Table S1. Clinic profiles of 25 healthy donors

Variable	Mean ± SEM / Count	Normal Range	Within normal range
Age	43 ± 12	-	-
Gender		-	-
Male	13	-	-
Female	12	-	-
Erythrocyte count	4.38 ± 0.51	3.5 - 5.5× 10^{12}/L	Yes
Hemoglobin	14.51 ± 1.33	11 – 16 g/dL	Yes
Platelet count	226.41 ± 38.58	100-300 × 10^9/L	Yes
White blood cell count	6.75 ± 1.52	4 – 10 × 10^9/L	Yes
Percentage of neutrophil	54.41 ± 7.15	40 – 70 %	Yes
Percentage of lymphocyte	35.65 ± 6.37	20 – 50 %	Yes
Percentage of monocyte	7.15 ± 1.83	3 – 10 %	Yes
Percentage of eosinophil	4.12 ± 1.54	0.4 – 8 %	Yes
Percentage of basophil	0.61 ± 0.31	0 – 1 %	Yes
Absolute neutrophil count	3.45 ± 1.68	1.8 – 6.3 × 10^9/L	Yes
Absolute lymphocyte count	1.73 ± 0.57	1.1 – 3.2 × 10^9/L	Yes
Absolute monocyte count	0.31 ± 0.12	0.1- 0.6 × 10^9/L	Yes
Absolute eosinophil count	0.15 ± 0.06	0.02- 0.52 × 10^9/L	Yes
Absolute basophil count	0.01 ± 0.01	0 - 0.006 × 10^9/L	Yes
K^+	4.54 ± 0.57	3.5 – 5.5 mmol/L	Yes
Na^+	141.35 ± 3.17	135 – 145 mmol/L	Yes
Cl^-	103.57 ± 2.64	99 - 110 mmol/L	Yes
Ca^{2+}	2.33 ± 0.09	2.11 – 2.52 mmol/L	Yes
Blood urea nitrogen	4.15 ± 1.49	2.5 – 7.14 mmol/L	Yes
Creatinine	67.93 ± 16.11	40 -106 μmol/L	Yes
Blood glucose level	5.15 ± 0.37	4.16 – 5.83 mmol/L	Yes
Alanine transaminase	19.81 ± 8.15	7 – 50 U/L	Yes
Aspartate transaminase	26.51 ± 8.94	13 – 40 U/L	Yes
Alkaline phosphatase	56.23 ± 11.41	35 – 135 U/L	Yes
Gamma-glutamyltransferase	19.73 ± 6.41	7 – 60 U/L	Yes
Total protein	73.32 ± 5.94	65 - 85 g/L	Yes
Albumin	47.81 ± 4.23	40 - 55 g/L	Yes
Globulin	28.84 ± 2.14	25 – 35 g/L	Yes
Total bilirubin	13.41 ± 3.62	0 - 20.5 g/L	Yes
Urine RBC	Negative	Negative	Yes
Fecal occult blood test	Negative	Negative	Yes
HIV test	Negative	Negative	Yes
HBsAg	Negative	Negative	Yes
Chest radiograph	Negative	Negative	Yes
Abdominal ultrasonography	Negative	Negative	Yes

Table S2. Primers for RT-qPCR

Gene symbol	Forward primer	Reverse primer
ENST00000560647	GGTGTGGAGGAGGAAGACTG	ATCCCTTGAACCCAGCAA
lnc-G0S2-3:2	TGGGAGGAGAATGGGAAAG	CGTTGGTGATGTGGTTGAGA
ENST00000512538	CCCCAATAGGATTTGAATGAC	CATACTTGCCTCTCTTGAGCA
lnc-C1orf137-1:1	GTCAGAAGGGACTGGTGAGG	AATGGTGGGCCTCTGTTTC
lnc-SPINK7-1:4	GAACAGCAGGTGGGGATAGA	TGACAGACAGGAACTGGAGGT
lnc-HSPA6-2:4	GGCTGTATTGATTGGGGTGT	CCTGAAGTTTGCCTTTCTGAC
lnc-ITPK1-3:1	GAACCAAAATAGGGCAAGAGC	CTGGGAGAAAACAAACGAGAA
lnc-ASZ1-3:1	GAAGAATAAGGCAGAGCACATCA	TGTTCAGTTTCCCCATCAGC
lnc-ADIPOR2-3:1	CTTCCGCTGTTCCATTCATT	GCTGTCAACCTTCTGCTTCA
lnc-CXCR2-1:4	CTTCCGCTGTTCCATTCATT	GCTGTCAACCTTCTGCTTCA
CTTN	GCTTTGAGTATCAAGGCAAAACG	CCAAGGGCACATTTGTCTTGT
MYO1B	TCAAATTGTTTCTTATTTGGGAGGA	TGTTTGGATTGTAAAACCTTTCTGA
WNT5A	CTTCGCCCAGGTTGTAATTGAAGC	CTGCCAAAAACAGAGGTGTTATCC
WNT5B	GCTTCTGACAGACGCCAACT	CACCGATGATAAACATCTCGGG
LGMN	GATGAACCACCTGCCGGATAA	CATCATAGTAACAGGCGTAGGACGA
FCGR2B	AGCCAATCCCACTAATCCTGA	GGTGCATGAGAAGTGAATAGGTG
FCGR2A	TGCATCACCTTGAAACAATCACT	TTCCACATCCACACAGCCAA
CXCR2	AGGTCAGAAGTTTCATCGTCAAG	AAAGCTGTCACTCTCCATGTTAA
CTTNBP2	AGTTGGCTTAGATAACTTGTACCAT	ACCAAATGGCAATGTAACCACT
SIM2	AAGGAAAATGGCGAGTTTTACGA	CGCGTCTCCTAAACCTTCGG

