Supplemental Material to:

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Small regulatory RNAs controlled by genomic imprinting and their contribution to human disease

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Name	Chromosome	Start *	End *	strand	Precursor transcript	Parental chromosome	References
miR-770	chr14	101318727	101318824	+	GTL2 (MEG3)	maternal	
miR-493	chr14	101335397	101335485	+		maternal	
miR-337	chr14	101340830	101340922	+		maternal	
miR-665	chr14	101341370	101341441	+		maternal	
miR-431	chr14	101347344	101347457	+	RTL1as	maternal	Mouse miR-431 is specifically expressed in the central nervous system. [1]
miR-433	chr14	101348223	101348315	+	RTL1as	maternal	Human miR-433 expression level is decreased by five-fold in gastric carcinoma compared with normal gaster samples. [2] Analysis of 160 paired samples of non-tumour mucosa and gastric cancer demonstrated that the low expression level of miR-433 is associated with an unfavourable outcome. [3]
miR-127	chr14	101349316	101349412	+	RTL1as	maternal	miR-127 levels are decreased by 27-fold in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4] miR-127 expression can be increased by 3-fold in cancer cell-lines upon histone deacetylase inhibition and DNA methylation inhibition by reactivating cryptic promoters.[5]
miR-432	chr14	101350820	101350913	+	RTL1as	maternal	miR-432 levels are decreased by 6-fold in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4]
miR-136	chr14	101351039	101351120	+	RTL1as	maternal	Murine miR-136 was overexpressed more than 100-fold in murine lung adenocarcinoma compared to adjacent normal lung tissues. [6] The mouse miR-136 is highly expressed in the brain compared to pooled microRNAs from 8 different mouse

							organs. [7]
SNORD112 (14q(0))	chr14	101364257	101364333	+	MEG8	maternal	C/D snoRNA specifically expressed in the mouse brain. [8]
miR-370	chr14	101377476	101377550	+		maternal	Human miR-370 expression levels were (on average) 4-fold increased in 40 samples of gastric cancers compared to 12 normal controls. [9] miR-370 increased the metastatic potential in xenograft assays, and is able to inhibit the translation of TGFβ-RII. [9] Human miR-370 was 20-fold increased, on average, in 100 samples of Acute Myeloid Leukemia compared to 2 normal bone marrow samples. [10] The human miR-370 is 15-fold increased during epithelial to mesenchymal transition of endometrial carcinosarcoma. [11]
SNORD113-1 (14q(I-1))	chr14	101391158	101391227	+		maternal	C/D snoRNA with marked expression in the brain. [8] This snoRNA is the precursor of piR-31650 in human testis. [12]
SNORD113-2 (14q(I-2))	chr14	101393679	101393749	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-3 (14q(I-3))	chr14	101396256	101396327	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-4 (14q(I-4))	chr14	101402828	101402901	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-5 (14q(I-5))	chr14	101404524	101404600	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-6 (14q(I-6))	chr14	101405893	101405966	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-7 (14q(I-7))	chr14	101407463	101407538	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-8 (14q(I-8))	chr14	101409788	101409860	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD113-9	chr14	101411986	101412056	+		maternal	C/D snoRNA with marked expression in the

(14q(I-9))							brain. [8]
SNORD114-1 (14q(II-1))	chr14	101416170	101416240	+		maternal	C/D snoRNA with marked expression in the brain. [8] This snoRNA is the precursor of piR-34456, piR-33510 and piR-34420 in human testis. [12] SNORD114-1(14q(II-1)) 50-fold over-expression promoted cell growth through cell cycle modulation in cell lines. [13]
SNORD114-2 (14q(II-2))	chr14	101418193	101418269	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-3 (14q(II-3))	chr14	101419686	101419759	+		maternal	C/D snoRNA with marked expression in the brain. [8] This snoRNA is the precursor of piR-34372 in human testis. [12]
SNORD114-4 (14q(II-4))	chr14	101420711	101420784	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-5 (14q(II-5))	chr14	101421707	101421775	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-6 (14q(II-6))	chr14	101423503	101423573	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-7 (14q(II-7))	chr14	101429391	101429466	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-8 (14q(II-8))	chr14	101431118	101431188	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-9 (14q(II-9))	chr14	101432366	101432436	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-10 (14q(II-10))	chr14	101433389	101433459	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-11 (14q(II-11))	chr14	101434448	101434521	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-12 (14q(II-12))	chr14	101435285	101435358	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-13 (14q(II-13))	chr14	101438440	101438513	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-14	chr14	101438440	101438513	+		maternal	C/D snoRNA with marked expression in the

