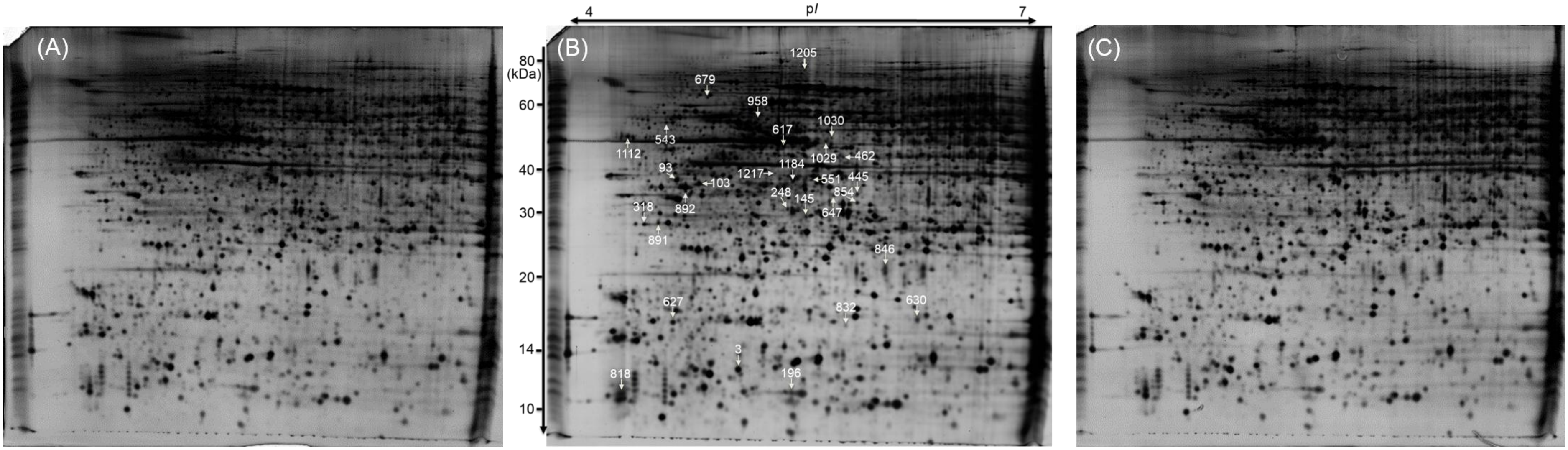

Supplementary Figure 1:

A representative silver stained 2-DE gel image of total proteins extracted from hESCs in absence of ROCKi (A), hESCs treated with soluble ROCKi (B), and immobilized ROCKi (C). Differentially accumulated proteins are shown in gel image of soluble ROCKi treated cells using arrows and numbers which refer to spot IDs as shown in table 1.

Supplementary table 1: Differentially expressed proteins in hESCs upon addition of Y-23632 (ROCKi) to the culture medium (Soluble ROCKI, S), to matrigel substratum (Immobilized ROCKi, I), and in the absence of ROCKi (Control, C).

Spot ID[1]	Protein name	Accession No[2]	% Cov./ Scor[3]	PMF/MS-MS[4]	Sequences of matched peptide
958	Tubulin, beta	P07437	31/92	11/3	K.TAVCDIPPR.G R.YLTVAAVFR.G K.DMMAACDPR.H K.IREEYPDR.I R.FPGQLNADLR.K K.LAVNMVPFPR.L R.ISEQFTAMFR.R R.AILVDLEPGTMDSVR.S R.LHFFMPGFAPLTSR.G K.GHYTEGAELVDSVLDVVR.K R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
93	Tropomyosin alpha-1 chain	P09493	32/447	12/8	K.YEEVARK.L K.HIAEDADR.K K.LDKENALDR.A K.LVIIESDLER.A K.EDRYEEEIK.V R.IQLVEEELDR.A R.KLVIIESDLER.A K.ATDAEADVASLNR.R R.RIQLVEEELDR.A K.KATDAEADVASLNR.R K.ENALDRAEQAEADK.K K.GTEDELDKYSEALK.D
892	Tropomyosin 1 alpha variant 6	B7Z596	33/135	12/4	K.SIDDLEGK.I K.YEEVARK.L R.QLEEQLR.I K.HIAEDADR.K R.AELSEGQVR.Q -.MAGSSSLEAVR.R K.LVIIESDLER.A K.EDRYEEEIK.V R.IQLVEEELDR.A R.KLVIIESDLER.A R.RIQLVEEELDR.A

