Sample	f1*	f2*	Sample	f1*	f2*
HDFa_I	58718762	58718762	MPS3D_I	49250436	49250436
HDFa_II	47756883	47756883	MPS3D_II	54197694	54197694
HDFa_III	54168450	54168450	MPS3D_III	52067506	52067506
HDFa_IV	41614258	41614258	MPS3D_IV	56947314	56947314
MPS1_I	45793517	45793517	MPS4A_I	55486056	55486056
MPS1_II	52769993	52769993	MPS4A_II	53613161	53613161
MPS1_III	57129332	57129332	MPS4A_III	52384107	52384107
MPS1_IV	49847130	49847130	MPS4A_IV	51577667	51577667
MPS2_I	57537368	57537368	MPS4B_I	53972180	53972180
MPS2_II	40457828	40457828	MPS4B_II	45196042	45196042
MPS2_III	48051766	48051766	MPS4B_III	49530863	49530863
MPS2_IV	52908488	52908488	MPS4B_IV	50709120	50709120
MPS3A_I	52050375	52050375	MPS6_I	58345020	58345020
MPS3A_II	61670273	61670273	MPS6_II	60052676	60052676
MPS3A_III	43882338	43882338	MPS6_III	50965223	50965223
MPS3A_IV	50595389	50595389	MPS6_IV	44087469	44087469
MPS3B_I	54088730	54088730	MPS7_I	44555814	44555814
MPS3B_II	43987340	43987340	MPS7_II	47253718	47253718
MPS3B_III	60018865	60018865	MPS7_III	55918102	55918102
MPS3B_IV	44837985	44837985	MPS7_IV	46516804	46516804
MPS3C_I	59767727	59767727	MPS9_I	60501009	60501009
MPS3C_II	43732902	43732902	MPS9_II	43414644	43414644
MPS3C_III	53819135	53819135	MPS9_III	49440837	49440837
MPS3C_IV	47165191	47165191	MPS9_IV	45087234	45087234

Table S1. Number of reads in RNA-seq analysis. MPS types are indicated by Arabic numbers.

f1. f2 - number of reads from one and the other end

Cell death Cell cycle process 80 80 No. of transcripts No. of transcripts 60 60 40 40 20 20 0 0 I Π IIIA IIIB IIIC IIID IVA IVB VI VII IX Ι Π IIIA IIIB IIIC IIID IVA IVB VI VII IX up-regulated down-regulated up-regulated down-regulated Secretion by cell Cell activation 60 60 No. of transcripts 50 No. of transcripts 50 40 40 30 30 20 20 10 10 0 0 I II IIIA IIIB IIIC IIID IVA IVB VI VII IX I Π IIIA IIIB IIIC IIID IVA IVB VI VII IX down-regulated up-regulated up-regulated down-regulated Actin filament-based process Multi-organism cellular process 40 40 No. of transcripts No. of transcripts 30 30 20 20 10 10 0 0 I II IIIA IIIB IIIC IIID IVA IVB VI VII IX I Π IIIA IIIB IIIC IIID IVA IVB VI VII IX down-regulated down-regulated up-regulated up-regulated Cellular homeostasis Cell division 30 30 No. Of transcripts 25 25 No. of transcripts 20 20 15 15 10 10 5 5 0 0 I Π IIIA IIIB IIIC IIID IVA IVB VI VII IX I Π IIIA IIIB IIIC IIID IVA IVB VI VII IX up-regulated down-regulated up-regulated down-regulated

**Figure S1.** Number of up (red)- and down (blue)-regulated transcripts with division into various cellular processes (not included in Figure 2) in different MPS types relative to control cells (HDFa)

















**Figure S2.** Heat maps indicating transcripts of genes which products are involved in various cellular processes and which expression is significantly changed in different MPS types relative to control HDFa line (S2-1 to S2-49 for particular processes, with FDR<0.1 in panels A, FDR<10<sup>-6</sup> in panels B, if relevant, and number of the changed transcripts in panels B or C). Because of the complexity of panels, and indication of numbers of biological repetitions (Roman numbers), names of MPS types are indicated atypically by Arabic numbers.





C

Transcripts in Cell Cycle		Significant changes in particular MPS type vs HDFa line													
Checkpoint process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX				
Up-regulated (FDR<0.1)	0	0	2	0	1	1	0	2	1	1	2				
Up-regulated (FDR<0.000001)	0	0	1	0	0	0	0	0	0	0	1				
Down-regulated (FDR<0.1)	11	1	3	6	4	16	2	2	1	10	15				
Down-regulated (FDR<0.000001)	0	0	0	1	0	0	0	0	0	0	1				



## В

Transcripts in <b>Septum</b>	Significant changes in particular MPS type vs HDFa line													
digestion after cytokinesis process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			
Down-regulated (FDR<0.1)	0	0	0	2	0	0	0	0	0	0	0			
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			



Transcripts in	Significant changes in particular MPS type vs HDFa line													
process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	18	16	19	33	24	16	8	29	8	25	22			
Up-regulated (FDR<0.000001)	7	5	8	9	9	7	3	10	4	9	9			
Down-regulated (FDR<0.1)	35	11	38	27	32	18	10	47	11	20	31			
Down-regulated (FDR<0.000001)	6	1	6	6	4	5	2	8	0	5	6			



C

Transcripts in		Significant changes in particular MPS type vs HDFa line														
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX					
Up-regulated (FDR<0.1)	4	3	3	6	2	3	1	4	1	4	2					
Up-regulated (FDR<0.000001)	2	2	0	3	1	0	0	3	1	2	2					
Down-regulated (FDR<0.1)	12	5	12	8	10	4	3	11	4	5	9					
Down-regulated (FDR<0.000001)	1	1	2	0	1	0	0	1	1	1	0					



Transcripts in	Significant changes in particular MPS type vs HDFa line														
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX				
Up-regulated (FDR<0.1)	0	0	0	2	0	0	0	0	1	0	0				
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0				
Down-regulated (FDR<0.1)	5	3	7	2	2	1	3	5	3	6	б				
Down-regulated (FDR<0.000001)	3	1	2	1	1	0	1	3	0	3	3				

