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Supplemental Data

Gene Expression Profiles in Alveolar Macrophages Induced by Lipopolysaccharide in Humans

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Supplementary Table S1.

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203504_s_at	ABCA1	3.81E-03	856.6	582.9	1291.6	1255.9	1360.6	913.2	1958.8	1072.8	952.5	2096.5	1993.5	1702.8	1530.9	2073.6	1255.9	1702.8	1.4
203505_at	ABCA1	1.80E-03	30.5	26.9	33.5	42.7	47.2	31.4	53.5	48.6	34.0	72.9	71.4	67.4	52.0	63.9	33.5	63.9	1.9
217504_at	ABCA6	1.38E-04	24.4	23.9	20.3	27.6	19.6	24.0	25.8	38.6	65.8	120.1	88.9	63.7	66.5	86.6	24.0	66.5	2.8
1569072_s_at	ABCB5	3.93E-03	89.8	59.8	51.0	59.1	61.7	27.2	93.4	106.0	172.3	275.9	106.6	91.8	99.3	172.6	59.8	106.6	1.8
243167_at	ABCB5	3.61E-03	48.0	24.9	25.6	27.7	35.7	22.1	65.0	59.1	74.9	255.7	108.5	75.4	62.9	111.4	27.7	75.4	2.7
209027_s_at	ABI1	9.84E-03	988.4	786.0	1143.8	1170.9	1396.6	1230.6	1489.7	1396.9	1456.0	2406.6	1701.4	1473.6	1475.1	1779.5	1170.9	1475.1	1.3
206411_s_at	ABL2	2.72E-04	131.5	96.4	119.0	110.7	171.4	103.3	160.9	174.8	195.3	257.2	171.2	292.0	240.0	287.4	119.0	240.0	2.0
226893_at	ABL2	1.29E-03	667.4	569.4	611.9	689.6	1124.2	642.6	1104.1	958.3	1043.6	1509.7	996.2	1430.8	1393.2	1681.4	667.4	1393.2	2.1
231907_at	ABL2	1.98E-03	141.7	113.0	193.5	192.7	291.3	151.9	294.1	223.4	198.3	455.6	264.8	318.9	272.8	469.7	192.7	272.8	1.4
213497_at	ABTB2	4.55E-05	123.5	69.2	58.7	54.6	89.0	69.4	80.5	242.3	390.6	528.4	258.4	389.9	381.5	532.4	69.4	389.9	5.6
221641_s_at	ACOT9	1.05E-04	1000.2	899.4	944.6	840.3	1163.7	970.7	1007.5	1396.2	1664.6	1915.7	1547.3	1786.4	1725.5	1876.9	970.7	1725.5	1.8
202767_at	ACP2	1.91E-03	220.0	136.7	177.9	190.0	194.9	143.1	203.1	329.2	142.5	302.8	373.8	388.2	347.4	319.8	190.0	329.2	1.7
201963_at	ACSL1	6.46E-03	2186.3	1256.1	2587.0	2763.4	3056.2	1805.5	4740.0	3026.7	3723.7	5173.5	4733.9	3428.9	3981.4	5356.6	2587.0	3981.4	1.5
207275_s_at	ACSL1	1.78E-03	2703.0	1373.7	2358.6	2221.4	3076.3	1414.8	3721.9	3866.1	4097.9	4499.1	4665.2	4243.8	4592.6	5270.9	2358.6	4499.1	1.9
202422_s_at	ACSL4	1.72E-03	125.3	112.8	198.6	254.7	250.2	242.2	326.3	201.6	296.0	582.0	438.0	350.0	341.8	484.9	242.2	350.0	1.4
218322_s_at	ACSL5	3.83E-04	517.5	353.2	502.0	545.9	740.8	533.0	624.8	732.2	648.5	1119.8	794.2	1070.6	899.7	1028.0	533.0	899.7	1.7
222592_s_at	ACSL5	4.37E-05	408.9	221.8	371.3	401.3	505.6	327.0	516.6	814.4	955.1	1787.0	1049.7	1382.6	1315.6	1411.0	401.3	1315.6	3.3
200720_s_at	ACTR1A	3.68E-03	484.1	451.0	426.5	494.6	550.6	444.4	486.9	573.1	579.2	649.9	619.9	644.3	608.5	705.9	484.1	619.9	1.3
205327_s_at	ACVR2A	5.19E-04	226.2	221.2	245.9	221.3	312.6	212.1	238.1	357.7	275.7	369.3	418.1	445.8	323.8	418.2	226.2	369.3	1.6
204639_at	ADA	2.42E-06	46.1	34.3	63.9	50.7	46.7	35.3	64.2	301.4	210.5	602.4	226.9	231.5	279.0	414.2	46.7	279.0	6.0
216705_s_at	ADA	5.75E-06	66.3	50.4	92.5	85.5	56.2	44.1	76.2	300.3	189.0	590.3	263.8	231.7	251.6	388.0	66.3	263.8	4.0
205746_s_at	ADAM17	1.58E-03	248.6	269.3	213.4	318.3	342.0	293.2	339.4	401.3	374.2	440.0	401.9	452.7	433.5	472.6	293.2	433.5	1.5
209765_at	ADAM19	1.15E-05	136.6	108.3	76.2	168.7	159.4	65.6	140.0	595.4	387.2	622.1	668.9	1047.8	550.3	1308.9	136.6	622.1	4.6
205180_s_at	ADAM8	2.14E-04	105.7	101.4	109.7	118.7	145.1	101.7	105.5	227.4	226.8	352.8	235.7	460.4	338.7	703.6	105.7	338.7	3.2
201786_s_at	ADAR	1.78E-03	2554.1	2716.0	2539.5	2551.3	2439.5	2257.9	2236.7	3128.3	3265.4	3712.1	3377.0	3481.7	3244.5	3712.2	2539.5	3377.0	1.3
228000_at	ADC	5.95E-03	52.2	39.8	58.3	46.2	51.2	45.6	55.9	58.9	55.2	82.8	65.8	65.5	86.5	65.0	51.2	65.5	1.3
202912_at	ADM	1.16E-05	80.5	40.3	82.3	36.7	125.8	32.2	114.5	365.4	814.5	1234.2	618.6	1008.6	727.5	1013.0	80.5	814.5	10.1
205013_s_at	ADORA2A /// CYTSA	2.65E-06	70.1	52.2	69.4	70.7	100.1	37.6	73.9	541.7	676.3	1318.4	740.5	1402.0	1045.2	1475.9	70.1	1045.2	14.9
223097_at	ADPRHL2	7.38E-04	966.3	1004.5	801.7	843.8	888.3	859.4	866.0	1205.5	1334.3	1523.1	1210.2	1451.7	1361.7	1419.9	866.0	1361.7	1.6
210250_x_at	ADSL	6.12E-03	582.5	482.2	520.4	555.6	549.1	534.7	601.2	663.7	654.5	743.1	642.2	711.8	800.7	708.0	549.1	708.0	1.3
219723_x_at	AGPAT3	2.22E-03	275.2	215.4	229.5	259.5	240.2	233.1	231.8	318.0	278.0	376.6	326.7	337.6	330.6	345.8	233.1	330.6	1.4
224282_s_at	AGPAT3	2.35E-03	276.5	228.6	322.6	327.3	294.3	275.7	288.8	343.0	286.5	415.2	403.7	445.1	455.0	462.7	288.8	415.2	1.4
225440_at	AGPAT3	9.14E-03	540.1	516.0	462.4	565.5	560.7	460.3	469.3	646.4	554.0	653.5	649.8	693.8	662.5	705.1	516.0	653.5	1.3
212285_s_at	AGRN	1.67E-03	459.3	377.5	433.3	451.3	327.9	300.0	261.9	563.6	575.7	845.8	547.4	600.2	663.4	601.3	377.5	600.2	1.6
217419_x_at	AGRN	3.31E-04	221.4	201.9	232.0	235.5	183.9	161.9	155.9	311.8	307.3	503.8	348.0	406.2	370.6	338.0	201.9	348.0	1.7
220199_s_at	AIDA	1.78E-03	168.2	147.3	228.6	216.3	217.1	248.1	225.5	258.2	286.2	492.5	323.7	290.0	293.1	332.4	217.1	293.1	1.4
226801_s_at	AIDA	3.16E-04	1325.6	1534.1	1399.2	1260.4	1496.6	1488.4	1372.6	2076.2	2183.3	2417.7	1904.0	2055.5	2022.4	2225.4	1399.2	2076.2	1.5
224461_s_at	AIFM2	4.03E-04	108.8	49.0	83.7	101.2	92.4	56.9	93.3	153.8	129.1	365.8	190.9	245.5	224.1	217.2	92.4	217.2	2.4
206513_at	AIM2	7.57E-06	369.6	400.1	303.8	259.0	387.9	215.8	242.8	794.3	1074.7	871.4	704.5	866.1	691.9	740.1	303.8	794.3	2.6
208967_s_at	AK2	5.92E-03	1397.5	1202.1	1159.3	1230.2	1185.3	1201.9	1053.3	1421.8	1660.5	1815.1	1513.4	1531.9	1670.0	1577.2	1201.9	1577.2	1.3
212173_at	AK2	1.39E-03	185.1	131.6	135.4	165.8	164.9	138.9	153.6	248.1	179.6	250.6	212.5	220.4	203.0	214.1	153.6	214.1	1.4
204347_at	AK3L1	1.44E-03	56.8	48.8	43.8	55.9	60.1	22.6	60.3	107.2	73.9	87.5	92.8	99.4	102.8	133.6	55.9	99.4	1.8
204348_s_at	AK3L1	4.59E-03	79.6	52.5	38.7	37.2	30.2	32.5	59.5	72.3	84.7	66.6	54.7	50.5	53.1	86.6	38.7	66.6	1.7
225342_at	AK3L1	2.03E-04	62.9	76.3	50.0	64.7	54.5	31.7	123.7	203.6	102.9	132.8	203.0	161.1	153.7	329.1	62.9	161.1	2.6

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Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
202759_s_at	AKAP2 /// PALM2-AKAP2	8.85E-05	59.3	45.2	28.3	30.8	54.8	69.0	259.3	190.0	205.5	373.8	178.7	186.7	346.5	742.6	54.8	205.5	3.7
226694_at	AKAP2 /// PALM2-AKAP2	5.15E-04	94.7	23.8	28.9	50.0	84.4	109.2	546.4	299.3	437.2	665.1	278.4	291.4	663.7	1545.0	84.4	437.2	5.2
222458_s_at	AKIRIN1	1.17E-03	204.9	185.5	249.7	239.7	240.7	216.3	253.8	285.2	255.8	357.1	285.3	337.3	306.5	333.9	239.7	306.5	1.3
204151_x_at	AKR1C1	5.57E-03	2114.5	3094.5	933.2	2416.9	1281.8	1035.9	1000.2	2416.9	4691.0	4055.2	3261.7	2194.6	2746.3	2336.1	1281.8	2746.3	2.1
216594_x_at	AKR1C1	8.35E-03	1524.1	1951.6	548.5	1502.4	760.0	679.6	492.1	1729.6	2272.0	2457.6	2129.0	1391.9	1873.6	1404.9	760.0	1873.6	2.5
209699_x_at	AKR1C2	6.35E-03	2906.2	2976.9	1119.6	2335.2	1552.6	1296.2	1000.4	3369.8	4483.8	6516.6	3261.5	2984.0	3742.8	3127.9	1552.6	3369.8	2.2
211653_x_at	AKR1C2	8.45E-03	751.7	804.6	288.1	615.2	399.7	402.7	360.6	817.9	993.8	1276.4	915.2	757.9	957.9	705.9	402.7	915.2	2.3
212607_at	AKT3	7.56E-04	509.3	491.3	595.4	559.0	722.2	628.0	717.7	778.0	930.3	1695.1	956.0	988.1	970.7	1285.1	595.4	970.7	1.6
219393_s_at	AKT3	8.40E-04	242.9	216.2	313.6	276.6	328.7	299.6	334.5	380.7	357.4	797.6	430.6	406.0	534.2	579.8	299.6	430.6	1.4
222880_at	AKT3	7.71E-04	730.2	590.7	892.6	848.8	944.6	893.2	895.3	1196.0	1337.6	2541.3	1321.5	1250.6	1430.6	1898.2	892.6	1337.6	1.5
224229_s_at	AKT3	8.92E-04	378.5	386.2	576.5	465.6	622.9	516.2	585.6	612.3	708.5	1218.3	670.5	719.7	809.8	1029.3	516.2	719.7	1.4
201951_at	ALCAM	5.49E-03	1118.6	1139.0	1551.7	1054.7	1089.3	1349.6	1682.7	1412.1	1734.3	2407.0	1630.6	1283.1	1449.3	2212.4	1139.0	1630.6	1.4
201952_at	ALCAM	3.32E-03	2889.0	2803.9	3142.5	2397.0	2222.7	2651.1	3094.3	3579.2	3535.0	4390.8	3042.2	3085.5	3145.2	3896.7	2803.9	3535.0	1.3
201196_s_at	AMD1	1.55E-03	1839.4	1885.6	1915.0	1835.7	1552.7	1661.0	1949.2	2085.5	2765.0	3199.4	2716.3	2115.9	2206.4	2923.3	1839.4	2716.3	1.5
207992_s_at	AMPD3	1.72E-03	54.4	85.7	47.4	83.7	86.7	39.1	73.5	142.2	88.0	140.5	170.1	142.4	90.5	127.8	73.5	140.5	1.9
209491_s_at	AMPD3	2.94E-04	38.7	38.6	51.2	57.8	52.2	49.2	61.1	69.5	55.0	82.8	116.8	98.1	68.0	91.4	51.2	82.8	1.6
223967_at	ANGPTL6	7.16E-04	81.5	51.2	89.9	73.8	68.1	76.7	72.5	92.2	107.2	180.7	117.6	117.7	179.7	128.1	73.8	117.7	1.6
219868_s_at	ANKFY1	1.45E-03	404.0	346.4	409.1	372.1	388.1	366.6	359.2	485.8	461.7	588.9	490.7	521.2	572.2	601.7	372.1	521.2	1.4
224900_at	ANKFY1	1.12E-03	643.9	653.1	602.7	572.2	683.3	568.1	554.9	897.4	786.8	980.2	892.1	850.4	860.2	862.9	602.7	862.9	1.4
1553138_a_at	ANKLE1	2.94E-04	116.1	64.2	125.1	171.3	150.6	86.2	239.7	223.0	135.7	236.4	367.6	194.6	236.8	403.2	125.1	236.4	1.9
212200_at	ANKLE2	8.83E-03	598.3	592.6	748.7	725.0	700.7	620.0	1485.5	689.8	816.1	1423.4	982.2	749.2	880.0	1918.3	700.7	880.0	1.3
212201_at	ANKLE2	1.02E-03	214.6	181.4	211.3	209.3	200.4	166.4	345.7	272.8	284.1	436.4	266.2	380.0	374.4	584.2	209.3	374.4	1.8
213962_s_at	ANKLE2	6.07E-04	168.3	118.0	176.9	187.4	172.8	157.8	299.1	250.8	210.3	433.9	225.2	322.1	293.6	565.6	172.8	293.6	1.7
238439_at	ANKRD22	9.08E-06	49.6	51.6	72.5	50.3	65.9	39.8	82.3	244.3	177.7	333.6	421.3	244.0	145.3	328.0	51.6	244.3	4.7
239196_at	ANKRD22	1.12E-05	42.7	27.8	57.2	40.1	67.3	24.8	81.0	248.2	153.1	328.6	377.8	209.6	106.5	316.4	42.7	248.2	5.8
202888_s_at	ANPEP	4.52E-03	349.5	455.3	99.6	550.3	522.3	234.4	557.4	418.0	563.6	197.0	655.4	881.8	521.9	833.6	455.3	563.6	1.2
1555536_at	ANTXR2	1.09E-03	60.0	50.6	51.9	52.5	51.6	48.3	40.9	80.3	66.6	90.6	105.0	104.9	71.7	106.5	51.6	90.6	1.8
225524_at	ANTXR2	3.96E-05	152.1	86.7	74.2	95.5	85.0	66.9	84.2	292.9	221.2	269.5	233.5	323.4	186.6	371.9	85.0	269.5	3.2
1568126_at	ANXA2	9.33E-03	1767.7	1473.5	1384.6	1516.3	1564.1	1038.4	1622.8	1813.5	1967.8	2229.1	1718.9	2320.0	2129.1	2278.2	1516.3	2129.1	1.4
209369_at	ANXA3	7.21E-05	20.5	34.3	43.6	74.1	59.5	26.4	78.0	65.4	129.8	252.8	175.4	122.3	111.1	200.4	43.6	129.8	3.0
203300_x_at	AP1S2	6.42E-03	646.2	623.3	538.5	499.5	690.3	560.3	584.9	644.2	798.5	886.5	673.7	927.3	755.6	850.0	584.9	798.5	1.4
230264_s_at	AP1S2	5.90E-03	1134.8	1070.3	1146.9	1005.2	1421.5	1116.0	1134.8	1228.6	1602.6	1852.7	1328.9	1708.7	1338.7	1769.5	1134.8	1602.6	1.4
219465_at	APOA2	2.81E-04	111.5	84.8	176.2	125.9	139.5	123.9	176.9	181.2	121.1	311.3	166.6	243.5	206.8	256.9	125.9	206.8	1.6
219466_s_at	APOA2	9.23E-03	61.3	52.6	67.2	53.3	52.6	55.8	65.0	69.3	59.5	93.1	72.8	87.5	67.3	79.4	55.8	72.8	1.3
210873_x_at	APOBEC3A	6.17E-06	52.9	47.8	90.4	46.4	84.6	37.7	46.2	394.7	1358.8	2685.7	1206.8	816.2	1282.7	1084.0	47.8	1206.8	25.2
214994_at	APOBEC3F	1.07E-04	67.6	71.9	69.2	78.0	80.9	83.0	87.2	119.1	128.8	169.5	122.8	126.2	150.6	179.5	78.0	128.8	1.7
214995_s_at	APOBEC3F /// APOBEC3G	1.15E-05	109.1	109.6	163.0	132.9	146.6	160.5	146.0	235.8	245.7	389.3	256.6	357.5	307.7	380.2	146.0	307.7	2.1
204205_at	APOBEC3G	6.50E-05	192.5	247.0	370.8	362.4	365.4	396.3	372.3	550.9	562.6	992.3	661.2	828.7	614.3	924.3	365.4	661.2	1.8
221653_x_at	APOL2	1.64E-03	7542.0	7749.9	8588.9	8934.5	6030.3	5999.6	8009.1	8443.4	11485.1	13371.0	11350.3	8770.3	9163.2	11666.5	7749.9	11350.3	1.5
221087_s_at	APOL3	2.11E-05	488.0	529.0	729.6	664.5	723.0	490.5	732.5	1038.4	1567.1	2178.0	1911.8	1327.5	1164.5	1664.1	664.5	1567.1	2.4
1557236_at	APOL6	7.04E-03	635.8	804.0	1113.2	1004.5	909.4	1204.5	1296.6	840.2	1497.3	2575.1	1839.7	1168.5	1181.8	1940.5	1004.5	1497.3	1.5
219716_at	APOL6	1.87E-04	600.5	790.8	754.9	719.6	808.1	811.7	863.7	1188.4	1471.9	1925.4	1380.8	1331.7	1106.4	1929.2	790.8	1380.8	1.7
241869_at	APOL6	2.45E-03	105.4	138.1	174.6	147.9	107.1	142.5	143.7	220.9	158.2	407.3	198.5	170.8	205.5	227.4	142.5	205.5	1.4
221620_s_at	APOO	3.46E-03	294.5	310.3	263.9	259.2	305.4	276.9	269.0	451.2	351.1	446.0	382.6	420.7	390.9	306.7	276.9	390.9	1.4
205568_at	AQP9	1.23E-04	1499.8	909.1	941.9	1106.1	2563.7	692.2	2068.6	3864.6	5451.1	6421.6	4849.5	5620.4	5276.0	6000.9	1106.1	5451.1	4.9
214102_at	ARAP2	5.60E-03	66.4	45.0	84.0	77.6	79.7	65.6	78.2	78.8	65.1	129.3	102.0	98.4	83.5	87.5	77.6	87.5	1.1
218950_at	ARAP3	2.01E-04	50.5	34.7	49.7	58.0	40.3	35.0	42.2	73.1	64.6	103.8	109.9	102.3	51.6	83.9	42.2	83.9	2.0
205239_at	AREG	1.52E-03	32.3	33.1	19.4	17.9	21.3	18.7	29.7	42.5	63.3	98.4	36.3	104.2	45.4	64.6	21.3	63.3	3.0
201096_s_at	ARF4	8.28E-04	315.5	375.6	368.2	378.1	456.1	418.0	471.4	535.8	613.8	864.0	699.5	611.1	593.2	653.8	378.1	613.8	1.6
203311_s_at	ARF6	7.31E-03	588.9	360.8	454.4	508.1	517.2	434.0	540.9	655.6	437.6	599.0	592.3	861.9	777.6	748.8	508.1	655.6	1.3
202211_at	ARFGAP3	1.17E-03	740.2	824.6	980.0	960.2	1138.9	1003.0	1230.0	1180.2	1441.4	2297.3	1518.1	1448.7	1417.1	1735.0	980.0	1448.7	1.5
226638_at	ARHGAP23	4.81E-03	60.0	67.5	45.3	37.4	48.2	51.6	37.9	66.3	86.1	104.1	58.6	73.0	68.4	81.9	48.2	73.0	1.5
225618_at	ARHGAP27	2.55E-03	457.2	392.8	445.0	448.0	429.0	474.2	388.8	548.4	544.1	650.2	528.4	674.6	647.8	703.4	445.0	647.8	1.5
202913_at	ARHGEF11	4.02E-03	437.2	397.0	475.0	574.8	557.6	444.3	448.7	603.4	494.9	676.6	601.7	743.3	660.0	687.3	448.7	660.0	1.5
202914_s_at	ARHGEF11	2.95E-03	313.7	247.7	260.1	286.6	314.2	240.4	279.7	344.4	338.9	406.2	349.8	448.9	397.2	398.6	279.7	397.2	1.4
207629_s_at	ARHGEF2	9.08E-03	231.8	219.6	248.7	245.5	265.5	242.6	253.9	270.1	250.3	350.2	277.4	331.8	330.8	322.0	245.5	322.0	1.3
214139_at	ARID4B	8.01E-03	371.7	338.9	555.0	560.3	554.9	516.2	478.7	579.6	482.7	764.9	621.2	604.0	615.9	702.6	516.2	615.9	1.2
223111_x_at	ARID4B	9.51E-03	266.3	208.4	323.7	266.0	299.6	291.5	278.9	313.6	337.0	375.0	316.6	359.8	369.1	360.1	278.9	359.8	1.3
1558000_at	ARID5B	7.51E-04	68.7	70.9	57.4	63.0	73.7	53.6	69.3	114.9	85.9	142.7	172.2	135.5	126.3	113.4	68.7	126.3	1.8
1558001_s_at	ARID5B	1.02E-04	89.4	84.5	74.2	66.4	92.4	68.6	79.0	164.2	119.3	186.3	185.1	204.5	167.3	178.7	79.0	178.7	2.3
212614_at	ARID5B	7.57E-06	69.1	75.5	97.3	106.4	171.4	80.2	108.1	318.3	302.0	489.3	511.7	391.9	335.8	465.0	97.3	391.9	4.0
235404_at	ARID5B	3.33E-04	45.4	49.4	40.8	45.8	56.2	32.4	42.1	86.0	60.8	102.3	140.0	123.5	101.2	106.6	45.4	102.3	2.3
201228_s_at	ARIH2	5.19E-03	48.1	47.8	71.3	56.6	63.5	67.0	76.3	71.6	68.6	117.6	93.0	82.9	78.4	80.3	63.5	80.3	1.3

