

Table SI. Clinical characteristics of the DS subjects recruited.

Variables	Yes	No	Missing
HEAD at examination			
Hypotonia	10	1	4
%	66.67	6.67	26.67
Brachycephaly	11	3	1
%	73.33	20.00	6.67
Flat occipit	12	3	0
%	80.00	20.00	0.00
Flat facial profile	11	4	0
%	73.33	26.67	0.00
Flattened nose	11	4	0
%	73.33	26.67	0.00
Small ears	7	6	2
%	46.67	40.00	13.33
Folded helix	6	6	3
%	40.00	40.00	20.00
Hearing loss	2	11	2
%	13.33	73.33	13.33
Mouth permanently open	8	7	0
%	53.33	46.67	0.00
Protruding tongue	7	8	0
%	46.67	53.33	0.00
Furrowed tongue	11	4	0
%	73.33	26.67	0.00
High arched palate	12	2	1
%	80.00	13.33	6.67
Small teeth	7	6	2
%	46.67	40.00	13.33
Narrow palade	13	1	1
%	86.67	6.67	6.67
Conical teeth	5	6	4
%	33.33	40.00	26.67
Upslanting palpebral fissures	14	1	0
%	93.33	6.67	0.00
Epicanthus	11	1	3
%	73.33	6.67	20.00
Nystagmus	2	13	0
%	13.33	86.67	0.00
Strabismus	3	10	2
%	20.00	66.67	13.33
Congenital heart defect	9	5	1
%	60.00	33.33	6.67
Murmur	7	6	2
%	46.67	40.00	13.33
Heart surgery	5	8	2
%	33.33	53.33	13.33
Separation of the abdominal muscle	4	10	1
%	26.67	66.67	6.67
Umbilical hernia	3	11	1
%	20.00	73.33	6.67
Short neck	9	6	0
%	60.00	40.00	0.00
Joint laxity	13	2	0
%	86.67	13.33	0.00
Short and broad hands	10	4	1
%	66.67	26.67	6.67

Table SI. Continued.

Variables	Yes	No	Missing
Fifth Finger Mid-Phalanx Hypoplasia	9	5	1
%	60.00	33.33	6.67
5th incurved finger	8	7	0
%	53.33	46.67	0.00
Single transverse palmar crease	6	9	0
%	40.00	60.00	0.00
Hallux separated	11	4	0
%	73.33	26.67	0.00
Mental retardation	12	0	3
%	80.00	0.00	20.00
Celiac disease	2	13	0
%	13.33	86.67	0.00
Masticatory dysfunction	4	10	1
%	26.67	66.67	6.67
Constipation	5	10	0
%	33.33	66.67	0.00
Diarrhea	2	13	0
%	13.33	86.67	0.00
Small genitalia	2	10	3
%	13.33	66.67	20

Table SII. Non-parametric Wilcoxon signed-rank test (or Kruskal Wallis test^a-when the subgroups are more than two) between miR expression levels and DS pathologies.