(14q(II-14))							brain. [8]
SNORD114-15 (14q(II-15))	chr14	101439007	101439077	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-16 (14q(II-16))	chr14	101439932	101440000	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-17 (14q(II-17))	chr14	101441143	101441216	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-18 (14q(II-18))	chr14	101442162	101442232	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-19 (14q(II-19))	chr14	101442814	101442887	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-20 (14q(II-20))	chr14	101447341	101447411	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-21 (14q(II-21))	chr14	101448312	101448382	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-22 (14q(II-22))	chr14	101449263	101449333	+		maternal	C/D snoRNA with marked expression in the brain. [8] This snoRNA is the precursor of piR-33372 and piR-34929 in human testis. [12]
SNORD114-23 (14q(II-23))	chr14	101450213	101450283	+		maternal	C/D snoRNA with marked expression in the brain. [8] This snoRNA is the precursor of piR-34291 in human testis. [12]
SNORD114-24 (14q(II-24))	chr14	101451114	101451184	+		maternal	C/D snoRNA with marked expression in the

							brain. [8]
SNORD114-25 (14q(II-25))	chr14	101452394	101452464	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-26 (14q(II-26))	chr14	101453383	101453453	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-27 (14q(II-27))	chr14	101454498	101454566	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-28 (14q(II-28))	chr14	101455467	101455537	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-29 (14q(II-29))	chr14	101456428	101456496	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-30 (14q(II-30))	chr14	101458256	101458326	+		maternal	C/D snoRNA with marked expression in the brain. [8]
SNORD114-31 (14q(II-31))	chr14	101459573	101459646	+		maternal	C/D snoRNA with marked expression in the brain. [8]
miR-379	chr14	101488403	101488469	+		maternal	miR-379 levels are decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4]
miR-411	chr14	101489662	101489757	+		maternal	
miR-299	chr14	101490131	101490193	+		maternal	
miR-380	chr14	101491354	101491414	+		maternal	Expressed in ES cells and provides a constitutive cell survival function by repressing the expression of p53. Its overexpression in neuroblastoma correlates with a poor outcome in individuals with

						MYCN-amplified disease. [14]
miR-1197	chr14	101491901	101491988	+	maternal	
miR-323	chr14	101492069	101492154	+	maternal	
miR-758	chr14	101492357	101492444	+	maternal	
miR-329-1	chr14	101493122	101493201	+	maternal	miR-329 levels are decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4]
miR-329-2	chr14	101493437	101493520	+	maternal	miR-329 levels are decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4]
miR-494	chr14	101495971	101496051	+	maternal	miR-494 expression level is 4-fold increased during neoplasic transformation of non-human primate cells. [15] miR-494 levels are decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts. [4] The 1.5 to 3.5-fold increased expression of miR-494 in a human lung cancer cell line was enough to target and inhibit (by 50%) the translation of the insulin-like growth factor 2 binding-protein 1 (IGFBP1) mRNA and maintains elevated (10 to 20-fold) IGF2 mRNA levels. [16] miR-494 can inhibit the growth of gastrointestinal stromal tumours cell lines by inhibiting the translation of the KIT receptor known to be overexpressed or activated by gain-of-function mutations in this cancer type.[17] The mouse miR-494 serum quantity presents diurnal oscillations in mouse. [18]
miR-1193	chr14	101496389	101496466	+	maternal	
miR-543	chr14	101498324	101498401	+	maternal	miR-543 expression level is 5-fold increased during neoplasic transformation of non-human primate cells. [15]