#### A GO:0006928 movement of cell or subcellular component







ENST00000262498

ENST00000337273

ENST00000296511

ENST00000342988

113 ENST00000375571

141 ENST00000229758

169 ENST00000356142

197 ENST00000264021

225 ENST00000275364

253 ENST00000263895

281 ENST00000395598

309 ENST00000254722

337 ENST00000336689

365 ENST00000562924

393 ENST00000422544

421 ENST00000412232

449 ENST00000357681

477 ENST00000397033

505 ENST00000344697

533 ENST00000419235

561 ENST00000319653

589 ENST00000425280

617 ENST00000244050

645 ENST00000379359

673 ENST00000559488

701 ENST00000552692

729 ENST00000374259

757 ENST00000369124

785 ENST00000316409

813 ENST00000230538

841 ENST00000372874

29

57

85

CFAP20

TNPO1

ANXA5

SMAD4

MAPRE1

FBXO5

RAC1

IFT46

GNA12

RND3

RABL2B

ASAP3

PDGFC

ADGRA2

ATP2B4

DUSP22

FMN2

LDB1

SNAI1

RGCC

ITGB3

CD63

FOXO4

PLEKHO1

FAM89B

Ι ΔΜΔ4

ADA

POMGNT2

ITGA4

NPTN

SERPINF1



MPS1 MPS2 MPS3A MPS3B MPS3C MPS3D MPS4A MPS4B MPS6 MPS7 MPS9 heatmap color key transcript biotype protein\_coding

Transcripts in <b>Movement of cel</b>	Significant changes in particular MPS type vs HDFa line												
or subcellular component process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	46	22	52	51	46	37	12	50	19	54	51		
Up-regulated (FDR<0.000001)	16	8	19	18	11	16	5	17	8	13	19		
Down-regulated (FDR<0.1)	35	9	43	49	46	21	20	57	17	40	41		
Down-regulated (FDR<0.000001)	10	4	12	12	12	9	4	10	5	13	10		



#### В

Transcripts in <b>Syncytium</b>	Significant changes in particular MPS type vs HDFa line													
formation process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	0	0	0	3	0	1	1	0	0	0			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			
Down-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	1	0			
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			



A

## GO:0007017 microtubule-based process



1	ENST00000418115	RHOA
14	ENST00000336083	RAB6A
27	ENST00000327761	RASSF1
40	ENST00000238497	VPS4B
53	ENST00000257430	APC
66	ENST00000327892	TUBB
79	ENST00000282058	HAUS1
92	ENST00000563694	CNTROB
105	ENST00000377818	MZT1
118	ENST00000301633	BIRC5
131	ENST00000397066	CCNF
144	ENST00000587309	KIF18B
157	ENST00000300403	TPX2
170	ENST00000330137	SKA2
183	ENST00000356142	RAC1
196	ENST00000519449	RNF19A
209	ENST00000260746	ARL3
222	ENST00000409197	DYNC1I2
235	ENST00000553286	KLC1
248	ENST00000408948	MARK2
261	ENST00000252050	CUL9
274	ENST00000325542	CEP57
287	ENST00000319653	FMN2
300	ENST00000527446	RPS3
313	ENST00000251412	TUBG2
326	ENST00000266254	TTLL1
339	ENST00000373151	MAP7D1
352	ENST00000370223	LZTS2
365	ENST00000591463	TUBB6
378	ENST00000245925	EML2

biotype



Hdfa\_I Hdfa\_I MPS1\_I MPS1\_I MPS1\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS3\_I MP





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- 2	-	

Transcripts in Microtubule-	Significant changes in particular MPS type vs HDFa line												
based process process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	5	4	14	8	8	12	3	12	4	10	12		
Up-regulated (FDR<0.000001)	1	0	4	2	0	2	1	2	0	0	4		
Down-regulated (FDR<0.1)	9	2	12	13	7	10	5	17	2	11	19		
Down-regulated (FDR<0.000001)	2	1	2	2	3	2	1	1	0	1	1		

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Fig. S2-9
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ENST0000012443 1 PPP5C ENST00000349556 FGFR10P 36 NUP62 71 ENST00000597029 106 ENST00000489288 RHNO1 141 ENST0000394818 INCENF 176 ENST00000352433 PTTG1 211 ENST0000350030 NASP 246 ENST00000303887 MCM7 281 ENST00000338193 PRIM1 316 ENST00000299130 BCCIP 351 ENST0000394287 MED1 386 ENST00000275034 PHIP 421 ENST0000368277 PMF1 456 ENST0000246166 FNTB 491 ENST0000261574 IPO5 526 ENST00000283109 RIOK2 561 ENST00000265678 RPS6KA2 596 ENST00000234296 ORC2 631 ENST00000394464 NR3C1 666 ENST00000373493 RBBP4 701 ENST00000369014 ENSA 736 ENST00000375213 МАРЗК20 771 ENST0000302182 UBB 806 ENST00000261692 CDK2AP1 841 ENST00000439235 CHD3 876 ENST00000265992 CCNI 911 ENST0000262891 MARK4 946 ENST00000375664 WAC 981 ENST00000368223 NES 1016ENST00000396290 ID2 1051ENST00000381410 SNX18

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17

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24

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biotype



ENST00000371222 JUN ENST00000397088 GPER 1 ENST00000502704 KIF13A group ENST00000407439 MRE11 Hdfa ENST00000378578 DYNLT3 MPS1 ENST00000618072 CDK2AP1 MPS2 ENST00000265339 UBE2B MPS3A ENST00000592299 SPHK1 ENST00000358208 MPS3B SRC ENST00000331129 ID2 MPS3C 11 ENST0000272164 WNT9A MPS3D ENST00000534313 SIPA1 MPS4A RPS6KA2 ENST00000265678 MPS4B ENST00000380122 TXLNG MPS6 15 ENST0000397624 MEIS2 MPS7 16 ENST0000373647 RABGAP1 MPS9 ENST00000522111 TRNP1 18 ENST00000394166 NR2F2 heatmap color key 19 ENST00000421109 NR2F2 4 20 ENST0000356208 RBM38 2 21 ENST00000220772 SFRP1 0 ENST00000423777 ATF5 -2 23 ENST00000585809 WDR18 ANAPC13 ENST00000354910 -4 ENST00000268613 CDH13 transcript biotype 26 ENST00000294304 LRP5 protein\_coding 27 ENST0000355680 PRMT2 28 ENST0000307407 CXCL8 29 ENST00000425032 USP8

~	Hdfa_I Hdfa_II Hdfa_III Hdfa_IIV MPS1_I MPS1_II	MPS1_III MPS1_IV MPS2_I	MPS2_III MPS2_IV MPS3A_I	MPS3A_II MPS3A_III MPS3A_IV	MPS3B_II MPS3B_II	MPS3B_IV MPS3C_I MPS3C_II	MPS3C_III MPS3C_IV MPS3D_I	MPS3D_II MPS3D_III MPS3D_IV	MPS4A I MPS4A II	MPS4A_III MPS4A_IV MPS4A_IV	MPS4B II MPS4B III	MPS4B_IV MPS6_I	MPS6_II MPS6_III MPS6_IV	MPS7_I MPS7_II	MPS7_III MPS7_IV	MPS9_I	MPS9_III MPS9_IV
(																	