Continued

Supplementary Table S1. *Continued..*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
216008_s_at	ARIH2	4.68E-03	148.0	115.0	167.8	141.7	159.5	144.6	149.4	185.6	147.4	231.3	179.3	180.3	176.6	200.5	148.0	180.3	1.2
202091_at	ARL2BP	1.36E-03	255.5	222.6	284.1	275.7	324.4	276.3	319.1	379.7	305.1	426.5	431.3	393.4	361.9	407.1	276.3	393.4	1.4
202207_at	ARL4C	1.34E-03	70.8	42.1	71.4	72.6	72.6	48.5	39.3	114.7	56.2	83.1	127.8	133.8	76.7	88.6	70.8	88.6	1.3
242727_at	ARL5B	4.14E-04	56.9	61.9	128.0	109.8	127.6	117.5	161.5	130.9	268.6	794.8	207.7	304.8	222.5	484.2	117.5	268.6	2.3
222442_s_at	ARL8B	1.09E-03	1865.2	1860.6	1700.5	1735.3	1968.4	1643.5	2354.9	2272.7	3595.6	4620.0	2746.0	2932.8	2990.2	4046.9	1860.6	2990.2	1.6
218694_at	ARMCX1	2.20E-03	253.6	351.0	367.8	295.0	332.0	222.8	302.6	349.8	640.7	801.3	394.4	399.7	303.3	562.1	302.6	399.7	1.3
220658_s_at	ARNTL2	1.50E-04	33.8	19.2	22.7	20.5	30.1	12.4	35.6	62.0	38.9	104.4	86.8	75.3	57.1	99.2	22.7	75.3	3.3
223586_at	ARNTL2	1.35E-03	62.4	52.1	47.1	39.5	71.2	53.9	80.5	95.9	75.2	120.2	126.7	105.5	106.5	125.2	53.9	106.5	2.0
224204_x_at	ARNTL2	1.02E-03	61.8	44.0	48.4	45.2	61.5	35.3	77.2	113.0	62.7	195.7	160.3	134.5	129.6	122.4	48.4	129.6	2.7
224797_at	ARRDC3	1.29E-03	69.8	70.7	113.6	90.1	110.5	130.1	94.0	129.4	117.3	273.4	392.0	239.5	174.8	175.6	94.0	175.6	1.9
231791_at	ASAH2B	1.62E-04	29.6	23.7	39.1	42.5	23.9	29.2	33.6	59.1	86.1	168.5	80.4	52.5	80.3	66.6	29.6	80.3	2.7
224796_at	ASAP1	7.32E-03	1141.5	913.7	1108.4	1085.2	1308.0	1129.7	1219.0	1572.1	1025.0	1434.3	1523.4	1601.7	1464.7	1366.4	1129.7	1464.7	1.3
236533_at	ASAP1	1.92E-03	388.5	239.7	316.2	304.1	347.3	288.2	333.1	448.8	299.3	545.0	408.4	548.1	459.0	476.5	316.2	459.0	1.5
229215_at	ASCL2	1.65E-03	74.2	61.9	79.6	87.1	106.5	90.4	62.4	112.9	162.2	134.9	141.7	161.8	109.5	157.7	79.6	141.7	1.8
206130_s_at	ASGR2	8.55E-03	82.1	52.7	75.4	61.2	72.6	64.4	70.0	85.1	79.5	90.5	73.3	141.8	91.2	119.5	70.0	90.5	1.3
244519_at	ASXL1	6.94E-03	117.6	87.8	164.4	164.7	168.4	141.5	158.9	159.0	131.7	254.9	196.9	167.0	202.8	218.4	158.9	196.9	1.2
1554980_a_at	ATF3	4.69E-05	90.7	53.6	79.8	82.4	96.1	75.3	101.3	190.8	200.9	354.9	170.3	230.9	261.4	330.4	82.4	230.9	2.8
202672_s_at	ATF3	1.39E-05	256.6	123.9	191.1	141.4	265.8	155.0	242.2	603.3	776.7	1342.2	686.2	1084.9	796.5	1100.9	191.1	796.5	4.2
204998_s_at	ATF5	9.85E-05	429.7	282.6	325.4	391.9	432.4	262.5	427.5	681.8	808.6	1214.0	827.7	935.7	864.9	1192.4	391.9	864.9	2.2
204999_s_at	ATF5	2.27E-05	86.5	53.4	111.5	103.7	139.8	77.2	147.3	205.5	185.7	350.5	220.8	360.0	305.7	336.4	103.7	305.7	2.9
217389_s_at	ATF5	2.83E-05	194.5	102.1	170.8	145.0	207.5	168.7	191.2	349.6	307.1	495.3	312.9	441.0	350.5	473.2	170.8	350.5	2.1
203454_s_at	ATOX1	8.65E-03	2475.8	2394.6	2590.7	2334.8	2525.8	2137.7	2379.3	3641.3	2474.3	3177.5	3030.6	3528.3	2857.4	2829.1	2394.6	3030.6	1.3
1554556_a_at	ATP11B	8.12E-03	110.8	72.1	133.6	179.2	187.0	169.7	174.0	163.5	144.5	275.4	215.4	230.6	191.7	225.1	169.7	215.4	1.3
1564063_a_at	ATP11B	9.46E-03	411.8	278.0	269.9	353.0	345.2	301.9	349.3	392.7	519.6	574.7	422.4	460.3	455.5	558.3	345.2	460.3	1.3
212297_at	ATP13A3	3.76E-03	1242.6	1183.9	1347.4	1452.2	1730.0	1486.8	2317.0	1694.1	1654.7	2362.5	2114.1	1922.0	1938.0	2885.8	1452.2	1938.0	1.3
219558_at	ATP13A3	1.58E-04	2889.9	2481.2	2391.4	2518.3	2854.5	2195.1	3455.2	4046.1	3724.9	4415.3	4031.5	5152.7	4600.1	6241.2	2518.3	4415.3	1.8
209186_at	ATP2A2	9.67E-03	2551.5	2782.4	2686.5	2751.3	2748.0	2596.2	3279.2	3283.8	3703.6	3837.0	3730.0	2987.7	3181.1	3600.7	2748.0	3600.7	1.3
209281_s_at	ATP2B1	9.25E-04	574.8	415.1	552.9	617.2	983.4	683.4	746.0	894.2	1073.4	2383.9	1018.4	1522.9	1518.0	1678.7	617.2	1518.0	2.5
215716_s_at	ATP2B1	2.77E-03	774.5	584.9	1007.5	953.3	1369.0	1121.9	1315.9	1020.9	1521.6	3553.1	1452.6	1818.7	2050.2	2358.1	1007.5	1818.7	1.8
209934_s_at	ATP2C1	7.17E-03	1293.1	1563.4	1436.7	1544.6	1569.5	1207.7	1667.1	1357.4	2031.9	2182.0	2155.5	1792.4	1818.5	2182.5	1544.6	2031.9	1.3
1557523_at	ATP6AP1L	8.95E-03	333.9	209.9	297.9	476.5	482.2	515.4	744.1	553.8	540.9	1349.8	788.6	567.5	744.0	993.9	476.5	744.0	1.6
221504_s_at	ATP6V1H	1.57E-03	1881.9	1521.0	1291.5	1405.1	1561.5	1000.8	1277.2	2145.8	2250.8	2576.0	1967.0	2667.2	2333.1	2193.8	1405.1	2250.8	1.6
214343_s_at	ATXN7L1	1.48E-03	79.2	81.9	94.3	86.2	99.4	81.0	90.7	124.6	93.2	232.1	131.8	167.3	129.1	152.2	86.2	131.8	1.5
227732_at	ATXN7L1	1.62E-03	68.0	77.4	116.4	107.9	107.1	129.3	89.4	92.9	133.6	182.0	134.8	139.9	161.5	130.4	107.1	134.8	1.3
232311_at	B2M	5.68E-04	140.1	120.0	217.0	181.0	185.8	134.9	187.9	195.8	194.9	510.5	286.7	272.6	229.1	275.4	181.0	272.6	1.5
1556134_a_at	B3GNT5	5.08E-03	62.8	65.2	85.4	88.7	156.6	97.3	122.5	126.8	121.3	277.5	174.7	141.5	153.1	202.9	88.7	153.1	1.7
201882_x_at	B4GALT1	8.13E-03	101.2	79.7	100.7	122.0	131.9	95.6	140.9	125.4	91.9	188.4	147.2	178.2	154.0	166.6	101.2	154.0	1.5
201883_s_at	B4GALT1	1.24E-03	5811.4	4893.8	5400.4	5810.6	7346.9	5603.6	7286.9	7554.6	8570.3	10556.8	9459.9	8805.8	9091.9	10128.7	5810.6	9091.9	1.6
211631_x_at	B4GALT1	2.48E-04	2445.0	1630.8	1624.1	1915.2	2975.3	1656.5	2883.0	3549.8	4025.2	5087.1	4394.1	5101.8	5009.2	5493.2	1915.2	5009.2	2.6
216627_s_at	B4GALT1	4.11E-04	1619.5	988.2	974.0	1182.3	1878.5	1092.0	1716.2	2267.4	2487.3	3469.5	2977.8	3030.4	3509.0	3617.5	1182.3	3030.4	2.6
229403_at	B4GALT1	3.42E-05	582.2	342.1	446.3	470.9	779.9	436.6	717.7	1058.7	963.7	1511.6	1263.8	1756.0	1525.3	1581.7	470.9	1511.6	3.2
238987_at	B4GALT1	5.25E-03	84.0	41.8	73.4	70.4	79.5	73.2	76.0	111.7	124.5	244.5	123.7	79.0	133.2	145.7	73.4	124.5	1.7
221484_at	B4GALT5	5.84E-04	3398.9	2218.2	2438.0	3394.9	3635.1	2685.9	4043.3	4800.0	6806.0	7283.3	5404.3	6129.7	6536.3	7810.8	3394.9	6536.3	1.9
221485_at	B4GALT5	2.55E-03	502.1	303.9	793.1	939.0	1165.4	759.6	1160.6	848.7	1493.2	2880.6	1516.3	1614.6	1601.1	2123.7	793.1	1601.1	2.0
204194_at	BACH1	1.49E-03	1573.4	1779.8	2441.6	1938.8	2327.8	2095.5	2882.3	2107.7	2849.6	4422.3	2744.6	2862.8	2814.6	3886.4	2095.5	2849.6	1.4
210818_s_at	BACH1	2.69E-03	524.1	377.7	509.0	490.9	533.3	416.8	577.9	600.6	764.7	935.7	551.7	902.0	949.4	1009.4	509.0	902.0	1.8
234938_at	BACH1	4.42E-03	49.9	59.9	47.2	38.3	47.2	31.7	50.3	62.8	58.6	79.5	83.2	78.5	54.0	79.8	47.2	78.5	1.7
202387_at	BAG1	6.91E-04	1530.3	1516.9	1311.6	1304.1	1149.9	1168.8	1091.5	1887.0	2171.4	2152.1	1745.0	2075.9	1967.0	1947.7	1304.1	1967.0	1.5
211475_s_at	BAG1	3.48E-03	2151.3	1939.8	1748.0	1796.1	1556.7	1699.3	1380.0	2240.8	2716.1	2728.1	2234.0	2438.1	2536.0	2445.1	1748.0	2445.1	1.4
203728_at	BAK1	4.05E-03	158.7	138.1	182.9	219.0	182.2	176.6	208.0	191.2	169.4	258.2	256.1	240.1	223.9	282.1	182.2	240.1	1.3
205345_at	BARD1	8.33E-03	358.8	273.1	243.6	292.1	188.4	223.8	200.5	424.4	315.5	317.0	324.3	275.2	303.8	343.9	243.6	317.0	1.3
202391_at	BASP1	5.13E-05	472.0	411.0	459.7	590.6	778.7	469.3	1012.0	1181.1	2559.0	3524.4	1728.1	2404.5	2111.9	3635.1	472.0	2404.5	5.1
205965_at	BATF	2.83E-05	99.2	86.7	93.3	86.0	114.2	60.4	99.3	232.2	202.0	344.3	247.6	451.3	319.4	433.5	93.3	319.4	3.4
228439_at	BATF2	3.37E-05	157.4	160.5	189.1	173.8	147.1	99.4	148.2	329.0	560.4	1012.7	442.8	491.5	363.9	720.8	157.4	491.5	3.1
220358_at	BATF3	3.36E-04	513.9	158.1	266.7	296.4	373.5	263.0	344.9	654.1	766.7	1192.5	720.4	1023.8	1085.3	1312.6	296.4	1023.8	3.5
217985_s_at	BAZ1A	5.78E-04	951.8	871.1	1233.0	1324.0	1720.3	1187.5	1708.2	1594.2	2397.7	3682.6	2222.8	2432.0	2097.0	3169.9	1233.0	2397.7	1.9
217986_s_at	BAZ1A	1.75E-03	536.5	464.0	840.0	792.5	931.2	819.1	992.5	836.4	1317.6	2221.9	1475.1	1114.5	1221.0	1697.6	819.1	1317.6	1.6
210347_s_at	BCL11A	4.50E-03	34.0	53.9	82.5	66.3	69.3	41.8	111.5	63.5	64.8	134.2	101.4	77.9	61.2	136.0	66.3	77.9	1.2
219498_s_at	BCL11A	7.86E-03	32.4	42.7	53.8	40.0	55.0	33.7	53.8	54.8	60.4	122.5	112.8	61.7	35.1	108.0	42.7	61.7	1.4
207004_at	BCL2	5.87E-03	158.2	104.6	118.2	113.4	118.5	131.2	146.1	162.0	137.7	214.8	158.8	153.4	190.5	198.9	118.5	162.0	1.4
207005_s_at	BCL2	2.93E-03	64.6	33.1	59.1	62.0	76.3	58.3	77.1	94.3	37.1	92.2	79.3	92.9	82.5	115.6	62.0	92.2	1.5
221241_s_at	BCL2L14	1.58E-04	35.3	33.1	21.9	10.4	20.8	20.0	24.7	74.3	132.9	291.2	113.4	85.7	98.7	134.3	21.9	113.4	5.2
204907_s_at	BCL3	5.18E-03	54.7	53.8	69.6	53.8	59.5	53.8	63.7	69.5	65.4	101.8	79.2	107.2	84.4	67.1	54.7	79.2	1.4
204908_s_at	BCL3	3.94E-04	433.4	184.3	375.0	438.0	627.4	244.1	527.3	793.7	790.5	1059.4	853.9	1081.1	1137.5	1330.7	433.4	1059.4	2.4
203140_at	BCL6	5.12E-04	1779.2	1393.1	1609.8	1795.0	2682.5	1790.8	2660.6	3016.0	3182.5	3717.8	3714.7	3497.8	3477.7	3682.6	1790.8	3497.8	2.0
215990_s_at	BCL6	1.52E-05	313.4	216.2	283.3	313.1	462.4	264.3	405.8	726.6	557.5	739.1	722.3	864.0	793.1	832.8	313.1	739.1	2.4

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
228758_at	BCL6	1.78E-03	177.8	110.7	141.1	149.9	186.5	119.4	176.0	203.9	210.2	348.9	237.9	257.3	285.1	291.0	149.9	257.3	1.7
1554442_at	BEST1	3.83E-04	420.2	373.0	392.1	413.1	406.1	371.2	387.5	513.6	566.6	781.9	649.8	715.6	676.9	730.1	392.1	676.9	1.7
1554443_s_at	BEST1	2.93E-04	337.6	227.8	320.4	350.4	319.7	285.1	310.1	412.2	397.4	627.9	540.7	553.8	510.6	565.0	319.7	540.7	1.7
204493_at	BID	7.40E-05	359.7	207.6	338.7	317.1	505.9	370.1	497.0	679.5	387.7	710.2	653.4	831.8	598.3	748.5	359.7	679.5	1.9
211725_s_at	BID	5.21E-05	773.8	495.5	654.7	795.0	936.3	619.1	968.3	1270.4	1092.2	1529.6	1420.7	1891.0	1591.1	1718.4	773.8	1529.6	2.0
227143_s_at	BID	2.14E-04	485.2	324.4	426.3	508.3	626.7	444.0	554.9	824.9	560.2	682.6	762.7	879.1	829.1	779.5	485.2	779.5	1.6
210538_s_at	BIRC3	1.14E-04	65.1	75.4	97.9	72.8	152.9	55.3	138.5	161.2	146.3	237.2	261.8	246.9	175.5	290.9	75.4	237.2	3.1
203840_at	BLZF1	2.78E-03	36.4	44.5	73.9	75.5	96.7	93.0	95.3	107.3	87.1	249.5	147.5	132.7	114.2	143.3	75.5	132.7	1.8
32088_at	BLZF1	6.12E-04	46.9	62.0	101.7	98.0	134.9	129.0	104.3	150.0	126.2	318.9	202.3	211.8	175.7	206.4	101.7	202.3	2.0
205290_s_at	BMP2	2.95E-03	51.1	41.9	36.9	40.6	35.5	35.5	40.8	61.8	86.7	153.5	59.6	62.2	61.1	109.7	40.6	62.2	1.5
209920_at	BMPR2	2.77E-04	753.5	682.6	638.2	681.2	723.7	703.5	649.0	1052.1	1057.1	1073.8	940.2	1169.9	1087.6	1262.1	682.6	1073.8	1.6
210214_s_at	BMPR2	6.93E-04	482.3	500.0	446.4	462.2	512.6	477.5	489.4	759.4	665.5	886.4	669.4	721.8	665.6	904.9	482.3	721.8	1.5
204930_s_at	BNIP1	2.45E-03	87.5	82.6	110.6	111.0	105.4	85.9	97.1	120.4	104.5	152.9	132.5	162.4	108.1	125.7	97.1	125.7	1.3
238724_at	BPGM	2.23E-03	100.0	127.5	73.1	104.2	90.3	67.4	86.5	124.0	175.7	180.3	180.4	123.2	98.6	141.7	90.3	141.7	1.6
206044_s_at	BRAF	2.47E-03	117.1	82.7	145.0	90.9	120.8	113.0	129.4	151.5	107.0	180.6	159.7	178.6	148.5	166.0	117.1	159.7	1.4
200920_s_at	BTG1	2.49E-04	354.3	463.5	475.4	457.2	600.2	465.8	471.3	849.3	628.5	994.6	722.5	1408.7	789.1	931.0	465.8	849.3	1.8
200921_s_at	BTG1	1.65E-03	985.1	1434.0	1497.2	1156.1	1751.7	1471.9	1491.0	1612.0	1781.2	3036.9	2252.3	2582.8	1774.3	2288.6	1471.9	2252.3	1.5
201235_s_at	BTG2	1.43E-03	123.9	96.6	200.2	148.4	154.2	192.3	188.1	159.6	162.7	309.6	188.1	401.4	384.0	367.9	154.2	309.6	2.0
201236_s_at	BTG2	1.55E-03	795.6	914.0	1587.8	1056.8	1544.0	1501.5	1398.5	1056.9	1896.6	2924.3	1433.9	2047.0	2017.9	2763.3	1398.5	2017.9	1.4
205548_s_at	BTG3	3.44E-04	277.8	248.9	286.6	247.4	634.4	257.0	528.7	487.7	861.0	1248.1	767.4	983.0	1008.8	1140.3	277.8	983.0	3.5
213134_x_at	BTG3	2.72E-04	268.4	196.6	265.0	233.7	578.3	237.3	488.1	501.1	788.0	1258.1	707.1	939.2	839.0	1094.4	265.0	839.0	3.2
203944_x_at	BTN2A1	4.91E-03	596.9	544.5	693.2	631.5	647.7	633.3	544.7	835.9	782.3	935.0	791.5	703.1	751.5	815.8	631.5	791.5	1.3
215493_x_at	BTN2A1	4.46E-03	683.9	541.4	590.8	569.0	612.2	539.6	543.8	778.7	709.6	853.1	687.4	729.5	737.6	779.5	569.0	737.6	1.3
200776_s_at	BZW1 /// BZW1L1	4.01E-03	137.8	114.0	206.4	245.7	265.0	224.2	286.9	212.5	174.9	398.3	320.1	340.6	271.1	338.8	224.2	320.1	1.4
217905_at	C10orf119	1.14E-03	151.9	96.4	195.7	205.4	242.1	256.5	264.3	307.6	138.2	293.1	353.3	309.6	359.8	353.9	205.4	309.6	1.5
222464_s_at	C10orf119	2.76E-04	701.2	536.5	555.6	557.8	835.0	656.2	718.5	1266.3	664.7	1017.1	1019.4	1293.4	1184.4	1136.6	656.2	1136.6	1.7
238795_at	C10orf18	3.42E-03	63.6	81.6	87.4	87.4	97.2	89.6	103.1	115.2	103.5	162.1	122.8	113.2	118.6	136.5	87.4	118.6	1.4
1557312_at	C12orf61	3.04E-03	43.7	41.8	54.1	49.9	67.0	52.6	64.4	68.2	76.0	235.2	87.8	97.0	83.1	109.7	52.6	87.8	1.7
1553141_at	C13orf31	6.27E-03	107.2	77.0	113.9	97.8	140.7	77.7	132.3	158.1	113.7	254.8	200.8	183.7	174.7	126.0	107.2	174.7	1.6
219563_at	C14orf139	5.63E-03	697.1	499.6	216.8	460.5	702.0	383.8	498.5	757.5	699.8	681.0	817.9	866.0	867.8	1304.3	498.5	817.9	1.6
227544_at	C14orf83	2.01E-03	94.5	57.0	84.8	80.5	80.7	83.3	80.3	118.6	95.6	126.7	93.9	156.5	118.1	117.4	80.7	118.1	1.5
242649_x_at	C15orf21	7.01E-05	25.2	22.4	31.9	33.4	38.1	18.5	87.2	74.3	85.8	317.9	177.5	132.0	97.6	219.3	31.9	132.0	4.1
215087_at	C15orf39	4.84E-03	75.2	63.7	65.9	85.1	83.6	71.3	67.5	83.8	102.3	127.4	95.3	110.7	110.3	125.3	71.3	110.3	1.5
223484_at	C15orf48	1.36E-04	815.5	116.8	372.9	380.3	795.6	95.5	1225.8	3655.8	3513.1	5866.1	3949.0	4021.4	3140.7	5492.1	380.3	3949.0	10.4
1554016_a_at	C16orf57	7.36E-03	196.1	197.9	213.0	220.7	236.9	191.1	261.5	288.7	236.9	275.7	318.1	293.3	279.1	270.5	213.0	279.1	1.3
226608_at	C16orf87	7.93E-03	50.8	55.1	96.2	99.3	90.7	93.1	96.3	93.0	126.7	211.0	142.2	95.7	100.9	143.9	93.1	126.7	1.4
224574_at	C17orf49	7.35E-03	421.1	296.8	355.3	444.3	421.8	320.2	437.6	534.8	333.2	524.4	512.1	801.0	687.4	615.7	421.1	534.8	1.3
214696_at	C17orf91	8.76E-04	586.7	479.6	490.2	550.8	648.5	415.5	726.3	741.1	788.5	1369.2	903.9	1089.7	784.5	1191.7	550.8	903.9	1.6
228066_at	C17orf96	1.17E-04	61.4	45.0	64.2	62.3	76.6	38.2	62.7	108.4	113.9	300.8	129.2	235.2	145.0	262.5	62.3	145.0	2.3
1553686_at	C18orf25	9.92E-03	106.3	76.5	80.9	96.3	88.9	98.6	115.8	111.4	89.7	113.7	131.4	124.2	113.7	154.5	96.3	113.7	1.2
223983_s_at	C19orf12	5.51E-03	251.1	238.8	358.6	263.7	367.2	291.6	377.4	392.0	295.2	539.1	344.1	386.4	433.6	469.8	291.6	392.0	1.3
221764_at	C19orf22	1.54E-04	257.1	230.8	293.8	347.7	282.3	258.7	317.6	376.0	394.9	624.0	506.2	558.4	494.9	525.3	282.3	506.2	1.8
1555491_a_at	C19orf66	2.79E-04	254.4	158.3	284.1	306.1	241.9	219.5	246.4	389.6	389.4	763.3	423.4	611.1	631.6	705.4	246.4	611.1	2.5
218429_s_at	C19orf66	1.76E-05	243.1	202.8	336.0	287.0	230.4	236.5	268.9	468.1	569.3	923.9	549.5	645.6	608.6	790.1	243.1	608.6	2.5
53720_at	C19orf66	9.03E-06	368.9	401.2	431.7	412.8	434.1	372.2	408.1	874.7	1010.9	1493.3	939.5	1129.3	898.1	1332.1	408.1	1010.9	2.5
219439_at	C1GALT1	2.15E-03	125.1	173.5	249.6	177.7	174.9	210.8	223.4	244.0	292.6	498.3	378.9	236.2	231.8	310.8	177.7	292.6	1.6
206721_at	C1orf114	5.56E-03	44.4	43.7	50.6	53.2	52.2	58.0	47.3	53.6	79.3	75.8	55.9	75.5	80.0	63.1	50.6	75.5	1.5
225480_at	C1orf122	9.97E-05	321.4	278.2	295.0	340.3	379.9	325.7	402.4	502.5	463.6	556.9	546.5	753.2	726.7	641.6	325.7	556.9	1.7
223063_at	C1orf198	9.63E-03	134.6	124.6	177.9	162.6	197.2	171.3	193.7	205.1	149.4	251.3	191.7	222.2	225.4	220.7	171.3	220.7	1.3
244379_at	C1orf224	3.99E-04	40.2	27.8	35.5	49.2	49.0	38.0	34.9	67.5	47.7	105.2	68.4	106.1	100.0	102.4	38.0	100.0	2.6
1555225_at	C1orf43	4.73E-03	150.1	126.0	231.8	234.3	227.5	190.2	219.8	211.8	200.2	379.1	308.0	235.1	300.1	267.2	219.8	267.2	1.2
225564_at	C1QTNF9 /// SPATA13	5.35E-03	695.0	793.2	1027.7	624.7	994.3	725.0	1068.2	1002.9	1087.9	1380.8	1038.4	1261.8	785.3	1282.2	793.2	1087.9	1.4
212067_s_at	C1R	6.41E-03	88.5	68.7	80.6	77.1	72.6	68.4	77.3	94.8	92.4	128.5	98.2	98.9	81.0	102.2	77.1	98.2	1.3
202357_s_at	C2 /// CFB	3.58E-06	184.9	179.3	234.4	226.8	315.5	160.1	200.9	808.3	1188.9	1442.1	1005.7	1301.3	1079.1	1648.8	200.9	1188.9	5.9
231991_at	C20orf160	1.06E-04	96.2	65.2	35.3	72.7	99.1	31.7	107.4	396.7	227.5	591.9	471.2	424.2	525.3	536.0	72.7	471.2	6.5
229899_s_at	C20orf199	7.85E-03	46.1	55.2	92.1	64.5	67.7	48.7	63.2	79.1	57.2	127.3	104.9	94.2	79.3	67.8	63.2	79.3	1.3
221211_s_at	C21orf7	1.45E-04	55.4	231.1	82.1	105.2	95.9	86.1	121.2	135.1	425.7	296.9	413.5	196.5	174.4	492.1	95.9	296.9	3.1
1556414_at	C21orf71	9.23E-03	78.6	65.9	62.8	57.8	61.8	48.3	54.3	74.9	113.6	302.2	105.8	96.0	82.7	116.0	61.8	105.8	1.7
200042_at	C22orf28	9.01E-05	762.3	707.7	718.5	692.8	708.9	685.5	685.9	1185.0	1292.7	1483.0	1159.6	1138.5	1071.2	1404.1	707.7	1185.0	1.7
1556072_at	C22orf37	3.46E-03	39.7	41.4	46.9	30.2	41.9	42.5	45.8	46.4	46.7	61.3	44.8	74.9	67.5	77.4	41.9	61.3	1.5
217767_at	C3	5.02E-03	356.9	269.0	316.1	329.5	756.1	228.2	439.9	801.0	317.6	423.9	730.7	1325.7	750.8	543.0	329.5	730.7	2.2
209906_at	C3AR1	5.39E-04	3661.6	1209.8	1345.9	2811.6	1846.3	1722.8	2415.8	4883.6	3318.8	4817.6	5085.0	3856.5	6112.8	4965.8	1846.3	4883.6	2.6
223004_s_at	C3orf1	3.62E-03	2028.0	2100.4	1851.6	2082.1	2188.9	2043.9	2085.9	2462.3	2279.6	3126.3	3100.8	2903.2	2888.5	3454.8	2082.1	2903.2	1.4
226524_at	C3orf38	4.68E-03	548.2	511.5	633.8	639.6	653.6	632.3	611.4	663.1	752.2	1105.7	801.3	830.8	721.1	893.7	632.3	801.3	1.3

