

Table S1: Differentially expressed ncRNAs in men with poor sperm quality relative to their normal controls.

miRNA species														
species	chr	start	end	logFC	logCPM	Pvalue	padj	FC						
hsa-mir-7110	chr3	123161794	123161879	1.04	13.89	2.1E-05	1.5E-03	2.06						
hsa-mir-4800	chr4	2250077	2250156	0.95	5.86	7.7E-05	2.8E-03	1.94						
hsa-miR-4488	chr11	61508596	61508657	0.71	8.25	3.2E-04	7.5E-03	1.63						
hsa-mir-4488	chr11	61508596	61508657	0.69	8.32	4.1E-04	7.5E-03	1.61						
hsa-mir-3916	chr1	247201967	247202060	0.90	9.80	1.1E-03	1.6E-02	1.87						
hsa-mir-4508	chr15	23562062	23562131	0.85	9.24	2.6E-03	3.2E-02	1.80						
circRNA species														
species	chr	start	end	ensemblID	gene_name	logFC	logCPM	Pvalue	padj	FC				
hsa_circ_0009013	chr3	195101737	195133645	NM_012287	ACAP2	2.37	6.96	9.19E-11	1.53E-07	5.16				
hsa_circ_0123184	chr3	195131435	195133645	NM_012287	ACAP2	2.31	6.93	5.37E-10	4.48E-07	4.95				
hsa_circ_0134168	chr1	78105133	78141374	ENST00000370801.3	ZZZ3	-3.03	10.00	1.08E-08	5.98E-06	0.12				
hsa_circ_0139507	chrX	102733063	102785825	ENST00000372633.1	RAB40A	1.80	5.79	5.08E-08	2.12E-05	3.48				
hsa_circ_0139505	chrX	102730028	102752541	ENST00000445990.1	LLOXNC01-250H12.3	1.56	5.19	7.69E-07	2.56E-04	2.94				
hsa_circ_0139508	chrX	102733063	102786112	TCONS_00017354	TCONS_00017354	1.49	5.23	1.75E-06	4.26E-04	2.81				
hsa_circ_0001488	chr5	59092885	59179746	NM_001104631	PDE4D	-2.29	6.73	1.79E-06	4.26E-04	0.20				
hsa_circ_0005447	chr3	194928153	194947585	NM_152531	XXYL1	1.15	6.14	4.24E-06	8.84E-04	2.21				
hsa_circ_0135261	chr8	100286425	100341142	ENST00000399596.1	VPS13B	1.10	4.68	5.83E-06	1.08E-03	2.14				
hsa_circ_0103367	chr15	36960311	37002162	ENST00000569302.1	C15orf41	-1.42	7.68	1.91E-05	3.18E-03	0.37				
hsa_circ_0126706	chr4	58094439	58179531	None	None	1.01	5.94	3.33E-05	5.05E-03	2.01				
hsa_circ_0009684	chr1	10093040	10241296	NM_001105562	UBE4B	-1.24	8.26	5.23E-05	7.27E-03	0.42				
hsa_circ_0096701	chr11	88301086	88386432	ENST00000418177.2	GRM5	0.86	6.80	8.47E-05	1.09E-02	1.82				
hsa_circ_0119752	chr2	32142994	32181667	NM_015955	MEMO1	-1.12	5.72	9.33E-05	1.11E-02	0.46				
hsa_circ_0130725	chr6	132539368	132564599	None	None	1.14	5.74	1.38E-04	1.53E-02	2.21				
hsa_circ_0132863	chr7	104306290	104377358	NM_199000	LHFPL3	-0.77	10.46	1.88E-04	1.96E-02	0.59				
hsa_circ_0056159	chr2	113856936	113891590	NM_173843	IL1RN	-1.76	7.06	2.18E-04	2.02E-02	0.30				
hsa_circ_0128521	chr5	167302990	167308471	NM_001122679	ODZ2	1.09	7.31	2.37E-04	2.08E-02	2.12				
hsa_circ_0063775	chr22	46449725	46494438	NR_027034	LOC150381	0.62	4.43	2.86E-04	2.35E-02	1.53				
hsa_circ_0098728	chr12	51001307	51034635	NM_173602	DIP2B	-1.24	13.53	2.96E-04	2.35E-02	0.42				
hsa_circ_0120217	chr2	48686954	48698323	NR_024188	PPP1R21	-1.58	7.36	3.16E-04	2.39E-02	0.34				
hsa_circ_0115951	chr21	37744829	37747401	ENST00000400485.1	MORC3	1.03	6.72	3.37E-04	2.44E-02	2.05				
hsa_circ_0036948	chr15	92397564	92671719	NM_013272	SLCO3A1	0.78	6.29	4.21E-04	2.93E-02	1.72				
hsa_circ_0123091	chr3	189983080	190032848	ENST00000295522.3	CLDN1	0.92	4.24	4.56E-04	3.04E-02	1.89				