Transcripts in			Sigr	nificant ch	anges in p	particular	MPS type	vs HDFa	line		
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	11	13	21	22	29	20	13	33	12	26	24
Up-regulated (FDR<0.000001)	0	2	3	5	4	4	4	5	3	3	5
Down-regulated (FDR<0.1)	41	10	40	33	30	79	12	32	8	53	83
Down-regulated (FDR<0.000001)	4	0	4	3	3	4	2	3	0	5	4





Transcripts in <b>Chromosome</b>			Sigr	nificant ch	anges in p	oarticular	MPS type	vs HDFa	line		
segregation process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	0	1	2	1	1	1	0	2	0	0	0
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0
Down-regulated (FDR<0.1)	2	2	2	4	6	11	1	2	0	6	12
Down-regulated (FDR<0.000001)	0	0	1	1	1	0	1	0	0	0	1



Transcripts in Cell			Sign	ificant ch	anges in J	oarticular	MPS type	vs HDFa	line		
Communication process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	98	59	120	135	102	100	34	139	50	119	127
Up-regulated (FDR<0.000001)	36	20	42	40	33	35	12	44	21	30	42
Down-regulated (FDR<0.1)	113	37	146	111	103	78	42	137	41	115	113
Down-regulated (FDR<0.000001)	20	13	26	23	22	14	9	28	10	26	18

Fig. S2-12 GO:0007163 establishment or maintenance of cell polarity



of cel polarity process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	4	1	7	1	5	3	1	5	1	3	3
Up-regulated (FDR<0.000001)	1	0	1	1	1	1	0	2	0	0	1
Down-regulated (FDR<0.1)	2	4	5	2	1	1	3	3	3	2	1
Down-regulated (FDR<0.000001)	1	1	1	1	0	0	1	0	2	2	1

#### Fig. S2-13 GO:0007165 signal transduction A



1	ENST00000375859	SPIN1
78	ENST00000585892	DNM2
155	ENST00000370508	GOT1
232	ENST00000243344	TTC21B
309	ENST00000405154	RASSF8
386	ENST00000318672	SLC38A9
463	ENST00000442253	PAQR8
540	ENST00000261797	NDST1
617	ENST00000526838	EEF1D
694	ENST00000481195	PPP2CA
771	ENST00000375370	TFDP1
848	ENST00000316626	GSK3B
925	ENST00000453744	UBE2D3
1002	2ENST00000576544	ACTG1
1079	9ENST00000458549	TMEM64
1156	5ENST00000376547	STK24
1233	3ENST00000222345	SIPA1L3
1310	DENST00000370971	WLS
1387	7ENST00000264245	ARHGAP31
1464	\$ENST00000268613	CDH13
1541	LENST00000371621	PTPN1
1618	3ENST00000413052	MOV10
1695	5ENST00000591349	GIPC1
1772	2ENST00000263734	EPAS1
1849	9ENST00000274311	PELO
1926	5ENST00000235382	RGS2
2003	3ENST00000373203	ENG
2080	DENST00000370113	EXTL2
2157	7ENST00000260130	SDCBP
2234	\$ENST00000253814	NDFIP1





SGK1



#### Hdfa\_I Hdfa\_I Hdfa\_I Hdfa\_I MPS1\_I MPS1\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS2\_I MPS3\_I MP biotype

Transcripts in Signal			Sign	nificant ch	anges in p	oarticular	MPS type	vs HDFa	line		
transduction process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	92	58	110	132	98	95	34	134	47	116	125
Up-regulated (FDR<0.000001)	33	20	38	37	32	32	12	42	19	29	41
Down-regulated (FDR<0.1)	112	33	141	108	101	74	43	133	43	112	110
Down-regulated (FDR<0.000001)	20	10	27	23	21	15	9	26	10	25	18



of neurons process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	1	4	б	7	4	4	2	8	2	3	4
Up-regulated (FDR<0.000001)	1	2	1	2	2	1	1	2	2	1	2
Down-regulated (FDR<0.1)	0	0	0	1	2	0	0	0	0	1	1
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0





Transcripts in <b>Cell recogniton</b>			Sigr	nificant ch	anges in p	particular	MPS type	vs HDFa	line		
process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	3	2	5	3	4	2	2	5	0	3	3
Up-regulated (FDR<0.000001)	3	2	3	2	2	2	2	2	0	2	2
Down-regulated (FDR<0.1)	3	1	0	1	3	2	1	1	3	3	3
Down-regulated (FDR<0.000001)	0	0	0	0	1	1	0	0	1	1	1





Transcripts in <b>Cell death</b>			Sigr	nificant ch	anges in p	oarticular	MPS type	vs HDFa	line		
process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	30	19	35	41	33	34	7	46	20	35	36
Up-regulated (FDR<0.000001)	7	6	12	10	7	6	3	9	6	8	9
Down-regulated (FDR<0.1)	47	15	58	45	43	39	19	63	14	52	47
Down-regulated (FDR<0.000001)	8	4	11	11	11	6	3	15	3	9	5

A

#### GO:0016043 cellular component organization



Transcripts in Cellular			Sigr	nificant ch	anges in p	oarticular	MPS type	vs HDFa	line		
component organisation process	Ι	ΙΙ	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	101	64	126	134	122	99	50	154	62	121	126
Up-regulated (FDR<0.000001)	28	19	36	35	27	26	13	40	26	29	37
Down-regulated (FDR<0.1)	123	41	161	132	111	120	48	138	40	136	172
Down-regulated (FDR<0.000001)	25	12	27	28	21	15	8	28	7	28	26





Transcripts in			Sigr	nificant ch	anges in p	particular	MPS type	vs HDFa	line		
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	7	2	14	15	14	7	4	11	6	10	14
Up-regulated (FDR<0.000001)	3	1	б	4	3	4	1	5	2	2	6
Down-regulated (FDR<0.1)	11	0	9	10	11	9	4	8	2	7	9
Down-regulated (FDR<0.000001)	4	0	4	6	4	4	2	4	0	3	4

Fig. S2-19



Transcripts in			Sigr	nificant ch	anges in J	particular	MPS type	vs HDFa	line		
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	2	1	2	3	4	2	0	4	0	3	4
Up-regulated (FDR<0.000001)	1	0	0	0	0	0	0	0	0	0	0
Down-regulated (FDR<0.1)	6	2	8	7	2	8	3	3	1	4	8
Down-regulated (FDR<0.000001)	0	0	1	0	1	0	1	0	0	1	0



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	Tropco

Transcripts in Cellular	Significant changes in particular MPS type vs HDFa line												
homeostasis process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	9	3	13	17	11	7	3	18	3	14	10		
Up-regulated (FDR<0.000001)	4	1	б	6	5	4	2	6	1	4	4		
Down-regulated (FDR<0.1)	23	4	19	13	12	22	8	15	2	19	21		
Down-regulated (FDR<0.000001)	2	1	1	1	2	2	1	1	1	3	2		