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
230405_at	C5orf56	1.93E-04	179.6	245.7	225.9	193.3	252.5	182.9	218.2	302.5	380.7	512.1	343.9	363.4	332.2	501.8	218.2	363.4	1.7
212923_s_at	C6orf145	4.56E-03	955.5	675.2	783.0	790.0	829.2	608.5	853.6	1023.1	1198.6	1304.2	943.2	1051.0	1083.0	1299.7	790.0	1083.0	1.4
1560838_at	C6orf146	8.26E-03	58.1	61.1	65.2	49.4	64.4	51.6	60.8	62.9	98.5	110.5	86.7	70.8	65.5	79.3	60.8	79.3	1.3
1559051_s_at	C6orf150	1.85E-04	237.8	269.7	360.3	358.2	339.7	260.0	329.6	425.7	596.9	967.5	557.4	526.0	528.7	566.4	329.6	557.4	1.7
222309_at	C6orf62	6.97E-03	40.3	34.6	83.7	70.1	66.6	74.0	82.0	79.0	43.7	207.7	113.1	90.4	92.2	93.2	70.1	92.2	1.3
220231_at	C7orf16	5.94E-03	70.5	73.9	22.2	50.2	31.0	42.6	44.1	50.3	112.5	465.1	323.3	192.9	302.5	525.0	44.1	302.5	6.9
231509_at	C7orf16	4.36E-03	44.5	32.5	27.4	25.2	30.0	20.2	23.8	37.5	53.9	201.1	119.0	87.1	143.4	223.2	27.4	119.0	4.3
208310_s_at	C7orf28A /// C7orf28B	2.04E-03	595.5	658.7	685.6	726.8	764.6	696.4	735.4	847.9	824.2	990.2	900.1	968.4	998.0	920.4	696.4	920.4	1.3
201973_s_at	C7orf28A /// C7orf28B /// LOC100133775	7.78E-03	3358.9	3807.4	3545.7	3573.5	4082.4	3788.1	4077.7	4148.6	4744.1	4785.4	4534.8	4544.1	4690.2	4849.0	3788.1	4690.2	1.2
225699_at	C7orf40	3.93E-05	113.5	139.0	172.5	156.0	159.2	157.4	173.7	244.8	236.0	360.4	274.3	267.1	278.0	381.7	157.4	274.3	1.7
228149_at	C7orf60	1.93E-04	171.3	140.2	309.9	242.8	412.7	228.2	421.3	404.0	368.9	882.2	651.8	605.1	526.1	646.1	242.8	605.1	2.5
1554228_a_at	C8orf56	4.02E-04	38.6	33.5	44.1	34.4	36.5	34.3	41.5	47.5	57.9	80.4	50.0	66.2	58.4	63.0	36.5	58.4	1.6
227534_at	C9orf21	2.18E-03	546.2	440.7	523.8	541.5	605.2	496.6	660.1	747.6	699.5	1126.6	693.8	787.9	824.4	860.7	541.5	787.9	1.5
218992_at	C9orf46	6.71E-04	105.7	95.8	138.7	124.9	141.1	116.7	163.2	204.5	114.7	270.5	194.0	206.8	185.1	258.5	124.9	204.5	1.6
221865_at	C9orf91	8.98E-06	59.7	70.8	129.3	112.7	102.8	82.9	110.8	173.1	212.4	497.9	271.2	256.0	192.3	296.2	102.8	256.0	2.5
203963_at	CA12	1.30E-03	35.8	22.1	27.2	22.9	42.9	21.4	53.0	72.3	47.8	57.7	122.5	62.6	131.4	145.9	27.2	72.3	2.7
210735_s_at	CA12	1.40E-03	46.7	41.0	31.5	28.8	33.6	36.8	45.1	49.2	68.2	47.0	52.2	57.3	64.5	66.0	36.8	57.3	1.6
214164_x_at	CA12	1.24E-04	64.6	55.2	46.3	56.5	49.1	47.0	78.4	101.5	97.5	85.4	116.9	79.1	126.5	165.0	55.2	101.5	1.8
215867_x_at	CA12	4.16E-04	47.2	46.5	32.1	37.6	39.5	37.6	60.2	95.5	61.4	69.0	136.9	78.7	104.7	121.7	39.5	95.5	2.4
214933_at	CACNA1A	3.79E-03	65.6	76.2	42.7	55.6	52.3	48.7	36.1	88.3	96.2	89.8	68.3	67.4	67.6	58.6	52.3	68.3	1.3
210817_s_at	CALCOCO2	4.50E-03	722.0	768.9	769.8	717.6	848.8	767.3	796.7	923.9	995.0	1210.7	927.4	959.3	960.0	1033.5	768.9	960.0	
1.2221732_at	CANT1	4.87E-03	160.7	161.5	254.4	224.2	288.9	217.4	265.9	340.0	242.9	343.8	270.1	361.0	303.0	335.2	224.2	335.2	1.5
208683_at	CAPN2	4.24E-04	1317.8	1391.9	1000.1	1263.7	1531.5	1015.3	1197.3	1892.4	1806.3	1859.4	1920.4	2321.1	1888.8	2315.8	1263.7	1892.4	1.5
209970_x_at	CASP1	7.59E-03	1885.4	2609.5	2709.1	2258.7	2585.7	2119.4	2283.3	2407.9	3349.0	4021.1	3011.7	2815.3	2397.4	3020.6	2283.3	3011.7	1.3
211367_s_at	CASP1	8.12E-03	1502.3	1830.1	1772.0	1736.9	1650.0	1457.1	1573.4	1673.0	2286.0	2762.6	2010.2	1977.9	1956.5	2105.4	1650.0	2010.2	1.2
205467_at	CASP10	5.52E-03	328.4	374.9	448.7	406.2	402.7	432.5	334.7	437.2	566.8	717.8	534.9	442.5	485.8	560.6	402.7	534.9	1.3
202763_at	CASP3	2.08E-03	74.3	85.7	106.5	107.1	119.9	102.0	92.9	119.6	92.0	163.8	149.9	156.7	153.9	152.9	102.0	152.9	1.5
209310_s_at	CASP4	9.56E-04	3131.1	2350.5	2553.6	2698.4	2821.8	2238.3	3012.4	3740.6	4132.0	4860.7	3523.7	4171.1	3832.2	4922.2	2698.4	4132.0	1.5
213596_at	CASP4	1.24E-03	417.8	419.6	399.8	439.9	329.2	292.4	425.4	469.4	671.7	850.7	679.7	468.8	486.0	729.2	417.8	671.7	1.6
207500_at	CASP5	5.61E-05	284.9	128.5	265.5	297.2	283.5	297.2	391.3	515.4	371.5	705.9	587.6	497.4	766.1	786.9	284.9	587.6	2.1
207181_s_at	CASP7	3.95E-03	710.6	1073.5	851.0	984.0	1017.1	858.8	1177.3	916.9	1594.9	2125.1	1763.4	1310.0	1047.0	1816.7	984.0	1594.9	1.6
243386_at	CASZ1	8.06E-03	43.8	44.7	34.5	43.4	60.6	41.4	47.3	96.7	49.5	89.0	59.3	67.4	64.3	76.6	43.8	67.4	1.5
235221_at	CBLN3	2.26E-03	44.1	73.5	74.4	101.1	89.6	63.5	77.1	87.6	114.1	139.9	158.3	125.3	76.3	91.9	74.4	114.1	1.5
226193_x_at	CBWD1	3.23E-03	2280.5	2364.2	2067.2	1948.1	2105.6	2244.8	2160.6	2637.2	3039.8	3265.1	2555.2	2740.4	2796.7	3023.5	2160.6	2796.7	1.3
202047_s_at	CBX6	1.10E-03	136.5	97.0	175.3	169.7	146.9	110.9	187.2	168.7	142.2	279.3	206.6	218.7	188.7	277.3	146.9	206.6	1.4
218655_s_at	CCDC49	4.89E-03	178.5	171.8	212.1	209.6	235.0	209.1	214.0	218.7	229.8	288.2	240.2	292.0	269.0	262.4	209.6	262.4	1.3
225331_at	CCDC50	6.54E-04	917.4	1164.3	1196.9	1046.7	1255.4	1150.8	1150.4	1368.5	2548.2	3557.3	1910.0	1999.2	1601.7	2341.4	1150.8	1999.2	1.7
235051_at	CCDC50	1.32E-03	132.4	213.7	254.9	243.7	276.3	258.2	225.9	231.6	343.2	533.1	338.9	366.1	315.0	354.5	243.7	343.2	1.4
219774_at	CCDC93	2.51E-03	279.1	232.7	232.2	216.9	291.1	254.6	227.5	346.5	310.6	502.3	327.1	398.0	339.5	345.6	232.7	345.6	1.5
210390_s_at	CCL14-CCL15 /// CCL15	8.48E-05	71.9	51.0	65.1	37.3	159.0	24.6	115.7	262.6	339.8	1254.9	226.5	465.4	181.6	613.6	65.1	339.8	5.2
210072_at	CCL19	1.24E-03	63.4	48.6	45.3	56.1	42.5	34.1	52.6	90.0	72.1	61.6	96.3	101.3	87.3	81.1	48.6	87.3	1.8
216598_s_at	CCL2	3.33E-05	1005.9	339.2	218.2	374.6	228.9	92.1	742.7	4754.5	2430.9	2280.2	3119.7	5778.3	2893.7	6358.4	339.2	3119.7	9.2
205476_at	CCL20	5.12E-04	586.7	69.0	428.4	291.6	1401.5	220.9	1399.0	2712.3	5705.1	7975.7	3611.3	5128.5	5171.0	6032.8	428.4	5171.0	12.1
207861_at	CCL22	3.91E-05	115.3	87.6	70.5	88.8	148.7	89.3	112.4	293.9	186.6	375.3	361.8	385.0	283.3	435.0	89.3	361.8	4.1
210548_at	CCL23	4.07E-05	298.1	156.8	305.5	315.0	732.8	124.1	503.4	880.6	520.8	1809.0	1412.4	2022.9	926.0	1474.0	305.5	1412.4	4.6
210549_s_at	CCL23	3.83E-04	1003.7	484.1	728.3	869.2	1757.6	226.9	1223.5	2116.7	1632.5	4006.3	3306.8	4073.2	2425.8	3413.6	869.2	3306.8	3.8
205114_s_at	CCL3 /// CCL3L1 /// CCL3L3	3.46E-04	564.2	95.1	488.2	439.8	1750.3	337.5	2629.2	3411.1	5254.6	8224.9	5004.2	6462.8	7365.3	8522.1	488.2	6462.8	13.2
204103_at	CCL4	9.46E-04	2691.4	521.6	2427.6	1777.2	5768.4	1338.0	5565.2	8562.9	9931.8	13337.0	10437.5	11312.7	10612.6	11792.1	2427.6	10612.6	4.4
1405_i_at	CCL5	8.15E-06	59.0	59.9	64.3	53.3	101.3	126.1	95.0	270.6	399.6	525.2	426.0	446.5	439.1	839.3	64.3	439.1	6.8
1555759_a_at	CCL5	1.08E-05	114.8	100.1	63.6	99.2	122.5	151.3	109.2	414.5	447.3	494.5	453.6	677.1	515.5	908.4	109.2	494.5	4.5
204655_at	CCL5	7.57E-06	51.5	68.4	88.5	78.7	97.4	117.1	77.9	227.4	327.1	455.4	368.7	421.7	330.3	604.2	78.7	368.7	4.7
208075_s_at	CCL7	1.15E-05	47.6	29.2	23.3	29.7	30.1	19.5	46.7	222.4	105.9	156.3	279.7	419.4	156.4	349.8	29.7	222.4	7.5
214038_at	CCL8	1.15E-05	74.3	85.0	55.6	21.9	31.2	23.4	75.2	558.3	652.7	1154.6	1051.3	804.8	508.3	2091.8	55.6	804.8	14.5
205899_at	CCNA1	1.12E-05	25.8	24.0	29.4	20.9	33.4	21.7	28.9	80.4	213.9	365.8	141.2	186.1	176.4	222.7	25.8	186.1	7.2
200953_s_at	CCND2	1.11E-03	251.0	235.0	264.2	381.4	262.6	163.9	290.4	382.6	272.5	409.5	767.4	432.8	367.8	692.9	262.6	409.5	1.6
227280_s_at	CCNYL1	5.65E-03	116.2	143.7	195.8	175.6	231.5	209.3	210.7	216.2	220.1	408.5	307.2	260.1	224.0	289.2	195.8	260.1	1.3
228810_at	CCNYL1	8.02E-05	39.1	40.6	83.0	72.6	83.3	67.9	74.0	108.1	108.9	242.1	167.2	137.9	122.2	140.2	72.6	137.9	1.9
205099_s_at	CCR1	7.14E-04	779.8	622.0	675.1	1089.0	879.4	637.0	1076.1	1043.4	1193.2	1425.2	1532.3	1235.3	1205.4	1608.5	779.8	1235.3	1.6
206978_at	CCR2	4.84E-04	109.1	68.5	59.3	67.6	77.3	68.6	68.2	275.8	103.8	182.2	169.5	296.8	207.0	523.9	68.5	207.0	3.0
206991_s_at	CCR5	3.00E-05	135.4	60.1	95.6	112.8	100.3	56.3	104.3	277.5	156.6	261.1	264.3	281.9	235.6	416.8	100.3	264.3	2.6
206337_at	CCR7	3.48E-04	31.3	24.6	25.0	40.1	41.4	24.3	19.1	65.2	118.6	209.1	84.4	134.9	85.2	168.5	25.0	118.6	4.7
211434_s_at	CCRL2	2.03E-04	1808.2	1035.5	1386.5	1185.5	2269.0	984.7	2085.1	3164.0	3408.9	4673.6	2178.5	4393.3	3312.9	4078.7	1386.5	3408.9	2.5

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1554283_at	CCRN4L	1.95E-04	73.0	111.4	75.1	93.6	108.6	91.3	106.3	139.9	348.7	390.4	213.5	339.3	175.5	489.4	93.6	339.3	3.6
220671_at	CCRN4L	3.91E-05	72.1	74.2	94.4	82.7	95.9	86.6	95.8	152.6	182.6	196.3	146.0	264.5	166.1	287.3	86.6	182.6	2.1
205987_at	CD1C	1.53E-03	109.1	64.6	38.3	84.7	87.0	72.7	121.1	239.7	79.1	78.3	209.3	179.5	96.4	171.6	84.7	171.6	2.0
207315_at	CD226	3.55E-03	64.1	51.6	39.6	59.0	48.1	48.0	38.3	72.8	62.8	53.1	88.2	76.1	67.7	75.2	48.1	72.8	1.5
208650_s_at	CD24	9.55E-03	39.3	78.4	44.1	55.0	24.4	41.6	25.2	81.8	168.2	52.6	101.0	92.0	50.0	29.2	41.6	81.8	2.0
210031_at	CD247	3.38E-03	53.8	67.1	47.8	77.0	51.7	51.6	53.9	81.9	68.7	65.2	130.9	71.9	75.6	102.5	53.8	75.6	1.4
223834_at	CD274	1.94E-04	1092.4	616.1	1088.8	1383.7	1294.6	862.2	1514.5	2105.5	3117.3	3894.5	2926.7	2540.5	2681.3	3557.3	1092.4	2926.7	2.7
203593_at	CD2AP	8.45E-03	159.1	165.3	254.6	246.6	260.1	262.1	299.1	273.5	358.2	488.5	380.5	307.2	278.6	347.8	254.6	347.8	1.4
205692_s_at	CD38	2.97E-05	128.2	141.2	101.8	96.1	113.0	101.3	86.8	292.4	763.6	978.7	494.7	527.1	534.1	694.5	101.8	534.1	5.2
205153_s_at	CD40	3.18E-05	417.2	268.7	315.1	453.3	474.1	198.2	399.5	895.7	1232.6	1452.0	1114.1	1606.1	1010.5	1322.8	399.5	1232.6	3.1
215346_at	CD40	8.08E-05	1612.5	1301.8	1168.0	1611.4	1891.9	764.4	1714.1	2891.8	4163.5	4403.8	3535.0	3926.9	2692.0	4003.8	1611.4	3926.9	2.4
222292_at	CD40	2.07E-04	123.9	89.3	180.7	187.7	178.0	87.3	180.3	214.4	220.8	556.5	323.0	279.8	231.6	352.8	178.0	279.8	1.6
35150_at	CD40	4.88E-05	418.7	290.3	294.6	448.0	428.2	195.2	403.7	798.9	1209.8	1412.2	1055.4	1479.7	894.0	1297.4	403.7	1209.8	3.0
1557905_s_at	CD44	1.16E-03	10023.8	7131.9	8254.4	10232.3	9999.3	9142.9	9810.3	12207.2	11658.5	13624.6	13371.5	13208.6	13094.2	14509.9	9810.3	13208.6	1.3
1565868_at	CD44	2.20E-04	51.9	65.0	78.9	95.5	96.0	87.2	94.1	77.5	131.2	246.8	243.6	162.4	183.3	174.2	87.2	174.2	2.0
204489_s_at	CD44	6.85E-03	5691.9	4203.2	5306.2	6422.1	6196.0	5862.0	6458.0	6579.9	7044.2	8490.8	8092.4	6951.4	7329.9	8714.0	5862.0	7329.9	1.3
204490_s_at	CD44	8.47E-04	8790.3	6243.5	7249.8	8412.9	8909.6	7760.0	8928.9	11014.3	11715.9	14059.0	12599.0	11869.8	12327.7	13359.0	8412.9	12327.7	1.5
209835_x_at	CD44	5.22E-04	8919.0	6302.3	7545.2	8395.3	8726.4	7710.2	8662.4	11112.3	11928.0	13463.7	12310.9	12263.3	12623.0	14206.2	8395.3	12310.9	1.5
210916_s_at	CD44	3.83E-04	5590.2	3416.7	4355.7	5082.0	5230.3	4443.8	5282.9	6957.6	6025.0	6984.7	7228.2	9063.0	8409.8	8590.7	5082.0	7228.2	1.4
212014_x_at	CD44	5.15E-04	9323.5	6794.6	7666.7	9189.3	8917.7	7935.0	8869.1	11598.6	12195.5	14383.7	12841.6	13096.7	13473.0	14792.8	8869.1	13096.7	1.5
212063_at	CD44	9.95E-03	4473.9	3941.6	5523.7	6527.0	6085.5	5868.3	6857.0	5903.8	6210.6	8118.9	8298.0	6612.0	6964.2	7762.5	5868.3	6964.2	1.2
216056_at	CD44	2.15E-04	90.2	96.9	114.3	146.7	133.4	118.8	145.6	116.5	202.9	332.7	367.9	264.6	248.7	293.3	118.8	264.6	2.2
217523_at	CD44	3.36E-05	77.8	49.7	106.4	128.4	142.6	106.0	141.6	137.0	137.9	318.0	294.6	283.4	233.2	294.0	106.4	283.4	2.7
229221_at	CD44	1.27E-05	70.8	62.3	100.3	115.5	157.4	104.5	140.9	260.9	457.0	650.6	385.6	486.4	456.3	544.4	104.5	457.0	4.4
234418_x_at	CD44	3.26E-04	59.1	35.0	109.4	119.6	117.5	80.2	107.4	88.0	130.8	245.8	240.2	250.1	189.4	180.5	107.4	189.4	1.8
211075_s_at	CD47	8.67E-04	4123.2	3173.1	3129.1	3090.5	3829.4	2808.2	3536.5	4843.2	5537.9	6445.3	5807.0	5152.1	5475.5	5764.6	3173.1	5537.9	1.7
213856_at	CD47	8.48E-03	21.9	40.1	61.5	43.3	68.4	57.9	61.2	63.6	62.8	144.4	111.4	72.3	68.9	81.0	57.9	72.3	1.2
213857_s_at	CD47	3.03E-03	4793.3	4966.5	5527.8	5152.6	5864.9	5154.8	6251.8	5737.2	7844.9	9233.1	8487.1	6638.6	7574.1	7984.7	5154.8	7844.9	1.5
227259_at	CD47	8.22E-03	621.2	398.1	462.3	752.7	519.1	594.6	538.1	683.8	493.8	576.4	904.7	635.1	864.6	686.1	538.1	683.8	1.3
242974_at	CD47	5.17E-04	91.8	113.1	182.8	149.3	199.8	158.5	204.7	180.8	175.8	416.3	300.8	280.0	222.6	309.7	158.5	280.0	1.8
204118_at	CD48	1.15E-05	298.7	206.2	256.2	160.7	499.2	174.8	281.3	741.4	535.2	718.2	643.8	1236.7	697.0	999.0	256.2	718.2	2.8
237759_at	CD48	6.73E-03	92.4	92.6	123.6	136.7	134.2	114.3	137.9	114.5	215.2	259.0	141.3	166.3	196.8	234.2	123.6	196.8	1.6
1555950_a_at	CD55	2.45E-03	1890.1	1124.1	1192.5	2056.2	2218.0	1349.6	1772.6	2367.9	2192.2	3743.4	2747.9	3475.8	3451.5	2932.8	1772.6	2932.8	1.7
201926_s_at	CD55	7.47E-04	1577.0	1023.3	986.6	1637.5	1923.5	1261.8	1501.3	2343.3	2059.2	3134.4	2454.0	3163.3	2972.9	2472.2	1501.3	2472.2	1.6
211744_s_at	CD58	1.69E-03	331.4	455.0	445.9	644.8	695.4	427.6	713.9	752.8	644.4	840.5	854.8	898.2	781.8	974.9	455.0	840.5	1.8
216322_at	CD58	5.50E-03	190.4	180.0	235.3	323.4	324.3	210.1	408.7	417.1	256.9	513.5	466.1	374.3	355.8	450.8	235.3	417.1	1.8
216942_s_at	CD58	2.34E-03	463.3	415.1	447.0	685.5	701.4	452.9	749.6	804.0	628.8	927.6	953.1	813.1	829.6	933.1	463.3	829.6	1.8
209795_at	CD69	2.16E-03	127.0	107.7	82.3	143.6	105.9	225.8	143.2	207.6	338.1	864.6	372.3	287.6	344.2	661.1	127.0	344.2	2.7
1554519_at	CD80	2.11E-05	907.9	947.4	810.0	989.6	1275.5	799.3	1075.8	2416.8	3887.0	5737.5	4600.6	3418.3	3847.5	4207.7	947.4	3887.0	4.1
1555689_at	CD80	2.18E-05	8.5	14.8	14.6	20.2	26.5	18.6	33.7	54.8	89.3	248.7	149.5	102.7	100.8	151.5	18.6	102.7	5.5
207176_s_at	CD80	6.17E-06	82.7	126.3	110.7	113.1	132.3	108.1	116.3	319.6	405.0	748.0	587.2	463.7	452.0	463.3	113.1	463.3	4.1
203904_x_at	CD82	2.17E-03	103.2	52.8	107.1	108.6	92.8	78.4	115.4	122.7	73.5	191.7	144.6	180.6	203.7	206.0	103.2	180.6	1.8
202877_s_at	CD93	1.10E-03	95.9	62.8	70.5	87.9	67.2	99.7	93.8	199.7	133.8	200.1	162.0	397.2	144.3	353.8	87.9	199.7	2.3
202878_s_at	CD93	2.98E-04	280.9	207.6	293.4	379.5	238.0	456.2	397.7	885.4	841.2	918.4	759.7	1581.2	756.5	1935.2	293.4	885.4	3.0
210232_at	CDC42	3.05E-03	116.7	107.2	147.6	141.7	146.3	126.3	161.9	162.1	181.8	263.1	220.6	159.5	159.9	218.8	141.7	181.8	1.3
209850_s_at	CDC42EP2	4.65E-05	58.0	44.2	63.6	61.8	75.1	58.8	73.7	91.5	94.8	154.5	110.7	151.7	133.3	189.4	61.8	133.3	2.2
1552612_at	CDC42SE2	2.67E-03	2149.7	1984.8	1904.1	1958.5	2293.7	1955.5	2161.1	2360.5	2683.1	3343.5	3017.6	2873.3	2895.4	3229.7	1984.8	2895.4	1.5
1552613_s_at	CDC42SE2	9.12E-04	723.1	767.7	921.5	862.9	968.1	918.5	1058.5	967.9	1169.4	1758.8	1584.1	1267.6	1326.2	1462.5	918.5	1326.2	1.4
226056_at	CDGAP	2.69E-03	552.8	357.0	462.3	638.4	611.5	549.3	725.6	773.4	513.1	908.9	805.3	704.6	969.8	1033.9	552.8	805.3	1.5
226057_at	CDGAP	4.37E-03	143.8	113.7	150.8	160.8	175.4	202.0	168.1	263.6	147.7	207.3	255.0	213.5	246.1	203.4	160.8	213.5	1.3
207766_at	CDKL1	2.57E-04	134.3	158.6	169.0	159.7	133.6	152.2	139.6	198.6	229.9	258.4	221.8	227.8	214.2	213.5	152.2	221.8	1.5
202284_s_at	CDKN1A	6.16E-03	1156.9	882.3	1697.9	1278.1	1003.1	1092.9	1324.3	1603.7	1312.0	1922.5	1381.1	1721.1	1440.2	1833.1	1156.9	1603.7	1.4
212862_at	CDS2	5.28E-03	541.4	417.1	489.4	504.3	505.8	417.2	411.6	601.1	665.1	681.9	540.9	698.1	643.6	618.3	489.4	643.6	1.3
203973_s_at	CEBPD	1.05E-04	120.5	196.8	248.4	241.3	257.8	205.9	207.6	286.5	402.3	528.6	336.5	454.1	424.8	524.3	207.6	424.8	2.0
213003_s_at	CEBPD	2.98E-05	124.9	193.9	215.1	202.8	200.6	184.4	185.6	265.0	368.1	496.5	320.8	436.5	431.6	461.6	193.9	431.6	2.2
222118_at	CENPN	2.68E-03	131.0	132.3	143.8	141.7	149.0	127.4	148.4	228.6	192.2	313.1	213.0	190.6	144.7	223.8	141.7	213.0	1.5
204373_s_at	CEP350	9.89E-03	151.6	264.3	346.9	340.5	417.5	421.5	501.8	254.5	337.7	484.8	491.8	469.3	541.1	523.2	346.9	484.8	1.4
213957_s_at	CEP350	3.62E-03	201.8	205.1	232.0	260.5	360.3	307.9	305.9	256.5	315.2	416.4	351.2	435.5	417.6	363.7	260.5	363.7	1.4
211920_at	CFB	2.14E-03	77.5	39.8	67.3	76.2	67.8	66.9	69.7	79.8	94.6	170.4	100.0	131.6	138.5	157.7	67.8	131.6	1.9
208485_x_at	CFLAR	7.57E-06	296.2	276.8	413.4	345.4	436.0	368.8	411.1	624.8	675.7	1170.5	735.6	943.7	868.3	935.2	368.8	868.3	2.4
209508_x_at	CFLAR	7.84E-05	524.0	454.8	499.2	480.9	585.3	484.2	517.4	798.7	944.8	1344.9	837.9	1106.4	1044.2	1137.2	499.2	1044.2	2.1
209939_x_at	CFLAR	5.51E-05	472.9	429.4	460.3	566.1	817.3	585.1	720.9	1297.8	2556.6	3329.9	2128.5	1982.8	1775.7	2775.9	566.1	2128.5	3.8
210563_x_at	CFLAR	2.75E-05	794.6	651.8	673.0	718.5	1015.7	683.6	895.7	1683.9	2744.1	3200.0	1952.3	2496.8	2261.7	2963.8	718.5	2496.8	3.5
210564_x_at	CFLAR	6.44E-05	844.2	679.3	832.7	851.4	1014.4	811.5	974.4	1402.7	2035.4	2799.4	1736.6	2114.5	2103.4	2365.5	844.2	2103.4	2.5
211316_x_at	CFLAR	1.73E-04	1013.5	880.9	1024.0	937.9	1145.8	1021.7	1084.2	1477.1	1963.4	2927.1	1680.3	1928.5	2047.7	2395.2	1021.7	1963.4	1.9
211317_s_at	CFLAR	2.52E-05	277.1	244.5	377.5	346.5	396.3	344.7	361.2	577.3	685.7	1119.3	599.7	869.2	843.0	898.6	346.5	843.0	2.4