Table S3. RT-qPCR validation of top 10 lncRNAs

lncRNA	*P* value	RT-qPCR mean	Gene chip mean	difference	SE of difference	t ratio	df
ENST00000560647	0.376231	7.15885	7.72483	-0.565984	0.626064	0.904035	21.0
lnc-G0S2-3:2	0.939727	5.68868	5.65671	0.0319633	0.417694	0.0765232	21.0
lnc-SPINK7-1:4	0.166247	3.49485	3.9216	-0.426746	0.297556	1.43417	21.0
ENST00000512538	0.31094	2.89594	3.17873	-0.282786	0.272355	1.0383	21.0
lnc-C1orf137-1:1	0.500443	3.01713	3.18776	-0.170632	0.248868	0.685635	21.0
lnc-ITPK1-3:1	0.686343	-2.91516	-3.01765	0.102494	0.250312	0.409467	21.0
lnc-HSPA6-2:4	0.243205	-2.38155	-2.68277	0.30122	0.250852	1.20078	21.0
lnc-ASZ1-3:1	0.130611	-3.25998	-2.86398	-0.396008	0.251716	1.57323	21.0
lnc-CXCR2-1:4	0.639109	-4.11044	-3.95686	-0.153584	0.322772	0.475828	21.0
lnc-ADIPOR2-3:1	0.137366	-4.61606	-5.2261	0.610033	0.394931	1.54466	21.0

Table S4. RT-qPCR validation of top 10 mRNAs

mRNA	*P* value	RT-qPCR mean	Gene chip mean	difference	SE of difference	t ratio	df
WNT5A (NM_003392.4)	0.615317	4.72016	4.94415	-0.223993	0.439136	0.510077	21.0
MYO1B (NM_001130158.1)	0.840076	4.24722	4.17301	0.0742083	0.363209	0.204313	21.0
FCGR2B (NM_004001.4)	0.69659	3.12638	3.00758	0.118799	0.30051	0.395325	21.0
CTTN (NM_005231.3)	0.669017	2.61218	2.73923	-0.127053	0.293035	0.433578	21.0
LGMN (NM_001008530.2)	0.457833	-2.99093	-3.23605	0.245125	0.324083	0.756364	21.0
Sim2 (NM_005069.4)	0.517908	-2.40093	-2.58083	0.179899	0.273548	0.65765	21.0
FCGR2A (NM_001136219.1)	0.260776	-3.11357	-2.76212	-0.35145	0.304097	1.15572	21.0
CTTNBP2 (NM_033427.2)	0.907564	-3.59566	-3.63786	0.0421976	0.359065	0.117521	21.0
WNT5B (NM_032642.2)	0.305416	-5.77127	-6.40372	0.63245	0.602032	1.05053	21.0
CXCR2 (NM_001557.3)	0.419297	-5.52842	-5.11913	-0.409288	0.496814	0.823826	21.0

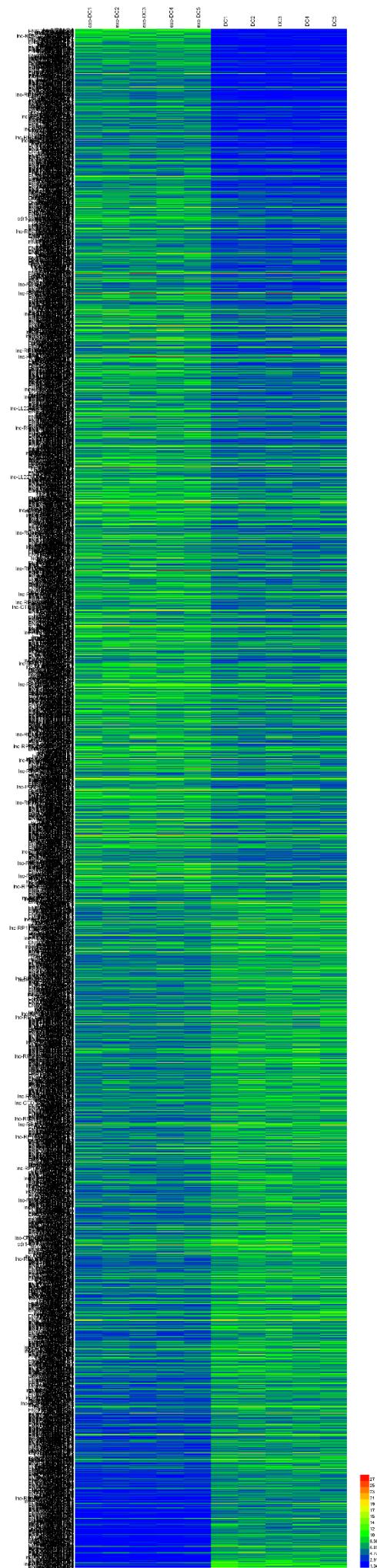Fig. S1. Hierarchical clustering of the differentially expressed lncRNAs.

Fig. S2. Hierarchical clustering of the differentially expressed mRNAs.