Transcripts in	Significant changes in particular MPS type vs HDFa line												
Cytolysis process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.1)	1	0	1	1	1	1	0	1	0	1	1		
Down-regulated (FDR<0.000001)	1	0	1	1	1	1	0	1	0	1	1		



Transcripts in	Significant changes in particular MPS type vs HDFa line													
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	9	7	17	12	21	13	6	21	5	17	15			
Up-regulated (FDR<0.000001)	0	1	2	2	0	2	1	0	1	1	3			
Down-regulated (FDR<0.1)	33	8	29	21	24	65	8	23	4	36	69			
Down-regulated (FDR<0.000001)	4	0	3	2	2	3	2	1	0	3	2			



Transcripts in	Significant changes in particular MPS type vs HDFa line													
docking process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	1	0	1	1	0	0	0	2	1	1	1			
Up-regulated (FDR<0.000001)	1	0	1	1	0	0	0	1	0	1	1			
Down-regulated (FDR<0.1)	6	1	5	1	3	1	2	4	2	3	5			
Down-regulated (FDR<0.000001)	0	1	0	0	0	0	0	0	0	0	1			

### ${f A}$ 022412 cellular process involved in reproduction in multicellular organism











Transcripts involved in	Significant changes in particular MPS type vs HDFa line													
reproduction in multicellular organism	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	3	4	3	3	4	3	2	3	2	5	1			
Up-regulated (FDR<0.000001)	1	1	2	2	2	2	1	1	1	0	1			
Down-regulated (FDR<0.1)	3	0	4	4	3	3	1	3	1	4	4			
Down-regulated (FDR<0.000001)	0	0	1	0	1	1	1	0	0	1	0			

#### GO:0030029 actin filament-based process



Transcripts in	Significant changes in particular MPS type vs HDFa line												
based process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	23	13	27	29	21	18	17	30	12	34	18		
Up-regulated (FDR<0.000001)	8	4	8	7	4	4	5	5	7	10	5		
Down-regulated (FDR<0.1)	7	16	13	13	13	3	5	18	4	8	12		
Down-regulated (FDR<0.000001)	2	1	1	2	2	2	1	2	2	3	1		



## В

Transcripts in <b>Transposition</b>	Significant changes in particular MPS type vs HDFa line												
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		

A

Hdfa\_I Hdfa\_II Hdfa\_II Hdfa\_II MPS1\_I MPS1\_II MPS1\_IV MPS1\_IV MPS1\_IV

≡ ≥

MPS2 NPS2

 $\equiv >$ 

**MPS3A MPS3A APS3A**  MPS3B

=,=>

# GO:0032940 secretion by cell



=,≡,≥

=.≡≥

MP53B.II MP53B.II MP53B.II MP53B.II MP53C.II MP53C.II MP53C.II MP53D.II MP53D.II MP53D.II MP54A.IV MP5

Z 1	EN2100000201225	ENSA
41	ENST00000264158	RAB3GAP1
61	ENST0000008527	CRY1
81	ENST00000373053	MCU
101	ENST00000336787	RAB27A
121	ENST00000356415	RAP1A
141	ENST00000355624	RAB11FIP2
161	ENST00000361891	ILF2
181	ENST00000275036	HMGN3
201	ENST00000289228	ACTR1B
221	ENST00000333896	SPTBN1
241	ENST00000329138	HGS
261	ENST00000515007	LHFPL2
281	ENST00000398409	CST3
301	ENST00000447182	SDCBP
321	ENST00000353047	CTSB
341	ENST00000371579	DPP7
361	ENST00000399231	MYO5A
381	ENST00000307767	TVP23B
401	ENST00000398529	RAB1A
421	ENST00000330452	PRKCD
441	ENST00000262424	CRISPLD2
461	ENST00000354124	C1QTNF1
481	ENST00000216962	PYGB
501	ENST00000371095	GNAS
521	ENST00000278505	ENDOD1
541	ENST00000262301	LMF1
561	ENST00000375068	MAGED2
581	ENST00000393110	STEAP3

ENST00000528499 APLP2

ENICA







Transcripts in	Significant changes in particular MPS type vs HDFa line												
process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	25	20	24	36	20	18	10	30	9	27	23		
Up-regulated (FDR<0.000001)	8	5	12	15	9	9	2	12	3	9	12		
Down-regulated (FDR<0.1)	31	11	53	26	39	28	14	46	9	28	35		
Down-regulated (FDR<0.000001)	6	2	9	5	7	7	3	13	1	5	6		

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MPS6 MPS6 MPS6 MPS7 MPS7 MPS7 MPS7 MPS7

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MPS9\_II MPS9\_III MPS9\_IV

MPS9





- 7		
	ISC	гн

Cellular	Significant changes in particular MPS type vs HDFa line													
pigmentation process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	1	0	0	0	0	0	0	0	0	0			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			
Down-regulated (FDR<0.1)	3	0	2	4	1	1	2	4	2	2	2			
Down-regulated (FDR<0.000001)	1	0	0	2	0	1	0	1	0	1	0			

A GO:0035212 cell competition in a multicellular organism



В											
Transcripts in Cell competition in a			Sigr	nificant ch	anges in p	particular	MPS type	e vs HDFa	line		
organism process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0
Down-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0





Transcripts in <b>Phenotypic</b>	Significant changes in particular MPS type vs HDFa line												
switching process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.1)	2	0	0	2	1	0	0	1	0	2	0		
Down-regulated (FDR<0.000001)	1	0	0	1	1	0	0	1	0	1	0		





## В

Transcripts in <b>Protein</b>	Significant changes in particular MPS type vs HDFa line												
unfolding process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0		





Hdfa\_Ti Hdfa\_Ti Hdfa\_Ti MPS1\_1 MPS1\_1 MPS1\_1 MPS2\_1 MPS2\_1 MPS2\_2 MPS2\_2 MPS2\_1 MPS2\_1 MPS3\_2 MPS3\_2

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С

1	ENST00002583	341	LAMC1
10	ENST00003103	380	XXYLT1
19	ENST00003950	074	LPXN
28	ENST00002479	933	IDUA
37	ENST0000374	694	FZD8
46	ENST00002650	016	BST1
55	ENST0000009	180	CD9
64	ENST00003149	922	PENK
73	ENST00003792	221	DNAJC15
82	ENST00005462	260	SOD2
91	ENST0000397	624	MEIS2
100	ENST0000318	607	PABPC1
109	ENST0000334	696	ENTPD5
118	ENST00001894	444	NFKB2
127	ENST00003584	432	EPHA2
136	ENST0000307	771	ZRSR2
145	ENST00005334	410	RNH1
154	ENST0000268	695	GALNS
163	ENST0000394	636	IRX5
172	ENST0000321	153	RPLP2
181	ENST00003706	659	FKBP1C
190	ENST0000371	625	PTGDS
199	ENST0000397	088	GPER1
208	ENST0000370	620	ARHGEF6
217	ENST00002433	108	HOXC6
226	ENST00000550	765	FKBP11
235	ENST00000582	743	SLC16A3
244	ENST00002748	B13	MUT
253	ENST0000530	797	RPLP2
262	ENST0000370	783	MOSPD1