DS pathologies	miR-16-5p	P-values	miR-144-3p	P-values	miR-99b-5p	P-values
Ipotonia						
<i>No</i>	2.20		4.51		2.98	
<i>Yes</i>	3.30	0.5455	5.27	0.9091	4.36	0.7273
Brachycephaly						
<i>No</i>	2.28		4.45		4.18	
<i>Yes</i>	3.77	0.5549	5.47	0.5549	4.53	0.5549
Flat occipit						
<i>No</i>	2.28		4.45		4.18	
<i>Yes</i>	3.52	0.7341	5.38	0.3648	3.89	1.0000
Flat facial profile						
<i>No</i>	3.91		5.27		4.70	
<i>Yes</i>	3.27	0.9495	5.29	0.8513	3.24	0.8513
Flattened nose						
<i>No</i>	4.18		5.28		4.70	
<i>Yes</i>	3.27	0.4117	5.29	0.8513	3.24	0.9495
Small ears						
<i>No</i>	2.99		4.79		2.97	
<i>Yes</i>	2.82	0.7308	5.29	0.7308	4.18	0.5338
Folded helix						
<i>No</i>	3.05		4.78		3.57	
<i>Yes</i>	3.56	0.6991	5.78	0.1797	4.23	0.3095
Hearing loss						
<i>No</i>	2.30		5.07		3.24	
<i>Yes</i>	3.05	0.9231	4.89	0.9231	4.18	0.9231
Mouth permanently open						
<i>No</i>	3.77		5.47		5.22	
<i>Yes</i>	2.55	0.2810	4.50	0.5358	2.97	0.3357
Protruding tongue						
<i>No</i>	4.30		5.78		4.88	
<i>Yes</i>	2.82	0.4634	4.51	0.5358	2.98	0.5358
Furrowed tongue						
<i>No</i>	3.73		5.15		4.62	
<i>Yes</i>	3.27	0.9495	5.29	0.8513	4.18	0.9495
High arched palate						
<i>No</i>	2.66		4.44		4.29	
<i>Yes</i>	3.83	0.3516	5.52	0.2637	4.36	0.7912
Small teeth						
<i>No</i>	3.30		4.79		3.76	
<i>Yes</i>	3.27	0.9452	5.29	0.8357	4.18	0.7308
Narrow palate						
<i>No</i>	3.27		5.29		5.99	
<i>Yes</i>	3.77	1.0000	5.47	1.0000	4.18	0.5714
Conical teeth						
<i>No</i>	4.30		5.58		4.88	
<i>Yes</i>	3.27	0.5368	5.29	0.6623	2.98	0.9307
Upslanting palpebral fissures						
<i>No</i>	7.68		6.71		7.89	
<i>Yes</i>	3.05	0.1333	5.18	0.5333	3.71	0.1333
Epicanthus						
<i>No</i>	3.77		5.07		4.53	
<i>Yes</i>	3.89	1.0000	5.57	1.0000	4.18	1.0000
Nystagmus						
<i>No</i>	3.77		5.47		4.53	
<i>Yes</i>	2.08	0.3048	4.20	0.2286	2.52	0.1143

Table SII. Continued.

DS pathologies	miR-16-5p	P-values	miR-144-3p	P-values	miR-99b-5p	P-values
<i>Strabismus</i>						
No	2.56		4.79		2.97	
Yes	3.27	0.5734	5.29	0.5734	5.40	0.1119
<i>Congenital heart defect</i>						
No	3.77		5.07		4.53	
Yes	2.30	0.5185	5.29	1.0000	4.18	0.8981
<i>Murmur</i>						
No	3.30		4.79		3.76	
Yes	3.27	0.9452	5.47	0.6282	5.22	0.9452
<i>Heart surgery</i>						
No	4.30		5.89		4.97	
Yes	2.30	0.2222	5.29	0.3543	3.24	0.4351
<i>Separation of the abdominal muscle</i>						
No	3.10		5.52		3.11	
Yes	3.52	0.7333	5.18	1.0000	4.97	0.4535
<i>Umbilical hernia</i>						
No	2.30		5.47		3.24	
Yes	3.77	0.5549	5.29	1.0000	5.22	0.4560
<i>Short neck</i>						
No	4.35		6.00		5.70	
Yes	2.82	0.4559	5.07	0.5287	2.98	0.1447
<i>Joint laxity</i>						
No	4.01		3.36		3.95	
Yes	3.27	1.0000	5.29	0.6857	4.18	1.0000
<i>Short and broad hands</i>						
No	1.81		4.19		3.43	
Yes	3.83	0.1878	5.52	0.1419	4.88	0.2398
<i>5th short</i>						
No	2.82		4.48		4.18	
Yes	3.27	0.8981	5.29	1.0000	3.24	0.7972
<i>5th incurved</i>						
No	2.82		4.48		2.96	
Yes	3.52	0.6943	5.38	0.3969	5.26	0.0939
<i>Single transverse palmar crease</i>						
No	2.28		4.51		2.98	
Yes	4.30	0.1810	5.69	0.2238	5.61	0.1810
<i>Hallux separated</i>						
No	1.81		4.19		3.43	
Yes	3.77	0.2799	5.47	0.1377	4.53	0.6608
<i>Mental retardation</i>						
No	-		-		-	
Yes	3.05	-	5.18	-	4.36	-
<i>Celiac disease</i>						
No	2.82		5.47		3.24	
Yes	3.52	0.9333	5.18	0.9333	5.26	0.4762
<i>Masticatory disfunction</i>						
No	3.52		5.38		3.89	
Yes	3.55	0.6354	5.70	1.0000	5.11	0.7333
<i>Constipation</i>						
No	3.83		5.52		4.88	
Yes	2.28	0.1292	4.45	0.0753	2.59	0.1292
<i>Diarrhea</i>						
No	2.82		5.07		3.24	
Yes	5.18	0.2286	6.51	0.2286	5.63	0.3048

Table SII. Continued.