miR-495	chr14	101500092	101500173	+		maternal	miR-495 expression level is 4-fold increased during neoplasic transformation of non-human primate cells. [15] miR-495 is 32-fold increased in breast cancer stem cell compared to breast cancer cells and is able to promote cell invasion and epithelial-mesenchymal transition *in-vivo* [19] miR-495 was 2.4-fold increased in human KRAS-positive lung adenocarcinomas. [20] Expressed during liver and pancreas development and targets HNF-6 to modulate the effects of this transcription factor in liver and pancreas organogenesis. [21]
miR-376c	chr14	101506027	101506092	+		maternal	miR-376c expression level is 6-fold increased during neoplasic transformation of non-human primate cells. [15] miR-376c levels are 56-fold decreased in osteosarcoma cell lines and human tumor tissues when compared with osteoblasts.[4] miR-376c promotes survival of ovarian cancer cells *in-vitro*. [22]
miR-376a-2	chr14	101506406	101506485	+		maternal	Human miR-376a can target CDK2 and Ago2 mRNAs. [23] miR-376a expression level is 8-fold increased during neoplasic transformation of non-human primate cells. [15] Murine miR-376a was overexpressed more than 30-fold in murine lung adenocarcinoma compared to adjacent normal lung tissues. [6] Mouse miR-376a is highly expressed in the brain compared to pooled microRNAs from 8 different mouse organs. [7] Human miR-376a expression level is 7-fold increased in a group of 28 pancreatic adenocarcinomas compared to

							15 adjacent healthy tissue biopsies. [24]
miR-654	chr14	101506556	101506636	+		maternal	miR-654 expression level is 7-fold increased during neoplasic transformation of non-human primate cells. [15]
miR-376b	chr14	101506773	101506872	+		maternal	miR-376b expression level is 5-fold increased during neoplasic transformation of non-human primate cells. [15] Human miR-376b expression level is frequently increased in breast cancer positive for the increased expression of the v-erb-b2 erythroblastic leukaemia viral oncogene homolog 2 receptor (HER2/*neu*). [25]
miR-376a-1	chr14	101507119	101507186	+		maternal	The human miR-376a targets CDK2 and Ago2 mRNAs. [23] miR-376a expression level is 8-fold increased during neoplasic transformation of non-human primate cells. [15] Murine miR-376a was overexpressed more than 30-fold in murine lung adenocarcinoma compared to adjacent normal lung tissues. [6] The mouse miR-376a is highly expressed in the brain compared to pooled microRNAs from 8 different mouse organs. [7] Human miR-376a expression level is 7-fold increased in a group of 28 pancreatic adenocarcinomas compared to 15 adjacent healthy tissue biopsies. [24]
miR-300	chr14	101507700	101507782	+		maternal	
miR-1185-1	chr14	101509314	101509399	+		maternal	
miR-1185-2	chr14	101510535	101510620	+		maternal	
miR-381	chr14	101512257	101512331	+		maternal	Mouse miR-381 is a repressor of *Mitf* expression and is downregulated by Kit signaling in systemic mastocytosis. [26]
miR-487b	chr14	101512792	101512875	+		maternal	Human miR-487b is downregulated in high-

						risk neuroblastoma group of patients. [27] miR-487b levels are 20-fold decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts.[4]
miR-539	chr14	101513658	101513735	+	maternal	Mouse miR-539 is a repressor of *Mitf* expression and is downregulated by Kit signalling in systemic mastocytosis. [26]
miR-889	chr14	101514238	101514316	+	maternal	
miR-544	chr14	101514995	101515085	+	maternal	Human miR-544 and other microRNAs from the 14q32 cluster are significantly downregulated in osteosarcoma compared to normal bone tissue. [28]
miR-655	chr14	101515887	101515983	+	maternal	
miR-487a	chr14	101518783	101518862	+	maternal	
miR-382	chr14	101520643	101520718	+	maternal	Human miR-382 is induced 8-fold in TGF-beta treated human renal epithelial cells (a model of epithelial-mesenchymal transition) compared to untreated cells. [29] Human miR-382 expression level is increased in t(15;17) acute myeloid leukemia.[30] miR-382 expression level is 3-fold increased during neoplasic transformation of non-human primate cells. [15] miR-382 levels are 11-fold decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts.[4]
miR-134	chr14	101521024	101521096	+	maternal	miR-134 negatively regulates the size of dendritic spines in rat hippocampal neurons.[31] miR-134 is involved in the translational repression of the Pumilio2 mRNA during activity-dependant dendritic outgrowth. [32] Its expression level is 3 fold increased in the mouse pyramidal neurons