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
211862_x_at	CFLAR	2.55E-05	500.4	412.4	483.0	494.5	619.9	485.1	586.3	915.4	1048.3	1555.3	999.1	1386.8	1241.1	1320.2	494.5	1241.1	2.5
214486_x_at	CFLAR	4.32E-05	1438.0	1196.8	1413.8	1362.2	1561.0	1238.6	1253.2	2448.1	2807.5	3898.9	2528.6	3014.1	2823.9	3401.1	1362.2	2823.9	2.1
237367_x_at	CFLAR	1.31E-03	130.8	124.1	162.5	144.7	161.1	135.6	155.2	163.3	158.7	253.0	191.0	214.6	218.1	223.1	144.7	214.6	1.5
239629_at	CFLAR	1.00E-03	45.9	44.6	60.2	50.9	64.0	71.0	68.7	71.4	94.4	210.3	113.2	104.7	97.5	123.1	60.2	104.7	1.7
206380_s_at	CFP	5.09E-03	98.4	59.7	108.0	160.3	202.9	247.8	147.7	157.1	95.9	159.9	174.4	516.6	302.1	336.0	147.7	174.4	1.2
206932_at	CH25H	6.29E-06	102.5	44.0	54.6	63.6	47.7	66.7	78.4	695.8	1428.6	1120.0	1036.8	421.7	830.2	943.0	63.6	943.0	14.8
209395_at	CHI3L1	2.48E-04	209.5	139.2	155.1	205.8	219.3	103.1	255.2	551.4	263.5	261.6	368.3	570.1	421.5	547.5	205.8	421.5	2.0
209396_s_at	CHI3L1	3.83E-04	216.2	133.8	143.7	174.1	164.6	96.2	243.1	422.7	263.2	244.0	295.8	501.0	372.6	475.9	164.6	372.6	2.3
213060_s_at	CHI3L2	1.17E-04	95.0	73.0	103.1	107.6	150.3	92.8	113.5	157.5	110.5	158.4	190.6	257.9	142.5	235.3	103.1	158.4	1.5
210069_at	CHKB-CPT1B /// CPT1B	8.21E-03	571.4	440.6	571.5	663.3	564.6	713.3	702.2	681.4	594.1	704.5	907.5	603.5	973.3	853.3	571.5	704.5	1.2
225119_at	CHMP4B	8.58E-03	1808.8	1391.6	1355.1	1615.1	1664.5	1303.3	1526.6	1899.2	1890.6	1966.6	1719.7	2626.3	2523.1	2393.9	1526.6	1966.6	1.3
225498_at	CHMP4B	5.08E-03	481.4	432.3	462.8	512.9	602.5	511.7	491.4	618.3	474.2	639.7	623.1	745.6	695.0	696.8	491.4	639.7	1.3
219356_s_at	CHMP5	8.63E-03	817.2	850.5	1159.7	1014.7	1006.4	1072.0	1128.0	1149.7	1297.3	1764.6	1336.7	1096.0	1166.8	1383.4	1014.7	1297.3	1.3
206703_at	CHRNB1	8.54E-03	40.5	31.0	75.1	54.4	51.3	50.5	67.1	55.8	47.9	98.7	51.2	73.5	71.0	88.0	51.3	71.0	1.4
219634_at	CHST11	6.72E-03	623.7	252.3	415.1	544.4	518.9	264.2	553.6	762.0	471.8	595.3	644.7	691.7	646.7	736.9	518.9	646.7	1.2
203066_at	CHST15	2.85E-04	31.1	67.5	30.5	22.1	23.3	19.5	24.9	74.5	132.9	225.6	90.3	241.0	118.6	258.2	24.9	132.9	5.3
203921_at	CHST2	4.66E-04	73.2	73.0	49.7	56.5	70.1	50.4	56.9	109.7	114.6	113.4	112.1	145.1	88.2	196.2	56.9	113.4	2.0
200998_s_at	CKAP4	1.35E-04	408.6	325.7	376.9	629.3	272.4	329.8	465.5	674.3	1419.1	1330.1	1171.5	1079.4	1223.7	1631.2	376.9	1223.7	3.2
200999_s_at	CKAP4	1.78E-05	670.9	583.8	574.1	871.3	490.4	476.4	716.5	1483.0	2167.4	1945.3	1821.4	1740.6	1822.1	2274.3	583.8	1822.1	3.1
238048_at	CLASP2	1.78E-03	77.2	68.1	102.3	117.8	108.0	102.1	100.8	112.5	88.1	151.9	148.3	140.7	124.6	137.6	102.1	137.6	1.3
220132_s_at	CLEC2D	4.07E-05	65.8	37.5	39.0	63.1	42.2	30.0	40.7	198.4	198.0	545.6	284.9	220.4	239.6	483.2	40.7	239.6	5.9
233500_x_at	CLEC2D	3.60E-05	50.3	32.3	32.4	56.6	34.2	43.1	38.3	155.2	157.2	414.9	221.2	191.3	200.2	342.3	38.3	200.2	5.2
1552772_at	CLEC4D	4.62E-04	81.4	51.4	167.7	280.7	219.5	220.9	262.5	199.7	162.4	556.5	356.7	358.7	618.9	636.5	219.5	358.7	1.6
1552773_at	CLEC4D	5.85E-04	108.1	53.0	158.6	251.3	266.9	190.7	285.3	212.9	207.3	469.4	381.3	398.8	502.8	609.5	190.7	398.8	2.1
219859_at	CLEC4E	5.03E-03	34.2	26.9	26.5	34.9	46.5	26.9	37.8	40.8	59.4	81.1	65.4	46.1	61.9	67.7	34.2	61.9	1.8
222934_s_at	CLEC4E	1.35E-04	627.1	252.8	365.4	653.8	936.1	477.1	661.8	1182.1	957.2	1445.3	1339.2	1809.8	1884.1	1828.1	627.1	1445.3	2.3
213415_at	CLIC2	8.45E-03	114.5	116.4	173.4	184.2	221.5	175.4	153.2	219.9	211.5	493.5	273.3	251.9	191.5	213.7	173.4	219.9	1.3
201559_s_at	CLIC4	6.42E-04	938.3	774.8	729.4	971.2	1090.0	854.2	978.3	1190.5	1295.7	1781.5	1553.3	1629.1	1471.5	1755.7	938.3	1553.3	1.7
201560_at	CLIC4	6.82E-03	4530.0	4364.1	4560.6	5164.6	5665.4	4596.0	5443.3	5151.7	6256.5	7917.4	7004.1	6098.2	6318.6	7206.3	4596.0	6318.6	1.4
221881_s_at	CLIC4	1.60E-04	1884.5	1588.4	1602.9	2019.0	2482.7	1591.4	2231.2	2931.6	3347.2	4345.6	3600.9	3941.8	4116.9	4511.8	1884.5	3941.8	2.1
201768_s_at	CLINT1	2.66E-04	989.7	923.4	1022.0	1078.2	1077.5	1062.9	1039.9	1412.5	1334.3	2061.6	1640.0	1600.0	1898.7	1768.7	1039.9	1640.0	1.6
201769_at	CLINT1	6.81E-03	1511.7	1509.1	2299.3	2324.2	2076.6	2379.9	2435.1	2022.6	2171.3	3869.0	3106.3	2149.4	2906.0	3170.7	2299.3	2906.0	1.3
1558924_s_at	CLIP1	4.45E-03	1206.3	1015.3	800.9	1015.8	1133.4	875.8	981.7	1436.8	1189.6	1153.8	1202.7	1545.7	1489.8	1417.9	1015.3	1417.9	1.4
207652_s_at	CMKLR1	1.40E-03	84.3	52.9	65.7	48.1	64.7	49.1	49.8	91.6	80.6	216.3	114.9	129.4	128.7	110.3	52.9	114.9	2.2
210659_at	CMKLR1	7.40E-04	95.9	69.9	88.0	56.0	97.1	40.2	56.5	126.7	149.5	425.4	216.8	213.1	232.7	176.5	69.9	213.1	3.0
229121_at	CMKLR1	4.36E-03	107.4	112.5	87.2	63.4	133.0	39.8	86.6	117.5	175.6	357.7	170.1	213.9	198.5	183.3	87.2	183.3	2.1
226702_at	CMPK2	4.93E-05	2540.2	2979.8	2566.9	2244.8	1943.2	1944.6	2431.6	4004.4	5926.6	7512.3	6488.1	5009.7	5250.0	7135.9	2431.6	5926.6	2.4
217947_at	CMTM6	7.78E-03	2223.3	1912.5	2602.9	2667.9	2492.0	2388.3	2662.6	2703.6	2835.4	3839.3	3348.8	2863.3	2689.1	3332.8	2492.0	2863.3	1.1
227953_at	CMTM6	3.14E-03	1238.5	1071.7	1215.3	1414.3	1228.2	1207.6	1239.5	1390.1	1514.2	1951.2	1792.8	1548.7	1615.0	1791.9	1228.2	1615.0	1.3
208912_s_at	CNP	4.93E-05	1242.3	1260.6	1234.0	1161.2	1021.5	951.0	1142.3	1836.0	2280.0	2639.7	2089.3	2102.8	2041.6	2418.9	1161.2	2102.8	1.8
1559005_s_at	CNTLN	3.18E-03	63.1	50.6	88.3	58.2	101.6	105.9	86.2	95.5	82.5	243.8	116.0	118.8	148.8	122.4	86.2	118.8	1.4
219397_at	COQ10B	2.75E-03	488.2	508.8	642.0	601.5	668.4	661.2	745.4	626.6	796.9	1077.2	901.2	763.5	826.1	1004.2	642.0	826.1	1.3
209083_at	CORO1A	4.20E-03	200.5	153.5	134.8	267.6	161.0	122.7	137.9	241.6	195.2	256.2	393.2	530.6	360.4	494.4	153.5	360.4	2.3
201940_at	CPD	1.78E-03	199.0	233.4	264.5	276.2	334.1	316.6	336.1	335.1	298.4	438.8	431.3	412.1	419.7	427.6	276.2	419.7	1.5
201942_s_at	CPD	5.11E-03	485.9	592.9	575.8	672.9	773.9	706.7	706.1	715.8	637.4	807.7	873.6	969.8	873.9	1136.5	672.9	873.6	1.3
201943_s_at	CPD	5.58E-03	126.6	149.6	186.7	190.4	216.6	199.5	251.6	186.6	205.2	398.9	270.1	224.9	267.5	366.1	190.4	267.5	1.4
229600_s_at	CPD	7.39E-04	119.5	123.3	154.3	193.1	211.3	167.1	171.8	183.1	204.5	321.7	235.4	296.3	266.1	313.6	167.1	266.1	1.6
226939_at	CPEB2	5.39E-03	457.4	450.0	595.3	532.2	607.3	635.1	634.2	564.5	952.9	1581.2	877.8	727.0	763.2	1101.6	595.3	877.8	1.5
235479_at	CPEB2	2.59E-04	207.8	174.3	220.4	168.1	209.1	204.6	194.2	305.8	318.9	482.8	324.4	297.2	316.2	423.2	204.6	318.9	1.6
206100_at	CPM	7.38E-06	295.3	314.1	390.8	336.7	434.7	432.2	446.9	851.4	725.7	1201.7	887.8	939.1	1127.6	1020.0	390.8	939.1	2.4
217557_s_at	CPM	1.03E-05	812.7	727.7	748.7	617.4	754.3	738.7	812.1	1613.8	1414.7	1707.1	1496.1	1637.0	1960.1	1828.6	748.7	1637.0	2.2
235019_at	CPM	6.17E-06	364.8	331.0	432.0	416.8	477.2	434.5	519.8	976.1	785.8	1248.9	1099.4	1075.6	1231.4	1156.0	432.0	1099.4	2.5
235706_at	CPM	1.08E-05	126.4	109.4	159.6	135.2	202.8	152.4	189.9	366.2	234.7	483.5	347.4	464.0	497.6	425.2	152.4	425.2	2.8
241765_at	CPM	6.17E-06	399.7	366.0	497.7	497.2	612.4	549.3	555.7	1138.9	1047.3	1526.6	1384.1	1254.2	1469.3	1381.1	497.7	1381.1	2.8
243403_x_at	CPM	2.11E-05	46.1	50.1	63.0	51.6	69.0	73.4	80.3	114.2	112.0	178.0	145.5	127.9	148.6	167.4	63.0	145.5	2.3
243727_at	CPNE8	2.99E-03	133.4	148.8	223.0	205.0	216.1	191.9	163.8	200.3	227.9	448.9	249.0	268.6	251.3	223.2	191.9	249.0	1.3
209432_s_at	CREB3	2.99E-03	186.5	127.3	210.4	217.3	209.9	151.6	210.7	231.2	175.5	325.7	283.8	394.6	390.5	319.5	209.9	319.5	1.5
207630_s_at	CREM	8.59E-05	147.2	143.6	174.5	167.3	255.3	120.9	185.4	230.6	363.2	450.7	321.0	445.6	306.8	502.1	167.3	363.2	2.2
209967_s_at	CREM	5.76E-04	48.8	58.1	59.7	58.1	95.6	57.6	74.9	86.0	76.2	162.7	125.7	136.8	108.4	166.5	58.1	125.7	2.2
214508_x_at	CREM	3.83E-04	254.7	215.1	178.3	196.4	295.9	152.6	212.1	350.0	455.4	520.6	354.3	551.7	435.7	714.3	212.1	455.4	2.1
230511_at	CREM	1.25E-03	64.4	41.8	47.1	40.7	75.8	45.1	51.6	71.4	85.0	127.0	93.4	105.7	92.6	105.1	47.1	93.4	2.0
221541_at	CRISPLD2	6.13E-04	23.3	21.9	14.6	13.6	10.2	12.3	9.7	34.3	64.6	103.7	50.0	105.4	66.6	127.1	13.6	66.6	4.9
226307_at	CRTC2	7.79E-03	133.0	166.0	224.9	198.0	237.6	224.6	214.8	230.0	186.4	295.8	227.9	327.6	308.1	258.2	214.8	258.2	1.2
207442_at	CSF3	8.25E-03	83.2	75.0	60.0	72.5	70.3	57.4	65.5	74.8	121.9	138.0	87.4	109.9	123.2	153.8	70.3	121.9	1.7
1553297_a_at	CSF3R	5.77E-03	103.6	90.9	155.2	154.1	121.8	152.1	101.2	122.8	139.1	274.8	152.4	284.3	259.9	226.4	121.8	226.4	1.9

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203591_s_at	CSF3R	8.12E-03	102.5	123.2	173.8	217.6	167.7	196.0	124.3	144.5	193.9	340.4	181.4	409.3	321.7	295.7	167.7	295.7	1.8
225557_at	CSRNP1	3.50E-04	108.6	87.2	111.4	93.3	100.5	98.2	94.3	149.1	224.7	464.4	195.8	281.1	187.3	272.2	98.2	224.7	2.3
225042_s_at	CSRNP2	6.03E-03	55.1	71.5	62.0	67.9	73.6	57.0	68.5	81.9	75.9	124.9	83.3	91.5	86.2	108.6	67.9	86.2	1.3
211126_s_at	CSRP2	5.51E-03	48.8	49.4	49.4	50.0	50.2	44.0	42.1	59.0	57.4	126.7	90.3	71.0	59.6	93.5	49.4	71.0	1.4
210140_at	CST7	4.85E-03	47.8	33.8	43.6	56.2	40.6	46.7	55.5	58.1	41.5	58.6	70.8	61.0	55.8	98.6	46.7	58.6	1.3
203947_at	CSTF3	6.96E-04	271.4	265.5	317.3	308.4	312.5	361.5	360.1	402.6	390.5	553.3	461.7	431.2	459.6	485.8	312.5	459.6	1.5
236341_at	CTLA4	9.76E-04	78.6	57.9	64.6	78.8	94.8	31.2	38.4	119.5	92.1	126.7	191.1	118.0	88.1	100.5	64.6	118.0	1.8
221021_s_at	CTNNBL1	4.71E-03	938.2	804.8	844.8	765.3	888.4	776.7	643.0	1087.4	1095.5	1103.7	867.3	1249.1	1121.8	1138.7	804.8	1103.7	1.4
1555467_a_at	CUGBP1	3.85E-03	191.7	171.3	170.1	186.4	201.7	173.9	183.7	225.1	240.5	270.6	206.0	269.2	272.1	252.4	183.7	252.4	1.4
209489_at	CUGBP1	5.14E-03	450.2	464.4	433.8	498.8	524.1	482.2	502.8	582.3	556.3	703.5	583.3	631.2	693.4	648.2	482.2	631.2	1.3
235297_at	CUGBP1	8.78E-03	173.2	140.2	182.7	175.8	196.4	172.1	198.4	258.8	140.9	270.3	218.4	300.2	252.1	226.3	175.8	252.1	1.4
235865_at	CUGBP1	5.10E-03	313.4	279.6	260.6	268.7	316.9	271.6	264.3	400.7	298.1	356.6	327.9	444.6	401.8	346.2	271.6	356.6	1.3
207614_s_at	CUL1	2.61E-03	1662.2	1598.0	1650.0	1512.1	1728.4	1407.9	1573.7	1951.6	2076.5	2345.8	1862.9	2189.3	2112.6	2262.3	1598.0	2112.6	1.3
238509_at	CUL1	9.56E-05	232.4	209.5	283.3	258.3	316.8	248.3	278.4	352.7	458.2	685.5	466.6	509.9	460.5	590.9	258.3	466.6	1.8
205898_at	CX3CR1	2.09E-03	40.3	36.1	13.4	15.2	11.4	17.2	20.7	70.3	44.0	69.2	39.4	75.7	36.9	86.2	17.2	69.2	4.0
204470_at	CXCL1	2.98E-05	202.1	84.1	310.1	274.0	694.1	100.1	576.8	1196.8	2553.3	6792.3	4895.7	3594.1	2979.6	5376.6	274.0	3594.1	13.1
204533_at	CXCL10	2.10E-05	1950.1	1016.0	1643.9	841.0	2763.0	862.9	2621.9	9776.6	15548.4	17869.5	14410.8	12305.9	12472.3	15444.0	1643.9	14410.8	8.8
210163_at	CXCL11	2.42E-06	18.2	84.3	147.8	27.4	144.7	30.9	79.3	300.5	3274.5	3440.3	1866.0	2271.2	1063.3	1898.4	79.3	1898.4	24.0
211122_s_at	CXCL11	3.58E-06	81.4	42.8	91.1	32.6	103.3	21.2	85.0	1351.9	2600.0	3964.6	2276.1	1712.5	1211.0	2235.0	81.4	2235.0	27.4
1569203_at	CXCL2	1.24E-03	23.2	26.3	33.1	24.7	51.1	31.5	39.7	46.8	40.7	128.6	74.9	90.6	51.5	61.1	31.5	61.1	1.9
209774_x_at	CXCL2	1.17E-03	312.7	196.8	493.9	386.2	941.4	234.9	673.9	570.3	1167.0	2446.5	1272.3	1209.9	1292.7	1584.1	386.2	1272.3	3.3
230101_at	CXCL2	2.48E-04	75.7	35.0	93.8	88.7	126.7	55.1	108.4	143.7	123.0	296.9	201.0	299.7	192.3	154.0	88.7	192.3	2.2
207850_at	CXCL3	5.18E-04	267.7	147.3	317.8	227.8	556.2	171.7	526.0	458.1	892.9	1634.6	970.8	1000.5	1145.4	1372.0	267.7	1000.5	3.7
207852_at	CXCL5	1.19E-03	44.3	9.6	16.2	28.7	64.2	10.1	52.1	75.8	71.4	182.4	147.0	114.5	118.0	160.1	28.7	118.0	4.1
214974_x_at	CXCL5	6.78E-03	1087.6	86.4	518.2	689.2	1409.9	266.8	1754.9	1431.9	1997.3	3688.5	2721.7	2078.3	2120.5	3360.9	689.2	2120.5	3.1
215101_s_at	CXCL5	1.33E-03	1487.9	64.5	302.3	474.7	1038.8	165.6	1021.2	2302.4	2103.1	3745.6	3012.9	3759.6	3417.5	3787.8	474.7	3417.5	7.2
206974_at	CXCR6	1.69E-03	75.0	72.5	73.0	85.5	95.1	99.6	87.2	129.0	97.8	102.0	149.2	118.3	121.5	129.7	85.5	121.5	1.4
230532_at	CXorf38	5.19E-03	299.5	381.8	514.1	493.4	496.6	564.6	462.3	582.6	581.6	748.5	601.0	616.0	614.4	794.5	493.4	614.4	1.2
228809_at	CXorf40A	8.68E-03	89.5	73.4	77.9	86.7	96.9	91.1	99.4	103.2	90.9	109.5	97.7	130.4	112.9	118.6	89.5	109.5	1.2
220230_s_at	CYB5R2	7.99E-05	213.3	161.7	346.4	133.8	105.8	124.8	365.0	423.5	269.2	635.3	247.6	154.0	240.5	573.2	161.7	269.2	1.7
201885_s_at	CYB5R3	7.99E-03	929.2	905.1	786.3	986.6	1040.2	836.9	972.8	1173.4	1019.7	1221.9	1126.4	1223.7	1143.8	1336.3	929.2	1173.4	1.3
221903_s_at	CYLD	6.65E-05	343.0	313.7	392.3	338.9	452.5	295.4	384.4	530.3	704.2	921.0	628.3	783.5	744.9	851.4	343.0	744.9	2.2
222142_at	CYLD	6.91E-04	46.8	53.7	87.3	79.0	107.6	63.6	84.4	95.2	76.3	186.9	131.1	129.1	128.7	141.3	79.0	129.1	1.6
60084_at	CYLD	2.97E-03	92.8	106.8	113.1	104.3	157.9	104.6	127.7	146.0	163.9	319.0	179.7	168.5	198.1	197.5	106.8	179.7	1.7
202436_s_at	CYP1B1	4.62E-03	62.5	53.7	68.7	68.8	42.8	28.6	40.7	85.0	63.9	116.0	123.5	134.1	67.8	197.1	53.7	116.0	2.2
219565_at	CYP20A1	3.66E-03	293.7	274.4	296.9	339.5	364.6	334.4	388.6	385.2	414.5	653.4	436.9	421.7	491.5	600.0	334.4	436.9	1.3
205676_at	CYP27B1	1.16E-05	4.9	11.6	26.1	23.2	17.8	10.2	29.0	65.5	73.5	226.8	95.3	86.9	48.9	147.4	17.8	86.9	4.9
205999_x_at	CYP3A4	3.16E-04	32.5	19.6	37.2	36.1	60.1	37.2	60.4	64.2	91.6	291.3	119.0	147.5	96.4	143.8	37.2	119.0	3.2
208367_x_at	CYP3A4	1.40E-03	42.0	39.6	39.0	30.7	40.6	28.4	41.4	51.3	76.3	125.8	68.3	73.3	64.6	57.0	39.6	68.3	1.7
211441_x_at	CYP3A43	7.04E-03	47.6	47.6	54.5	28.9	47.6	45.3	60.2	49.3	71.7	66.2	64.8	61.4	75.3	101.2	47.6	66.2	1.4
211442_x_at	CYP3A43	3.95E-03	49.1	53.6	49.7	39.1	52.7	40.9	62.2	45.3	121.6	114.7	92.9	76.6	108.0	95.6	49.7	95.6	1.9
205765_at	CYP3A5	1.03E-04	88.2	70.5	154.3	127.1	239.8	159.7	279.4	187.8	400.6	1158.1	464.4	636.1	863.3	818.6	154.3	636.1	4.1
214234_s_at	CYP3A5	7.66E-04	115.8	133.9	157.2	137.2	255.3	155.6	295.4	143.6	477.5	1244.7	485.8	618.4	780.2	901.7	155.6	618.4	4.0
214235_at	CYP3A5	9.97E-05	40.6	39.7	74.5	57.8	111.8	58.3	117.0	82.3	141.2	478.0	231.3	247.0	225.4	324.9	58.3	231.3	4.0
205939_at	CYP3A7	2.54E-04	95.1	64.6	78.4	85.5	209.6	40.3	184.3	240.0	366.7	1240.3	605.6	606.1	476.5	660.7	85.5	605.6	7.1
211843_x_at	CYP3A7	2.20E-04	95.7	73.9	96.2	119.5	236.7	39.6	193.7	331.5	437.8	1277.3	627.1	614.8	695.7	781.8	96.2	627.1	6.5
243609_at	CYP3A7	4.66E-03	61.0	42.4	58.9	37.7	78.5	40.4	71.7	83.2	76.4	318.1	171.2	109.8	144.2	110.2	58.9	110.2	1.9
216607_s_at	CYP51A1	2.07E-03	612.3	490.4	277.6	291.9	504.0	392.1	602.1	744.4	688.0	468.7	438.4	598.9	597.1	789.7	490.4	598.9	1.2
237234_at	CYTH2	5.98E-03	146.2	101.4	140.7	126.7	118.4	116.8	115.0	195.4	151.0	144.7	153.9	167.1	171.6	148.1	118.4	153.9	1.3
1560633_a_at	D21S2089E	6.92E-03	54.7	55.1	61.0	67.0	49.4	48.0	50.5	58.1	80.8	80.3	75.0	67.1	81.8	75.6	54.7	75.6	1.4
222858_s_at	DAPP1	1.09E-03	840.3	946.2	879.1	879.7	1116.3	1022.9	960.1	1393.5	1284.3	1128.8	1435.8	1479.3	1347.0	1338.6	946.2	1347.0	1.4
1553768_a_at	DCBLD1	6.07E-03	145.8	126.1	88.1	132.0	130.1	92.4	111.7	170.2	186.5	260.1	167.0	178.0	153.9	198.9	126.1	178.0	1.4
226609_at	DCBLD1	2.44E-03	83.7	71.6	68.1	93.8	86.5	62.8	74.9	109.4	149.5	230.0	131.8	115.6	136.7	143.5	74.9	136.7	1.8
218508_at	DCP1A	1.08E-04	449.6	373.5	399.1	375.7	478.2	497.3	526.5	687.1	692.1	947.0	686.6	859.3	760.5	963.1	449.6	760.5	1.7
225443_at	DCP1A	4.56E-04	476.1	456.8	513.8	520.7	667.9	617.5	645.7	722.7	919.1	1335.3	841.4	923.1	1004.3	1225.2	520.7	923.1	1.8
204296_at	DCTN1	2.24E-03	102.1	51.2	82.1	90.9	112.4	50.3	142.5	129.4	139.6	220.3	168.9	158.6	154.0	198.2	90.9	158.6	1.7
209231_s_at	DCTN5	1.59E-03	227.4	220.6	263.9	265.6	288.7	197.5	212.2	311.6	277.8	423.9	338.5	430.3	264.7	269.1	227.4	311.6	1.4
239648_at	DCUN1D3	3.24E-03	297.1	156.7	350.6	325.5	577.7	275.2	555.4	389.7	504.0	1215.0	576.5	674.6	717.3	950.2	325.5	674.6	2.1
218260_at	DDA1	9.74E-03	115.1	98.4	118.5	123.3	121.9	130.9	134.6	168.4	103.7	172.6	139.9	183.4	207.9	152.9	121.9	168.4	1.4
202887_s_at	DDIT4	3.02E-04	461.4	864.6	330.4	242.8	424.5	345.6	440.9	869.3	1157.1	1102.5	741.6	1537.3	1180.8	1868.6	424.5	1157.1	2.7
210749_x_at	DDR1	9.61E-03	83.2	75.7	45.5	63.8	69.1	71.0	71.5	102.1	127.8	51.3	75.9	139.4	88.9	96.1	71.0	96.1	1.4
227485_at	DDX26B	5.77E-03	95.8	114.0	108.1	126.1	102.4	86.5	103.5	118.7	145.9	156.1	140.1	125.9	129.5	127.5	103.5	129.5	1.3
201584_s_at	DDX39	8.19E-03	255.4	186.5	229.7	270.7	259.9	202.6	281.3	332.2	226.7	385.7	285.0	392.8	409.9	355.8	255.4	355.8	1.4
201211_s_at	DDX3X	1.47E-03	1047.1	983.9	1030.4	1076.8	1096.2	974.5	1207.2	1210.9	1433.9	1810.6	1344.6	1641.0	1561.7	1918.3	1047.1	1561.7	1.5
212514_x_at	DDX3X	4.16E-03	1854.8	2444.5	2350.3	2427.4	2557.8	2371.7	2706.9	2419.0	3222.1	4124.4	3059.6	3082.5	3003.7	3489.2	2427.4	3082.5	1.3
212515_s_at	DDX3X	9.86E-03	735.7	742.3	1008.6	973.8	1036.0	963.6	1202.0	972.2	1061.4	1649.9	1158.5	1220.1	1131.8	1345.5	973.8	1158.5	1.2

