

Table S3. Details for the annotation used for transcript identifiers.

Probe Name	Gene Symbol	Ensembl	Accession	Probe Seq
A_23_P38816	<i>AIBG</i>	ENST00000598345	NM_130786	CCTGGTGGCAGAAAGCTGATGCAGCCGCGGG CCCAGAGGTGCTGTTGGTGTCTCAGAAG
A_23_P117599	<i>AHSA1</i>	ENST00000556866	NM_012111	ATTAGTGTGAGCCTTGCCAAAGATGAGCCTG ACACAAATCTCGTGGCCTTAATGAAGGAA
A_23_P155509	<i>AHSG</i>	ENST00000411641	NM_001622	CATGATTGTGTTCTCTGCCTCTGGTTGACCTT ACAAAAACCATTGGAACCTGTGACTTTGA
A_23_P205959	<i>ALDH1A3</i>	ENST00000329841	NM_000693	ATATAGACACTAACCTTGATAGTGATACGTT AGAGGGTTCCTATTCTTCCATTGTACGAT
A_32_P148345	<i>ANXA2</i>	ENST00000421017	NM_001002857	TAAGCCAAAGAAATGTACATTCCAAGCAGTT GGAAGTGAAATCTATGATGTGAAACACTT
A_23_P48217	<i>APOLD1</i>	ENST00000326765	NM_030817	GAGTGGTTGTAGAAGTCTCCATAAATCAGAC ATGTCAAGCAATCAGCCAACGTGGTGTAT
A_32_P162183	<i>C2</i>	ENST00000299367	NM_000063	GGTTGACTTGACTCATGCTTGTTTCACTTTCA CATGGAATTTCCAGTTATGAAATTAAT
A_23_P42282	<i>C4B</i>	ENST00000463249	NM_001002029	GCTTTCGCCTCTTTGAGACCAAGATCACCCA AGTCCTGCACTTCACCAAGGATGTCAAG
A_24_P228130	<i>CCL3L3</i>	ENST00000621940	NM_001001437	TTCCACAGAATTTTCATAGCTGACTACTTTGAG ACGAGCAGCCAGTGCTCCAAGCCCAGTG
A_23_P207564	<i>CCL4L2</i>	ENST00000613947	NM_001291470	CAGGAAGTCTTCAGGGAAGGTCACCTGAGCC CGGATGCTTCTCCATGAGACACATCTCCT
A_23_P138760	<i>CLCF1</i>	ENST00000312438	NM_013246	TGGCAATTCTACACAAAAAGAGATGAGATTA ACAGTGCAGGGTTGGGGTCTGCATTGGAG
A_23_P254522	<i>COL4A4</i>	ENST00000396625	NM_000092	TCCTAAAAGTTCAACCTGTTTCATCTGAACTT GGCCTGAGAACATTTTCTGGGAAGAGGT
A_23_P26021	<i>COPS2</i>	ENST00000299259	NM_004236	TGCTTTTTTGATCAACTGGTTTGTGTTTTGCTG CTGCATTTATCCCAAGAAAAACAGCTT
A_23_P414793	<i>CP</i>	ENST00000463556	NM_000096	TCACGGCCATAGCTTCCAATACAAGCACAGG GGAGTTTATAGTTCTGATGTCTTTGACAT
A_23_P7144	<i>CXCL1</i>	ENST00000395761	NM_001511	CATACTGCCTTGTTTAATGGTAGTTTTACAGT GTTTCTGGCTTAGAACAAAGGGGCTTAA
A_23_P315364	<i>CXCL2</i>	ENST00000508487	NM_002089	CAATGTGACGGCAGGGAAATGTATGTGTGTC TATTTTGTAAGTGTAAAGATGAATGTCAG
A_23_P108415	<i>DARS</i>	ENST00000537273	NM_001349	TTGATTTGGAGAAAATTAAGGCTTACATTGAT TCCTCCGCTTTGGAGCCCCCTCCTCATG
A_23_P12405	<i>ESPN</i>	ENST00000377828	NM_031475	GCCTCATTTCTTATCCCCGCCAAGGGTTTCCT CTCAGTCATTTGTTTACCAGAAACATGA
A_23_P375372	<i>FGA</i>	ENST00000403106	NM_021871	GGAGAGAGTACCACACAGAAAACTGGTCAC TTCTAAAGGAGATAAAGAGCTCAGGACTG
A_23_P93027	<i>FGF18</i>	ENST00000274625	NM_003862	GGGTGATAAGGATTTTATTGTTGACTTGAAAC CCCCGATGACAAAAGACTCACGCAAAGG
A_24_P99244	<i>FGF7</i>	ENST00000560765	NM_002009	TCTACAGATCATGCTTTCACATTATCTGTCTA GTGGGTACTATATCTTTAGCTTGCAATG
A_23_P96568	<i>FLNA</i>	ENST00000498491	NM_001456	TCCCTCGGGAGAATGGCGTTTACCTGATTGAC GTCAAGTTCAACGGTACCACATCCCTG
A_23_P167349	<i>GC</i>	ENST00000503472	NM_000583	CTTTACTGTGATTTCAGAGATTGATGCTGAATT GAAGAATATCCTGTAGTCTGAAGCATG
A_24_P140608	<i>HBEGF</i>	ENST00000230990	NM_001945	CCCATCTGTAGTAATTTATTGTCTGTCTACAT