hsa_circ_0136453	chr8	35828130	35902033	ENST00000523748.1	RP11-473J6.1	-0.86	7.99	5.05E-04	3.23E-02	0.55				
hsa_circ_0004923	chr2	109389501	110598981	NM_001099289	SH3RF3	-0.69	7.35	5.40E-04	3.33E-02	0.62				
hsa_circ_0108420	chr18	39661086	39739441	ENST00000262039.4	PIK3C3	0.73	8.56	6.49E-04	3.86E-02	1.66				
hsa_circ_0129336	chr5	64493019	64509953	ENST00000314351.5	ADAMTS6	-0.75	11.11	7.35E-04	4.09E-02	0.60				
hsa_circ_0132209	chr6	72816211	72892852	ENST00000348717.5	RIMS1	0.81	4.76	8.18E-04	4.26E-02	1.76				
hsa_circ_0139547	chrX	109263579	109352374	NM_032227	TMEM164	0.74	5.44	8.21E-04	4.26E-02	1.67				
hsa_circ_0113676	chr1	57120676	57140195	NM_006252	PRKAA2	-1.51	9.70	8.51E-04	4.26E-02	0.35				
hsa_circ_0100429	chr13	39311053	39358945	NM_207361	FREM2	-0.93	5.91	9.11E-04	4.26E-02	0.53				
hsa_circ_0024724	chr11	123430969	123465546	NM_020716	GRAMD1B	0.76	4.71	9.55E-04	4.30E-02	1.69				
hsa_circ_0113744	chr1	61195246	61231292	TCONS_000000081	TCONS_000000081	-0.99	5.45	1.11E-03	4.87E-02	0.50				
piRNA species														
species	chr	start	end	Ensembl geneID	genetype	genename	distance	logFC	logCPM	pvalue	padj	FC		
piR-hsa-26399	chr11	85195043	85195070	ENSG00000150672.18_1	protein_coding;	DLG2	0	-1.55	9.66	0.0001	0.008	0.34		
piR-hsa-28160	chr19	50607227	50607253	ENSG00000267890.1_1	lncRNA;	CTD-2126E3.4	-28069	1.36	8.27	0.0004	0.020	2.57		
piR-hsa-28478	chr2	230045585	230045613	ENSG00000153823.19_1	protein_coding;	PID1	0	-1.83	12.57	0.0001	0.008	0.28		
piR-hsa-1077	chr5	71146846	71146874	ENSG00000278824.1_1	processed_pseudogene	RP11-1315F8.2	0	-1.58	10.08	0.0002	0.009	0.33		
rRNA species														
RNAcentral_ID	chr	start	end	Gene_ID	Full Name	logFC	logCPM	pvalue	padj	FC				
URS00008C6BF7	chr21	8210477	8211461	RNA18S1	SSU	-1.31	8.08	0.0001	0.02	0.40				
URS00008C9E2E				AC090637.2	SSU	0.97	7.85	0.0006	0.03	1.96				
URS0000914753	chr8	68306274	68306589	RFO2543	LSU	-0.68	4.41	0.0007	0.03	0.63				
URS0000CADD60	chr21	8213888	8218941	RNA28S	LSU	0.73	8.46	0.0008	0.03	1.66				
URS00008CE4BC				AC079965.5	SSU	0.98	8.11	0.0010	0.03	1.97				
URS00008CBFC	chr21	8210483	8211470	SSURNA	SSU	-1.12	6.96	0.0016	0.04	0.46				
lncRNA species														
RNAcentral_ID	chr	start	end	Name	Source	EnsembleGene	Type	Name	Dist	logFC	logCPM	pvalue	padj	FC
URS00005G6E09	chr1	214274503	214281505	Lnc-PTPN14-2-6	LNCipedia	ENSG0000028351	lncRNA	LINC02775	0	1.33	9.49	0.0002	0.020	2.51
URS00005AE24	chr1	214279570	214281505	Lnc-PTPN14-2-7	LNCipedia	ENSG0000028351	lncRNA	LINC02775	0	1.34	9.39	0.0002	0.020	2.53
URS0000A7764F	chr10	42871521	42874060	LINC02623	HGNC	ENSG0000021514	Unprocessed_pseudogene	RP11-313J2.1	-8100	0.74	11.47	0.0004	0.029	1.67
ENST00000631211.1	chr21	8210384	8211306	Lnc-KCNE1B	LNCipedia	ENSG0000027999	processed_pseudogene	RPSAP68	1281074	0.72	13.15	0.0002	0.020	1.64
ENST00000629969.1	chr21	8254592	8255514	KCNE1B-157	LNCipedia	ENSG0000027999	processed_pseudogene	RPSAP68	1236866	0.78	13.03	0.0001	0.020	1.72
URS0000EABF79	chr6	5778210	5779345	HSALNT0100579	LncBook	ENSG0000014598	protein_coding	FARS2	0	1.41	9.33	0.0001	0.020	2.65
URS0000E9C93	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1.13	7.74	0.0006	0.039	0.46