ENST00000375203

ATF6B

HSF1

SPRY2

LAMP2

ADH5

**ZNF706** 

MGAT1

ANKRD9

ZNF287

SMAD3

ZNF384

томм20

MTREX

PACS2

RAP2A

PPP6C

XRCC1

ARL6IP1

CHTF18

RECQL4

RPL15

TPCN1

RPS2

CSNK1E

ZNF354A

DKK3

SYNCRIP

SDHA

AES

TMEM129

ATP6V0E1

group

Hdfa

MPS1

MPS2

MPS3A

MPS3B

MPS3C

MPS3D

MPS4A

MPS4B

MPS6

MPS7

MPS9

2

0

-2

-4

heatmap color key

transcript biotype

non\_stop\_decay

protein\_coding

nonsense\_mediated\_decay



Transcripts in <b>Cellular</b>	Significant changes in particular MPS type vs HDFa line													
metabolic process	Ι	ΙΙ	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	132	96	148	185	148	126	61	205	74	158	179			
Up-regulated (FDR<0.000001)	37	30	43	50	37	34	16	50	20	39	52			
Down-regulated (FDR<0.1)	213	67	264	226	208	217	89	221	71	250	285			
Down-regulated (FDR<0.000001)	44	18	49	50	56	38	21	54	21	56	47			

biotype

A

#### GO:0044764 multi-organism cellular process



ENST0000221566 SGTA 1 HNRNPA1 16 ENST00000340913 ENST00000397239 DEK 31 46 ENST00000423485 TOP2A ENST00000295119 NUP35 61 76 ENST00000340648 RRP1B 91 ENST00000400000 VAPA 106 ENST00000371317 MCTS1 121 ENST00000537981 RTN3 136 ENST00000379965 TRIM22 RHOA 151 ENST00000418115 166 ENST00000468812 PPIA 181 ENST00000542575 SLC1A5 196 ENST00000374429 CXCL12 211 ENST0000315872 ROCK2 226 ENST00000284049 CHD1 241 ENST00000261017 ABI2 256 ENST00000371795 IFIT5 271 ENST0000358514 PSMB10 286 ENST00000354258 TAP1 301 ENST00000318524 NFX1 316 ENST00000376281 HNRNPK 331 ENST00000380629 BNIP3L 346 ENST00000426155 SNX3 361 ENST00000296181 ITGB5 376 ENST00000399808 **IFITM3** 391 ENST00000425762 PSMB5 406 ENST00000405442 EIF3D 421 ENST00000344836 USP7 436 ENST00000290921 CTBP1 451 ENST00000379389 ISG15



Hdfa\_I Hdfa\_I Hdfa\_I MP51\_I MP51\_I MP51\_I MP52\_I MP52\_I MP52\_I MP52\_I MP52\_I MP53\_I MP biotype

#### GO:0044764 multi-organism cellular process



1	ENST00000343575	CXCL12
2	ENST00000356286	RBCK1
3	ENST00000616316	IFITM2
4	ENST00000399817	IFITM2
5	ENST00000315274	MMP1
6	ENST00000360534	DPP4
7	ENST00000412585	HLA-B
8	ENST00000358208	SRC
9	ENST00000371222	JUN
10	ENST00000265097	THOC3
11	ENST00000261693	SCARB1
12	ENST00000521381	PIK3R1
13	ENST00000286713	STOM
14	ENST00000407439	MRE11
15	ENST00000334464	PDZD8
16	ENST00000367429	CFH
17	ENST00000307407	CXCL8
18	ENST00000331817	KRT7
19	ENST00000318607	PABPC1
20	ENST0000358432	EPHA2
21	ENST00000553286	KLC1



Transcripts in Multi-organism	Significant changes in particular MPS type vs HDFa line												
cellular process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	12	8	15	16	15	12	9	18	6	14	17		
Up-regulated (FDR<0.000001)	3	3	4	2	2	4	3	1	2	4	4		
Down-regulated (FDR<0.1)	21	9	25	22	13	28	10	24	8	27	26		
Down-regulated (FDR<0.000001)	3	1	3	4	1	1	0	2	1	5	6		



GO:0045103 intermediate filament-based process



GO:0045103 intermediate filament-based process





B

Transcripts in <b>Intermediate</b>	Significant changes in particular MPS type vs HDFa line												
filament-based process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	1	0	2	0	0	0	0	0	0	0	0		
Up-regulated (FDR<0.000001)	0	0	1	0	0	0	0	0	0	0	0		
Down-regulated (FDR<0.1)	0	5	2	0	1	0	0	2	1	1	0		
Down-regulated (FDR<0.000001)	0	2	0	0	1	0	0	1	1	1	0		

#### A GO:0048522 positive regulation of cellular process



group

Hdfa

MPS1

MPS2

MPS3A

MPS3B

MPS3C

MPS3D

MPS4A

MPS4B

MPS6

MPS7

MPS9

4

2

0

-2

-4

MPS1

MPS2

MPS3A

MPS3B

MPS3C

MPS3D

MPS4A

MPS4B

MPS7

MPS9

4

2

0

-2

-4

heatmap color key

transcript biotype

protein\_coding

nonsense mediated decay

Transcripts in <b>Positive</b>	Significant changes in particular MPS type vs HDFa line										
regulation of cellular process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	77	50	94	109	86	85	37	131	37	96	105
Up-regulated (FDR<0.000001)	21	14	32	28	23	23	12	32	12	26	34
Down-regulated (FDR<0.1)	96	26	112	108	100	93	47	130	37	120	134
Down-regulated (FDR<0.000001)	16	6	17	23	26	18	9	29	7	19	25

# Fig. S2-36 A GO:0048523 negative regulation of cellular process



Negative	Significant changes in particular MPS type vs HDFa line											
regulation of cellular process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX	
Up-regulated (FDR<0.1)	75	54	84	108	84	81	35	116	45	100	104	
Up-regulated (FDR<0.000001)	26	21	34	32	25	24	14	34	18	25	37	
Down-regulated (FDR<0.1)	87	31	119	104	81	90	37	110	35	104	117	
Down-regulated (FDR<0.000001)	15	8	19	20	23	16	8	25	8	24	19	