							during epilepsy and its silencing can protect mice from epileptic seizure. [33] miR-134 expression level is 2 fold increased in absence of the NAD-dependent deacetylase sirtuin-1 (SIRT1).[34] It downregulates Sox2 during Retinoic acid induced ES cell differentiation. [35] miR-134 expression level is 3-fold increased during neoplasic transformation of non-human primate cells. [15] miR-134 levels are 6-fold decreased in osteosarcoma cell lines and human tumour tissues when compared with osteoblasts.[4]
miR-668	chr14	101521595	101521660	+		maternal	The ectopic expression of miR-668 induces senescence in rapidly proliferating keratinocytes. [36]
miR-485	chr14	101521756	101521828	+		maternal	Human miR-485 is a brain enriched microRNA involved in the regulation of synaptic development and function through inhibition of the presynaptic protein SV2A. [37] Human miR-485-5p expression level is 8-fold decreased in ovarian serous carcinoma compared to benign ovarian serous tumours. [38]
miR-323b	chr14	101522556	101522637	+		maternal	
miR-154	chr14	101526092	101526175	+		maternal	Murine miR-154 is 50% down-regulated after foetal ethanol exposure. [39] Human miR-154 was 43-fold increased, on average, in 100 samples of Acute Myeloid Leukemia compared to 2 normal bone marrow samples. [10] Its expression has been detected during the myeloid/erythroid progenitor commitment. [40] miR-154 is expressed in the stroma of foetal but not adult lung both in

							human and murine lungs.[41]
miR-496	chr14	101526910	101527011	+		maternal	Human miR-496 expression in peripheral blood mononuclear cells decreases by 50% with age, [42] or during embryonic development upon ethanol exposure responsible for brain development retardation which can be reversed by folic acid. [39]
miR-377	chr14	101528387	101528455	+		maternal	Human miR-377 expression level is increasing during the trans-differentiation of mesenchymal stem cells into neuronal progenitors *in-vitro*. [43] miR-377 expression level is increased by two fold during cell growth arrest. [44]
miR-541	chr14	101530832	101530915	+		maternal	
miR-409	chr14	101531637	101531715	+		maternal	Human miR-409-3p is two-fold decreased on average in 90 gastric cancer samples compared to non-tumorous samples, and it suppresses metastasis in mice. [45] Mouse miR-409 was found to be significantly down-regulated in the brain of *Mecp2*-null (KO) (a model of Rett syndrome) compared to wild-type littermates.[46]
miR-412	chr14	101531784	101531874	+		maternal	Human miR-412 expression level is 3.8-fold increased in squamous cell lung carcinoma. [47]
miR-369	chr14	101531935	101532004	+		maternal	This microRNA is used for iPS reprogramming. [48]
miR-410	chr14	101532249	101532328	+		maternal	Specifically expressed in the central nervous system. [1] miR-410 expression level is 4-fold decreased on average in a cohort of high-risk compared to low-risk neuroblastoma patients. [27] However, its high expression

