

Table S1. Potential Pdx1-interacting proteins identified by ReCLIP/MS (Ref. Table 1). Proteins and MS results illustrating percent protein coverage and number of peptides found after IgG or Pdx1 treatment.

| Factor | Hits | | % Coverage |
|--|------|------|------------|
| | IgG | Pdx1 | |
| Baf47 | 0 | 1 | 11 |
| Baf155 | 0 | 3 | 3 |
| Baf57 | 0 | 2 | 9 |
| Baf170 | 0 | 3 | 3 |
| Brg1 | 0 | 5 | 1.6 |
| Rbbp4 | 1 | 10 | 9 |
| Hdac1 | 0 | 5 | 5 |
| Mi2beta | 0 | 7 | 2.5 |
| Tif1beta | 0 | 6 | 14 |
| Spectrin beta chain, brain 1* | 1 | 12 | 3.76 |
| Myosin-9* | 1 | 14 | 3.94 |
| Microtubule-associated protein 1B | 1 | 8 | 1.96 |
| Importin-5 | 0 | 8 | 5.27 |
| Chaperonin subunit 2 (Beta), isoform CRA_a* | 2 | 8 | 6.07 |
| Glyceraldehyde-3-phosphate dehydrogenase* | 2 | 8 | 16.44 |
| Stip1 | 0 | 7 | 8.45 |
| 14-3-3 protein | 1 | 6 | 15.22 |
| ATP citrate lyase | 1 | 11 | 10.93 |
| DNA replication licensing factor MCM2 | 2 | 13 | 8.55 |
| DNA replication licensing factor MCM3 | 2 | 10 | 10.41 |
| DNA replication licensing factor MCM7 | 1 | 10 | 8.29 |
| DNA replication licensing factor MCM6 | 2 | 5 | 6.63 |
| DNA replication licensing factor MCM5 | 0 | 7 | 7.39 |
| DNA replication licensing factor MCM4 | 1 | 4 | 4.59 |
| heterogeneous nuclear ribonuclearprotein U* | 2 | 10 | 2.58 |
| heterogeneous nuclear ribonuclearprotein K* | 3 | 9 | 19.96 |
| heterogeneous nuclear ribonuclearprotein A1* | 1 | 3 | 16.06 |
| heterogeneous nuclear ribonuclearprotein C1/C2 | 1 | 3 | 7.23 |
| RuvBL1/2 | 0 | 5 | 7.99 |
| Nucleolin* | 1 | 9 | 14.69 |
| alpha actin* | 1 | 7 | 8.84 |
| Elongation factor 2 | 1 | 4 | 5.64 |
| Elongation factor 1 alpha | 1 | 4 | 10.88 |
| Polyadenylate-binding protein *1 | 1 | 2 | 5.47 |
| Serine hydroxymethyltransferase (Shmt2) | 0 | 3 | 5.67 |
| ATP-dependent RNA helicase Ddx39 | 0 | 2 | 4.4 |
| Actin-like protein 6A | 0 | 2 | 7.14 |
| DNA methyltransferase 1 | 0 | 4 | 0.79 |
| Peroxiredoxin 1 | 4 | 9 | 24.36 |
| Splicing factor 3B, subunit 3* | 1 | 9 | 5.65 |
| Cell division control protein 2 homolog | 0 | 8 | 6.25 |
| E3 ubiquitin-protein ligase NEDD4-like | 0 | 7 | 2.83 |
| Smc3 | 0 | 5 | 2.02 |
| Serine/threonine-protein phosphatase 2A | 1 | 4 | 5.91 |
| Triosephosphate isomerase | 1 | 5 | 11.56 |
| ATPase WRNIP1 | 1 | 3 | 2.51 |

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| | | | |
|--|---|---|-------|
| Delta-1-pyrroline-5-carboxylate synthase | 0 | 6 | 4.98 |
| Structural maintenance of chromosomes 1A | 0 | 4 | 1.82 |
| Alanyl-tRNA synthetase | 0 | 5 | 2.09 |
| Cell division cycle 5-related protein | 0 | 4 | 4.49 |
| Malate dehydrogenase | 0 | 6 | 8.21 |
| Heterogeneous nuclear ribonucleoprotein A3* | 1 | 6 | 12.51 |
| DNA topoisomerase 2-alpha | 1 | 3 | 1.45 |
| Histone deacetylase 6 | 0 | 3 | 1.53 |
| AP-2 complex subunit beta | 1 | 3 | 1.32 |
| Adenosylhomocysteinase | 0 | 4 | 5.92 |
| Sister chromatid cohesion protein PDS5 homolog | 0 | 3 | 1.08 |
| U4/U6.U5 tri-snRNP-associated protei | 0 | 3 | 1.74 |
| Thymopoietin | 0 | 2 | 3.58 |
| Epb4.113 protein | 0 | 3 | 2.24 |
| Probable ATP-dependent RNA helicase DDX46 | 0 | 2 | 1.9 |
| C-terminal-binding protein 1 | 0 | 2 | 2.72 |
| Ubiquitin carboxyl-terminal hydrolase 7 | 0 | 2 | 0.6 |
| Centrosomal protein of 170 kDa | 0 | 2 | 0.61 |
| Histone acetyltransferase MYST2 | 0 | 2 | 1.66 |
| NSFL1 cofactor p47 | 0 | 2 | 3.08 |
| Insulin-like growth factor 2 receptor | 0 | 1 | 0.27 |
| Serrate RNA effector molecule homolog | 0 | 2 | 3 |

* Indicates proteins found within the CRAPome
 (Mellacheruvu et al., 2013 Nature Methods)