#### GO:0048869 cellular developmental process Α



1	ENST	00000	53345	5	CTSB
52	ENST	00000	37980	2	DSP
103	ENST	00000	24679	2	RRAS
154	ENST	00000	29520	6	EN1
205	ENST	00000	30650	3	SOCS5
256	ENST	00000	41258	5	HLA-B
307	ENST	00000	26259	3	DOK5
358	ENST	00000	39304	0	BIN1
409	ENST	00000	39197	1	SEPT2
460	ENST	00000	362074	4	NOTCH2NLA
511	ENST	00000	48845	1	ITGB1BP1
562	ENST	00000	58817	3	IER2
613	ENST	00000	36063	2	WWTR1
664	ENST	00000	26035	6	THBS1
715	ENST	00000	27536	4	GNA12
766	ENST	00000	29812	5	WDFY2
817	ENST	00000	39675	1	ILK
868	ENST	00000	361924	4	GOLGA4
919	ENST	00000	38894	8	LRRK1
970	ENST	00000	374429	9	CXCL12
1021	LENST	00000	30638	5	BMP1
1072	2ENST	00000	41811	5	RHOA
1123	BENST	00000	40636	0	FOXO3
1174	ENST	00000	35469	5	HNRNPH3
1225	SENST	00000	33987	2	HMGB1
1276	SENST	00000	25896	2	SRSF1
1327	/ENST	00000	42827	8	ASH2L
1378	BENST	00000	61885	2	WASF2
1429	ENST	00000	30877	5	DAG1
1480	)ENST(	00000	33796	3	ZMYM5
1531	LENST	00000	216029	9	CBY1



Hdfa 1 Hdfa 1 Hdfa 1 Hdfa 1 Hdfa 1 MPS1 1 MPS2 1 MPS2 1 MPS2 1 MPS2 1 MPS2 1 MPS3 1 MP

#### GO:0048869 cellular developmental process







В

Transcripts in Cellular	Significant changes in particular MPS type vs HDFa line											
developmental process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX	
Up-regulated (FDR<0.1)	61	37	77	85	85	54	26	104	32	98	83	
Up-regulated (FDR<0.000001)	22	12	25	23	26	17	10	37	14	28	30	
Down-regulated (FDR<0.1)	59	23	84	67	67	46	33	82	26	62	77	
Down-regulated (FDR<0.000001)	9	4	14	17	18	11	8	15	4	14	12	

A

#### GO:0050794 regulation of cellular process



Transcripts in	Significant changes in particular MPS type vs HDFa line												
cellular process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	140	95	170	206	165	143	75	219	75	185	193		
Up-regulated (FDR<0.000001)	48	31	54	51	45	43	22	59	25	52	59		
Down-regulated (FDR<0.1)	179	67	241	190	168	161	74	209	60	199	233		
Down-regulated (FDR<0.000001)	35	21	44	44	46	31	18	54	16	49	41		





Transcripts in	Significant changes in particular MPS type vs HDFa line													
process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	9	2	7	б	б	5	2	10	1	10	2			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	1	0			
Down-regulated (FDR<0.1)	11	6	8	14	11	19	0	10	1	21	24			
Down-regulated (FDR<0.000001)	1	0	2	2	1	1	0	2	0	2	1			



Transcripts in Maintenance of	Significant changes in particular MPS type vs HDFa line													
location in cell process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	2	0	0	1	5	2	0	3	0	2	0			
Up-regulated (FDR<0.000001)	0	0	0	0	1	1	0	1	0	0	0			
Down-regulated (FDR<0.1)	3	2	5	4	1	0	3	7	0	2	4			
Down-regulated (FDR<0.000001)	0	1	1	0	0	0	0	0	0	0	1			



Transcripts in



Cellular	Significant changes in particular MPS type vs HDFa line										
response to stimulus process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX
Up-regulated (FDR<0.1)	102	64	127	147	113	107	43	153	55	126	142
Up-regulated (FDR<0.000001)	36	22	44	42	37	36	16	46	23	31	46
Down-regulated (FDR<0.1)	137	39	165	136	118	126	51	148	45	140	162
Down-regulated (FDR<0.000001)	23	11	28	28	22	15	9	27	1	29	22



Contact		Significant changes in particular MFS type vs HDFa line													
inhibition process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX				
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0				
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0				
Down-regulated (FDR<0.1)	0	0	0	1	0	0	0	1	0	0	1				
Down-regulated (FDR<0.000001)	0	0	0	1	0	0	0	1	0	0	0				



#### В

Transcripts in <b>Cell adhesion</b>	Significant changes in particular MPS type vs HDFa line													
molecule production process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	1	0	0	0			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			
Down-regulated (FDR<0.1)	1	0	0	2	0	0	1	4	0	0	0			
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			

### ${f A}$ GO:0061919 process utilizing autophagic mechanism



Process utilizing		Significant changes in particular MPS type vs HDFa line											
autohagic mechanism	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX		
Up-regulated (FDR<0.1)	11	8	5	15	7	11	2	13	б	7	13		
Up-regulated (FDR<0.000001)	4	3	2	3	1	2	1	4	2	3	2		
Down-regulated (FDR<0.1)	9	3	12	11	9	2	6	10	7	15	8		
Down-regulated (FDR<0.000001)	1	0	1	2	1	0	0	3	3	3	1		

Fig. S2-45

#### GO:0071804 cellular potassium ion transport



Cellular	Significant changes in particular MPS type vs HDFa line													
potassium ion transport process	Ι	Π	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	0	3	3	4	0	1	3	3	1	1			
Up-regulated (FDR<0.000001)	0	0	1	2	1	0	1	1	2	1	1			
Down-regulated (FDR<0.1)	4	1	3	5	2	5	2	7	0	4	3			
Down-regulated (FDR<0.000001)	1	1	1	1	1	1	0	1	4	1	1			



## В

Transcripts in <b>DNA clamp</b>	Significant changes in particular MPS type vs HDFa line													
unloading process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX			
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0			
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			
Down-regulated (FDR<0.1)	0	0	0	0	0	1	0	0	0	0	0			
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0			





#### C

Transcripts in <b>Execution phase</b>		Significant changes in particular MPS type vs HDFa line													
of apoptosis process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX				
Up-regulated (FDR<0.1)	0	1	0	2	1	1	0	2	0	1	2				
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0				
Down-regulated (FDR<0.1)	2	0	1	1	1	2	1	1	0	2	1				
Down-regulated (FDR<0.000001)	1	0	1	0	1	1	1	1	5	0	1				

biotype

Hdfa\_1 Hdfa\_1 Hdfa\_1 MPS1\_1 MPS1\_1 MPS1\_1 MPS2\_1 MPS2\_2 MPS2\_2 MPS2\_2 MPS3\_1 MPS3\_2 MP