							level is negatively associated with overall survival in advanced ovarian cancer.[49] miR-410 could inhibit cell-cycle progression through CDK1 translational inhibition.[50]
miR-656	chr14	101533061	101533138	+		maternal	
miR-1247	chr14	102026759	102026624	-	DIO3AS	ND	
miR-512-1	chr19	54169933	54170016	+		paternal	
miR-512-2	chr19	54172411	54172508	+		paternal	miR-512-2 is frequently deleted (33%) in meduloblastomas. Its deletion correlates with MYC overexpression in meduloblastomas due to its binding and translational inhibition of *MYCC* 3'UTR.[51] This study suggests that miR-512-2 is a tumour suppressor.
miR-1323	chr19	54175222	54175294	+		paternal	
miR-498	chr19	54177451	54177574	+		paternal	miR-498's high expression levels correlated with the probability of recurrence-free survival in human stage II colon cancer.[52] However, miR-498 was 3.6-fold increased in retinoblastoma compared to normal retinas.[53]
miR-520e	chr19	54178965	54179051	+		paternal	miR-520e is a tumour suppressor microRNA whose expression level is decreased by five-fold on average in hepatocellular carcinoma compared to non-tumorous liver. It may act through the targeting of NF-kB-inducing kinase (NIK) in hepatoma cells.[54]
miR-515-1	chr19	54182257	54182339	+		paternal	
miR-519e	chr19	54183194	54183277	+		paternal	
miR-520f	chr19	54185413	54185499	+		paternal	Expression correlates with the progesterone receptor status in breast cancer.[25]
miR-515-2	chr19	54188263	54188345	+		paternal	

miR-519c	chr19	54189723	54189809	+	paternal	
miR-1283-1	chr19	54191735	54191821	+	paternal	
miR-520a	chr19	54194135	54194219	+	paternal	miR-520a is expressed in the human placenta and is a pregnancy-associated microRNA detected in the maternal plasma. [55]
miR-526b	chr19	54197647	54197729	+	paternal	
miR-519b	chr19	54198467	54198547	+	paternal	
miR-525	chr19	54200787	54200871	+	paternal	Expressed in the human placenta and is a pregnancy-associated microRNA detected in the maternal plasma. [55]
miR-523	chr19	54201639	54201725	+	paternal	
miR-518f	chr19	54203269	54203355	+	paternal	
miR-520b	chr19	54204481	54204541	+	paternal	Induced by IFN-gamma and can downregulate NKG2D ligand MHC class I-related chain A (MICA), which binds to a receptor (NKG2D) used by NK cells to detect virally infected and transformed cells. [56] Expression levels are inversely correlated to the metastatic potential of breast cancer cells. [57]
miR-518b	chr19	54205991	54206073	+	paternal	Expressed in the human placenta and is a pregnancy-associated microRNA detected in the maternal plasma. [55]
miR-526a-1	chr19	54209506	54209590	+	paternal	Expressed in the human placenta and is a pregnancy-associated microRNA detected in the maternal plasma. [55]
miR-520c	chr19	54210707	54210793	+	paternal	Promotes tumour invasion and metastasis. [58] Increased during breast tumourigenesis and metastasis. [59]
miR-518c	chr19	54211989	54212089	+	paternal	Highly expressed in retinoblastoma. [53] Significantly upregulated in pre-eclanmptic placentas where it could downregulate the

							level of hydroxysteroid (17-β) dehydrogenase 1 (HSD17B1), a steroidogenic enzyme expressed in the placenta. [60]
miR-524	chr19	54214256	54214342	+		paternal	
miR-517a	chr19	54215522	54215608	+		paternal	Promotes tumorigenesis and metastasis *in vivo*. [61]
miR-519d	chr19	54216601	54216688	+		paternal	Overexpressed in adipose tissue of non-diabetic severely obese adults. Inhibits the translation of the peroxisome proliferator-activated receptor-α (PPARA). [62] Expression is activated by DNA hypomethylation and p53 mediated transcriptional activation in hepatocellular carcinoma cell line. [63]
miR-521-2	chr19	54219848	54219934	+		paternal	
miR-520d	chr19	54223350	54223436	+		paternal	
miR-517b	chr19	54224330	54224396	+		paternal	
miR-520g	chr19	54225420	54225509	+		paternal	Frequently amplified in a subtype of aggressive primitive neuroectodermal brain tumours where it acts as an oncogene. [64]
miR-516b-2	chr19	54228696	54228780	+		paternal	
miR-526a-2	chr19	54230176	54230240	+		paternal	
miR-518e	chr19	54233092	54233179	+		paternal	
miR-518a-1	chr19	54234260	54234344	+		paternal	
miR-518d	chr19	54238131	54238217	+		paternal	
miR-516b-1	chr19	54240099	54240188	+		paternal	
miR-518a-2	chr19	54242587	54242673	+		paternal	
miR-517c	chr19	54244567	54244661	+		paternal	Frequently amplified in a subtype of aggressive primitive neuroectodermal brain tumours were they act as oncogenes. [64]
miR-520h	chr19	54245766	54245853	+		paternal	Expressed in the human placenta and is a pregnancy-associated microRNA detected in the maternal plasma. [55] Overexpressed in