					K.MEIQEIQLKEAK.H + Oxidation (M)
551	F-actin capping protein alpha-1 subunit	P52907	25/187	5/3	K.FITHAPPGEFNEVFNDVR.L K.IEGYEDQVLITEHGDLGNSR.F K.ISFK.F R.LLLNNDNLLR.E K.DVQDSLTVSNEAQTAK.E
832	Transgelin 2	P37802	35/92	8/2	R.GPAYGLSR.E K.DVGRPQPGR.E R.ENFQNWLK.D R.KDVGRPQPGR.E R.TLMNLGGLAVAR.D R.DDGLFSGDPNWFPK.K K.QMEQISQFLQAAER.Y R.TLMNLGGLAVARDDGLFSGDPNWFPK.K + Oxidation (M)
318	Eukaryotic translation initiation factor 6	P56537	57/610	6/2	R.ASFENNCEIGCFAK.L K.LNEAQPSTIATSMR.D K.VEVFR.Q R.NSLPDTVQIR.R R.MCVGNR.H K.VEVFR.Q
1184	Keratin 10	P13645	30/283	19/5	R.LAADDFR.L K.SEITELR.R K.YENEVALR.Q K.IKEWYEK.H K.VTMQNLNDR.L K.DAEAWFNEK.S K.HGNSHQGEPR.D R.QSVEADINGLR.R R.LKYENEVALR.Q K.NHEEEMKDLR.N K.NHEEEMKDLR.N + Oxidation (M) R.QSVEADINGLRR.V R.SQYEQLAEQNR.K K.QSLEASLAETEGR.Y K.IRLENEIQTYR.S R.SQYEQLAEQNRK.D R.SGGGGGGGGCGGGGGVSSLR.I K.GSLGGGFSSGGFSGGSFSR.G K.NQILNLTTDNANILLQIDNAR.L
1217	Keratin 10	P13645	38/273	21/3	R.LAADDFR.L

					K.SEITELR.R K.YENEVALR.Q K.IKEWYEK.H -.MSVRYSSSK.H + Oxidation (M) K.VTMQNLNDR.L K.DAEAWFNEK.S K.HGNSHQGEPR.D R.QSVEADINGLR.R R.LKYENEVALR.Q R.SLLEGEGSSGGGGR.G K.NHEEEMKDLR.N + Oxidation (M) R.QSVEADINGLRR.V R.SQYEQLAEQNR.K K.QSLEASLAETEGR.Y K.IRLENEIQTYR.S R.SQYEQLAEQNRK.D K.GSLGGGFSSGGFSGGSFSR.G R.NVQALEIELQSQLALK.Q K.NQILNLTTDNANILLQIDNAR.L R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S
1205	Keratin 10	P13645	38/284	21/5	R.LAADDFR.L K.SEITELR.R K.YENEVALR.Q K.IKEWYEK.H -.MSVRYSSSK.H + Oxidation (M) K.VTMQNLNDR.L K.DAEAWFNEK.S K.HGNSHQGEPR.D R.QSVEADINGLR.R R.LKYENEVALR.Q R.SLLEGEGSSGGGGR.G K.NHEEEMKDLR.N + Oxidation (M) R.QSVEADINGLRR.V R.SQYEQLAEQNR.K K.QSLEASLAETEGR.Y K.IRLENEIQTYR.S R.SQYEQLAEQNRK.D K.GSLGGGFSSGGFSGGSFSR.G R.NVQALEIELQSQLALK.Q K.NQILNLTTDNANILLQIDNAR.L R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S
196	Keratin 10	P13645	32/155	18/3	R.LAADDFR.L

					K.YENEVALR.Q K.IKEWYEK.H K.VTMQNLNDR.L K.DAEAWFNEK.S K.HGNSHQGEPR.D R.QSVEADINGLR.R R.LKYENEVALR.Q R.YSSSKHYSSSR.S K.NHEEEMKDLR.N + Oxidation (M) R.QSVEADINGLRR.V R.SQYEQLAEQNR.K K.QSLEASLAETEGR.Y K.IRLENEIQTYR.S R.SQYEQLAEQNRK.D K.GSLGGGFSSGGFSGGSFSR.G K.NQILNLTTDNANILLQIDNAR.L R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S
617	Keratin, type I cytoskeletal 19	P08727	61/275	26/3	R.LAADDFR.T R.FGPGVAFR.A R.QNQEYQR.L K.FETEQALR.M R.APSIHGGSGGR.G K.IRDWYQK.Q R.VLDELTLAR.T R.IVLQIDNAR.L K.ILGATIENSR.I K.DAEAWFTSR.T K.LTMQNLNDR.L R.LEQEIATYR.S R.MSVEADINGLR.R R.KDAEAWFTSR.T R.TKFETEQALR.M K.NHEEEISTLR.G R.TDLEMQIEGLK.E R.SQYEVMAEQNR.K K.SRLEQEIATYR.S K.AALEDTLAETEAR.F R.EVAGHTEQLQMSR.S R.QSSATSSFGGLGGGSVR.F R.DYSHYYTTIQDLR.D R.SLLEGQEDHYNNLSASK.V