Fig. S2-48



#### В

Transcripts in		Significant changes in particular MPS type vs HDFa line													
Exocytic process	Ι	II	IIIA	IIIB	IIIC	IIID	IVA	IVB	VI	VII	IX				
Up-regulated (FDR<0.1)	0	0	0	0	0	0	0	0	0	0	0				
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0				
Down-regulated (FDR<0.1)	0	0	1	0	1	0	0	0	0	0	0				
Down-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0				



Up-regulated (FDR<0.1)	1	1	1	4	0	1	1	2	0	2	2
Up-regulated (FDR<0.000001)	0	0	0	0	0	0	0	0	0	0	0
Down-regulated (FDR<0.1)	5	0	б	7	1	1	0	2	1	6	2
Down-regulated (FDR<0.000001)	3	0	2	4	1	0	0	1	6	3	0

MPS I		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	3.19	7.53 x 10 <sup>-13</sup>
CAPG	2.73	8.05 x 10 <sup>-15</sup>
CLU	2.82	1.55 x 10 <sup>-10</sup>
CLU	2.69	4.26 x 10 <sup>-12</sup>
ADAMTSL1	3.77	4.07 x 10 <sup>-11</sup>
MFGE8	2.70	4.64 x 10 <sup>-12</sup>
MFGE8	2.64	4.74 x 10 <sup>-13</sup>
MN1	2.69	1.29 x 10 <sup>-11</sup>
LY6K	-3.84	7.67 x 10 <sup>-15</sup>
LY6K	-3.45	1.56 x 10 <sup>-13</sup>
SERPINB2	-2.85	6.91 x 10 <sup>-9</sup>
SNHG5	-2.91	3.08 x 10 <sup>-13</sup>

**Table S2.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS I relative to control cells (HDFa).

**Table S3.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS II relative to control cells (HDFa).

MPS II			
transcript	log <sub>2</sub> fold change (log <sub>2</sub> FC)	p-value	
CLU	3.05	1.55 x 10 <sup>-10</sup>	
CLU	2.97	4.26 x 10 <sup>-12</sup>	
MN1	2.78	1.29 x 10 <sup>-11</sup>	
PFN1	3.70	1.04 x 10 <sup>-10</sup>	
LY6K	-2.57	7.67 x 10 <sup>-15</sup>	
SERPINB7	-3.83	1.63 x 10 <sup>-14</sup>	
CLEC2B	-2.86	1.24 x 10 <sup>-12</sup>	

MPS IIIA		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	3.88	7.53 x 10 <sup>-13</sup>
ADAMTSL1	3.32	4.07 x 10 <sup>-11</sup>
POSTN	5.27	2.33 x 10 <sup>-11</sup>
POSTN	5.14	8.84 x 10 <sup>-12</sup>
MFAP5	6.14	5.18 x 10 <sup>-17</sup>
MFGE8	3.70	4.64 x 10 <sup>-12</sup>
MFGE8	3.88	1.26 x 10 <sup>-8</sup>
MFGE8	3.90	4.74 x 10 <sup>-13</sup>
FAM167A	2.64	2.75 x 10 <sup>-12</sup>
PFN1	3.51	1.04 x 10 <sup>-10</sup>
ENPP2	-2.64	2.40 x 10 <sup>-13</sup>
CLEC2B	-2.66	1.23 x 10 <sup>-12</sup>
CTSC	-2.90	7.57 x 10 <sup>-11</sup>
PTGDS	-6.16	1.29 x 10 <sup>-8</sup>
PTGS1	-2.57	1.89 x 10 <sup>-16</sup>
COL18A1	-2.89	2.70 x 10 <sup>-11</sup>

**Table S4.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IIIA relative to control cells (HDFa).

MPS IIIB		
transcript	log <sub>2</sub> fold change (log <sub>2</sub> FC)	p-value
ADAMTSL1	3.64	4.08 x 10 <sup>-11</sup>
POSTN	7.74	8.84 x 10 <sup>-12</sup>
POSTN	7.25	2.33 x 10 <sup>-11</sup>
MFAP5	4.99	5.18 x 10 <sup>-17</sup>
PCOLCE2	3.21	5.71 x 10 <sup>-11</sup>
MFGE8	3.05	4.75 x 10 <sup>-13</sup>
MFGE8	2.72	4.65 x 10 <sup>-12</sup>
FAM167A	3.29	2.75 x 10 <sup>-12</sup>
NR2F2	3.13	1.92 x 10 <sup>-15</sup>
NR2F2	2.89	1.10 x 10 <sup>-14</sup>
CDH2	3.05	1.39 x 10 <sup>-12</sup>
OXTR	5.20	4.75 x 10 <sup>-11</sup>
MT1X	3.32	5.24 x 10 <sup>-10</sup>
AC004556.1	2.96	8.86 x 10 <sup>-12</sup>
ENPP2	-2.79	2.00 x 10 <sup>-13</sup>
ENPP2	-3.23	2.41 x 10 <sup>-13</sup>
SNHG5	-2.68	9.21 x 10 <sup>-11</sup>
PTGDS	-4.78	1.29 x 10 <sup>-8</sup>
TRPV2	-3.86	5.78 x 10 <sup>-14</sup>
KREMEN1	-3.05	2.00 x 10 <sup>-14</sup>
WISP2	-7.23	7.63 x 10 <sup>-10</sup>
TNFRSF11B	-2.84	3.10 x 10 <sup>-16</sup>

**Table S5.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IIIB relative to control cells (HDFa).

MPS IIIC		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	4.13	7.53 x 10 <sup>-13</sup>
CAPG	4.27	8.05 x 10 <sup>-15</sup>
CLU	2.95	4.26 x 10 <sup>-12</sup>
ADAMTSL1	3.31	4.07 x 10 <sup>-11</sup>
POSTN	5.41	2.33 x 10 <sup>-11</sup>
POSTN	5.63	8.84 x 10 <sup>-12</sup>
MFAP5	4.51	5.18 x 10 <sup>-17</sup>
FAM167A	2.87	2.75 x 10 <sup>-12</sup>
NR2F2	2.69	1.10 x 10 <sup>-14</sup>
CDH2	2.55	1.39 x 10 <sup>-12</sup>
TENM3	2.55	1.99 x 10 <sup>-11</sup>
PFN1	3.72	1.04 x 10 <sup>-10</sup>
OXTR	6.42	4.75 x 10 <sup>-11</sup>
LY6K	-3.61	7.67 x 10 <sup>-15</sup>
ENPP2	-2.59	2.40 x 10 <sup>-13</sup>
EPDR1	-3.40	2.97 x 10 <sup>-12</sup>
НОХВ6	-3.96	1.71 x 10 <sup>-16</sup>
HOXB5	-2.94	5.76 x 10 <sup>-15</sup>