						hematopoietic stem cells. [65] The tumour suppressing activities, such as cancer cell-mobility and in vitro invasion, mediated by the adenovirus type 5 E1A may be exerted in part by the E1A-mediated downregulation of miR-520h expression. [66]
miR-521-1	chr19	54251890	54251976	+	paternal	
miR-522	chr19	54254465	54254551	+	paternal	A polymorphism in the 3'UTR sequence of PLIN4, a member of the PAT family of lipid storage droplet protein, modulates the miR-522 seed sequence recognition and has an impact on obesity related phenotypes in humans. [67]
miR-519a-1	chr19	54255651	54255735	+	paternal	Upregulated in ovarian tumours. [38]
miR-527	chr19	54257272	54257356	+	paternal	
miR-516a-1	chr19	54259995	54260084	+	paternal	
miR-1283-2	chr19	54261486	54261572	+	paternal	
miR-516a-2	chr19	54264387	54264476	+	paternal	
miR-519a-2	chr19	54265598	54265684	+	paternal	Upregulated in ovarian tumours. [38]
miR-371	chr19	54290929	54290995	+	paternal	The miR-371-373 microRNA cluster is overexpressed in human testicular germ cells, [68] and downregulated in human non-obstructive azoospermia. [69] Expression of the miR-371-373 cluster is a hallmark of the human embryonic stem cells compared to human induced pluripotent stem cells. [70] Overexpressed in a rare embryonal neoplasm derived from liver progenitor cells in a c-Myc-dependent manner and could contribute to the invasiveness of the tumours and poor prognosis. [71] Expression level appears to have both a predictive and a

							functional role in determining human pluripotent stem cell neurogenic differentiation behaviour. [72]
miR-372	chr19	54291144	54291210	+		paternal	The miR-371-373 microRNA cluster is overexpressed in human testicular germ cells, [68] and downregulated in human non-obstructive azoospermia. [69] Expression of the miR-371-373 cluster is a hallmark of the human embryonic stem cells compared to human induced pluripotent stem cells. [70] Overexpressed in a rare embryonal neoplasm derived from liver progenitor cells in a c-Myc-dependent manner and could contribute to the invasiveness of the tumours and poor prognosis. [71] Expression level appears to have both a predictive and a functional role in determining human pluripotent stem cell neurogenic differentiation behavior. [72] Promotes somatic cell reprogramming by targeting multiple cellular processes such as cell-cycle, epithelial-mesenchymal transition, epigenetic regulation and vesicular transport. [73]
miR-373	chr19	54291959	54292027	+		paternal	Highly expressed in retinoblastoma. [53] Promotes tumour invasion and metastasis. [58] Increased during breast tumourigenesis and metastasis. [59] The miR-371-373 microRNA cluster is overexpressed in human testicular germ cells, [68] and downregulated in human non-obstructive azoospermia. [69] Expression of the miR-371-373 cluster is a hallmark of the human embryonic stem cells compared

							to human induced pluripotent stem cells. [70] Overexpressed in a rare embryonal neoplasm derived from liver progenitor cells in a c-Myc-dependent manner and could contribute to the invasiveness of the tumours and poor prognosis. [71] Expression level appears to have both a predictive and a functional role in determining human pluripotent stem cell neurogenic differentiation behavior. [72] Downregulates more than 30 proteins involved in the regulation of invasion and metastasis in breast cancer cell line. [74]
SNORD107 (HBII-436)	chr15	25227141	25227215	+	SNURF-SNRPN	paternal	C/D snoRNA.[75]
SNORD64 (HBII-13)	chr15	25230247	25230313	+	SNURF-SNRPN	paternal	C/D snoRNA. [75]
SNORD108 (HBII-437)	chr15	25232072	25232142	+	SNURF-SNRPN	paternal	C/D snoRNA. [75]
SNORD109A (HBII-438A)	chr15	25287121	25287187	+	SNURF-SNRPN	paternal	C/D snoRNA. [75]
SNORD116-1 (HBII-85-1)	chr15	25296623	25296719	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-2 (HBII-85-2)	chr15	25299356	25299452	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-3 (HBII-85-3)	chr15	25302006	25302102	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-4 (HBII-85-4)	chr15	25304684	25304781	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]