DS pathologies	miR-16-5p	P-values	miR-144-3p	P-values	miR-99b-5p	P-values
<i>Small genitalia</i>						
<i>No</i>	3.36		5.52		3.10	
<i>Yes</i>	4.60	0.7576	6.52	0.4848	5.59	0.3636
<i>Number of comorbidities (categorical)^a</i>						
<i>Low comorbidities</i>	4.00		5.58		4.79	
<i>Medium comorbidities</i>	2.56		4.79		2.97	
<i>High comorbidities</i>	4.82	0.4597	6.94	0.2051	6.04	0.05
<i>Neurologic severity^a</i>						
<i>Mild</i>	2.55		4.47		3.27	
<i>Moderate</i>	5.42		7.59		5.40	
<i>Severe</i>	2.56	0.5738	4.50	0.1178	3.60	0.5834

^aKruskal wallis test.

Table SIII. List of the miRNAs most abundant in the plasma secretome of DS (n=4) and C (n=4) subjects detected by at least 3 probes using agilent miRNA microarray.

miRNA_name	no. of probes	Chromosome
hsa-miR-16-5p	5	Chr3
hsa-miR-5009-5p	5	Chr15
hsa-miR-99b-5p	4	Chr19
hsa-miR-4452	4	Chr4
hsa-miR-4775	4	Chr2
hsa-miR-548am-3p	4	ChrX
hsa-miR-141-3p	3	Chr12
hsa-miR-302d-3p	3	Chr4
hsa-miR-3912-3p	3	Chr5
hsa-miR-3925-3p	3	Chr6
hsa-miR-4747-5p	3	Chr19
hsa-miR-548an	3	ChrX
hsa-miR-548aq-5p	3	Chr3
hsa-miR-548b-5p	3	Chr6
hsa-miR-581	3	Chr5

DS, Down syndrome subjects; C, healthy siblings; n, number; miR/miRNA, microRNA.

Table SIV. Descriptive statistics for quantitative variables available in the dataset.

Descriptive	Mother's age	Father's age	Birth weight (g)	Development sitting months	Development babbling months	Development walking months	Development Sphincter control months
Min	23.00	28.00	890.00	4.00	7.00	11.00	30.00
Q1	32.00	32.50	2337.50	6.00	13.50	19.50	30.00
Median	39.00	39.00	2890.00	7.50	21.00	24.00	36.00
Mean	36.00	37.60	2748.47	8.25	21.40	28.21	37.42
Std dev	5.52	5.60	960.67	3.13	11.90	13.08	8.93
Q3	40.00	41.50	3167.50	9.75	24.00	34.50	37.50
Max	43.00	48.00	4210.00	15.00	48.00	60.00	60.00
Missing (%)	0.00 (0.00%)	0.00 (0.00%)	0.00 (0%)	1.00 (7.00%)	5.00 (33.00%)	1.00 (7.00%)	3.00 (20.00%)

Table SV. Number of comorbidities for each DS subject and the corresponding categorical classification.

ID	Number of comorbidities for each DS subject	Number of comorbidities for each DS subject (categorical)
DS01	17	Low comorbidities
DS02	21	High comorbidities
DS03	21	High comorbidities
DS04	20	Medium comorbidities
DS05	25	High comorbidities
DS06	19	Medium comorbidities
DS07	11	Low comorbidities
DS08	15	Low comorbidities
DS09	24	High comorbidities
DS10	22	High comorbidities
DS11	21	High comorbidities
DS12	21	High comorbidities
DS13	11	Low comorbidities
DS14	18	Medium comorbidities
DS15	18	Medium comorbidities

DS, Down syndrome.

Table SVI. Descriptive statistics for miRs expression levels on all the subjects, DS subjects and C subjects respectively.