					R.GQVGGQVSVEVDSAPGTDLAK.I R.VLDELTLARTDLEMQIEGLK.E + Oxidation (M)
891	14-3-3 protein zeta/delta	P63104	40/467	12/6	K.NELVQK.A R.YDDMAACMK.S+ Oxidation (M) R.NLLSVAYK.N K.FLIPNASQAESK.V R.YLAEVAAGDDK.K K.EMQPTHPIR.L+ Oxidation (M) K.ACSLAK.T K.DSTLIMQLLR.D+ Oxidation (M) R.EYR.E K.VFYLK.M R.DICNDVLSLLEK.F R.SSWR.V
647	Toll interacting protein	Q9H0E2	34/151	8/2	R.GPVYIGELPQDFLR.I R.ITPTQQQR.Q K.NYGMTR.M+ Oxidation (M) R.LR.L K.VIHCTVPPGVDSFYLEIFDER.A R.IAWTHITIPESLR.Q K.VEDK.W R.SVLEAQR.G
1030	ILF3 protein	Q12906	25/73	7/3	R.VPTWGPLR.G K.CLAALASLR.H K.EATDAIGHLDR.Q R.EDITQSAQHALR.L K.SIGTANRPMGAGEALR.R K.EPPLSLTIHLTSPVVR.E K.VLAGETLSVNDPPDVLDR.Q
1029	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1, SMARCB1, (Ini1)	Q12824	37/158	11/2	R.YPSLWR.R R.YPSLWRR.L R.GQLSWHQK.T K.AVSISTEPPTYLR.E K.TYAFSENPLPTVEIAIR.N R.QQIESYPTDSILEDQSDQR.V K.FQLEDDGEFYMIGSEVGNYLR.M R.NSQWVPTLSNSSHHLDAVPCSTTINR.N K.FQLEDDGEFYMIGSEVGNYLRMFR.G + Oxidation (M) K.RNSQWVPTLSNSSHHLDAVPCSTTINR.N R.TFPLCFDDHDPAVIHENASQPEVLVPIR.L

627	Dpy-30-like protein	Q9C005	34/177	4/3	K.AQFEDRN.- K.VDLQSLPTR.A K.QKVDLQSLPTR.A K.ERPPNPIEFLASYLLK.N
1112	Calumenin	O43852	47/333	5/2	R.QFLMCLSLCTAFALSK.P+ Oxidation (M) R.VHHEPQLSDK.V K.VHNDAQSFDYDHDAFLGAEEAK.T K.IVSK.I K.DIVVQETMEDIDK.N+ Oxidation (M)s
679	Ubiquilin 1 isoform 2	Q9UMX0	19/121	11/3	R.NPAMMQEMMR.N R.NPAMMQEMMR.N + Oxidation (M) R.ALSNLESIPGGYNALR.R R.NPEISHMLNNPDIMR.Q R.NPEISHMLNNPDIMR.Q + Oxidation (M) R.QLIMANPQMQQLIQR.N R.QLIMANPQMQQLIQR.N + Oxidation (M) R.FQQQLEQLSAMGFLNR.E R.FQQQLEQLSAMGFLNR.E + Oxidation (M) K.EKEEFAVPENSSVQQFK.E R.EANLQALIATGGDINAAIER.L
248	Cathepsin D preproprotein	P07339	34/101	7/2	R.YYTVFDR.D K.LSPEDYTLK.V K.FDGILGMAYPR.I K.FDGILGMAYPR.I + Oxidation (M) K.LVDQNIFSFYLSR.D K.AYWQVHLDQVEVASGLTLCK.E K.EGCEAIVDTGTSLMVGPVDEVR.E
846	Dipeptidyl peptidase 1	B4DJQ8	33/183	10/3	K.MKEDCFR.Y K.MKEDCFR.Y + Oxidation (M) R.NVHGINFVSPVR.N R.DVNCSVMGPQEK.K + Oxidation (M) K.ILHLPTSWDWR.N R.NQASCGSCYSFASMGMLEAR.I K.VTTYCNETMTGWVHDVLGR.N R.YYSSEYHYVGGFYGGCNEALMK.L K.YAQDFGLVEEACFPYTGTDSPCK.M K.LELVHHGPMAVAFEVYDDFLHYK.K
854	Proteasome activator subunit 3	P61290	50/437	15/8	R.LIISELR.N K.LKVDSFR.E K.YPHVEDYR.R K.MWVQLLIPR.I

