9	80%
5518	PPP2R1A	R1A_1	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	TCCCATCTTGGGCAAAGACAA	SI00103733	Hs_PPP2R1A_1	94%
5518	PPP2R1A	R1A_5	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	CTGGTGTCCGATGCCAACCAA	SI02225811	Hs_PPP2R1A_5	91%
5518	PPP2R1A	R1A_6	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	ACGGCTGAACATCATCTCTAA	SI02225818	Hs_PPP2R1A_6	71%
5518	PPP2R1A	R1A_7	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	GACCAGGATGTGGACGTCAAA	SI04436495	Hs_PPP2R1A_7	95%
5518	PPP2R1A	R1A_8	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	ATCGCGGTGCTCATAGACGAA	SI04436502	Hs_PPP2R1A_8	89%
5518	PPP2R1A	R1A_9	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	NM_014225	CACCTTGCAGAGTGAAGTCAA	SI04436509	Hs_PPP2R1A_9	97%
5520	PPP2R2A	R2A_1	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	CTCGCCGTGTCTGGCACTGAA	SI00041895	Hs_PPP2R2A_1	72%
5520	PPP2R2A	R2A_3	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	AAGCGAGACATAACCCTAGAA	SI00041909	Hs_PPP2R2A_3	76%
5520	PPP2R2A	R2A_5	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	CTGCAGATGATTTGCGGATTA	SI02225825	Hs_PPP2R2A_5	95%
5520	PPP2R2A	R2A_6	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	ATGGAAGGTATAGAGATCCTA	SI02225832	Hs_PPP2R2A_6	94%
5520	PPP2R2A	R2A_7	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	CCCGGTCTTGGTGGTGGTATA	SI04436516	Hs_PPP2R2A_7	77%
5520	PPP2R2A	R2A_8	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	NM_002717	CAGTCTCATAGCAGAGGAGAA	SI04436523	Hs_PPP2R2A_8	93%
55844	PPP2R2D	B55δ	protein phosphatase 2, regulatory subunit B, delta isoform	NM_001003656 NM_018461	CAGAGACTACCTGTCGGTGAA	SI00691523	Hs_PPP2R2D_1	72%
55844	PPP2R2D	B55δ	protein phosphatase 2, regulatory subunit B, delta isoform	NM_001003656 NM_018461	CCGCTCCATTAAGAACAGTGA	SI00691530	Hs_PPP2R2D_2	52%
55844	PPP2R2D	B55δ	protein phosphatase 2, regulatory subunit B, delta isoform	NM_001003656 NM_018461	TTCATCCATATCCGATGTAAA	SI02759148	Hs_PPP2R2D_5	82%
3837	KPNB1	Importin ß1	karyopherin (importin) beta 1	NM_002265	TCGGTTATATTTGCCAAGATA	SI00035490	Hs_KPNB1_1	89%
3837	KPNB1	Importin ß1	karyopherin (importin) beta 1	NM_002265	CAAGAACTCTTTGACATCTAA	SI00035497	Hs_KPNB1_2	90%
3837	KPNB1	Importin ß1	karyopherin (importin) beta 1	NM_002265	AAGGGCGGAGATCGAAGACTA	SI00035504	Hs_KPNB1_3	89%

red = used for single or triple knockdown, this study.

Supplementary Information Table 3. Plasmids generated for this study

For efficient generation of cell lines stably expressing fluorescently tagged marker proteins, the genes were subcloned into pIRES-puro2 and pIRES-neo3 vectors (Clontech) that allow expression of resistance genes and tagged proteins from a single transcript.

Table 3. Generated plasmids

Plasmid name	Tag	Source plasmids	Vector backbone	Backbone cloning sites
pIBB-mEGFP-IRES-puro2b	mEGFP[1]	pIBB-mEGFP[2]	pIRES-puro2b	EcoRI/NotI
pGalT-GFP-IRES-puro2b	GFP	pGalT-GFP (MluI blunted/EcoRI)[3]	pIRES-puro2b	(NotI blunted/EcoRI)
pEGFP-PCNA-IRES-puro2b	mEGFP[1]	pNLS-EGFP-PCNA[4]	pIRES-puro2b	(NdeI, XbaI)

mEGFP indicates monomeric EGFP.

Supplementary Information Table 4. Monoclonal fluorescent reporter cell lines

Stable cell lines were generated as described in [5].

Table 4. HeLa Kyoto monoclonal cell lines

Background	Cell line name	Plasmid 1	Plasmid 2
HeLa 'Kyoto'	H2B-mCherry	pH2B-mCherry-IRES-neo3	-
HeLa 'Kyoto'	H2B-mCherry and IBB-mEGFP	pH2B-mCherry-IRES-neo3	pIBB-mEGFP-IRES-puro2b
HeLa 'Kyoto'	H2B-mCherry and GalT-GFP	pH2B-mCherry-IRES-neo3	pGalT-GFP-IRES-puro2b
HeLa 'Kyoto'	H2B-mCherry and PCNA-mEGFP	pH2B-mCherry-IRES-neo3	pPCNA-mEGFP-IRES-puro2b
HeLa 'Kyoto'	H2B-mCherry and mEGFP-α-tubulin[6]	pH2B-mCherry-IRES-neo3	pmEGFP-α-tubulin-IRES-puro2b

Supplementary references

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