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
218943_s_at	DDX58	4.47E-06	680.9	687.8	605.3	590.8	582.5	492.5	612.5	2057.2	3238.5	3825.2	2720.0	2830.8	2824.9	3812.8	605.3	2830.8	4.7
222793_at	DDX58	6.17E-06	373.0	343.9	248.3	266.2	310.7	266.6	338.9	1129.2	1465.2	1835.7	1544.0	1378.2	1429.9	2115.7	310.7	1465.2	4.7
242961_x_at	DDX58	2.73E-05	112.2	562.9	844.6	701.5	530.7	616.6	425.8	223.5	2559.0	4361.3	3321.2	1726.1	2004.3	2173.6	562.9	2173.6	3.9
228385_at	DDX59	9.57E-03	369.8	303.1	351.1	442.3	440.3	388.6	352.8	417.8	423.1	671.3	586.7	453.9	627.3	482.2	369.8	482.2	1.3
228386_s_at	DDX59	1.57E-03	170.7	180.6	264.6	273.8	268.4	281.4	255.4	316.9	278.5	485.5	403.6	312.0	389.6	341.4	264.6	341.4	1.3
218986_s_at	DDX60	6.91E-05	577.7	853.5	1007.2	865.8	870.1	911.2	815.3	1093.2	1644.1	2884.1	1894.7	1420.3	1673.1	1955.2	865.8	1673.1	1.9
1559585_at	DDX60L	5.99E-04	147.2	186.4	252.2	131.6	175.6	217.6	193.2	239.5	411.2	939.5	335.0	325.7	301.4	411.5	186.4	335.0	1.8
228152_s_at	DDX60L	1.09E-04	1082.5	1706.9	1346.2	783.2	1211.7	1504.6	1303.7	1869.0	3249.1	4228.8	2129.1	2438.1	2624.4	2706.6	1303.7	2624.4	2.0
219763_at	DENND1A	7.96E-04	118.6	105.4	103.7	144.2	150.0	112.6	141.8	163.0	239.2	326.6	222.3	236.6	216.9	376.2	118.6	236.6	2.0
219696_at	DENND1B	6.73E-03	45.0	55.5	85.3	74.2	80.8	84.8	81.4	93.0	87.0	143.7	127.7	90.4	88.6	108.8	80.8	93.0	1.2
212974_at	DENND3	2.59E-04	48.4	47.0	62.2	62.2	71.7	47.8	71.8	76.7	66.9	81.9	102.6	131.1	89.3	128.7	62.2	89.3	1.4
212975_at	DENND3	4.38E-04	163.5	140.1	189.0	205.5	211.7	160.3	251.5	265.9	234.0	269.5	326.2	307.3	388.9	426.3	189.0	307.3	1.6
212561_at	DENND5A	1.39E-03	2967.6	2760.0	2654.4	2767.5	3404.6	2997.9	3117.5	3767.7	4094.4	5010.6	3858.3	4132.5	4560.8	5014.8	2967.6	4132.5	1.4
218333_at	DERL2	4.16E-03	1327.8	1234.6	1087.7	1119.7	1185.3	1014.7	1076.5	1555.2	1384.4	1505.0	1490.4	1576.3	1600.6	1470.1	1119.7	1505.0	1.3
1553300_a_at	DGKH	3.42E-04	34.7	33.2	59.2	41.5	74.8	47.2	69.7	90.3	90.8	237.0	90.1	103.6	119.6	124.5	47.2	103.6	2.2
225503_at	DHRSX	2.93E-03	252.2	252.0	291.4	277.5	263.9	242.5	262.7	328.0	278.6	368.8	383.7	380.8	361.8	355.1	262.7	361.8	1.4
201385_at	DHX15	3.94E-03	735.2	786.9	934.6	1002.4	975.9	915.6	1239.5	1035.2	1252.8	1637.9	1294.3	1080.9	1196.0	1576.6	934.6	1252.8	1.3
201386_s_at	DHX15	4.78E-03	1358.6	1094.6	1121.9	1205.9	1118.9	984.7	1226.8	1444.8	1521.0	1614.1	1403.1	1528.6	1526.0	1721.2	1121.9	1526.0	1.4
219364_at	DHX58	2.14E-05	140.1	113.0	129.9	125.2	142.9	110.1	129.6	236.3	244.1	369.6	284.3	357.9	290.6	339.8	129.6	290.6	2.2
216260_at	DICER1	6.88E-03	61.5	59.4	42.5	34.4	59.4	49.2	51.6	66.9	74.0	147.0	97.4	77.2	94.3	118.4	51.6	94.3	1.8
216280_s_at	DICER1	3.30E-03	126.6	102.2	116.2	129.6	120.0	126.4	156.1	166.0	125.3	177.6	154.2	165.0	166.2	191.6	126.4	166.0	1.3
231412_at	DKFZp686 L14188	9.31E-05	29.9	33.2	34.4	26.5	43.4	31.5	44.6	67.1	67.9	145.6	80.9	76.8	77.4	111.5	33.2	77.4	2.3
229715_at	DKFZp686 O24166	2.51E-04	107.4	90.2	104.1	136.6	179.8	74.3	167.6	236.6	170.2	403.1	237.2	331.4	237.9	341.0	107.4	237.9	2.2
209095_at	DLD	5.18E-04	2123.6	2886.9	2617.8	2488.2	2632.1	2548.4	2594.3	2906.8	3992.0	4597.4	4146.1	3700.7	3850.5	3509.8	2594.3	3850.5	1.5
1563229_at	DLEU2	6.36E-03	38.4	28.8	54.1	54.3	58.3	47.0	46.9	56.6	45.4	88.0	76.1	54.8	66.3	62.0	47.0	62.0	1.3
224215_s_at	DLL1	2.19E-03	93.8	117.1	73.0	64.0	93.3	67.1	70.8	126.9	224.8	129.2	72.5	157.4	94.2	169.1	73.0	129.2	1.8
215761_at	DMXL2	2.30E-03	42.1	40.0	86.4	62.1	79.2	70.5	90.5	88.2	73.2	259.1	179.5	99.2	107.6	119.7	70.5	107.6	1.5
215266_at	DNAH3	6.32E-03	41.4	45.8	42.6	39.1	38.4	43.2	46.3	45.5	59.0	57.2	62.9	49.1	69.4	53.7	42.6	57.2	1.3
1554334_a_at	DNAJA4	8.84E-03	398.6	378.6	393.2	303.2	324.8	276.1	333.7	381.6	735.7	816.9	382.1	422.9	415.4	506.3	333.7	422.9	1.3
212817_at	DNAJB5	7.64E-03	58.0	46.2	58.0	53.8	59.3	47.1	53.2	82.3	66.0	74.7	52.5	76.6	65.0	91.1	53.8	74.7	1.4
208811_s_at	DNAJB6 /// TMEM135	5.55E-03	1751.5	1877.0	1828.6	1738.0	1820.7	1902.7	1970.8	2104.4	2378.4	2922.9	2162.5	2153.7	2385.7	2544.8	1828.6	2378.4	1.3
1554462_a_at	DNAJB9	1.99E-03	130.4	229.0	283.9	271.2	288.9	261.3	296.4	294.8	343.7	754.3	535.5	360.1	379.6	410.2	271.2	379.6	1.4
202842_s_at	DNAJB9	9.49E-03	1114.6	1250.4	1371.0	1321.6	1348.9	1275.7	1522.7	1259.2	2061.2	2836.8	2509.2	1504.7	1568.9	1949.3	1321.6	1949.3	1.5
202843_at	DNAJB9	4.91E-03	111.1	169.7	182.6	150.1	180.8	171.6	251.1	201.7	289.2	472.4	430.6	210.1	250.7	295.2	171.6	289.2	1.7
222620_s_at	DNAJC1	8.67E-03	571.3	539.0	612.1	600.3	640.6	587.6	548.6	748.4	776.7	904.1	785.4	640.7	691.4	903.1	587.6	776.7	1.3
222621_at	DNAJC1	3.88E-03	214.4	227.9	240.8	235.8	278.5	249.6	234.8	364.4	281.5	389.8	331.3	321.5	290.8	375.2	235.8	331.3	1.4
238336_s_at	DNAJC21	5.32E-03	381.6	411.6	425.3	370.7	448.4	434.1	411.3	441.0	532.4	704.8	529.2	571.1	499.7	542.6	411.6	532.4	1.3
1558080_s_at	DNAJC3	2.36E-03	420.5	520.6	458.6	545.1	520.7	491.9	618.3	692.5	648.5	1243.5	815.7	753.6	733.2	949.0	520.6	753.6	1.4
208499_s_at	DNAJC3	1.34E-03	2135.6	1830.1	1649.2	1954.0	1966.3	1636.6	2195.8	2583.7	2743.2	3564.9	2753.5	2698.7	2829.9	3699.4	1954.0	2753.5	1.4
225284_at	DNAJC3	9.53E-03	2346.7	2711.2	2577.2	2610.6	2643.8	2524.8	3017.8	2690.9	3321.8	4484.4	3774.6	2968.8	3129.5	3899.0	2610.6	3321.8	1.3
235341_at	DNAJC3	2.15E-04	561.2	571.8	625.7	655.2	640.6	520.7	787.9	872.0	889.7	1446.1	1100.3	1067.5	831.5	1208.2	625.7	1067.5	1.7
224612_s_at	DNAJC5	9.54E-03	481.2	353.1	465.9	457.3	457.9	366.8	497.4	515.6	432.3	603.7	545.5	574.0	570.9	637.8	457.9	570.9	1.2
224613_s_at	DNAJC5	3.52E-03	158.7	106.9	159.2	158.8	142.8	132.3	180.9	207.5	177.0	272.3	183.8	180.2	195.0	221.8	158.7	195.0	1.2
1556053_at	DNAJC7	3.53E-03	104.5	109.3	188.2	177.3	170.2	150.0	214.1	145.3	179.4	302.3	232.8	245.8	201.4	222.9	170.2	222.9	1.3
202416_at	DNAJC7	3.59E-03	1056.2	1004.7	1027.6	1017.7	1110.8	930.3	1195.2	1358.7	1278.8	1505.7	1182.8	1392.8	1544.4	1564.8	1027.6	1392.8	1.4
38703_at	DNPEP	3.01E-03	1060.5	924.4	980.3	1051.7	941.0	871.5	919.8	1248.3	1218.7	1551.3	1199.2	1350.8	1210.5	1400.3	941.0	1248.3	1.3
1558691_a_at	DOCK4	1.38E-04	20.2	32.0	31.0	24.4	42.2	12.4	33.8	51.1	78.2	116.4	104.4	110.7	70.2	61.1	31.0	78.2	2.5
205003_at	DOCK4	4.03E-04	358.3	180.8	223.2	337.8	453.6	226.9	370.7	599.2	729.8	1315.3	1001.8	762.6	631.3	1195.6	337.8	762.6	2.3
244840_x_at	DOCK4	5.94E-03	93.9	58.4	50.0	59.1	78.9	54.9	61.0	88.0	78.2	106.5	128.4	114.7	106.3	91.9	59.1	106.3	1.8
225384_at	DOCK7	6.70E-03	302.7	281.2	393.4	358.2	401.1	416.8	462.1	445.8	417.2	521.2	478.3	453.4	462.2	565.4	393.4	462.2	1.2
231297_at	DOT1L	9.12E-05	55.2	51.5	53.7	62.9	69.5	49.1	68.2	91.4	80.0	131.8	132.7	124.8	93.9	117.8	55.2	117.8	2.1
218627_at	DRAM1	6.53E-04	3683.6	2477.3	2289.2	1566.6	3983.5	1811.4	4023.0	5381.0	5774.4	7110.7	3655.9	5804.9	5746.2	6832.5	2477.3	5774.4	2.3
218854_at	DSE	3.51E-03	2831.3	2797.3	2610.9	3231.7	4170.5	2531.4	4422.1	3922.6	4542.3	5485.5	5115.1	4461.8	4583.8	5549.0	2831.3	4583.8	1.6
208430_s_at	DTNA	4.27E-05	107.3	157.5	131.7	89.6	128.3	121.6	110.2	199.1	353.0	439.5	205.1	259.4	247.9	226.2	121.6	247.9	2.0
210091_s_at	DTNA	2.90E-04	31.6	36.0	66.0	30.2	48.1	66.6	45.0	63.7	133.1	253.3	121.5	105.3	98.6	110.7	45.0	110.7	2.5
210611_s_at	DTNA	6.72E-04	33.7	39.5	51.9	20.1	32.3	54.7	41.9	59.0	123.3	231.8	103.1	86.0	83.0	88.2	39.5	88.2	2.2
210736_x_at	DTNA	9.18E-05	123.1	175.7	139.9	111.6	146.9	135.3	126.7	202.9	433.8	500.9	222.1	299.1	296.0	296.3	135.3	296.3	2.2
211493_x_at	DTNA	2.47E-04	90.3	148.0	122.4	95.7	138.3	136.2	115.9	206.2	353.4	546.5	192.1	249.5	259.3	238.8	122.4	249.5	2.0
227084_at	DTNA	1.14E-04	386.0	625.1	399.8	253.1	418.1	436.3	373.5	619.2	1479.2	1447.4	616.8	836.4	839.7	947.2	399.8	839.7	2.1
215732_s_at	DTX2	1.69E-03	67.4	53.3	75.1	85.1	86.4	74.7	93.7	102.9	65.3	108.2	118.6	164.5	111.6	116.4	75.1	111.6	1.5
225415_at	DTX3L	2.37E-03	1759.0	1747.0	1874.5	1890.0	1778.7	2013.8	1976.5	2028.6	2855.5	3974.1	2719.4	2469.0	2627.4	3369.1	1874.5	2719.4	1.5
201041_s_at	DUSP1	9.31E-05	1197.8	2225.6	1312.2	783.2	1161.9	869.3	1362.5	1735.4	3675.4	2954.9	1685.6	2901.8	1974.0	3055.4	1197.8	2901.8	2.4
226578_s_at	DUSP1	1.45E-04	92.7	143.8	147.5	109.1	116.5	93.2	136.0	198.9	255.6	321.2	172.6	398.6	249.3	283.4	116.5	255.6	2.2

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
224336_s_at	DUSP16	3.32E-04	59.6	87.5	64.6	54.7	104.0	51.4	90.2	102.6	120.4	186.3	119.9	181.6	111.7	154.5	64.6	120.4	1.9
224832_at	DUSP16	2.63E-03	165.9	193.9	125.1	120.4	265.2	96.8	161.5	194.5	271.2	351.5	213.0	372.5	209.1	273.2	161.5	271.2	1.7
204794_at	DUSP2	6.50E-05	43.4	35.8	58.6	41.5	51.7	37.5	39.2	79.3	72.5	170.2	112.8	217.9	110.1	149.2	41.5	112.8	2.7
209457_at	DUSP5	4.69E-05	113.6	102.6	163.1	123.2	173.8	113.6	144.2	250.9	515.6	932.4	406.4	451.4	310.2	584.0	123.2	451.4	3.7
208892_s_at	DUSP6	7.59E-03	625.2	560.8	553.3	895.5	1022.0	900.4	1214.9	725.6	960.6	1193.5	1337.7	1357.8	1015.8	1548.3	895.5	1193.5	1.3
208893_s_at	DUSP6	1.07E-03	632.9	520.0	372.1	595.1	847.4	611.9	837.6	730.6	846.8	819.2	1136.4	1245.8	964.1	1321.8	611.9	964.1	1.6
206374_at	DUSP8	8.18E-03	153.7	156.1	115.8	126.2	174.3	125.4	151.8	144.1	185.3	318.8	220.7	278.5	376.5	334.9	151.8	278.5	1.8
203590_at	DYNC1LI2	1.53E-03	234.9	189.4	184.5	180.8	212.8	189.6	186.0	290.3	259.8	301.7	249.3	270.4	258.7	250.7	189.4	259.8	1.4
201999_s_at	DYNLT1	6.48E-05	1213.0	1257.5	1135.1	1042.3	1111.6	932.1	1116.1	1910.5	2629.7	3523.3	2066.3	2533.0	2379.2	3003.7	1116.1	2533.0	2.3
218660_at	DYSF	5.29E-03	80.2	70.2	61.8	64.4	61.0	62.8	57.7	84.1	91.4	143.9	81.8	138.8	101.7	115.7	62.8	101.7	1.6
203692_s_at	E2F3	8.78E-04	212.9	168.1	279.3	291.2	318.2	245.3	313.8	313.0	258.4	482.3	382.7	428.5	431.5	400.2	279.3	400.2	1.4
219424_at	EBI3	1.76E-05	61.6	45.4	62.7	61.2	76.0	59.2	56.6	133.1	99.2	237.3	179.6	216.6	176.6	219.7	61.2	179.6	2.9
201750_s_at	ECE1	4.56E-03	50.3	39.5	65.3	72.2	67.6	58.7	61.6	66.7	51.4	86.9	74.6	121.2	101.3	102.4	61.6	86.9	1.4
203279_at	EDEM1	1.41E-03	587.1	435.8	535.8	565.6	699.3	664.3	734.0	769.0	795.6	1124.3	911.5	895.2	893.0	1087.9	587.1	895.2	1.5
1564630_at	EDN1	1.17E-04	68.9	46.8	42.5	36.0	50.4	35.1	41.9	132.5	367.8	691.9	222.4	251.3	223.3	432.4	42.5	251.3	5.9
218995_s_at	EDN1	2.19E-05	64.6	51.2	56.7	58.2	61.8	51.9	70.2	219.3	748.2	1312.3	529.7	559.1	389.9	896.5	58.2	559.1	9.6
222802_at	EDN1	1.24E-05	20.6	20.8	19.6	20.6	27.8	20.3	37.2	116.7	334.4	802.2	250.0	245.5	224.2	511.2	20.6	250.0	12.1
222483_at	EFHD2	7.45E-03	1225.0	1080.5	999.0	1278.2	1258.4	902.7	1090.1	1242.1	1467.0	1660.0	1499.8	1720.0	1785.2	1796.4	1090.1	1660.0	1.5
201693_s_at	EGR1	5.30E-03	63.0	45.5	69.9	49.2	74.9	65.1	75.7	79.0	75.3	163.1	84.8	95.1	72.7	109.8	65.1	84.8	1.3
206115_at	EGR3	5.76E-05	25.3	29.8	21.3	23.3	38.8	29.8	29.8	74.6	154.2	356.2	133.0	191.8	156.4	327.9	29.8	156.4	5.3
212650_at	EHBP1	2.09E-03	314.8	321.5	345.8	394.0	375.4	367.1	310.0	483.3	600.2	666.2	449.7	506.5	494.5	647.1	345.8	506.5	1.5
212653_s_at	EHBP1	1.58E-03	129.4	178.8	230.1	198.5	214.3	228.0	219.1	262.8	322.1	460.7	303.1	261.9	274.4	344.2	214.3	303.1	1.4
1557749_at	EHBP1L1	7.87E-03	128.5	109.8	239.3	196.6	192.9	170.0	192.8	207.2	165.7	328.0	260.8	220.6	188.0	225.7	192.8	220.6	1.1
91703_at	EHBP1L1	8.88E-03	162.6	124.9	169.5	168.2	164.0	154.2	165.0	249.0	133.5	209.3	205.6	268.5	254.3	190.5	164.0	209.3	1.3
208112_x_at	EHD1	7.06E-04	267.7	104.4	204.2	274.0	358.3	183.2	450.4	434.3	598.4	740.9	490.7	833.5	857.7	1005.2	267.7	740.9	2.8
209037_s_at	EHD1	4.11E-05	128.8	91.4	87.2	101.8	205.9	107.1	219.4	346.7	463.1	859.3	436.7	657.1	730.6	870.9	107.1	657.1	6.1
209038_s_at	EHD1	4.66E-04	93.7	58.2	78.9	92.5	118.5	80.6	136.0	143.6	112.3	207.5	155.8	337.8	334.9	281.8	92.5	207.5	2.2
209039_x_at	EHD1	1.28E-04	365.7	164.4	273.5	366.3	567.4	322.9	724.7	811.2	847.3	1141.7	742.8	1381.8	1409.1	1735.1	365.7	1141.7	3.1
222221_x_at	EHD1	1.67E-04	211.5	122.9	161.7	224.8	294.9	163.0	352.8	389.0	448.2	594.8	403.3	702.5	695.2	823.0	211.5	594.8	2.8
209536_s_at	EHD4	7.07E-03	1793.5	1888.5	1588.3	1654.7	1639.2	1536.6	1483.8	1904.7	2154.2	2155.9	2230.0	2086.6	2130.8	2184.3	1639.2	2154.2	1.3
233660_at	EHD4	9.87E-04	405.2	483.4	471.9	536.0	492.6	406.2	484.5	576.5	705.1	734.3	676.2	644.2	540.2	654.8	483.4	654.8	1.4
212225_at	EIF1	2.72E-03	157.7	130.7	226.0	169.7	182.8	169.3	187.7	212.9	230.5	448.8	253.1	223.0	200.3	273.3	169.7	230.5	1.4
204211_x_at	EIF2AK2	8.89E-05	825.2	1262.7	1204.4	1007.6	1062.3	1102.3	1237.6	1357.5	2035.7	2403.9	2250.0	1676.1	1814.3	2398.9	1102.3	2035.7	1.8
225827_at	EIF2C2	3.64E-05	143.4	113.6	183.0	185.6	227.1	145.4	207.7	357.5	241.6	543.0	341.1	393.0	328.2	476.6	183.0	357.5	2.0
225940_at	EIF4E3	7.57E-06	60.7	52.7	104.6	123.4	113.0	84.3	75.4	133.9	145.4	245.4	241.7	267.6	203.9	197.6	84.3	203.9	2.4
225941_at	EIF4E3	4.19E-04	31.4	37.2	55.3	55.3	58.6	41.6	30.8	50.9	56.2	108.7	122.8	76.5	83.0	75.7	41.6	76.5	1.8
238461_at	EIF4E3	1.22E-04	103.4	147.2	173.3	190.3	174.0	121.3	112.3	150.5	303.3	485.2	391.2	427.4	321.7	378.6	147.2	378.6	2.6
208624_s_at	EIF4G1	5.99E-03	738.4	592.5	605.3	680.2	686.6	608.0	694.4	794.2	740.5	814.9	815.7	923.9	961.0	944.4	680.2	815.7	1.2
201122_x_at	EIF5A	5.92E-03	662.9	513.8	600.6	653.1	573.6	539.0	652.3	687.7	679.5	846.9	774.1	813.5	809.8	873.5	600.6	809.8	1.3
201123_s_at	EIF5A	1.55E-03	293.3	231.8	266.3	328.3	278.9	273.3	317.8	391.2	288.2	490.8	430.4	494.1	543.9	456.1	278.9	456.1	1.6
213753_x_at	EIF5A	9.78E-03	669.0	578.4	588.0	696.0	592.0	509.2	634.1	760.2	651.6	804.6	768.1	770.5	704.2	916.4	592.0	768.1	1.3
203490_at	ELF4	7.69E-04	564.4	573.4	541.3	535.1	583.2	533.4	558.7	800.2	680.7	791.6	750.0	869.3	855.2	913.9	558.7	800.2	1.4
31845_at	ELF4	1.20E-03	776.8	866.7	770.2	789.3	882.1	768.8	823.7	1100.1	1038.7	1427.9	1101.7	1190.5	1174.9	1284.2	789.3	1174.9	1.5
1565254_s_at	ELL	1.83E-03	58.2	84.8	91.8	97.5	78.8	79.5	108.5	86.8	88.4	138.3	170.6	174.7	142.9	186.5	84.8	142.9	1.7
220363_s_at	ELMO2	3.55E-03	264.2	191.3	260.3	288.2	265.3	267.3	274.7	321.4	240.0	316.6	361.2	469.9	389.7	422.1	265.3	361.2	1.4
221528_s_at	ELMO2	4.24E-04	684.4	625.8	690.5	714.2	738.4	726.6	762.5	964.1	1019.2	1049.6	1023.5	991.6	969.6	1175.3	714.2	1019.2	1.4
55692_at	ELMO2	1.41E-03	324.8	353.8	426.3	417.0	443.3	485.2	490.1	613.1	473.7	661.1	707.8	619.4	582.4	674.7	426.3	619.4	1.5
215082_at	ELOVL5	5.57E-03	61.0	53.0	64.6	65.2	73.6	74.3	68.7	88.2	63.6	103.3	72.8	101.6	86.1	111.3	65.2	88.2	1.4
227180_at	ELOVL7	1.54E-04	45.9	36.2	60.4	68.9	280.5	101.4	161.2	305.4	559.2	1110.5	462.8	626.7	555.1	748.3	68.9	559.2	8.1
226789_at	EMB	1.15E-03	96.4	88.8	45.8	73.2	68.5	61.8	61.9	129.6	108.7	100.4	149.2	140.3	92.1	148.0	68.5	129.6	1.9
234464_s_at	EME1	3.77E-03	613.9	674.3	654.7	737.0	757.5	679.9	779.4	844.6	843.2	1081.7	939.3	983.3	870.9	913.3	679.9	913.3	1.3
224374_s_at	EMILIN2	5.98E-03	3186.7	2441.0	2800.7	3748.7	2936.8	2542.4	2835.5	3361.8	2931.6	4712.6	5029.5	3873.3	4405.2	3933.3	2835.5	3933.3	1.4
242288_s_at	EMILIN2	2.63E-03	1402.5	1076.9	1075.0	1694.0	1141.8	1069.7	1507.8	1622.3	1511.3	2070.5	2062.6	1820.0	2188.5	2334.4	1141.8	2062.6	1.8
201324_at	EMP1	1.42E-04	441.7	225.3	253.1	262.4	303.5	74.4	357.5	747.6	1767.9	1863.3	1486.9	1393.7	966.0	1869.8	262.4	1486.9	5.7
201325_s_at	EMP1	2.95E-04	322.5	139.8	110.0	168.0	162.4	62.0	168.7	390.8	657.7	523.1	501.3	608.9	351.9	736.8	162.4	523.1	3.2
213895_at	EMP1	1.55E-03	51.8	45.1	34.6	44.2	45.1	28.2	38.2	59.0	80.3	91.3	64.1	73.1	54.0	92.7	44.2	73.1	1.7
203729_at	EMP3	2.33E-03	566.5	305.6	404.7	505.2	451.2	341.9	518.7	699.8	603.6	861.4	635.7	1313.0	1218.8	979.3	451.2	861.4	1.9
207111_at	EMR1	4.79E-04	2222.1	995.9	1058.2	716.1	2884.8	1689.1	2664.2	4476.3	2230.6	2683.0	2463.0	4204.7	3854.8	3824.3	1689.1	3824.3	2.3
207610_s_at	EMR2	7.57E-06	271.3	103.6	129.0	173.4	192.6	138.0	364.6	649.9	342.2	379.3	410.6	699.5	511.7	1005.9	173.4	511.7	3.0
212570_at	ENDOD1	1.46E-04	161.8	80.4	92.7	106.9	97.7	109.5	84.0	232.2	216.6	170.1	225.0	210.8	212.9	141.1	97.7	212.9	2.2
212573_at	ENDOD1	5.61E-05	132.7	144.7	139.1	115.3	121.4	157.3	129.4	322.7	286.9	241.6	355.7	309.3	323.1	240.7	132.7	309.3	2.3
209392_at	ENPP2	1.67E-04	194.7	125.8	575.0	385.6	242.6	234.2	405.6	529.9	630.3	1174.9	1199.7	461.8	649.6	791.0	242.6	649.6	2.7
210839_s_at	ENPP2	6.58E-05	59.7	63.1	124.4	91.4	57.6	64.8	94.0	157.6	117.2	223.3	261.9	164.2	143.2	166.7	64.8	164.2	2.5
205757_at	ENTPD5	4.37E-03	159.8	139.6	163.0	140.8	114.3	190.8	119.5	175.1	169.0	241.1	201.4	185.7	247.1	224.7	140.8	201.4	1.4
206710_s_at	EPB41L3	1.46E-03	289.7	306.0	429.2	366.6	436.0	353.2	451.8	501.6	456.0	696.8	723.3	534.2	489.3	572.4	366.6	534.2	1.5
211776_s_at	EPB41L3	2.09E-03	516.9	478.2	512.5	597.1	677.2	523.3	604.5	630.7	705.9	944.2	966.2	778.2	784.0	867.8	523.3	784.0	1.5

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
212681_at	EPB41L3	2.58E-03	159.3	165.6	241.2	233.6	265.9	234.1	253.3	264.7	258.8	405.4	368.0	283.8	307.5	332.7	234.1	307.5	1.3
220977_x_at	EPB41L5	8.85E-03	82.5	126.9	100.1	83.3	129.1	110.0	79.6	129.1	142.0	198.1	149.9	125.4	149.4	155.0	100.1	149.4	1.5
229292_at	EPB41L5	2.86E-04	34.4	39.9	68.7	42.2	73.0	46.9	66.9	78.9	98.3	290.4	74.9	122.3	131.2	125.2	46.9	122.3	2.6
202609_at	EPS8	4.58E-04	181.8	142.2	199.3	201.1	195.7	166.1	198.4	338.6	322.0	371.9	307.0	281.5	223.7	317.7	195.7	317.7	1.6
227609_at	EPSTI1	7.13E-05	1265.4	1217.9	996.8	943.9	928.9	513.4	872.0	2010.1	3589.4	4107.0	3216.9	2585.4	2269.6	3712.9	943.9	3216.9	3.4
235276_at	EPSTI1	4.66E-04	323.6	261.8	232.7	256.9	251.6	182.9	189.0	457.7	423.5	643.1	573.2	590.1	537.8	769.6	251.6	573.2	2.3
209701_at	ERAP1	4.78E-03	1012.0	862.9	873.2	948.1	977.7	1007.3	814.9	1316.9	1137.4	1154.2	1217.6	1093.9	1206.6	1071.4	948.1	1154.2	1.2
1569583_at	EREG	7.68E-03	54.2	61.9	51.3	44.1	55.1	41.3	49.0	54.2	81.1	86.1	56.2	86.1	51.2	86.1	51.3	81.1	1.6
205767_at	EREG	1.14E-03	41.5	28.7	14.7	24.4	51.2	12.3	46.8	55.6	120.6	407.5	136.0	209.8	106.4	274.2	28.7	136.0	4.7
207061_at	ERN1	3.14E-03	72.1	69.9	71.2	84.2	77.7	81.7	82.1	86.4	99.5	123.4	106.5	122.2	103.5	102.2	77.7	103.5	1.3
235745_at	ERN1	1.67E-03	51.9	64.0	52.2	57.8	61.7	47.3	56.6	69.3	88.1	110.0	96.3	76.0	68.3	85.8	56.6	85.8	1.5
220012_at	ERO1LB	4.91E-03	46.4	73.1	75.5	56.6	81.6	64.1	88.9	74.5	82.3	126.5	116.9	96.3	86.8	118.9	73.1	96.3	1.3
201573_s_at	ETF1	8.11E-03	641.9	711.0	704.8	694.9	787.1	675.2	861.4	756.8	948.7	1179.5	890.3	853.9	928.5	1059.9	704.8	928.5	1.3
224453_s_at	ETNK1	3.02E-03	60.5	62.0	84.1	74.7	84.2	78.1	74.9	96.9	95.8	133.7	98.1	93.7	99.5	96.5	74.9	96.9	1.3
1555355_a_at	ETS1	2.04E-03	37.2	35.2	26.2	36.2	41.8	26.7	41.4	51.0	47.9	76.0	127.9	59.0	57.8	92.7	36.2	59.0	1.6
201328_at	ETS2	2.63E-04	251.9	192.5	310.0	268.0	254.9	287.5	344.7	358.3	292.5	641.6	392.3	391.3	471.8	614.6	268.0	392.3	1.5
201329_s_at	ETS2	1.24E-04	200.0	136.5	230.5	197.4	233.3	212.1	301.7	295.2	286.6	650.8	340.8	481.3	541.8	609.4	212.1	481.3	2.3
241193_at	ETS2	1.05E-04	286.9	275.0	379.7	207.3	252.0	201.6	318.3	399.3	633.3	1282.9	537.1	648.4	461.6	896.8	275.0	633.3	2.3
1552423_at	ETV3	3.42E-03	45.2	52.3	63.3	66.3	70.3	63.3	50.9	83.7	67.2	109.3	93.7	114.6	64.0	84.4	63.3	84.4	1.3
203348_s_at	ETV5	1.03E-04	36.3	44.0	38.4	44.6	51.7	26.2	67.0	116.4	98.9	189.9	137.9	101.9	124.4	153.3	44.0	124.4	2.8
203349_s_at	ETV5	2.84E-05	204.2	105.3	103.1	122.3	152.1	78.6	254.3	530.7	663.3	877.3	694.8	558.0	578.5	917.9	122.3	663.3	5.4
216375_s_at	ETV5	4.08E-05	74.5	62.4	62.8	68.2	67.3	55.4	73.4	141.2	119.2	149.7	105.9	127.5	119.6	138.2	67.3	127.5	1.9
230102_at	ETV5	1.40E-04	228.8	58.5	104.7	168.6	237.2	86.2	381.9	695.2	874.1	1100.6	917.8	799.1	930.3	1291.1	168.6	917.8	5.4
205585_at	ETV6	1.52E-04	210.2	165.2	250.6	263.1	257.0	197.0	262.7	343.2	263.2	379.1	358.4	408.5	316.6	392.9	250.6	358.4	1.4
221680_s_at	ETV7	1.73E-04	39.1	31.2	42.3	33.9	22.4	45.5	32.5	75.5	82.3	355.1	94.8	131.6	211.2	152.4	33.9	131.6	3.9
210011_s_at	EWSR1	3.01E-03	467.2	311.5	423.3	438.0	401.6	339.8	419.7	506.3	451.0	609.6	563.3	629.2	630.4	580.8	419.7	580.8	1.4
205061_s_at	EXOSC9	3.60E-03	1031.0	1191.1	1422.6	1466.6	1226.4	1340.2	1359.7	1378.4	2251.7	3089.5	2236.2	1240.5	1970.1	2481.6	1340.2	2236.2	1.7
201995_at	EXT1	6.71E-06	289.9	188.4	221.1	226.0	245.6	213.5	275.6	1053.6	1866.3	2114.9	1076.5	1786.9	1790.0	1744.8	226.0	1786.9	7.9
230183_at	EXT1	2.81E-03	42.7	33.7	24.7	35.2	36.1	26.3	34.5	54.8	42.6	80.9	54.5	59.9	58.1	69.4	34.5	58.1	1.7
203358_s_at	EZH2	5.38E-04	105.7	124.1	182.9	164.3	165.7	109.2	137.4	175.8	175.6	310.1	286.4	200.8	161.8	211.2	137.4	200.8	1.5
208621_s_at	EZR	6.51E-03	399.7	268.2	287.2	385.5	379.8	317.2	358.7	416.4	414.8	436.8	432.8	493.8	502.6	516.5	358.7	436.8	1.2
208622_s_at	EZR	2.60E-03	351.1	281.3	263.0	342.4	353.3	273.1	359.7	421.6	407.8	389.7	393.7	514.5	467.0	480.2	342.4	421.6	1.2
204363_at	F3	4.66E-04	146.1	132.5	184.3	198.4	239.4	126.2	273.9	253.0	387.1	863.0	455.5	377.4	278.6	589.8	184.3	387.1	2.1
220643_s_at	FAIM	7.83E-03	400.3	249.5	299.5	335.1	318.3	236.2	468.5	457.7	404.4	808.5	522.8	387.0	380.8	584.8	318.3	457.7	1.4
224783_at	FAM100B	4.19E-03	455.5	380.4	396.3	385.2	394.1	360.3	508.8	558.7	498.7	709.2	472.2	655.4	841.2	684.7	394.1	655.4	1.7
226905_at	FAM101B	8.10E-03	111.6	91.8	153.6	140.3	110.8	108.6	86.8	123.2	159.0	343.3	158.5	284.5	209.3	422.3	110.8	209.3	1.9
228382_at	FAM105B	4.53E-03	136.5	128.9	162.1	148.4	163.0	171.2	161.4	182.4	141.8	221.5	194.4	191.5	232.4	231.1	161.4	194.4	1.2
229196_at	FAM111A	6.63E-03	43.3	49.7	70.5	66.2	80.0	65.1	59.6	64.9	67.0	104.2	84.5	91.2	74.5	70.6	65.1	74.5	1.1
213861_s_at	FAM119B	7.83E-03	210.5	241.7	376.3	259.9	333.9	170.9	388.6	272.5	379.5	674.4	329.2	385.6	250.9	414.3	259.9	379.5	1.5
1552323_s_at	FAM122C	1.66E-03	50.4	60.7	57.1	45.6	53.2	45.6	40.0	60.2	86.8	99.1	73.5	69.1	62.8	53.2	50.4	69.1	1.4
230067_at	FAM124A	5.50E-03	35.4	38.9	32.3	38.9	31.8	31.3	34.7	45.9	39.1	158.7	109.0	78.9	67.8	67.5	34.7	67.8	2.0
230519_at	FAM124A	6.73E-03	60.3	64.5	67.4	62.5	69.4	61.5	70.6	62.0	75.5	223.3	174.5	122.2	132.0	114.7	64.5	122.2	1.9
221687_s_at	FAM125B	1.07E-03	262.7	273.1	235.8	227.1	347.1	289.5	187.9	371.0	337.7	527.3	340.2	563.1	428.4	329.6	262.7	371.0	1.4
221828_s_at	FAM125B	4.30E-03	66.7	65.9	92.9	91.7	113.0	83.3	98.2	113.4	75.8	156.7	122.0	153.3	149.6	110.7	91.7	122.0	1.3
52975_at	FAM125B	1.00E-03	169.5	192.4	188.2	213.8	240.1	198.3	116.7	269.0	249.7	376.6	292.8	358.4	286.6	248.4	192.4	286.6	1.5
217966_s_at	FAM129A	4.04E-04	5096.2	5251.4	4588.2	5843.1	6223.1	5225.4	6560.2	7214.2	9305.5	10059.6	9372.3	8205.4	8657.4	11435.2	5251.4	9305.5	1.8
217967_s_at	FAM129A	2.61E-04	1911.6	1740.6	1933.3	2601.6	2410.4	1884.2	2144.7	3153.2	3355.3	5046.0	4084.0	3466.6	3310.3	4117.9	1933.3	3466.6	1.8
233971_at	FAM166A	3.09E-03	175.9	109.6	193.4	211.2	148.7	180.0	245.9	233.2	181.1	323.7	247.8	317.5	430.3	316.0	180.0	316.0	1.8
1554509_a_at	FAM188A	4.28E-03	254.4	271.9	358.9	361.0	456.9	350.9	385.4	446.0	398.1	726.2	575.4	486.1	496.6	464.1	358.9	486.1	1.4
1554132_a_at	FAM190B	1.36E-03	116.7	115.9	151.9	137.3	154.2	138.8	171.8	161.9	202.8	350.6	226.7	182.3	305.8	263.5	138.8	226.7	1.6
209378_s_at	FAM190B	1.35E-04	235.1	233.4	206.0	200.9	217.3	236.0	252.6	369.7	386.2	456.4	319.9	328.1	395.3	466.4	233.4	386.2	1.7
228362_s_at	FAM26F	6.35E-04	121.3	61.8	156.2	59.2	234.1	164.5	133.5	322.3	200.1	450.5	217.9	296.1	259.9	313.4	133.5	296.1	2.2
229390_at	FAM26F	2.51E-03	322.9	166.6	587.2	107.6	571.1	465.2	462.5	909.9	483.1	1560.7	731.5	809.7	658.0	902.5	462.5	809.7	1.8
229391_s_at	FAM26F	1.46E-04	183.2	83.0	196.3	81.7	241.9	164.0	155.4	360.7	210.0	454.4	223.6	352.6	267.8	339.6	164.0	339.6	2.1
229543_at	FAM26F	2.44E-03	165.3	85.8	304.3	61.4	311.4	250.2	266.9	440.7	270.6	927.7	378.4	405.1	374.3	485.0	250.2	405.1	1.6
208092_s_at	FAM49A	3.73E-04	311.7	326.4	411.3	354.3	498.4	500.7	406.9	574.1	649.6	820.4	657.0	920.7	595.6	1036.1	406.9	657.0	1.6
223038_s_at	FAM60A /// LOC728115	2.63E-03	349.0	261.8	275.7	386.9	360.0	273.4	283.9	495.9	305.2	362.5	460.2	497.0	437.2	414.3	283.9	437.2	1.5
206707_x_at	FAM65B	2.43E-05	58.0	57.6	74.2	90.0	54.3	67.3	89.2	146.6	156.6	342.3	217.1	218.2	284.3	456.6	67.3	218.2	3.2
209829_at	FAM65B	1.55E-04	34.8	32.1	25.9	46.7	12.4	34.5	37.5	62.1	106.0	141.0	123.8	71.9	89.3	108.2	34.5	106.0	3.1
225834_at	FAM72A /// FAM72B /// FAM72C /// FAM72D	2.77E-03	70.0	86.4	139.5	150.0	107.2	122.3	133.2	181.9	203.0	465.1	266.5	136.1	155.9	201.4	122.3	201.4	1.6
204780_s_at	FAS	6.97E-05	238.8	211.8	350.5	448.5	517.5	319.4	193.2	480.3	665.0	1020.3	1044.6	888.6	668.3	365.7	319.4	668.3	2.1
204781_s_at	FAS	2.56E-05	169.0	182.3	272.0	356.5	321.3	259.9	159.5	293.7	457.1	714.0	768.7	626.0	498.0	348.1	259.9	498.0	1.9
215719_x_at	FAS	2.64E-04	77.7	68.3	182.2	177.6	224.7	153.0	96.7	230.1	238.0	486.2	489.2	355.2	292.2	154.6	153.0	292.2	1.9
216252_x_at	FAS	6.81E-05	90.4	87.3	185.1	214.6	209.5	145.4	102.6	245.1	254.5	543.6	586.1	367.5	302.1	175.0	145.4	302.1	2.1