SNORD116-5 (HBII-85-5)	chr15	25307479	25307575	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-6 (HBII-85-6)	chr15	25310172	25310269	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-7 (HBII-85-7)	chr15	25312934	25313030	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-8 (HBII-85-8)	chr15	25315578	25315674	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-9 (HBII-85-9)	chr15	25318253	25318349	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-10 (HBII-85-10)	chr15	25319260	25319363	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-11 (HBII-85-11)	chr15	25321075	25321168	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-12 (HBII-85-12)	chr15	25322197	25322290	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-13 (HBII-85-13)	chr15	25324204	25324297	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-14 (HBII-85-14)	chr15	25325288	25325381	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-15 (HBII-85-15)	chr15	25326433	25326526	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]

SNORD116- 16 (HBII-85-16)	chr15	25327914	25328007	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-17 (HBII-85-17)	chr15	25328734	25328827	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-18 (HBII-85-18)	chr15	25330531	25330624	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-19 (HBII-85-19)	chr15	25331673	25331766	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-20 (HBII-85-20)	chr15	25332808	25332901	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-21 (HBII-85-21)	chr15	25333950	25334043	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-22 (HBII-85-22)	chr15	25335069	25335162	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-23 (HBII-85-23)	chr15	25336932	25337025	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-24 (HBII-85-24)	chr15	25339183	25339276	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-25 (HBII-85-25)	chr15	25342809	25342902	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-26 (HBII-85-26)	chr15	25344645	25344742	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]

SNORD116-27 (HBII-85-27)	chr15	25346721	25346814	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-28 (HBII-85-28)	chr15	25349788	25349880	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD116-29 (HBII-85-29)	chr15	25351667	25351751	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Gene-candidate for PWS. Ubiquitously-expressed. [8]
SNORD115-1 (HBII-52-1)	chr15	25415870	25415951	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing)”. Specifically expressed in the brain. [8]
SNORD115-2 (HBII-52-2)	chr15	25417782	25417863	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-3 (HBII-52-3)	chr15	25420074	25420155	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-4 (HBII-52-4)	chr15	25421979	25422060	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-5 (HBII-52-5)	chr15	25423885	25423966	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing,

