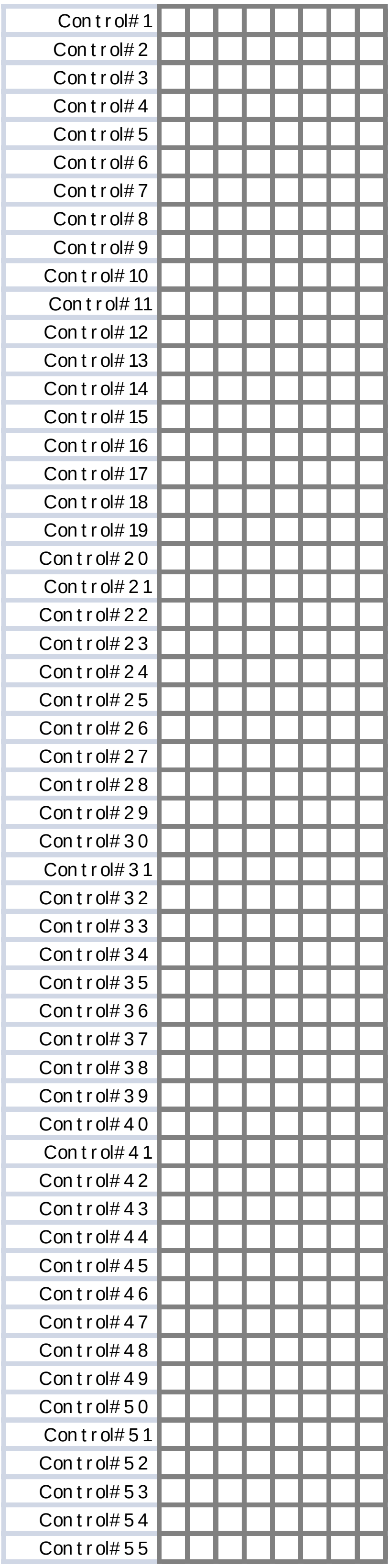
Muthusamy et al., Supplementary Fig. 1



Supplementary Figure 1. (**a**) Methylation status of LXN promoter region in control normal blood samples. Blank squares indicates lack of methylation.

Table 1. RT-QPCR Primer sequences

Gene	Primer Sequence
LXN	F - ATTTAGCCTGGGTTGCCTGT
	R - TTAGTGCCGTATTGTGGATGC
OCT4	F - GTGAGAGGCAACCTGGAGAAT
	R - GTTACAGAACCACACTCGGACC
NANOG	F - AAGAACTCTCCAACATCCTGAAC
	R - CTGGGGTAGGTAGGTGCTGA
SOX2	F - GCACACTGCCCCTCTCAC
	R - ATGCTGTTTCTTACTCTCCTCTTT
KLF4	F - CGCCGCTCCATTACCAA
	R - ACAGCCGTCCCAGTCACAG
MYC	F - TCCTCGGATTCTCTGCTCTC
	R - GATTTCTTCCTCATCTTCTTGTTC

Melanoma Sample	Absent (-)	Weak (+)	Moderate (++)	Strong (> +++)
1		90%		
2	20%		80%	
3		90%		
4	>90%			
5	>90%			
6	>90%			
7		>90%		
8	>90%			
9	40%	60%		
10	20%			80%
11	70%	30%		

Table 2. Expression of LXN in melanoma tissue sections interpreted from The Human Protein Atlas (http://www.proteinatlas.org/) staining with validated antibody – HPA014179

Primary cultured melanocytes	Melanocytes1 *	
	Melanocytes c261	
	Melanocytes c264	
	Melanocytes c293	
	Melanocytes c295	
	HFSC	
	HMAP	
Congenital Nevi	YUOPE	
	YUVATI	
	YUCLIR	
Melanoma cell lines	MelJuSo *	▨
	UACC903 *	▨
	C8161 *	▨
	Neo6/C8161 *	
	WM1205 *	▨
	WM455 *	▨
	WM1366 *	▨
	WM293A *	▨
	WM35 *	░
	Roth*	▨
	Carney *	▨
	WM793 *	▨
	Swift-Mel *	▨
	YULAC	▨
	YURIF	▨
	YUSIK	▨
	WW165	▨
	MEL501	▨
	YUCAL	▨
	YUMAC	▨
Melanoma tumor tissues	86002 *	▨
	86008 *	▨
	86016 *	▨
	86060 *	▨
	86075 *	▨
	86134 *	▨
	86140 *	▨
	86187 *	▨
	86221 *	
	86233 *	▨
	86246 *	▨
	86296 *	▨
	86304 *	▨
	86307 *	▨
	86335 *	▨
	86338 *	▨
	86392 *	▨
	86393 *	▨
	86396 *	▨
	86397 *	▨
	YURER	▨
	YUTUR	
	YUKIL	▨
	YUPAO	▨
	YUROL	▨
	YUPER	▨
	YUHUY	▨
	YUBUNE	▨
	YUKOLI	▨
	YUCHER	▨
	YUFIT	▨
	YUHOIN	▨
	YUKAY	▨
	YUMUT	▨

Table 3. List of samples analyzed for promoter hypermethylation of LXN. Gray shading indicates presence of methylation. Light gray indicates partial methylation . Star indicates – methylation previously reported in Muthusamy et al 2006.