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
219608_s_at	FBXO38	7.54E-03	297.9	242.0	311.1	319.8	366.3	330.0	285.4	425.4	296.5	381.9	410.2	428.6	405.2	328.4	311.1	405.2	1.3
231769_at	FBXO6	1.12E-05	114.1	102.8	178.3	179.0	181.1	158.5	166.8	297.3	194.0	426.7	371.5	368.8	367.2	361.2	166.8	367.2	2.2
218941_at	FBXW2	3.18E-03	303.3	249.5	304.2	313.2	293.4	277.7	314.4	375.8	305.1	432.8	371.3	449.6	376.7	402.6	303.3	376.7	1.2
207674_at	FCAR	8.13E-03	200.4	27.1	19.0	223.7	349.9	275.7	85.8	262.3	359.0	477.5	498.6	668.0	559.0	603.9	200.4	498.6	2.5
211307_s_at	FCAR	2.09E-03	140.9	64.5	70.0	109.4	144.9	113.0	67.7	167.5	125.9	180.9	147.3	375.1	292.2	289.4	109.4	180.9	1.7
211816_x_at	FCAR	4.12E-03	76.2	46.1	32.7	77.3	89.1	70.0	54.8	83.0	87.5	117.2	90.3	183.7	159.5	158.3	70.0	117.2	1.7
205237_at	FCN1	2.65E-04	55.0	43.2	161.5	103.6	112.9	112.2	150.9	294.5	127.7	283.7	222.2	748.6	328.3	648.5	112.2	294.5	2.6
221345_at	FFAR2	6.25E-05	41.9	49.4	51.4	51.8	59.7	40.4	57.0	110.7	155.7	365.2	135.4	316.7	317.5	294.4	51.4	294.4	5.7
215602_at	FGD2	9.86E-03	178.7	176.1	264.9	223.7	174.1	149.3	203.3	257.6	189.7	364.2	228.5	241.8	212.2	279.1	178.7	241.8	1.4
205014_at	FGFBP1	7.22E-03	56.9	59.0	45.5	64.4	48.2	46.0	34.1	86.3	99.0	53.4	72.5	66.5	51.2	51.3	48.2	66.5	1.4
219910_at	FICD	1.94E-03	77.1	63.8	80.5	74.9	89.9	82.9	98.7	112.7	81.2	126.4	133.6	137.9	131.7	108.1	80.5	126.4	1.6
219522_at	FJX1	3.02E-04	92.7	84.7	56.5	113.1	86.6	51.5	82.1	131.5	239.6	415.5	383.2	270.1	205.1	395.2	84.7	270.1	3.2
206857_s_at	FKBP1B	7.44E-03	71.7	61.3	46.7	82.9	61.1	31.8	39.9	79.4	92.1	126.8	88.0	93.8	76.1	92.4	61.1	92.1	1.5
204560_at	FKBP5	6.24E-03	562.7	495.2	452.9	596.0	421.7	380.5	352.9	718.7	564.5	578.0	716.6	587.6	731.2	515.3	452.9	587.6	1.3
224840_at	FKBP5	4.68E-03	1455.5	1275.7	1365.0	1817.5	1326.1	1199.4	1225.9	1941.0	1523.2	1810.0	2256.1	1540.6	1768.1	1519.8	1326.1	1768.1	1.3
224856_at	FKBP5	7.14E-03	686.8	736.6	731.9	864.9	673.4	639.2	618.1	1095.8	793.6	897.2	1100.8	868.6	974.4	755.9	686.8	897.2	1.3
227882_at	FKRP	4.17E-04	83.2	79.0	108.2	108.7	131.4	126.8	112.9	127.5	111.5	191.1	161.9	169.9	183.3	173.7	108.7	169.9	1.6
219906_at	FLJ10213	1.67E-03	104.1	87.9	132.2	141.3	122.8	113.9	138.9	133.2	114.3	254.0	175.6	189.8	168.5	209.0	122.8	175.6	1.4
241627_x_at	FLJ10357	8.59E-04	209.4	163.2	103.1	116.5	163.2	108.1	112.6	251.8	269.2	164.9	168.7	253.8	147.1	214.4	116.5	214.4	1.8
233210_at	FLJ12120	2.45E-03	36.9	11.2	48.0	43.8	57.0	91.8	66.5	88.2	64.6	792.1	174.6	116.2	182.8	149.0	48.0	149.0	3.1
235291_s_at	FLJ32255	3.13E-03	419.9	398.6	476.0	408.3	515.4	576.3	518.5	569.8	596.3	971.4	500.1	627.1	764.7	824.1	476.0	627.1	1.3
238432_at	FLJ35776	6.91E-03	221.5	203.6	159.4	175.3	280.0	164.5	217.4	255.9	221.8	218.8	224.1	391.7	298.0	306.4	203.6	255.9	1.3
239421_at	FLJ35776	1.83E-03	48.2	38.9	50.1	46.4	54.8	42.3	44.0	52.7	55.6	90.4	70.9	78.3	58.0	72.9	46.4	70.9	1.5
229521_at	FLJ36031	1.11E-03	192.3	167.3	267.4	248.2	338.5	243.0	280.5	296.0	411.8	594.4	372.5	419.0	405.5	443.9	248.2	411.8	1.7
1558234_at	FLJ36644	2.96E-03	39.1	39.6	33.8	35.2	51.6	32.8	30.5	49.9	56.5	156.8	68.7	82.3	87.0	81.9	35.2	81.9	2.3
238874_at	FLJ43663	2.38E-03	48.1	49.5	40.8	45.0	37.5	53.3	40.8	56.1	65.5	66.7	61.2	53.9	66.1	56.1	45.0	61.2	1.4
208748_s_at	FLOT1	3.08E-04	68.3	85.3	63.5	87.0	103.7	81.1	105.1	122.3	130.5	163.8	175.3	143.7	187.2	182.7	85.3	163.8	1.9
222033_s_at	FLT1	2.40E-03	46.0	39.7	34.3	40.0	39.0	23.2	49.4	73.2	69.9	272.8	108.8	67.5	75.1	110.9	39.7	75.1	1.9
226497_s_at	FLT1	2.88E-05	15.9	7.1	23.9	10.8	22.7	13.9	31.2	71.7	44.5	403.9	120.7	91.2	70.5	174.6	15.9	91.2	5.7
226498_at	FLT1	3.96E-04	27.6	25.7	22.8	23.2	24.7	18.3	30.1	81.0	52.8	275.0	86.2	110.6	44.9	122.4	24.7	86.2	3.5
232249_at	FMNL3	2.58E-03	1725.2	1659.7	1403.1	1315.5	1602.2	1532.1	1811.7	2304.3	1845.3	2298.1	2075.5	2308.5	2139.5	2277.0	1602.2	2277.0	1.4
212288_at	FNBP1	8.22E-03	466.7	524.8	494.6	602.0	622.1	530.8	604.7	602.3	611.5	943.2	726.6	714.6	744.9	850.8	530.8	726.6	1.4
218618_s_at	FNDC3B	1.76E-03	823.8	712.4	542.0	817.5	921.5	738.0	863.5	1014.6	1073.8	1239.3	1195.9	1313.7	1334.1	1186.4	817.5	1195.9	1.5
222692_s_at	FNDC3B	8.53E-03	931.5	773.8	785.9	932.5	1016.6	879.7	1305.7	981.2	1403.8	1843.5	1441.4	1197.2	1247.2	1730.8	931.5	1403.8	1.5
229865_at	FNDC3B	3.26E-05	202.8	166.6	267.3	312.3	322.8	216.2	342.5	551.4	748.7	1387.0	906.0	651.4	844.1	1211.0	267.3	844.1	3.2
242029_at	FNDC3B	5.80E-03	88.1	70.2	77.4	81.9	96.5	77.4	87.7	90.8	89.7	126.3	127.6	114.1	112.4	131.4	81.9	114.1	1.4
225922_at	FNIP2	4.68E-03	547.9	398.3	995.5	685.6	984.5	670.8	1407.1	887.7	1009.5	2328.0	974.1	1098.3	979.9	1850.8	685.6	1009.5	1.5
225924_at	FNIP2	3.51E-03	268.6	160.3	365.5	286.2	424.7	319.5	486.0	394.0	414.5	865.3	406.9	559.4	411.9	706.3	319.5	414.5	1.3
226460_at	FNIP2	1.67E-03	551.8	327.1	715.1	532.9	820.3	439.3	1003.8	821.8	930.9	1921.5	779.7	1146.1	837.1	1468.5	551.8	930.9	1.7
202768_at	FOSB	3.47E-03	112.1	74.6	97.4	92.8	108.1	112.1	97.1	119.8	107.3	155.7	112.4	188.9	169.5	189.6	97.4	155.7	1.6
204420_at	FOSL1	7.14E-05	36.2	40.9	43.2	40.5	41.1	30.9	51.7	62.5	59.3	89.9	73.1	93.0	64.6	98.1	40.9	73.1	1.8
218880_at	FOSL2	3.91E-04	143.6	132.6	146.8	173.0	232.0	151.7	218.7	229.5	193.9	376.4	258.3	431.2	328.0	355.7	151.7	328.0	2.2
218881_s_at	FOSL2	1.63E-03	71.9	64.6	87.1	110.8	150.8	95.1	125.1	128.9	82.7	162.6	140.3	206.7	172.5	166.0	95.1	162.6	1.7
225262_at	FOSL2	6.36E-03	129.2	123.5	191.3	196.4	293.9	221.4	253.0	210.6	164.8	367.9	260.5	342.2	247.7	340.0	196.4	260.5	1.3
205119_s_at	FPR1	2.95E-04	1152.6	585.0	753.6	998.0	1100.0	429.0	975.6	1843.9	1506.8	2773.5	2006.4	2412.3	2066.6	2353.6	975.6	2066.6	2.1
210772_at	FPR2	6.81E-05	238.9	256.1	282.2	275.0	464.5	241.5	518.6	594.1	1342.4	2034.8	1071.0	1009.6	1223.6	1810.4	275.0	1223.6	4.4
210773_s_at	FPR2	1.15E-05	175.5	207.8	219.7	179.3	309.8	139.4	328.4	564.0	1120.8	1509.5	804.6	1053.0	1155.1	1469.2	207.8	1120.8	5.4
214560_at	FPR3	4.25E-03	3071.3	2333.0	670.1	1041.9	1987.7	475.3	1038.2	3510.5	3310.8	1141.7	1848.1	2948.9	1681.1	2315.7	1041.9	2315.7	2.2
230422_at	FPR3	4.53E-03	1373.7	916.3	323.2	423.1	896.2	206.0	489.5	1443.4	1649.2	578.0	742.5	1146.0	677.8	1060.5	489.5	1060.5	2.2
229893_at	FRMD3	2.93E-04	42.5	68.7	51.5	44.2	49.9	41.8	45.9	87.7	157.1	167.5	138.6	90.5	56.6	110.9	45.9	110.9	2.4
230645_at	FRMD3	2.60E-03	30.2	44.2	26.5	27.2	30.2	28.0	30.2	61.5	67.7	102.7	73.7	48.4	31.2	73.2	30.2	67.7	2.2
210933_s_at	FSCN1	1.48E-04	31.9	26.8	19.6	48.6	69.1	25.1	31.4	86.6	55.2	107.2	97.6	146.7	84.3	103.2	31.4	97.6	3.1
242586_at	FSD1L	2.39E-03	28.8	47.8	53.5	73.4	63.0	66.7	100.1	63.1	76.6	171.9	157.4	96.3	77.7	152.3	63.0	96.3	1.5
242807_at	FSD1L	2.66E-03	42.7	38.0	50.0	60.2	60.9	60.2	57.3	56.8	61.7	125.4	143.1	81.5	72.7	116.1	57.3	81.5	1.4
212380_at	FTSJD2	6.48E-05	225.4	263.9	321.8	275.9	263.5	260.3	261.5	376.1	390.5	624.8	485.0	471.3	527.9	556.0	263.5	485.0	1.8
203091_at	FUBP1	2.92E-03	1113.6	889.3	1108.7	990.9	1199.5	1065.7	1212.4	1494.4	1252.0	1505.1	1181.4	1496.8	1420.7	1460.6	1108.7	1460.6	1.3
1565716_at	FUS	5.91E-03	283.8	222.1	303.6	283.5	279.1	237.9	246.5	364.7	273.3	473.3	352.7	361.3	259.0	340.5	279.1	352.7	1.3
209892_at	FUT4	9.30E-05	336.6	289.8	497.0	427.3	496.8	410.9	546.1	739.7	890.3	1597.2	956.7	792.3	812.1	1156.4	427.3	890.3	2.1
209893_s_at	FUT4	4.69E-05	683.2	603.1	751.2	586.7	726.8	603.1	697.9	1167.2	1566.7	2298.1	1607.2	1301.1	1389.0	1751.5	683.2	1566.7	2.3
224641_at	FYTTD1	5.41E-04	430.7	555.7	702.0	603.8	680.7	645.3	854.9	804.7	1041.8	1613.5	1186.5	1003.9	892.4	1155.6	645.3	1041.8	1.6
224642_at	FYTTD1	1.35E-03	501.2	573.8	682.8	643.5	699.2	749.3	762.4	760.8	1056.1	1473.1	1015.5	891.4	936.5	1149.8	682.8	1015.5	1.5
221245_s_at	FZD5	7.09E-03	212.8	264.2	249.5	211.9	279.8	241.6	256.9	249.2	397.8	378.9	330.4	299.9	276.2	389.4	249.5	330.4	1.3
213524_s_at	G0S2	6.04E-05	258.0	88.0	230.1	145.4	581.3	272.1	762.9	1168.1	4106.9	6565.8	1320.0	4122.0	5571.6	7778.8	258.0	4122.0	16.0
201514_s_at	G3BP1	9.85E-03	1084.6	828.5	1014.8	1050.0	1010.3	853.8	1106.7	1142.7	1100.0	1407.4	1359.0	1144.6	1167.0	1357.6	1014.8	1167.0	1.2
203853_s_at	GAB2	2.07E-04	647.4	664.1	817.6	694.6	870.0	801.0	740.2	970.1	1313.9	2109.1	1186.9	1420.3	1529.3	1954.8	740.2	1420.3	1.9
203146_s_at	GABBR1	1.61E-03	47.7	38.0	26.5	45.5	38.9	31.5	30.8	56.0	53.3	71.3	68.8	72.4	66.8	70.8	38.0	68.8	1.8

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
206173_x_at	GABPB1	2.99E-03	143.3	105.0	161.6	191.7	234.5	177.7	189.8	217.5	190.6	318.0	260.3	260.5	245.4	252.5	177.7	252.5	1.4
207574_s_at	GADD45B	6.41E-03	823.0	771.6	1041.6	928.0	1040.7	850.2	828.3	1069.6	1450.7	1490.9	859.4	1690.0	1264.7	1458.5	850.2	1450.7	1.7
209305_s_at	GADD45B	7.01E-03	246.8	173.0	258.2	253.3	275.1	220.0	238.8	278.0	295.2	412.0	243.1	612.7	436.2	408.7	246.8	408.7	1.7
213560_at	GADD45B	7.81E-03	768.7	667.0	1010.6	923.8	957.4	847.9	875.1	944.1	1311.0	1517.0	868.8	1716.4	1178.4	1388.9	875.1	1311.0	1.5
204121_at	GADD45G	5.52E-04	61.3	40.2	72.1	55.7	84.3	42.0	65.5	81.8	68.8	138.8	121.4	118.8	65.6	98.1	61.3	98.1	1.6
220442_at	GALNT4 /// WDR51B	9.62E-03	96.2	90.7	97.4	115.0	153.0	118.9	117.9	117.6	117.7	176.5	159.8	151.3	162.4	165.9	115.0	159.8	1.4
202269_x_at	GBP1	1.12E-04	6421.0	4447.9	4830.7	4359.5	6875.0	3459.5	7241.3	11982.3	14845.6	17039.3	14186.9	12458.7	13198.8	15139.6	4830.7	14186.9	2.9
202270_at	GBP1	3.61E-05	138.9	120.3	247.7	224.5	318.1	168.0	440.2	547.4	790.1	1788.8	983.9	765.7	818.8	1235.5	224.5	818.8	3.6
231577_s_at	GBP1	1.25E-04	4628.5	3382.8	4100.8	3907.2	4983.8	2588.3	6033.9	8340.1	11477.8	13095.6	10855.7	9356.9	10176.6	11979.7	4100.8	10855.7	2.6
231578_at	GBP1	1.05E-04	46.1	46.4	64.4	46.4	46.4	32.8	42.3	85.8	124.0	448.3	215.7	148.0	113.9	216.7	46.4	148.0	3.2
202748_at	GBP2	3.14E-04	5640.6	6444.1	6113.0	6544.7	6876.0	5516.0	5634.5	7838.2	10459.8	12001.3	10405.0	9415.8	10876.1	11157.8	6113.0	10459.8	1.7
223434_at	GBP3	2.45E-03	173.6	275.1	564.5	312.3	110.7	438.0	672.4	415.2	491.2	1497.3	587.9	144.4	501.6	1029.2	312.3	501.6	1.6
235175_at	GBP4	4.18E-06	360.5	324.8	435.8	380.4	448.1	317.1	443.0	1080.7	1480.1	2020.6	1472.9	1294.2	1162.5	1770.2	380.4	1472.9	3.9
235574_at	GBP4	2.65E-06	301.9	397.2	483.1	413.8	537.2	373.5	431.2	1124.7	1468.5	2308.5	1479.0	1507.3	1321.9	1805.0	413.8	1479.0	3.6
229625_at	GBP5	7.57E-06	812.0	1336.0	1162.3	935.5	1370.4	662.1	1301.8	2325.2	4348.1	6060.6	4733.1	4583.0	3629.8	5135.1	1162.3	4583.0	3.9
238581_at	GBP5	6.71E-06	97.4	252.1	247.8	268.4	348.0	180.7	322.4	375.9	896.5	1442.6	1689.0	1051.2	701.2	1370.1	252.1	1051.2	4.2
204224_s_at	GCH1	5.39E-04	2718.1	961.4	1624.4	1752.2	3913.0	774.3	4438.7	6600.0	9690.2	12641.8	10204.3	8779.9	9460.9	10596.7	1752.2	9690.2	5.5
211020_at	GCNT2	1.30E-03	89.6	94.1	103.6	82.1	106.2	109.9	99.6	145.7	105.5	163.4	135.4	146.6	148.9	161.6	99.6	146.6	1.5
230788_at	GCNT2	3.77E-03	423.4	552.6	374.9	325.9	370.8	465.8	476.9	573.2	729.2	807.6	575.6	485.9	541.3	697.9	423.4	575.6	1.4
220831_at	GCNT4	2.77E-04	50.0	49.7	24.5	11.8	15.5	17.7	24.9	76.3	163.8	314.3	84.5	110.9	96.7	150.3	24.5	110.9	4.5
202721_s_at	GFPT1	6.82E-03	741.7	705.1	578.1	664.8	696.1	667.2	555.2	819.8	891.5	841.1	847.2	777.0	923.7	786.5	667.2	841.1	1.3
205582_s_at	GGT5	3.17E-03	44.1	28.7	53.7	42.1	53.3	40.5	56.2	59.3	38.1	64.1	58.5	66.5	57.2	66.3	44.1	59.3	1.3
223278_at	GJB2	1.05E-04	38.3	43.9	42.8	43.7	143.2	26.1	95.5	193.0	253.8	997.9	220.5	605.8	400.9	403.1	43.7	400.9	9.2
207387_s_at	GK	6.94E-03	3074.4	2035.0	2699.4	2600.3	3309.6	2602.1	3969.6	3195.0	3250.0	4399.9	3601.6	4018.2	3670.5	4793.9	2699.4	3670.5	1.4
215975_x_at	GK	1.07E-03	1552.0	968.8	1091.6	1072.8	1593.3	1089.1	1731.7	1903.4	1647.2	2514.4	1608.9	2408.0	1998.3	2482.7	1091.6	1998.3	1.8
215977_x_at	GK	4.22E-03	1082.9	552.8	767.0	729.3	996.5	673.6	1115.3	1125.5	1046.1	1459.0	945.0	1444.5	1398.3	1532.2	767.0	1398.3	1.8
217167_x_at	GK	3.18E-03	1050.3	537.6	732.3	733.5	979.8	626.9	1092.1	1150.9	1037.7	1403.6	952.5	1426.4	1340.6	1519.7	733.5	1340.6	1.8
216316_x_at	GK /// GK3P	4.86E-03	230.6	137.3	241.0	214.6	267.4	218.1	341.2	286.4	297.7	470.1	280.2	335.9	349.8	410.9	230.6	335.9	1.5
215966_x_at	GK3P	1.73E-03	235.9	137.8	176.9	174.5	250.8	169.6	285.1	284.5	244.9	374.4	258.5	357.6	334.6	368.4	176.9	334.6	1.9
1553772_at	GK5	2.68E-04	77.6	82.5	99.5	83.0	88.4	101.9	97.5	135.9	100.5	166.4	143.2	181.7	182.3	177.9	88.4	166.4	1.9
227376_at	GLI3	1.73E-03	91.8	43.5	60.2	56.7	63.0	50.0	70.6	115.8	71.4	82.2	78.0	76.0	68.9	118.7	60.2	78.0	1.3
230258_at	GLIS3	2.07E-03	61.4	71.1	92.6	94.5	48.0	91.9	80.0	124.9	78.1	221.8	195.0	86.8	182.6	97.3	80.0	124.9	1.6
209080_x_at	GLRX3	5.91E-03	426.8	384.9	407.2	475.3	483.1	406.2	447.4	524.3	474.1	632.9	558.9	586.5	539.7	550.5	426.8	550.5	1.3
211414_at	GLS	6.39E-03	25.9	37.5	44.5	42.6	41.9	55.5	42.4	46.6	60.2	68.0	89.0	70.5	51.2	53.1	42.4	60.2	1.4
223079_s_at	GLS	1.46E-03	432.2	439.0	644.9	623.4	549.2	619.3	696.9	629.9	704.6	1219.5	896.0	689.7	789.9	938.6	619.3	789.9	1.3
219920_s_at	GMPPB	5.65E-03	211.7	155.2	192.5	195.9	182.9	201.6	214.4	235.7	170.4	248.7	289.7	262.5	306.7	290.7	195.9	262.5	1.3
204187_at	GMPR	6.62E-04	732.1	288.3	347.2	359.5	239.5	251.4	185.0	864.8	916.5	1006.4	769.1	1075.9	1112.9	964.8	288.3	964.8	3.3
221737_at	GNA12	2.71E-03	319.3	245.5	255.6	283.1	355.7	234.3	320.7	453.3	315.3	347.4	368.3	424.4	362.0	387.7	283.1	368.3	1.3
224681_at	GNA12	5.37E-03	230.9	184.4	254.4	293.4	341.5	248.3	367.9	385.8	216.8	406.9	384.7	436.7	430.3	402.6	254.4	402.6	1.6
206917_at	GNA13	9.25E-03	507.3	412.5	471.8	456.5	546.3	478.6	476.5	552.5	561.8	720.9	544.0	662.6	590.1	591.1	476.5	590.1	1.2
201179_s_at	GNAI3	7.59E-03	2054.8	1510.7	1755.1	1876.7	2066.3	1664.4	2107.8	2297.0	2157.2	2585.5	2253.6	2275.6	2361.1	2758.9	1876.7	2297.0	1.2
223487_x_at	GNB4	1.24E-03	171.9	227.7	260.5	257.8	245.5	241.5	265.5	241.5	319.1	549.1	388.8	379.5	294.8	417.3	245.5	379.5	1.5
223488_s_at	GNB4	1.64E-04	693.1	528.2	625.3	532.2	578.5	557.8	552.8	887.6	990.7	1212.2	890.4	972.5	1015.9	1089.3	557.8	990.7	1.8
1555766_a_at	GNG2	1.30E-04	40.1	29.0	24.1	33.4	38.0	19.9	37.2	62.1	104.7	151.8	99.3	155.4	99.6	200.9	33.4	104.7	3.1
223943_s_at	GNG2	4.87E-04	36.6	45.6	31.5	29.7	35.0	24.8	32.3	50.7	67.0	79.3	72.8	87.5	81.9	107.7	32.3	79.3	2.5
224964_s_at	GNG2	3.03E-04	37.3	59.6	45.0	53.7	50.4	54.8	28.9	116.0	139.2	214.2	177.5	288.8	174.7	424.8	50.4	177.5	3.5
224965_at	GNG2	1.75E-05	33.7	30.6	40.4	55.0	68.6	35.8	43.4	106.3	148.1	287.7	193.2	291.0	177.0	413.5	40.4	193.2	4.8
205495_s_at	GNLY	3.01E-03	39.9	36.5	44.7	63.8	44.4	126.1	53.4	57.4	39.8	63.1	143.4	93.1	176.4	94.0	44.7	93.1	2.1
37145_at	GNLY	3.27E-03	42.0	40.9	41.6	51.1	41.4	108.9	44.9	46.4	49.5	58.9	118.3	86.9	203.3	83.6	42.0	83.6	2.0
201567_s_at	GOLGA4	3.53E-03	329.9	335.2	425.2	425.3	474.6	425.3	457.4	412.0	625.8	763.2	569.7	542.3	552.1	711.0	425.3	569.7	1.3
218193_s_at	GOLT1B	8.10E-03	1137.5	816.7	982.0	1061.1	1107.5	1025.9	1209.0	1188.8	1273.0	2021.0	1570.3	1316.7	1333.0	1666.7	1061.1	1333.0	1.3
210009_s_at	GOSR2	2.93E-03	143.0	126.7	154.9	151.0	145.0	127.5	156.0	199.2	146.2	225.7	192.1	200.1	183.7	186.2	145.0	192.1	1.3
223705_s_at	GPBP1	3.14E-03	1097.6	1356.0	1475.8	1158.1	1496.0	1310.6	1388.0	1454.1	1836.4	2407.8	1655.2	1751.0	1541.6	1889.7	1356.0	1751.0	1.3
209220_at	GPC3	1.61E-04	38.1	53.5	22.9	30.6	28.2	32.4	22.0	74.2	125.3	169.6	95.4	102.6	98.1	107.1	30.6	102.6	3.4
204983_s_at	GPC4	3.37E-05	118.7	78.3	125.8	88.9	126.6	48.0	94.0	249.4	203.4	684.2	357.9	367.6	209.0	336.7	94.0	336.7	3.6
204984_at	GPC4	9.39E-05	60.7	57.3	85.6	59.2	101.6	33.9	83.1	138.9	123.7	377.6	208.9	187.2	119.8	199.6	60.7	187.2	3.1
210007_s_at	GPD2	2.09E-04	1368.5	1078.5	1087.2	1369.8	1618.3	1109.5	1713.5	2245.6	2948.7	3544.4	2720.3	2691.3	2817.9	3103.3	1368.5	2817.9	2.1
211613_s_at	GPD2	1.32E-04	347.8	210.1	264.9	357.8	364.3	277.8	392.5	586.7	687.4	1029.0	662.7	840.6	828.2	889.6	347.8	828.2	2.4
225447_at	GPD2	6.39E-04	803.9	528.5	752.6	831.3	1113.2	829.7	1385.5	1409.0	1689.1	2843.6	1990.3	1831.0	1596.8	2128.0	829.7	1831.0	2.2
220265_at	GPR107	7.51E-03	93.1	103.9	109.2	132.9	137.0	120.8	110.5	140.5	148.4	226.0	174.7	134.4	169.8	153.4	110.5	153.4	1.4
223887_at	GPR132	3.32E-04	53.3	39.8	23.1	48.2	55.5	42.5	52.9	106.0	89.9	177.7	135.2	148.4	103.7	207.0	48.2	135.2	2.8
227970_at	GPR157	2.77E-03	417.7	368.1	315.1	291.3	364.4	301.3	391.4	471.3	455.7	640.6	412.2	559.5	585.2	619.7	364.4	559.5	1.5
214104_at	GPR161	2.64E-04	75.3	53.2	63.4	63.0	67.3	55.7	79.6	109.9	98.5	153.0	98.7	156.8	128.4	124.5	63.4	124.5	2.0
232350_x_at	GPR161	1.82E-03	158.2	121.2	148.7	138.8	128.8	135.2	148.0	205.1	160.4	182.5	199.1	157.9	196.0	230.7	138.8	196.0	1.4