**Table S6.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IIIC relative to control cells (HDFa).

MPS IIID		
transcript	log <sub>2</sub> fold change (log <sub>2</sub> FC)	p-value
COL8A2	4.36	7.53 x 10 <sup>-13</sup>
POSTN	4.97	8.84 x 10 <sup>-12</sup>
POSTN	5.00	2.33 x 10 <sup>-11</sup>
PCOLCE2	2.90	5.71 x 10 <sup>-11</sup>
AC004556.1	3.14	8.86 x 10 <sup>-12</sup>
LY6K	-4.79	1.56 x 10 <sup>-13</sup>
LY6K	-5.34	7.67 x 10 <sup>-15</sup>
SERPINB7	-2.54	1.63 x 10 <sup>-14</sup>
RPL10	-2.92	9.84 x 10 <sup>-15</sup>
RPL10	-4.61	9.95 x 10 <sup>-12</sup>

**Table S7.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IIID relative to control cells (HDFa).

**Table S8.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IVA relative to control cells (HDFa).

MPS IVA		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	3.26	7.54E-13
CAPG	4.17	8.05E-15

**Table S9.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IVB relative to control cells (HDFa).

MPS IVB		
transcript	log <sub>2</sub> fold change (log <sub>2</sub> FC)	p-value
CAPG	4.14	8.05 x 10 <sup>-15</sup>
CLU	3.45	4.27 x 10 <sup>-12</sup>
CLU	3.42	1.55 x 10 <sup>-10</sup>
CLU	3.83	2.39 x 10 <sup>-11</sup>
POSTN	5.83	8.84 x 10 <sup>-12</sup>
POSTN	5.68	2.33 x 10 <sup>-11</sup>
MFAP5	4.10	5.18 x 10 <sup>-17</sup>
PCOLCE2	3.21	5.71 x 10 <sup>-11</sup>
MFGE8	2.77	4.74 x 10 <sup>-13</sup>
FAM167A	3.77	2.75 x 10 <sup>-12</sup>
NR2F2	3.19	1.93 x 10 <sup>-15</sup>
NR2F2	2.98	1.10 x 10 <sup>-14</sup>
CDH2	2.94	1.39 x 10 <sup>-12</sup>
TENM3	3.16	1.99 x 10 <sup>-11</sup>
OXTR	6.07	4.75 x 10 <sup>-11</sup>
MT1X	3.49	5.24 x 10 <sup>-10</sup>
LY6K	-4.28	7.67 x 10 <sup>-15</sup>
LY6K	-3.94	1.56 x 10 <sup>-13</sup>
SERPINB7	-2.72	1.63 x 10 <sup>-14</sup>
ENPP2	-2.54	2.00 x 10 <sup>-13</sup>
ENPP2	-2.86	2.41 x 10 <sup>-13</sup>
CLEC2B	-3.08	1.23 x 10 <sup>-12</sup>
SERPINB2	-3.55	6.91 x 10 <sup>-9</sup>
KREMEN1	-2.54	2.00 x 10 <sup>-14</sup>
WISP2	-2.83	7.63 x 10 <sup>-10</sup>
НОХВ6	-3.35	1.71 x 10 <sup>-16</sup>
HOXB5	-3.21	5.76 x 10 <sup>-15</sup>

MPS VI		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	3.60	7.53 x 10 <sup>-13</sup>
CAPG	3.82	8.05 x 10 <sup>-15</sup>
CLU	2.58	4.26 x 10 <sup>-12</sup>
CLU	2.68	1.55 x 10 <sup>-10</sup>
ADAMTSL1	2.69	4.07 x 10 <sup>-11</sup>
LY6K	-2.69	7.67 x 10 <sup>-15</sup>
SERPINB7	-3.09	1.63 x 10 <sup>-14</sup>

**Table S10.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS VI relative to control cells (HDFa).

**Table S11.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS VII relative to control cells (HDFa).

MPS VII		
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
CAPG	4.27	8.05 x 10 <sup>-15</sup>
MFAP5	4.19	5.18 x 10 <sup>-17</sup>
PCOLCE2	3.99	5.71 x 10 <sup>-11</sup>
TENM3	3.72	1.99 x 10 <sup>-11</sup>
NOTCH3	3.32	7.27 x 10 <sup>-9</sup>
LY6K	-3.84	7.67 x 10 <sup>-15</sup>
LY6K	-2.90	1.56 x 10 <sup>-13</sup>
CLEC2B	-2.83	1.23 x 10 <sup>-12</sup>
SNHG5	-2.82	3.08 x 10 <sup>-13</sup>
CTSC	-3.02	7.57 x 10 <sup>-11</sup>
PTGS1	-5.21	1.89 x 10 <sup>-16</sup>
PTGS1	-4.31	1.19 x 10 <sup>-12</sup>
TNFRSF11B	-5.51	3.10 x 10 <sup>-16</sup>
RPL10	-3.90	9.84 x 10 <sup>-15</sup>

	MPS IX	
transcript	$\log_2$ fold change ( $\log_2$ FC)	p-value
COL8A2	3.21	7.53 x 10 <sup>-13</sup>
CLU	3.46	3.56 x 10 <sup>-10</sup>
CLU	3.43	4.26 x 10 <sup>-12</sup>
CLU	3.56	2.39 x 10 <sup>-11</sup>
ADAMTSL1	2.89	4.07 x 10 <sup>-11</sup>
POSTN	5.83	2.33 x 10 <sup>-11</sup>
POSTN	5.70	8.84 x 10 <sup>-12</sup>
MFAP5	4.40	5.18 x 10 <sup>-17</sup>
PCOLCE2	3.93	5.71 x 10 <sup>-11</sup>
NR2F2	2.51	1.92 x 10 <sup>-15</sup>
CDH2	2.98	1.39 x 10 <sup>-12</sup>
TENM3	3.69	1.99 x 10 <sup>-11</sup>
MN1	3.31	1.29 x 10 <sup>-11</sup>
NOTCH3	2.70	7.27 x 10 <sup>-9</sup>
LY6K	-3.24	1.56 x 10 <sup>-13</sup>
LY6K	-4.01	7.67 x 10 <sup>-15</sup>
SERPINB7	-3.84	1.63 x 10 <sup>-14</sup>
ENPP2	-3.52	2.00 x 10 <sup>-13</sup>
ENPP2	-3.70	2.41 x 10 <sup>-13</sup>
COL18A1	-2.53	2.70 x 10 <sup>-11</sup>
TRPV2	-3.40	5.78 x 10 <sup>-14</sup>
EPDR1	-2.77	2.97 x 10 <sup>-12</sup>

**Table S12.** Statistical analysis of results of gene expression level estimation with  $\log_2 FC > 2.5$  in MPS IX relative to control cells (HDFa).