							splicing). Specifically expressed in the brain. [8]
SNORD115-6 (HBII-52-6)	chr15	25425644	25425725	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-7 (HBII-52-7)	chr15	25427532	25427613	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-8 (HBII-52-8)	chr15	25429453	25429534	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-9 (HBII-52-9)	chr15	25430778	25430859	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-10 (HBII-52-10)	chr15	25432683	25432763	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-11 (HBII-52-11)	chr15	25434561	25434642	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-12 (HBII-52-12)	chr15	25436563	25436644	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-13 (HBII-52-13)	chr15	25438468	25438549	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-14 (HBII-52-14)	chr15	25440068	25440148	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-15 (HBII-52-15)	chr15	25442723	25442803	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-16 (HBII-52-16)	chr15	25444595	25444676	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-17 (HBII-52-17)	chr15	25446470	25446551	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-18 (HBII-52-18)	chr15	25448374	25448455	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-19 (HBII-52-19)	chr15	25449504	25449585	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-20 (HBII-52-20)	chr15	25451409	25451490	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-21 (HBII-52-21)	chr15	25453230	25453310	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-22 (HBII-52-22)	chr15	25455065	25455146	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-23 (HBII-52-23)	chr15	25456943	25457024	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-24 (HBII-52-24)	chr15	25458806	25458876	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-25 (HBII-52-25)	chr15	25460688	25460769	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-26 (HBII-52-26)	chr15	25463764	25463845	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-27 (HBII-52-27)	chr15	25465650	25465725	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-28 (HBII-52-28)	chr15	25467501	25467574	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-29 (HBII-52-29)	chr15	25468393	25468474	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-30 (HBII-52-30)	chr15	25470350	25470431	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-31 (HBII-52-31)	chr15	25472256	25472337	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-32 (HBII-52-32)	chr15	25474114	25474195	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-33 (HBII-52-33)	chr15	25475985	25476066	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-34 (HBII-52-34)	chr15	25477534	25477615	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-35 (HBII-52-35)	chr15	25479394	25479475	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-36 (HBII-52-36)	chr15	25481232	25481313	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-37 (HBII-52-37)	chr15	25483133	25483214	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-38 (HBII-52-38)	chr15	25484985	25485066	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-39 (HBII-52-39)	chr15	25486893	25486974	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-40 (HBII-52-40)	chr15	25488761	25488842	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-41 (HBII-52-41)	chr15	25490625	25490706	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD115-42 (HBII-52-42)	chr15	25492492	25492573	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-43 (HBII-52-43)	chr15	25494345	25494426	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-44 (HBII-52-44)	chr15	25496006	25496087	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-45 (HBII-52-45)	chr15	25509674	25509726	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-47 (HBII-52-47)	chr15	25513664	25513696	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
SNORD115-48 (HBII-52-48)	chr15	25514930	25515005	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain.

							[8]
SNORD109B (HBII-438B)	chr15	25523490	25523556	+	SNURF-SNRPN	paternal	C/D snoRNA [75] Post-transcriptional regulator of 5-HT2C pre-mRNA (editing, splicing). Specifically expressed in the brain. [8]
miR-675	chr11	2017989	2018061	-	H19	maternal	The expression of miR-675 and its H19 ncRNA precursor are controlled by SOX9 in human articular chondrocytes and are necessary for the down regulation of an unreported negative regulator of a Type II collagen protein (COL2A1). [76] miR-675 and H19 are overexpressed in colorectal cancer cell lines and primary human colorectal cancer samples and could target the pRB tumour suppressor mRNA. [77] The pre-miR-675 and H19 exon structure are conserved in marsupials. [78]
miR-483	chr11	2155364	2155439	-	IGF2	paternal	Overexpressed in Wilms' tumors, where it has anti-apoptotic effects by targeting the BBC3/PUMA mRNA, [79] and is induced by the Wnt/β-catenin pathway. [80]
miR-335	chr7	130135952	130136045	+	MEST	paternal	Prognostic marker in colorectal cancer. [81] Overexpression of miR-335 led to decreased cell viability and an increase in apoptosis, supporting its tumour-suppressive function.[82] It is frequently inactivated in human breast cancer. [83] It directly targets pRb mRNA 3' UTR and activate the p53 tumour suppressor pathway to limit cell proliferation and neoplasic cell transformation. [84] miR-335 supresses metastasis and migration through targeting

							of the progenitor cell transcription factor SOX4 and extracellular matrix component tenascin C. [85]
miR-296	chr20	57392670	57392749	-	NESPAS	paternal	Expressed from the paternally expressed long non-coding antisense transcript Nespas which regulates in *cis* imprinted gene expression at the Gnas imprinted domain. [86] Targets p21WAF1 3'UTR. [87] Regulator of cell migration, invasion and tumourigenicity trough inhibition of Scrib. [88] Elevated levels in human brain tumours where it contributes to angiogenesis. [89] miR-296 targets the coding sequence of the Nanog mRNA to inhibit its translation. The silent mutation of its binding sequence can partially reverse the expression of differentiation markers induced upon miR-296 overexpression. [35]
miR-298	chr20	57393281	57393368	-	NESPAS	paternal	Expressed from the paternally expressed long non-coding antisense transcript Nespas which regulate in *cis* imprinted gene expression at the *Gnas* imprinted domain. [86] Recognizes and inhibits the translation of the β-amyloid precursor protein converting enzyme (BACE1). [90]

*: hg19 human coordinates.

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