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
235961_at	GPR161	8.59E-04	44.8	35.5	51.3	64.4	66.8	67.9	77.5	79.3	65.9	85.5	89.9	77.5	98.8	130.5	64.4	85.5	1.3
207651_at	GPR171	4.07E-05	48.6	60.0	72.0	64.8	63.0	71.1	56.1	105.1	156.4	190.9	238.3	140.4	173.4	252.9	63.0	173.4	2.8
231871_at	GPR180	4.60E-04	148.5	212.2	224.3	186.7	192.0	226.5	178.2	261.1	424.3	512.9	360.3	260.9	293.8	361.6	192.0	360.3	1.9
205419_at	GPR183	2.59E-05	29.7	30.5	18.9	36.6	39.5	24.6	29.0	112.7	84.6	104.2	122.9	239.9	99.4	259.2	29.7	112.7	3.8
223767_at	GPR84	1.71E-05	73.6	27.7	42.5	43.6	272.9	32.7	107.8	512.7	606.5	623.2	405.1	1156.4	632.2	904.8	43.6	623.2	14.3
220404_at	GPR97	3.16E-04	20.6	18.7	34.5	36.6	48.2	35.1	28.9	43.7	57.1	175.2	57.6	94.2	97.8	101.3	34.5	94.2	2.7
224807_at	GRAMD1A	1.16E-05	134.3	75.2	119.2	130.8	176.7	103.7	197.0	323.3	284.5	629.5	378.0	551.6	459.7	681.3	130.8	459.7	3.5
244808_at	GRAMD1A	2.43E-05	232.8	154.2	258.9	138.0	300.9	99.3	265.7	623.5	616.1	1853.4	611.0	941.8	746.7	1241.9	232.8	746.7	3.2
218706_s_at	GRAMD3	9.58E-04	121.8	97.8	141.8	122.1	134.6	116.0	145.6	166.3	202.4	414.0	208.1	187.8	206.4	243.5	122.1	206.4	1.7
228263_at	GRASP	8.22E-03	62.2	53.5	57.6	62.3	67.0	59.2	56.2	64.2	64.9	76.5	77.4	85.0	84.2	79.6	59.2	77.4	1.3
202554_s_at	GSTM3	4.00E-03	43.8	76.5	88.3	73.3	83.1	37.8	120.8	80.0	101.0	162.1	91.3	106.8	66.2	136.4	76.5	101.0	1.3
208066_s_at	GTF2B	5.57E-04	1525.8	1529.5	1227.3	1301.6	1376.8	1272.6	1230.7	1953.2	2438.7	2928.8	1939.5	2446.8	2159.0	2549.6	1301.6	2438.7	1.9
202680_at	GTF2E2	1.39E-03	509.9	526.9	492.3	533.2	504.3	496.7	576.4	631.1	866.2	908.1	710.0	691.1	725.0	775.9	509.9	725.0	1.4
205274_at	GTPBP1	3.08E-04	39.0	27.6	50.1	40.1	35.7	37.6	46.3	51.5	45.3	90.5	61.3	61.2	78.7	69.2	39.0	61.3	1.6
219357_at	GTPBP1	3.91E-05	154.0	110.9	175.4	153.1	183.7	171.4	161.7	277.1	236.0	341.2	246.2	296.6	325.1	300.2	161.7	296.6	1.8
226359_at	GTPBP1	4.70E-03	67.9	52.7	82.3	72.7	65.4	71.1	77.1	92.4	58.2	119.6	98.1	135.1	145.4	101.2	71.1	101.2	1.4
221050_s_at	GTPBP2	5.45E-03	489.3	579.9	409.1	444.7	625.9	581.6	671.5	785.2	595.3	792.1	705.2	862.2	814.5	818.0	579.9	792.1	1.4
218238_at	GTPBP4	4.38E-03	1003.3	882.8	1111.4	955.2	1047.2	963.7	1104.0	1220.1	1308.5	1666.3	1462.0	1154.6	1239.2	1381.6	1003.3	1308.5	1.3
218239_s_at	GTPBP4	8.28E-03	748.1	895.4	1303.4	1109.6	1134.4	1155.7	1339.5	991.5	1237.7	2046.4	1736.1	1169.1	1377.0	1631.2	1134.4	1377.0	1.2
220577_at	GVIN1	2.94E-03	82.9	71.8	88.0	114.7	91.3	107.1	105.8	118.5	108.6	243.6	248.2	122.0	148.8	146.7	91.3	146.7	1.6
205488_at	GZMA	4.31E-03	37.4	42.4	46.1	54.1	89.0	96.5	62.7	111.0	58.5	78.2	197.8	104.9	150.1	116.1	54.1	111.0	2.1
210164_at	GZMB	6.93E-04	35.2	48.2	47.1	28.9	58.6	52.9	59.6	124.3	50.9	218.2	123.8	156.5	141.8	274.2	48.2	141.8	2.9
206666_at	GZMK	3.61E-03	65.2	56.4	33.7	44.5	35.3	35.1	45.5	75.4	80.8	46.7	132.1	63.3	56.9	77.7	44.5	75.4	1.7
209069_s_at	H3F3B	1.49E-03	3423.7	2897.8	2839.6	3181.8	3350.1	2729.2	3425.5	3894.0	4413.4	4495.8	3989.9	5333.0	4879.2	5290.0	3181.8	4495.8	1.4
211997_x_at	H3F3B	3.64E-03	2882.3	2216.1	2085.8	2697.8	2560.8	2161.2	2530.3	3019.7	3515.3	3638.9	3077.0	4484.2	4236.9	4670.8	2530.3	3638.9	1.4
220491_at	HAMP	1.41E-03	165.3	169.7	146.5	100.0	119.8	101.0	135.4	400.9	208.5	244.5	171.0	503.0	297.2	459.5	135.4	297.2	2.2
227262_at	HAPLN3	2.22E-04	57.8	64.1	68.2	69.6	77.8	57.0	86.2	118.4	94.6	168.1	144.1	109.4	115.1	152.9	68.2	118.4	1.7
1554285_at	HAVCR2	2.99E-03	923.7	1112.8	879.5	812.4	804.5	733.2	843.3	969.9	1430.3	1364.8	1143.8	1142.8	1268.2	1370.5	843.3	1268.2	1.5
1555628_a_at	HAVCR2	4.74E-03	3115.8	3497.2	2325.9	2432.5	2761.8	2349.4	2535.9	3279.6	4432.5	3771.6	3228.5	3617.0	3993.8	4621.5	2535.9	3771.6	1.5
1555629_at	HAVCR2	6.05E-03	59.0	51.4	66.8	55.8	70.1	45.8	66.9	65.7	68.0	102.4	90.5	74.7	68.2	93.5	59.0	74.7	1.3
214414_x_at	HBA1 /// HBA2	9.19E-03	308.3	63.2	57.2	74.3	74.8	47.9	164.5	105.7	1081.0	2476.0	229.1	1950.6	256.4	2575.0	74.3	1081.0	14.6
244322_at	hCG_ 2038586	5.78E-04	42.1	39.3	45.5	38.6	37.3	42.5	44.2	70.6	88.5	265.8	112.8	112.6	69.7	120.5	42.1	112.6	2.7
208018_s_at	HCK	3.42E-03	4362.5	2733.2	3131.0	4402.2	4278.4	3357.3	4782.7	4792.4	4655.1	5073.5	5461.7	7114.8	7102.9	6393.6	4278.4	5461.7	1.3
211722_s_at	HDAC6	7.17E-04	62.8	39.4	51.3	50.0	59.8	49.1	67.8	69.4	69.4	97.5	81.6	105.4	77.5	134.8	51.3	81.6	1.6
216484_x_at	HDGF	9.94E-03	146.3	105.0	127.6	155.3	160.5	124.7	158.9	164.8	149.0	220.5	186.5	175.4	173.8	203.9	146.3	175.4	1.2
230582_at	HECA	1.49E-03	75.4	74.4	92.8	104.7	86.1	95.3	78.7	98.6	95.9	131.7	135.2	110.1	123.6	117.5	86.1	117.5	1.4
212822_at	HEG1	2.46E-03	372.6	249.6	190.5	289.5	175.1	193.5	250.5	371.8	425.8	539.8	432.1	361.8	506.8	650.7	249.6	432.1	1.7
213069_at	HEG1	1.06E-03	796.3	678.7	568.6	838.2	492.6	526.0	709.1	928.8	1379.6	1625.1	1204.5	943.0	1088.8	1770.4	678.7	1204.5	1.8
1552787_at	HELB	3.61E-03	57.0	82.2	77.2	108.8	107.2	75.4	28.6	68.9	107.1	149.0	184.1	150.8	93.3	37.1	77.2	107.1	1.4
1552788_a_at	HELB	3.73E-03	48.6	58.1	75.9	74.4	89.2	62.5	65.8	77.8	68.0	119.4	123.5	116.1	82.8	75.0	65.8	82.8	1.3
219863_at	HERC5	1.16E-05	999.0	941.2	978.9	797.1	769.6	892.2	626.7	2395.9	3667.2	4231.0	2881.9	3039.4	2796.0	3780.7	892.2	3039.4	3.4
1563659_at	HERC6	2.06E-04	66.7	66.1	76.8	65.6	49.1	49.6	62.7	90.2	112.2	179.1	134.3	79.2	86.9	116.8	65.6	112.2	1.7
219352_at	HERC6	7.57E-06	357.3	444.9	357.6	330.5	275.4	291.9	245.2	1037.9	1358.9	1933.2	1357.2	1264.6	1183.9	1482.5	330.5	1357.2	4.1
203394_s_at	HES1	3.59E-03	66.1	56.2	36.7	40.1	46.3	42.8	66.5	101.4	64.0	110.6	70.7	200.9	71.1	151.7	46.3	101.4	2.2
203395_s_at	HES1	4.34E-03	83.7	67.3	68.4	80.9	82.7	67.9	106.5	94.9	100.4	151.5	92.5	165.8	103.5	252.0	80.9	103.5	1.3
211267_at	HESX1	6.17E-06	71.9	45.1	75.9	49.2	42.1	33.5	37.0	240.8	360.2	632.9	326.0	326.9	250.6	406.1	45.1	326.9	7.3
218839_at	HEY1	3.31E-04	110.7	60.7	61.6	87.0	187.7	78.6	196.4	196.9	429.0	668.7	374.1	609.0	722.6	607.3	87.0	607.3	7.0
44783_s_at	HEY1	3.55E-04	162.8	152.4	110.9	131.7	379.8	125.8	373.1	357.3	868.7	1385.8	667.6	880.2	1249.7	1291.1	152.4	880.2	5.8
225222_at	HIAT1	7.24E-04	497.8	524.7	559.7	497.9	668.0	574.2	695.3	814.1	929.0	1319.7	925.7	904.9	757.9	1078.0	559.7	925.7	1.7
200989_at	HIF1A	6.81E-05	814.2	724.6	956.6	845.5	1471.5	908.1	1509.6	1600.4	2346.5	3570.1	2403.7	2583.5	2177.4	3541.4	908.1	2403.7	2.6
218279_s_at	HIST2H2AA3	1.14E-03	401.8	235.0	568.5	459.8	369.8	555.9	433.0	585.0	581.7	844.3	602.1	884.9	867.3	1006.3	433.0	844.3	1.9
214290_s_at	HIST2H2AA3 /// HIST2H2AA4	3.46E-03	628.2	603.5	1046.0	814.5	596.3	952.6	782.0	964.0	1048.0	1182.8	1007.5	1559.1	1556.7	1749.1	782.0	1182.8	1.5
218280_x_at	HIST2H2AA3 /// HIST2H2AA4	5.58E-04	505.7	451.4	859.9	663.9	574.7	823.8	632.0	831.0	868.7	1198.5	914.0	1341.7	1307.5	1430.6	632.0	1198.5	1.9
204512_at	HIVEP1	9.51E-04	242.2	166.4	258.3	236.8	408.4	263.9	448.0	393.7	425.4	777.5	503.2	503.6	569.7	689.4	258.3	503.6	1.9
212641_at	HIVEP2	4.38E-04	75.5	41.5	101.7	75.6	161.8	61.8	127.2	143.2	156.6	285.5	158.0	219.8	212.7	268.5	75.6	212.7	2.8
212642_s_at	HIVEP2	1.75E-03	154.6	103.6	169.1	133.8	290.7	144.8	300.5	250.2	282.8	545.6	288.0	326.0	455.5	483.1	154.6	326.0	2.1
243254_at	HIVEP2	1.61E-04	86.8	96.7	100.6	90.9	198.9	83.2	169.7	190.0	239.7	429.7	206.1	344.7	316.3	359.2	96.7	316.3	3.3
232581_x_at	HIVEP3	5.01E-03	99.5	69.8	81.5	98.7	85.7	55.6	97.0	117.3	104.0	134.8	121.1	120.5	141.4	142.4	85.7	121.1	1.4
235122_at	HIVEP3	1.71E-03	52.8	45.8	45.7	84.8	87.3	44.0	90.8	117.0	53.7	218.2	222.7	136.9	165.9	220.6	52.8	165.9	3.1
221978_at	HLA-F	4.28E-05	235.7	309.3	376.6	331.7	340.6	208.9	324.7	373.1	527.2	694.5	578.1	667.0	462.1	601.7	324.7	578.1	1.8
206074_s_at	HMGA1	1.20E-04	291.5	217.3	278.1	287.5	291.3	197.8	287.4	454.3	406.9	554.7	401.5	549.2	441.8	551.8	287.4	454.3	1.6
210457_x_at	HMGA1	2.45E-03	92.7	72.0	105.9	83.7	111.8	78.9	114.7	126.9	94.0	135.7	113.2	165.4	136.9	134.5	92.7	134.5	1.5

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
205822_s_at	HMGCS1	9.75E-04	117.5	100.3	98.9	92.6	153.9	94.9	137.3	187.9	136.9	182.6	150.8	179.7	153.7	196.1	100.3	179.7	1.8
1554303_at	HNMT	7.28E-04	191.0	179.3	185.9	149.2	232.9	197.9	222.7	244.1	345.5	427.7	414.7	333.0	402.0	385.2	191.0	385.2	2.0
211732_x_at	HNMT	2.93E-03	2356.4	2268.5	2118.3	1916.4	2374.6	2000.5	2115.3	2794.5	2659.3	2961.9	2636.6	3104.2	2992.4	2778.1	2118.3	2794.5	1.3
200751_s_at	HNRNPC	1.05E-03	1156.0	988.0	1334.0	1415.0	1429.6	1218.8	1385.5	1531.8	1513.6	2356.2	1865.5	1846.4	1771.5	1905.3	1334.0	1846.4	1.4
211597_s_at	HOPX	5.96E-04	24.5	20.4	15.5	21.7	35.1	24.5	14.7	53.7	74.9	257.2	82.3	92.1	91.5	58.2	21.7	82.3	3.8
204934_s_at	HPN	2.38E-03	63.1	79.2	66.8	72.3	77.0	64.7	72.1	77.5	96.9	104.6	94.4	100.8	93.8	126.5	72.1	96.9	1.3
219403_s_at	HPSE	1.96E-03	153.4	105.4	203.3	117.8	122.8	220.9	194.7	232.0	202.0	278.4	153.7	184.5	252.7	300.6	153.4	232.0	1.5
205579_at	HRH1	4.84E-04	123.6	103.5	114.3	134.4	181.6	134.1	223.7	198.0	278.7	337.8	289.6	261.2	342.3	346.9	134.1	289.6	2.2
205580_s_at	HRH1	2.86E-04	58.9	43.4	52.8	60.9	81.7	55.5	98.4	120.8	77.1	120.9	138.5	111.3	154.9	158.4	58.9	120.9	2.1
1561908_a_at	HS3ST3B1	7.57E-06	202.8	113.0	124.6	73.8	260.7	100.9	207.5	1037.0	1037.2	2449.5	1004.1	1494.6	911.7	2355.8	124.6	1037.2	8.3
221062_at	HS3ST3B1	8.37E-06	43.4	27.3	42.1	18.7	81.3	26.6	78.2	299.1	260.1	1088.5	364.6	495.8	349.1	865.6	42.1	364.6	8.7
227361_at	HS3ST3B1	9.18E-05	79.5	10.5	110.3	51.7	262.4	31.9	253.3	830.2	1234.5	3258.0	1249.2	1375.3	999.8	2236.7	79.5	1249.2	15.7
205404_at	HSD11B1	2.64E-04	118.8	84.3	148.4	64.0	111.9	120.8	187.1	326.4	147.6	349.4	179.4	200.0	373.5	268.1	118.8	268.1	2.3
1552623_at	HSH2D	2.39E-03	57.0	33.8	33.5	45.5	24.4	33.4	22.9	63.2	62.1	146.7	92.1	125.3	94.0	146.6	33.5	94.0	2.8
202557_at	HSPA13	5.29E-03	699.9	777.4	779.2	875.3	958.6	836.5	1133.3	919.1	1201.7	1672.9	1395.9	1134.4	1058.3	1376.4	836.5	1201.7	1.4
202558_s_at	HSPA13	6.85E-03	53.4	53.5	118.8	108.1	134.1	110.4	154.6	104.6	112.3	286.0	157.8	144.0	146.9	181.9	110.4	146.9	1.3
211538_s_at	HSPA2	3.32E-03	72.0	96.7	96.1	92.1	151.7	106.4	84.7	146.4	144.7	169.5	115.8	161.2	189.8	120.7	96.1	146.4	1.5
204883_s_at	HUS1	5.98E-03	417.0	469.6	510.4	512.4	500.7	484.2	461.6	551.5	642.3	773.0	628.5	557.7	646.4	533.9	484.2	628.5	1.3
207370_at	IBSP	2.64E-03	111.4	111.9	115.7	91.2	97.3	101.7	104.7	134.2	163.1	192.4	122.6	120.8	199.4	220.7	104.7	163.1	1.6
236028_at	IBSP	1.66E-03	26.2	56.3	13.8	10.7	13.3	19.5	21.1	40.7	93.4	115.9	23.2	36.3	97.3	74.0	19.5	74.0	3.8
202637_s_at	ICAM1	7.00E-04	1356.1	370.9	882.2	1131.5	2008.2	495.6	2042.9	2908.7	2543.1	3438.6	2962.5	3750.5	3215.8	4072.5	1131.5	3215.8	2.8
202638_s_at	ICAM1	1.45E-03	722.4	134.7	499.9	554.3	1106.3	261.5	1140.5	1465.3	1304.4	2170.1	1693.8	1868.6	1746.5	2202.8	554.3	1746.5	3.2
215485_s_at	ICAM1	8.20E-04	414.1	96.9	320.7	372.3	567.8	159.6	653.5	817.9	629.7	1081.2	852.5	1454.4	1330.3	1317.5	372.3	1081.2	2.9
204949_at	ICAM3	6.11E-03	188.3	124.4	312.5	361.3	283.8	513.8	434.9	279.8	348.7	485.2	367.0	580.6	682.5	706.8	312.5	485.2	1.6
211197_s_at	ICOSLG	1.31E-04	77.8	50.6	87.8	92.4	84.4	74.4	108.4	140.5	75.3	188.1	143.8	179.9	140.5	170.1	84.4	143.8	1.7
211198_s_at	ICOSLG	8.26E-03	38.6	42.0	51.6	50.0	53.0	43.7	64.2	57.7	44.1	61.7	61.0	69.8	58.2	83.7	50.0	61.0	1.2
211199_s_at	ICOSLG	2.64E-03	46.6	46.4	54.9	62.4	57.9	57.5	46.1	55.2	53.2	102.8	87.7	93.8	84.9	82.4	54.9	84.9	1.5
213450_s_at	ICOSLG	1.28E-04	92.0	65.4	105.3	135.9	132.9	82.3	131.1	158.4	112.4	260.8	207.9	271.3	176.9	211.6	105.3	207.9	2.0
228976_at	ICOSLG	2.58E-03	113.2	47.9	121.8	112.7	113.7	108.6	131.8	207.5	57.9	170.1	136.6	175.5	193.8	171.6	113.2	171.6	1.5
210029_at	IDO1	2.42E-06	64.6	41.5	97.4	58.5	77.2	48.0	64.0	1628.9	1878.9	3282.6	1646.7	1625.8	567.9	2786.1	64.0	1646.7	25.7
201631_s_at	IER3	7.51E-04	2922.2	2791.1	853.0	2409.3	5912.9	2956.2	5548.2	7390.5	12809.0	11356.3	8923.4	11377.4	10485.3	14057.0	2922.2	11356.3	3.9
208965_s_at	IFI16	3.93E-03	3209.7	2950.5	2865.8	3360.2	3080.5	2589.7	3184.1	3552.8	3841.4	4206.2	4158.7	3868.2	4061.2	4564.4	3080.5	4061.2	1.3
208966_x_at	IFI16	7.72E-03	2621.1	2425.9	2864.7	2913.1	2851.7	2643.0	2989.9	2911.7	3255.7	4063.6	3552.3	3218.0	3498.4	3817.9	2851.7	3498.4	1.2
209417_s_at	IFI35	9.69E-05	700.9	574.0	547.8	609.8	426.0	452.3	473.1	1197.8	1422.7	1738.1	1243.2	1734.1	1655.0	1819.4	547.8	1655.0	3.0
214059_at	IFI44	2.02E-04	418.6	557.1	507.2	475.0	287.3	341.1	222.2	626.3	960.6	1427.9	1025.7	659.0	793.5	777.9	418.6	793.5	1.9
214453_s_at	IFI44	2.75E-05	2790.3	3636.9	3513.6	2911.5	2495.2	2547.5	2611.8	4768.8	7109.4	9052.6	6391.0	5644.7	5844.5	7520.8	2790.3	6391.0	2.3
204439_at	IFI44L	2.12E-05	402.6	807.9	800.1	607.1	455.9	485.1	307.3	1038.1	1887.5	2587.4	1846.8	1127.0	1420.4	1522.7	485.1	1522.7	3.1
1555464_at	IFIH1	4.32E-05	38.7	50.5	49.7	40.6	44.7	39.8	44.3	88.6	142.9	312.9	150.6	124.5	113.9	195.8	44.3	142.9	3.2
216020_at	IFIH1	1.15E-05	82.9	70.8	135.0	88.8	159.7	75.6	101.1	249.0	277.2	660.6	396.1	352.4	315.4	435.1	88.8	352.4	4.0
219209_at	IFIH1	1.16E-05	524.8	461.0	580.6	538.0	597.6	361.3	655.7	1373.4	2129.5	3593.9	1893.2	1780.6	1757.3	2803.8	538.0	1893.2	3.5
203153_at	IFIT1	3.07E-05	2198.6	2156.1	1559.7	1398.7	941.8	1148.5	1000.1	4516.4	7533.1	7847.2	5645.5	4977.1	5460.4	7123.0	1398.7	5645.5	4.0
217502_at	IFIT2	1.25E-05	1369.0	1304.1	1211.5	866.8	937.4	925.6	801.4	3506.7	5614.9	7708.7	3576.6	4706.2	3942.9	6048.8	937.4	4706.2	5.0
226757_at	IFIT2	2.25E-05	3586.9	3567.8	3652.4	2912.0	2570.5	3069.1	2867.1	6155.7	10215.1	11530.2	7938.1	8247.6	7892.9	9788.1	3069.1	8247.6	2.7
204747_at	IFIT3	3.49E-05	1690.1	1531.0	1438.5	1293.3	1173.2	995.2	1051.4	3248.8	4943.0	6631.3	3655.6	4748.2	4262.1	5534.6	1293.3	4748.2	3.7
229450_at	IFIT3	2.62E-05	1251.6	1245.3	1346.8	1208.4	936.7	934.7	1073.2	2263.6	3880.9	5270.2	3043.6	2838.6	2744.7	4080.2	1208.4	3043.6	2.5
203595_s_at	IFIT5	5.75E-04	249.9	219.0	383.7	438.1	344.4	306.9	409.6	441.8	604.8	1081.9	689.2	494.4	503.1	782.1	344.4	604.8	1.8
203596_s_at	IFIT5	2.15E-04	366.9	478.3	562.6	571.0	496.5	464.1	497.2	530.9	746.7	998.1	807.7	786.0	682.5	922.7	496.5	786.0	1.6
201601_x_at	IFITM1	1.96E-04	223.5	184.5	203.0	173.5	123.1	88.2	97.2	426.2	603.5	760.9	551.2	651.7	678.8	943.0	173.5	651.7	3.8
214022_s_at	IFITM1	1.96E-06	27.8	18.1	30.4	34.7	26.8	30.8	29.0	172.9	161.9	375.7	293.7	251.9	241.9	344.6	29.0	251.9	8.7
201315_x_at	IFITM2	1.34E-03	716.2	302.0	650.7	847.0	546.6	212.9	263.9	983.8	1132.6	1743.6	1321.2	2056.1	1348.3	1727.0	546.6	1348.3	2.5
212203_x_at	IFITM3	1.09E-03	2783.6	1837.4	3069.8	2842.1	1229.1	851.3	986.9	4534.5	4488.4	6242.1	4994.2	5704.3	4804.5	5778.1	1837.4	4994.2	2.7
201642_at	IFNGR2	5.91E-05	1432.0	1078.1	1315.8	1289.7	2129.2	1390.2	1894.2	3257.3	2446.3	3078.5	3337.5	3550.0	3188.0	2979.0	1390.2	3188.0	2.3
218100_s_at	IFT57	1.46E-03	545.0	515.1	585.1	524.6	621.1	684.9	569.0	706.9	664.9	810.5	765.9	757.2	1053.9	766.1	569.0	765.9	1.3
203819_s_at	IGF2BP3	3.41E-05	138.1	116.2	171.8	171.1	132.0	108.1	142.7	381.6	726.8	1128.5	540.8	431.2	304.4	753.5	138.1	540.8	3.9
203820_s_at	IGF2BP3	3.55E-05	75.0	82.1	147.3	111.2	99.5	105.7	123.0	256.2	589.6	1245.1	463.1	355.8	273.5	578.5	105.7	463.1	4.4
216493_s_at	IGF2BP3	8.16E-05	45.7	63.4	50.3	38.1	55.7	44.6	39.8	112.4	161.9	294.0	175.6	127.5	121.0	191.8	45.7	161.9	3.5
201508_at	IGFBP4	1.10E-03	99.0	65.8	71.7	89.0	75.0	46.6	70.4	114.9	316.4	488.2	193.1	200.1	152.1	371.2	71.7	200.1	2.8
206420_at	IGSF6	4.68E-03	3552.4	2410.9	4079.2	4632.2	4776.7	4129.6	5114.5	4784.1	5001.0	7503.6	5702.0	5466.7	6288.7	6648.4	4129.6	5702.0	1.4
204549_at	IKBKE	4.26E-04	91.5	81.1	96.9	90.0	116.4	66.4	144.2	191.8	114.7	212.4	259.9	235.7	198.6	211.9	91.5	211.9	2.3
214398_s_at	IKBKE	6.86E-04	68.2	51.0	66.6	62.0	61.2	57.1	67.9	84.5	67.2	102.9	93.9	100.1	106.8	110.6	62.0	100.1	1.6
1565816_at	IKZF1	2.63E-03	223.4	201.2	188.6	217.4	186.7	193.9	217.9	251.7	260.6	274.0	283.1	245.3	283.4	292.5	201.2	274.0	1.4
1565818_s_at	IKZF1	2.59E-03	563.9	516.8	509.3	559.1	517.1	529.9	625.6	725.6	707.8	791.1	652.5	652.8	864.4	828.9	529.9	725.6	1.4
204912_at	IL10RA	2.13E-04	1527.5	1685.0	1338.9	1527.3	1817.5	1070.9	1116.8	2289.5	3185.7	3641.8	2807.8	3203.5	2432.4	3401.9	1527.3	3185.7	2.1
207901_at	IL12B	1.51E-03	19.6	17.1	12.4	10.9	10.5	30.1	33.3	48.6	92.3	995.3	39.3	110.2	133.7	410.4	17.1	110.2	6.5
205992_s_at	IL15	4.79E-04	165.4	179.7	292.4	240.3	310.5	293.2	309.6	310.4	346.1	682.6	438.4	429.9	380.1	524.3	292.4	429.9	1.5
217371_s_at	IL15	2.61E-04	59.5	64.8	87.2	70.3	84.7	84.6	100.4	102.3	114.5	240.2	141.0	144.9	118.7	187.8	84.6	141.0	1.7