Descriptive (all)	miR-16-5p	miR-144-3p	miR-99b-5p
Min	0.00	0.00	0.00
Q1	2.22	4.03	2.61
Median	2.97	4.87	4.11
Mean	3.22	5.01	3.96
Std dev	1.76	1.76	1.91
Q3	4.27	6.14	5.36
Max	7.68	7.97	7.89
Missing (%)	0.00 (0%)	0.00 (0%)	0.00 (0%)

Descriptive (DS)	miR-16-5p	miR-144-3p	miR-99b-5p
Min	0.34	0.00	0.00
Q1	2.24	4.47	2.82
Median	3.27	5.29	4.18
Mean	3.56	5.18	4.18
Std dev	1.96	1.94	2.05
Q3	5.12	6.40	5.70
Max	7.68	7.97	7.89
Missing (%)	0.00 (0%)	0.00 (0%)	0.00 (0%)

Descriptive (C)	miR-16-5p	miR-144-3p	miR-99b-5p
Min	0.00	1.88	1.11
Q1	2.17	3.91	2.26
Median	2.97	4.62	4.04
Mean	2.88	4.84	3.74
Std dev	1.51	1.61	1.80
Q3	3.65	6.10	4.72
Max	5.49	7.59	7.35
Missing (%)	0.00 (0%)	0.00 (0%)	0.00 (0%)

miR, microRNA.

Table SVII. Descriptive statistics (Mean, Median, Min-Max) on miRNA expression levels for the 2 clusters obtained on DS and C subjects with the Partitioning Around Medoids algorithm. The median expression levels of miRNAs are compared in the two clusters using the Wilcoxon signed-rank test.

	Cluster 1 (C ₁)	Cluster 2 (C ₂)
Number of healthy siblings (%)	11 (55%)	4 (40%)
Number of DS	9 (45%)	6 (60%)
miR-16-5p		
Mean	2.31	5.04
Median	2.33 ^a	5.33 ^a
Min-Max	0.00-3.89	2.81-7.68
miR-144-3p		
Mean	4.19	6.64
Median	4.46 ^a	6.54 ^a
Min-Max	0.00-7.59	5.29-7.97
miR-99b-5p		
Mean	2.97	5.94
Median	2.91 ^a	5.70 ^a
Min-Max	0.00-5.99	4.47-7.89

^aP<0.05. miR/miRNA, microRNA DS, Down syndrome; C, control.

Table SVIII. Gene target prediction performed by miRWALK. The expression levels in peripheral blood leucocytes are also reported.

A, miR-99b-5p			
Gene name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
FZD5	9,173197885	8,48830639	1,08
LIF	13,43677518	12,97990478	1,04
PPM1H	7,377761361	7,603011092	0,97

B, miR-16-3p			
Gene_name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
ADAMTS3	1,782850161	1,852815197	0,96
ASH1L	196,5940289	197,8829887	0,99
BCAS1	22,16839026	23,72249889	0,93
BCL2L2	339,9058115	352,9397435	0,96
BTG2	421,6781692	437,9353887	0,96
C1orf21	45,29182185	29,08559174	1,56
CACUL1	47,94503021	48,96900027	0,98
CAPRIN1	117,749783	122,4261628	0,96
CAPZA2	289,8590265	301,8449506	0,96
CBX2	11,92518344	11,57341461	1,03
CBX4	507,511527	496,6656402	1,02
CC2D1B	34,95527472	35,85438783	0,97
CCDC6	160,1968777	179,0429061	0,89
CD2AP	70,50144413	72,4134998	0,97
CLCN4	7,845742618	8,356192267	0,94
CNOT6L	215,9380156	195,7648517	1,10
DVL3	78,61796377	72,05784327	1,09
EZH1	96,15704691	104,8020726	0,92
FOXK1	50,19344801	49,65154753	1,01
FSTL4	8,734681479	8,687189665	1,01
GABARAPL1	68,14901818	69,24004415	0,98
GALNT1	187,7197903	187,7780644	1,00
IHH	16,0424799	15,40365499	1,04
IRAK2	25,2175894	22,55530924	1,12
KDSR	48,56795978	52,78949262	0,92
KIF5C	31,17863493	30,85904598	1,01
KLHDC8B	32,89384806	41,53126791	0,79
LAMP3	19,27496358	18,42682266	1,05
LRP6	6,271889687	7,831806432	0,80
MASP1	11,51389032	11,03790824	1,04
MGAT4A	202,886157	216,817676	0,94
MKNK1	164,3931261	146,1047588	1,13
MYO5A	64,76157863	63,58263929	1,02
N4BP1	168,5954089	159,5117707	1,06
NEBL	8,554425748	6,849586804	1,25
PAFAH1B1	180,0077546	173,2690752	1,04
PAPPA	5,40188175	5,185052957	1,04
PCMT1	384,9500502	341,7391708	1,13
PDK4	52,17409835	36,89163843	1,41
PLAG1	12,15647102	22,42429832	0,54
PLD1	11,59448225	10,85816499	1,07
POLR3F	36,79321461	43,58865671	0,84
PRDM4	103,5350442	123,9595979	0,84
PTCD3	133,6457611	152,6841469	0,88

Table SVIII. Continued.