					K.MWVQLLIPR.I + Oxidation (M) K.KLLELDSFLK.E K.YPHVEDYRR.T K.SNQQLVDIIEK.V R.LDECEEAFQGTK.V R.NQYVTLHDMILK.N R.NQYVTLHDMILK.N + Oxidation (M) R.RLDECEEAFQGTK.V R.TVESEAASYLDQISR.Y R.ITSEAEDLVANFFPK.K R.IEDGNNFGVSIQEETVAELR.T
543	Proteasome 26S non-ATPase subunit 4	P55036	10/90	6/3	R.NGDFLPTR.L R.ILSK.L K.ITFCTGIR.V K.VNVDIINFGEEEVNTEK.L R.VSMEEQR.Q+ Oxidation (M) K.DGK.K
103	Charged multivesicular body protein 4b	Q9H444	48/290	9/4	R.AALQALKR.K K.QEFLEKK.I K.KIEQELTAAK.K K.GGPTPQEAIQR.L R.LRDTEEMLSK.K R.LRDTEEMLSK.K + Oxidation (M) K.QLAQIDGTLSTIEFQR.E R.EALENANTNTEVLKNMGYAAK.A + Oxidation (M) K.NLLEISGPETVPLPNVPSIALPSKPAK.K
145	Hexosaminidase B (beta polypeptide)	P07686	35/176	11/4	K.IQDFMR.Q K.IQDFMR.Q + Oxidation (M) K.CWESNPK.I R.DMDDAYDR.L K.KLESFYIQK.V K.DSAYPEELSR.V K.VEPLDFGGTQK.Q K.LAPGTIVEVWK.D K.GSIVWQEVFDDK.A K.EISEVFPDQFIHLGGDEVEFK.C K.QLFIGGEACLWGEYVDATNLTPR.L
630	Prefoldin subunit 2	Q9UHV9	56/183	10/3	K.ELNEFR.E R.LRQEQR.G R.MVGGVLVER.T R.MVGGVLVER.T + Oxidation (M)

					K.EVLPALENNK.E R.LMGEDEKPAAK.E K.IIETLTQQLQAK.G K.GAVSAEQVIAGFNR.L K.AAELEMELNEHSLVIDTLK.E K.AAELEMELNEHSLVIDTLK.E + Oxidation (M)
445	Dnaj homolog, subfamily C, member 9	Q8WXX5	53/357	12/6	R.RFQILGK.V K.QAYLDFK.G K.VYSVLSDR.E R.EASDGEVRR.G R.DWEAYWR.L K.VSLQVHPDR.V R.VGEGDKEDATR.R K.ISLEDIQAFEK.T K.EMDNFLAQMEAK.Y M.GLLDLCEEVFGTADLYR.V R.AVYDEQGTVDEDSPVLTQDR.D K.GDMDQIMESVLCVQYTEEPR.I
3	Galectin-1	P09382	78/322	9/3	K.SFVLNLGK.D K.LPDGYEFK.F R.VRGEVAPDAK.S K.DGGAWGTEQR.E K.DSNNLCLHFNPR.F R.FNAHGDANTIVCNSK.D R.LNLEAINYMAADGDFK.I R.LNLEAINYMAADGDFK.I + Oxidation (M) R.EAVFPFQPGSVAEVCITFDQANLTVK.L
818	Chain a of human saposin b	1N69_A	37/79	2/1	R.LGPGMADICK.N M.DGDVCQDCIQMVTDIQTAVR.T
462	MYG1 protein precursor	Q9HB07	46/204	13/5	R.YDHHQR.S K.EPHSFQSR.L R.LPLPEPWR.G R.YALTTTLSAR.V R.ALVEEALAQR.F R.AMDLVQEEFLQR.L R.LDFYQHSWLPAR.A K.LSSAGLIYLHFGHK.L K.LASCDIVVDVGGEYDPR.R R.LNPTWNHPDQDTEAGFK.R R.IGTHNGTFHCDEALACALLR.L K.LMAPPRIGTHNGTFHCDEALACALLR.L

					R.DEALDQVSGIPGCIFVHASGFIGGHHTREGALSMAR.A + Oxidation (M)

[1]The numbering corresponds to the 2-DE gel; [2]Accession number in Uni-Prot; [3]Percent coverage and MASCOT score resulted from combined MS-MS/MS search; [4]Number of peptide identified by PMF and MS/MS.