				TTCTGCAGATCTTCCGTGGTCAGAGTGC
A_24_P311926	<i>HLA-G</i>	ENST00000428701	NM_002127	TTCCTGTTCCAGAAAAGGGGCTGGGATGTCT CCGTCTCTGTCTCAAATTTGTGGTCCACT
A_23_P206760	<i>HP</i>	ENST00000566821	NM_005143	GATAAGATGTGGTTTGAAGCTGATGGGTGCC AGCCCTGCATTGCTGAGTCAATCAATAAA
A_23_P71037	<i>IL6</i>	ENST00000485300	NM_000600	ATTGTTGTTGTTAATGGGCATTCTTCTTCTG GTCAGAAACCTGTCCACTGGGCACAGAA
A_23_P5131	<i>ISYNA1</i>	ENST00000577820	NM_016368	TACCCTATGTTGAACAAGAAAGGACCGGTAC CCGCTGCCACCAATGGCTGCACCGGTGAT
A_24_P416489	<i>MAP2K6</i>	ENST00000590474	U39657	TGGGTAAATATACCCACAGGTTCTATGATTTG TAGCTCTAGGTTTCTTGATGATCAAGGA
A_23_P207699	<i>MAPT</i>	ENST00000621329	NM_016835	ACCAGTCTCTTTGTAAGGACTTGTGCCTCTT GGGAGACGTCCACCCGTTTCCAAGCCTG
A_23_P52761	<i>MMP7</i>	ENST00000260227	NM_002423	TTGGGTATGGGACATTCTCTGATCCTAATGC AGTGATGTATCCAACCTATGAAATGGA
A_24_P279797	<i>MRI1</i>	ENST00000319545	NM_001031727	TTTTATGTGTAAGATCATAAAACGTTGTAAG TTTTCTAAAACACATAAGCTCTCAATAA
A_23_P77529	<i>MSLN</i>	ENST00000545450	NM_005823	GTGGAATGTGACGTCCCTGGAGACCCTGAAG GCTTTGCTTGAAGTCGACAAAGGGCACGA
A_24_P408772	<i>NAMPT</i>	ENST00000354289	NM_005746	ACAGGCACCACTAATAATCAGACCTGATTCT GGAAACCCTCTTGACACTGTGTTAAAGGT
A_23_P127584	<i>NNMT</i>	ENST00000299964	NM_006169	CTGCTGTGAAAGAGGCTGGCTACACAATCGA ATGGTTTGAGGTGATCTCGCAAAGTTATT
A_24_P252364	<i>NRCAM</i>	ENST00000351718	NM_001037132	GTGGTTTTAAAAGTTCCTCTCTCTTTTGTAAAT TATGTTCCCAATTGAGTGTGAATGTCC
A_23_P9485	<i>ORM2</i>	ENST00000431067	NM_000608	GTTTGGTTCCTACCTGGACGATGAGAAGAAC TGGGGGCTGTCTTCTATGCTGACAAGCC
A_23_P257129	<i>PAEP</i>	ENST00000371768	NM_002571	TACGGTGGCGAACGAGGCCACGCTGCTCGAT ACTGACTACGACAATTTCTGTTTCTCTG
A_23_P74001	<i>S100A12</i>	ENST00000368737	NM_005621	TGAAGGCTTTTTACCCAGCAATGTCCTCAATG AGGGTCTTTTCTTCCCTCACAAAACC
A_23_P23048	<i>S100A9</i>	ENST00000368738	NM_002965	GAGCTGGTGCGAAAAGATCTGCAAAATTTTC TCAAGAAGGAGATAAGAATGAAAAGGTC
A_23_P87238	<i>SAA4</i>	ENST00000615694	NM_006512	GATATCCAATCACAAAATTCAAAACAGATAT CTCTATGCTCGGGGAAACTATGATGCTGC
A_23_P16944	<i>SDC1</i>	ENST00000381150	NM_001006946	ACCCTGGGCCCTGGGCTGGAATCAGGAATAT TTTCCAAAAGAGTGATAGTCTTTTGCTTTT
A_23_P134176	<i>SOD2</i>	ENST00000541573	NM_001024465	TTGATGTGTGGGAGCACGCTTACTACCTTCAG TATAAAAATGTCAGGCCTGATTATCTAA
A_23_P107206	<i>STAT3</i>	ENST00000404395	NM_213662	TCATCATGGGCTATAAGATCATGGATGCTAC CAATATCCTGGTGTCTCCACTGGTCTATC
A_23_P70168	<i>TARS</i>	ENST00000502553	NM_152295	CTGCAGGCGTAACTATTTTTGACCTAGTCAGT TTTTAAACAATGTGCATTTGAAGGAGTT
A_24_P142118	<i>THBS1</i>	ENST00000260356	NM_003246	AATAAGCTGCTCTGCCCTTGTGCTCAGAGTG GATGTTATGGGATTCTTTTTTCTCTGT
A_23_P376488	<i>TNF</i>	ENST00000376122	NM_000594	GGGGTATCCTGGGGGACCAATGTAGGAGCT GCCTTGGCTCAGACATGTTTCCGTGAAA
A_24_P152398	<i>TP53AIP1</i>	ENST00000621818	NM_001195195	ACACACACACCTGGCTGGGTTTCAGATCCCTT AGTTTTGGGTGCCCAAGTTCACGGAGGG
A_23_P26954	<i>VAT1</i>	ENST00000592388	NM_006373	TGCCCAACCATTGCAATGGGAGGTGGAGGG

A_23_P102113	<i>WNT10A</i>	ENST00000258411	NM_025216	ACAGGCTCAGCCTCCTCATTGTCTAAATG AACAAATATTTATTTGCACTCTCTTTGCGGC ACTCTGGGGGCGGTGGGGTGC GTGGGGG
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