B, miR-16-3p

Gene_name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
PTH	1,819919797	1,841387955	0,99
RAB10	506,9463519	505,9683616	1,00
RAB3B	4,139648558	4,147241963	1,00
RAD23B	262,5231114	264,6418531	0,99
RET	17,5051355	17,20688225	1,02
RFK	93,48119538	91,99537372	1,02
RSBN1	145,8086464	152,5156966	0,96
SESN1	143,5623765	241,4155565	0,59
SH3BGRL2	95,67576527	59,89642176	1,60
SLC12A2	29,25634817	27,50275182	1,06
SLC13A1	1,38446178	1,509111322	0,92
SLC1A2	8,794354023	8,621352041	1,02
SLC36A1	73,00016553	67,08462681	1,09
SNRNP48	51,34741198	56,08864206	0,92
SNTB2	33,93710607	27,63397519	1,23
SOCS6	5,049039313	6,323563028	0,80
SPRYD3	90,96905909	86,58101599	1,05
SSR1	421,1448657	410,8232823	1,03
ST8SIA3	2,46344795	2,55129299	0,97
SYNJ1	49,20697838	35,3854095	1,39
TAF5	75,44284391	81,64930231	0,92
TFCP2L1	15,09125942	14,13334953	1,07
TGFBR3	550,3754615	299,2779763	1,84
TLK1	65,62923442	72,88872716	0,90
UBE2Q1	224,0609239	204,6896099	1,09
UBL3	357,1651822	336,3211153	1,06
UHMK1	336,655075	309,6283507	1,09
USP25	108,8311359	77,23223383	1,41
USP31	25,51497224	22,3282164	1,14
VAPB	58,62849868	61,52107276	0,95
WEE1	41,98272252	40,55873691	1,04
YRDC	91,06081979	75,91098232	1,20
YWHAH	97,57898892	68,7091271	1,42
ZBTB39	39,4759048	35,77985934	1,10
SRPRA	254,3009577	224,8940243	1,13
SRPRB	103,2589731	102,8773326	1,00

C, miR-144-3p

Gene name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
ABCA1	23,86189104	30,6549565	0,78
ADAMTS17	9,521134419	10,59436954	0,90
ADAMTS3	1,782850161	1,852815197	0,96
AKAP11	171,9535236	212,0830338	0,81
ALDH1A3	3,75596824	3,954423962	0,95
APPBP2	74,17138991	79,40961533	0,93
ARID2	59,5088252	61,04714088	0,97
ARID5B	69,02871226	76,87136891	0,90
ARL4C	728,0116752	653,7684964	1,11
ATXN1	95,85845076	69,12537451	1,39
BACH2	66,93537687	137,8033943	0,49
BHLHE41	5,916538162	9,237500168	0,64

Table SVIII. Continued.

C, miR-144-3p

Gene name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
CAV2	6,143806975	6,973521317	0,88
CBX1	308,0881771	306,9356208	1,00
CD164	448,2738953	425,8269899	1,05
CD302	693,6094185	844,2498899	0,82
CDK19	70,05339798	69,7857109	1,00
CDS2	122,0108531	112,7052304	1,08
CEP68	87,92652829	96,87030287	0,91
CLDN8	1,923050061	2,062896416	0,93
CMTM6	510,0593684	492,9542653	1,03
CREBRF	203,7306459	235,7958278	0,86
CXCL11	2,779043674	2,042102555	1,36
CXCL12	3,977441275	3,593111088	1,11
DYRK1A	151,826792	116,6614094	1,30
E2F8	4,863043521	3,20264885	1,52
ELL2	37,94895148	31,68027394	1,20
FAM129A	372,2844779	269,3409864	1,38
FAM8A1	459,1912508	374,292582	1,23
FBN2	27,43902354	28,42618555	0,97
FGD6	9,776116922	12,13264414	0,81
FUBP3	32,86654368	31,36416614	1,05
FZD6	12,61466925	18,90477613	0,67
GLCCI1	125,3834064	102,002244	1,23
GNG12	5,648886688	5,323344806	1,06
HLTF	76,75121803	86,63725327	0,89
ITPRIPL2	44,0395844	40,19383314	1,10
KCND2	1,500324522	1,448311181	1,04
KCTD4	3,287080007	3,22704846	1,02
KIAA1024	3,032169748	3,449052459	0,88
KIAA1549L	3,49427052	3,48883542	1,00
KIDINS220	130,4666146	123,7841143	1,05
KIF14	6,090425934	4,56529141	1,33
KIF3A	39,93045014	38,02131639	1,05
KL	2,1104397	2,173141498	0,97
KLB	2,07231836	2,136753895	0,97
LARP4B	57,45296314	52,44383058	1,10
LCOR	83,30271888	79,64524245	1,05
LRAT	2,185275748	2,067049478	1,06
MAOB	4,382510941	4,373338362	1,00
MAP7D1	384,6691244	382,1154812	1,01
MED12L	3,636952782	3,709083367	0,98
MED4	70,2571741	63,87881158	1,10
MEGF9	248,383716	251,5814097	0,99
MFSD6	90,90805397	65,65282736	1,38
MGAT4A	202,886157	216,817676	0,94
MMGT1	408,0546838	423,5408534	0,96
MTMR9	96,95350843	100,075505	0,97
MYBL1	201,035806	167,7833111	1,20
MYO1E	27,61494126	29,26353567	0,94
NDFIP1	335,2224791	371,5697673	0,90
NECAB1	1,452384756	1,560596054	0,93
NETO2	36,19279911	39,32735728	0,92
NLN	38,8209324	39,164244	0,99
NPTX1	26,31839153	16,47824418	1,60
NR2F2	3,596957472	3,580073963	1,00

Table SVIII. Continued.

C, miR-144-3p

Gene name	Mean expression levels (DS)	Mean expression levels (C)	Ratio (DS/C)
NT5DC1	72,42333682	86,28621924	0,84
ONECUT2	3,659340668	3,592315636	1,02
PCDH20	1,710970283	1,639595221	1,04
PGRMC2	82,82650778	84,15708427	0,98
PPAT	25,54669911	30,1800601	0,85
PPP1R16B	143,1408736	115,1406195	1,24
PTPN9	26,33804968	25,5411439	1,03
QSER1	43,2513939	46,92395141	0,92
RAP2B	211,2917272	186,0963934	1,14
RASSF3	324,5019185	339,9002132	0,95
RAVER2	5,595842349	5,829916357	0,96
RET	17,5051355	17,20688225	1,02
RGL1	73,42317846	60,2050597	1,22
RNF125	221,8709583	207,9480939	1,07
SFRP1	11,21563825	12,21509191	0,92
SIM1	2,082095561	2,10342395	0,99
SLC26A2	88,78603185	90,78371583	0,98
SLC35A3	71,00908775	76,30730435	0,93
SLC7A11	6,621803716	6,474624719	1,02
SMARCA1	1,880926338	2,208738963	0,85
SNTB2	33,93710607	27,63397519	1,23
SOCS6	5,049039313	6,323563028	0,80
SPOPL	199,9317545	228,6225391	0,87
SRPK1	131,8592621	111,1707713	1,19
SUCLG2	127,5399445	145,5486043	0,88
SYT11	66,95651366	41,51716371	1,61
TEK	3,125133653	3,086186623	1,01
TMF1	81,09052196	85,47054288	0,95
TMTC3	14,80881552	18,80456389	0,79
TNKS2	114,4241168	117,4638287	0,97
TNS3	89,7844367	115,9790452	0,77
TSPAN12	9,696989542	9,467224387	1,02
TUBGCP5	11,64829296	13,62564333	0,85
UBE2G1	259,6751565	248,4071896	1,05
VANGL1	21,66765989	16,92019378	1,28
VPS4B	350,8871775	358,8912523	0,98
YWHAG	605,7599584	654,3746459	0,93
ZC3H6	38,41863303	43,62212345	0,88
ZNF148	93,32898369	105,9362651	0,88
ZNF260	26,68225303	38,49095501	0,69

Bold, differentially expressed genes between DS and C participants.