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
207375_s_at	IL15RA	2.42E-06	169.2	172.0	189.7	185.1	203.0	112.9	193.7	989.0	1708.1	2071.8	1224.3	1659.7	1384.7	2150.8	185.1	1659.7	9.0
206295_at	IL18	4.41E-03	212.9	157.8	319.9	276.1	461.6	366.5	498.0	478.8	326.8	927.6	717.7	624.4	526.8	499.0	319.9	526.8	1.6
206618_at	IL18R1	1.08E-03	37.2	32.9	25.6	29.0	36.2	23.4	25.3	48.0	46.4	87.1	81.0	63.8	62.9	63.4	29.0	63.4	2.2
207072_at	IL18RAP	5.16E-04	50.4	46.2	74.9	63.9	64.1	51.7	67.3	56.9	82.2	175.3	144.7	120.7	104.0	168.2	63.9	120.7	1.9
210118_s_at	IL1A	1.53E-04	1104.3	665.5	1203.0	827.6	2074.1	773.6	2129.8	2112.2	4212.1	7390.9	3625.7	5376.9	5657.2	6435.7	1104.3	5376.9	4.9
205067_at	IL1B	4.19E-05	1717.9	642.0	1117.0	937.5	2345.7	792.0	2762.5	5305.2	9601.2	12648.2	7875.8	11269.1	10828.5	13971.2	1117.0	10828.5	9.7
39402_at	IL1B	4.26E-05	2119.5	924.4	1356.7	1251.8	2893.5	1108.9	3139.6	5951.9	10499.8	13592.3	8443.0	11972.3	11802.5	14091.6	1356.7	11802.5	8.7
220322_at	IL1F9	1.66E-04	32.1	41.4	29.7	26.0	31.6	34.3	29.8	66.6	81.3	95.7	47.1	153.1	108.1	106.2	31.6	95.7	3.0
202948_at	IL1R1	1.58E-03	46.6	54.7	59.3	75.4	79.6	59.9	61.6	81.2	70.5	155.9	97.4	116.4	109.3	111.4	59.9	109.3	1.8
205403_at	IL1R2	1.85E-04	67.3	61.1	37.8	34.5	59.5	36.3	44.2	136.3	282.4	475.2	122.0	213.9	237.2	392.0	44.2	237.2	5.4
211372_s_at	IL1R2	1.99E-03	68.4	78.8	38.6	40.0	37.3	49.2	56.8	81.9	198.4	315.4	70.1	128.0	148.1	228.0	49.2	148.1	3.0
210233_at	IL1RAP	2.18E-03	82.2	51.8	71.8	90.0	74.5	78.6	92.1	166.2	91.0	260.6	135.4	135.4	126.9	116.3	78.6	135.4	1.7
212657_s_at	IL1RN	6.14E-05	4945.7	2439.0	3003.5	4183.1	6036.7	3536.8	5883.1	11305.9	15009.4	15981.3	13110.7	15185.1	14638.7	16591.4	4183.1	15009.4	3.6
212659_s_at	IL1RN	8.61E-06	497.4	144.5	273.4	352.4	483.1	234.4	558.1	2672.0	2770.1	3487.4	2398.9	4985.8	4568.4	4258.0	352.4	3487.4	9.9
216243_s_at	IL1RN	1.52E-05	1065.7	263.7	542.2	793.1	971.6	442.3	1139.3	5192.7	5776.0	6641.0	4714.1	9071.6	8411.1	8701.3	793.1	6641.0	8.4
216244_at	IL1RN	1.55E-05	41.1	23.6	14.6	35.5	14.8	15.7	28.9	129.1	94.1	99.3	182.3	74.0	114.3	316.6	23.6	114.3	4.8
216245_at	IL1RN	1.43E-05	173.5	47.5	83.7	126.3	160.8	66.4	169.9	749.7	848.7	1093.3	792.0	1026.7	1061.2	1426.0	126.3	1026.7	8.1
220054_at	IL23A	2.04E-03	81.4	64.0	84.3	94.5	85.5	77.4	92.9	118.6	1078.5	1181.4	172.5	341.1	317.6	897.5	84.3	341.1	4.0
1552995_at	IL27	1.22E-03	43.1	35.7	49.0	40.3	43.0	40.3	56.9	47.4	48.6	87.4	68.6	89.3	80.8	100.8	43.0	80.8	1.9
206341_at	IL2RA	7.99E-03	55.2	43.1	46.2	48.6	50.8	46.2	44.9	59.3	52.0	130.4	103.6	73.6	70.4	143.9	46.2	73.6	1.6
211269_s_at	IL2RA	7.75E-03	53.9	82.2	43.8	31.6	39.7	27.8	36.4	55.7	85.8	85.4	77.9	65.6	56.9	115.3	39.7	77.9	2.0
205291_at	IL2RB	7.20E-03	73.1	54.7	36.1	55.5	64.0	51.5	45.2	79.4	67.8	68.0	101.7	82.3	86.7	133.9	54.7	82.3	1.5
230966_at	IL4I1	1.21E-05	63.4	32.7	71.0	70.6	85.1	51.1	73.2	132.3	112.2	226.7	182.7	249.9	209.3	200.1	70.6	200.1	2.8
205207_at	IL6	4.90E-06	231.7	76.1	310.3	156.6	403.9	142.1	486.3	4279.8	9316.7	12716.8	6972.7	8322.5	7949.7	11178.5	231.7	8322.5	35.9
204864_s_at	IL6ST	4.10E-03	223.9	204.1	304.5	269.3	381.2	267.1	349.1	370.3	327.6	456.3	340.1	446.1	347.8	403.2	269.3	370.3	1.4
211000_s_at	IL6ST	5.49E-03	404.7	366.6	541.4	395.0	669.7	521.7	608.0	697.7	528.0	764.3	628.4	779.4	609.9	697.5	521.7	697.5	1.3
205798_at	IL7R	2.16E-04	1645.6	830.3	550.9	1598.1	1324.4	560.8	1293.0	2985.3	3785.1	4017.9	3984.7	4064.5	3894.7	4664.3	1293.0	3984.7	3.1
226218_at	IL7R	2.95E-04	2366.9	1768.5	906.3	2470.5	2157.2	1180.2	2684.4	4021.9	6428.9	5834.3	6071.7	5125.1	5875.3	7218.5	2157.2	5875.3	2.7
202859_x_at	IL8	2.00E-03	1362.0	138.9	763.8	785.7	2878.2	473.2	2937.1	3169.8	5518.1	9575.4	6641.8	5766.4	6135.5	7498.5	785.7	6135.5	7.8
211506_s_at	IL8	2.05E-04	767.8	83.0	339.8	381.4	1440.5	162.1	1148.8	3236.5	5187.4	9070.3	5714.1	7228.6	6293.4	7847.8	381.4	6293.4	16.5
229582_at	INO80C	4.45E-03	485.4	342.8	393.3	435.6	511.5	357.0	521.4	561.7	507.8	608.8	499.4	775.4	609.4	624.4	435.6	608.8	1.4
220165_at	INO80D	3.96E-03	161.2	155.7	225.2	206.5	228.7	206.3	218.8	212.7	198.9	288.3	232.1	297.8	270.8	280.3	206.5	270.8	1.3
202794_at	INPP1	1.41E-03	314.3	248.7	316.3	299.0	350.7	259.3	312.1	423.6	327.5	535.2	397.2	458.3	365.8	404.0	312.1	404.0	1.3
201625_s_at	INSIG1	7.22E-04	170.9	125.1	111.0	85.2	180.0	110.2	140.5	311.3	143.7	240.9	149.2	270.9	200.4	315.2	125.1	240.9	1.9
201627_s_at	INSIG1	3.63E-03	250.2	248.2	160.6	154.6	281.1	178.0	243.0	372.9	293.1	445.2	200.3	426.5	283.9	486.9	243.0	372.9	1.5
219092_s_at	IPPK	3.17E-03	533.2	463.3	503.7	442.5	544.3	449.9	466.8	614.8	631.6	749.2	807.2	636.6	639.1	706.5	466.8	639.1	1.4
1553740_a_at	IRAK2	4.92E-04	43.4	29.3	41.8	35.4	47.4	34.3	46.1	61.9	48.1	90.8	57.6	75.6	99.3	94.1	41.8	75.6	1.8
231779_at	IRAK2	5.52E-05	301.5	200.0	241.7	220.4	610.7	191.3	567.5	987.3	1490.2	2887.0	1350.6	1668.5	1489.5	2392.0	241.7	1490.2	6.2
1568830_at	IRAK3	1.49E-03	67.6	91.4	137.7	112.8	130.7	126.7	143.6	122.0	146.1	254.7	182.4	161.4	150.7	203.5	126.7	161.4	1.3
220034_at	IRAK3	6.98E-05	578.3	570.6	634.5	617.8	759.1	679.9	715.6	999.9	1042.7	1326.2	988.3	1221.9	1076.2	1195.0	634.5	1076.2	1.7
202531_at	IRF1	2.47E-04	342.1	274.1	377.0	342.4	420.5	295.8	364.0	456.4	486.9	938.0	614.7	708.9	640.5	853.4	342.4	640.5	1.9
238725_at	IRF1	4.87E-05	155.7	195.3	209.6	240.6	356.1	196.1	205.4	366.0	332.0	621.3	652.3	630.8	449.1	457.3	205.4	457.3	2.2
204562_at	IRF4	2.46E-03	44.1	49.2	39.1	49.7	37.6	41.6	36.4	62.0	95.7	52.9	76.6	59.9	55.3	103.8	41.6	62.0	1.5
208436_s_at	IRF7	2.38E-04	291.6	194.7	201.7	204.2	194.3	137.8	182.4	449.8	477.7	775.3	462.5	846.7	744.8	746.6	194.7	744.8	3.8
240287_at	IRG1	2.42E-06	40.5	26.7	55.4	35.2	176.2	34.3	73.0	731.9	1370.1	1828.5	1196.8	1894.9	1045.7	1883.1	40.5	1370.1	33.8
205483_s_at	ISG15	8.70E-05	752.2	691.2	541.4	535.4	319.1	288.3	334.9	1729.3	2449.0	3159.5	2122.2	3051.6	2755.3	3149.6	535.4	2755.3	5.1
204698_at	ISG20	2.65E-06	117.5	61.6	65.4	80.6	65.6	51.1	47.6	1227.5	2231.6	2627.7	1495.6	2176.9	2066.6	2367.8	65.4	2176.9	33.3
33304_at	ISG20	5.84E-06	171.7	96.7	93.9	109.0	65.3	61.7	66.4	1385.0	2873.5	3196.0	1848.3	2570.0	2517.0	3078.0	93.9	2570.0	27.4
209744_x_at	ITCH	6.61E-03	181.3	193.1	304.0	272.8	319.1	329.8	308.0	286.9	376.6	570.5	382.8	338.7	421.9	364.1	304.0	376.6	1.2
217094_s_at	ITCH	1.22E-03	412.7	435.9	546.2	484.9	539.0	583.8	543.5	577.0	716.6	980.5	652.1	671.8	816.1	731.8	539.0	716.6	1.3
202351_at	ITGAV	3.05E-03	741.7	707.8	807.8	897.6	1115.3	812.7	1294.7	1059.7	989.4	1462.4	1624.0	1293.0	1316.0	1488.9	812.7	1316.0	1.6
204627_s_at	ITGB3	4.41E-04	39.6	35.3	22.8	14.7	17.5	19.7	35.9	95.2	63.1	169.1	37.1	56.1	45.2	170.8	22.8	63.1	2.8
205816_at	ITGB8	2.37E-04	306.8	169.9	228.5	345.7	678.3	235.1	682.3	875.9	1108.6	1660.2	1203.1	1351.6	1273.7	1513.5	306.8	1273.7	4.2
211488_s_at	ITGB8	3.20E-04	592.3	340.4	379.0	515.3	1024.0	352.3	1129.3	1391.9	1642.6	2481.4	1646.4	1858.2	1944.9	2457.5	515.3	1858.2	3.6
226189_at	ITGB8	1.66E-03	96.6	49.9	115.7	136.5	293.4	111.4	387.0	269.8	369.7	826.9	526.0	395.2	425.7	600.7	115.7	425.7	3.7
242982_x_at	ITGB8	8.54E-04	232.0	135.4	108.7	154.5	317.0	128.3	342.4	384.9	524.1	675.6	468.4	533.8	577.9	669.5	154.5	533.8	3.5
206287_s_at	ITIH4	3.62E-03	446.6	858.9	748.4	952.9	448.9	755.0	432.8	770.2	1197.5	1311.3	1197.5	1416.2	1201.2	1567.3	748.4	1201.2	1.6
242720_at	ITIH4	3.20E-04	70.5	68.6	88.3	91.5	73.8	86.9	96.3	113.5	103.0	225.8	131.9	156.8	149.8	199.4	86.9	149.8	1.7
37201_at	ITIH4	9.12E-04	124.4	198.2	250.8	301.9	147.5	271.8	179.7	205.1	390.9	551.8	376.4	334.8	386.8	500.8	198.2	386.8	2.0
211360_s_at	ITPR2	3.94E-03	291.8	241.3	339.4	363.3	330.3	295.7	333.7	346.7	306.5	529.4	424.1	417.5	484.5	475.9	330.3	424.1	1.3
227954_at	ITPRIPL2	1.91E-03	632.8	599.5	622.6	610.2	605.5	622.4	659.4	825.6	745.2	970.0	818.0	867.8	740.4	1009.2	622.4	825.6	1.3
1552610_a_at	JAK1	1.18E-04	1135.7	892.0	961.7	980.1	1136.5	879.7	1021.4	1649.5	1654.3	2163.9	1562.5	1922.2	1913.2	2034.0	980.1	1913.2	2.0
1552611_a_at	JAK1	4.79E-05	811.4	672.1	717.2	818.9	937.5	759.2	808.5	1356.2	1209.2	1643.8	1323.8	1636.1	1465.1	1587.9	808.5	1465.1	1.8
201648_at	JAK1	1.03E-04	1130.5	1064.9	1273.5	1316.4	1552.0	1243.4	1404.3	1836.9	1866.4	2416.1	2092.3	2190.8	1974.0	2515.3	1273.5	2092.3	1.6
239695_at	JAK1	1.82E-03	48.0	46.9	47.1	35.9	47.6	37.2	45.5	61.7	50.5	108.0	72.2	86.5	66.2	90.5	46.9	72.2	1.5
240613_at	JAK1	6.65E-05	33.7	35.5	46.6	39.6	40.8	54.4	52.8	64.7	63.0	110.6	86.3	108.0	90.8	91.6	40.8	90.8	2.2

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1562031_at	JAK2	5.45E-03	59.5	76.4	80.2	79.4	68.6	69.0	61.2	84.2	90.4	150.6	139.5	101.2	71.0	127.9	69.0	101.2	1.5
205841_at	JAK2	5.12E-04	89.7	116.1	186.2	166.9	151.7	167.2	145.7	178.9	267.9	465.4	280.5	202.2	237.9	268.2	151.7	267.9	1.8
205842_s_at	JAK2	2.73E-05	269.1	358.6	448.3	404.3	435.2	361.8	378.6	580.4	724.0	968.3	729.5	683.8	715.9	787.5	378.6	724.0	1.9
207187_at	JAK3	1.93E-03	63.8	50.5	69.9	85.1	90.6	46.5	106.0	100.1	85.7	142.7	127.0	107.3	116.4	144.7	69.9	116.4	1.7
227677_at	JAK3	4.66E-04	312.6	91.4	174.3	327.0	272.0	75.3	348.5	617.5	275.4	521.4	545.7	824.3	519.1	849.5	272.0	545.7	2.0
201473_at	JUNB	1.06E-04	404.8	266.6	457.0	459.2	554.4	419.6	493.5	671.1	794.7	1064.8	733.9	1062.8	907.9	1091.3	457.0	907.9	2.0
201015_s_at	JUP	7.35E-03	85.7	78.8	81.5	77.9	59.5	70.9	117.3	103.9	132.1	155.3	78.8	123.6	102.1	347.8	78.8	123.6	1.6
227750_at	KALRN	4.31E-03	231.0	325.9	367.7	309.6	260.7	366.9	315.4	338.0	573.0	777.4	517.9	322.9	386.3	774.4	315.4	517.9	1.6
200079_s_at	KARS	6.50E-03	1121.6	1327.2	1273.8	1172.6	1277.6	1286.7	1178.9	1428.8	1491.7	1571.7	1469.7	1644.5	1527.9	1599.1	1273.8	1527.9	1.2
203845_at	KAT2B	5.62E-04	248.0	238.8	259.0	258.8	257.1	255.0	222.0	346.4	344.9	470.6	381.9	337.0	392.6	420.9	255.0	381.9	1.5
210119_at	KCNJ15	1.04E-04	65.5	71.6	38.0	29.8	43.6	44.2	34.9	141.1	192.8	282.4	107.6	251.7	159.9	262.7	43.6	192.8	4.4
211806_s_at	KCNJ15	5.66E-03	110.4	107.2	59.9	67.5	65.0	53.6	55.6	101.9	181.2	208.7	88.4	146.2	138.5	173.3	65.0	146.2	2.2
206765_at	KCNJ2	2.14E-05	53.7	57.7	128.1	97.8	228.3	95.5	147.1	203.8	610.7	1651.5	798.5	760.5	690.5	1177.1	97.8	760.5	7.8
1554710_at	KCNMB1	9.39E-05	68.5	28.0	71.0	50.3	76.2	37.9	65.2	145.8	46.7	139.9	130.6	155.8	73.3	96.7	65.2	130.6	2.0
209948_at	KCNMB1	1.59E-03	75.3	50.1	84.3	75.2	70.5	54.0	73.9	120.5	63.3	126.7	120.7	190.9	104.6	106.0	73.9	120.5	1.6
204401_at	KCNN4	1.51E-04	156.1	103.5	106.0	94.8	122.3	57.1	100.2	311.7	190.7	302.7	339.5	389.7	331.6	427.9	103.5	331.6	3.2
200700_s_at	KDELR2	8.92E-03	761.7	803.2	821.5	815.5	842.0	671.6	989.2	944.4	958.7	1081.4	1034.1	979.6	897.0	1096.1	815.5	979.6	1.2
1556067_a_at	KDM6B	4.33E-04	43.4	31.2	57.8	48.4	55.8	62.5	61.4	56.8	65.0	92.3	70.1	100.4	94.3	98.3	55.8	92.3	1.7
213146_at	KDM6B	2.04E-03	496.4	352.1	521.2	609.6	600.7	485.6	619.5	559.4	716.4	1304.5	723.1	1129.9	992.1	1307.9	521.2	992.1	1.9
41386_i_at	KDM6B	8.15E-04	515.5	340.2	473.2	519.9	549.9	408.3	559.4	653.4	832.6	1304.6	689.9	1078.4	994.5	1355.2	515.5	994.5	1.9
41387_r_at	KDM6B	2.96E-03	425.2	350.9	387.6	385.7	441.2	360.1	432.2	442.9	661.9	900.3	488.4	701.4	646.1	932.6	387.6	661.9	1.7
203143_s_at	KIAA0040	7.22E-05	153.0	107.0	148.9	158.4	144.0	130.5	174.7	262.0	402.0	580.0	392.8	336.3	297.4	513.2	148.9	392.8	2.6
203144_s_at	KIAA0040	1.99E-04	124.8	113.3	123.4	113.6	131.7	118.2	138.0	187.7	302.9	324.9	220.8	204.8	239.7	365.4	123.4	239.7	1.9
1554612_at	KIAA0226	4.24E-04	34.3	29.3	40.5	32.2	47.2	38.4	41.6	62.9	50.1	92.4	57.5	63.4	58.0	60.4	38.4	60.4	1.6
1554613_a_at	KIAA0226	2.45E-03	175.5	125.1	150.7	163.6	149.3	146.9	153.3	185.7	205.0	346.4	206.8	334.2	311.7	332.2	150.7	311.7	2.1
212733_at	KIAA0226	1.61E-04	269.1	287.0	343.2	376.2	332.4	391.5	359.3	477.6	692.7	1071.4	674.6	665.4	608.5	914.4	343.2	674.6	2.0
212735_at	KIAA0226	4.79E-05	114.8	127.3	207.9	155.3	229.5	182.0	176.7	293.6	245.6	559.6	331.7	385.1	343.4	481.4	176.7	343.4	1.9
202181_at	KIAA0247	4.33E-04	2909.5	2343.5	2539.7	2371.5	2873.2	2242.2	2939.3	3838.4	3489.3	3773.2	3389.3	3846.5	3738.3	4504.8	2539.7	3773.2	1.5
212946_at	KIAA0564	1.10E-03	336.3	334.1	300.7	344.9	471.6	503.6	482.8	544.8	816.9	1329.3	776.7	661.4	885.7	1030.7	344.9	816.9	2.4
215936_s_at	KIAA1033	7.45E-03	498.0	557.8	677.5	711.6	692.5	672.4	630.1	652.8	858.6	916.2	827.0	739.7	823.7	911.6	672.4	827.0	1.2
214929_s_at	KIAA1109	6.88E-03	93.5	129.0	151.1	146.8	200.6	197.2	161.5	161.0	142.3	214.5	196.6	241.9	228.1	239.8	151.1	214.5	1.4
216294_s_at	KIAA1109	1.67E-03	118.9	154.7	141.9	132.6	213.0	177.7	152.5	188.9	185.4	234.2	193.8	260.2	234.6	246.3	152.5	234.2	1.5
233227_at	KIAA1109	6.76E-03	219.4	275.9	289.8	256.5	356.8	367.0	328.8	337.0	366.7	535.6	362.3	434.6	366.6	501.3	289.8	366.7	1.3
226248_s_at	KIAA1324	4.84E-03	47.2	53.6	46.6	44.2	46.9	43.9	50.3	50.1	77.6	60.4	55.9	80.9	64.6	65.9	46.9	64.6	1.4
224746_at	KIAA1522	2.39E-03	85.2	113.0	84.3	90.1	96.3	81.2	81.7	113.0	129.0	163.0	115.3	156.0	119.1	131.3	85.2	129.0	1.5
231956_at	KIAA1618	6.44E-05	238.4	257.0	237.8	249.4	224.1	221.1	228.4	414.0	553.3	905.7	673.0	551.1	554.6	828.8	237.8	554.6	2.3
232155_at	KIAA1618	2.43E-05	123.9	186.2	143.2	158.7	113.1	157.5	154.9	262.6	450.9	528.3	463.8	300.2	308.5	480.7	154.9	450.9	2.9
241347_at	KIAA1618	4.25E-04	416.9	360.9	251.2	367.4	355.3	306.7	340.6	543.8	720.2	823.9	723.7	708.5	846.5	1124.9	355.3	723.7	2.0
224927_at	KIAA1949	7.04E-03	712.3	474.1	678.3	657.7	766.3	624.6	755.0	778.7	749.3	860.3	774.2	935.3	890.6	1018.0	678.3	860.3	1.3
230166_at	KIAA1958	3.40E-03	42.2	47.8	47.2	42.4	51.4	63.4	38.7	54.2	71.6	85.3	77.7	62.1	71.6	60.4	47.2	71.6	1.5
226968_at	KIF1B	7.29E-03	452.2	307.6	361.2	398.6	417.2	378.2	444.8	569.6	481.9	733.8	450.1	515.0	479.1	608.6	398.6	515.0	1.3
212877_at	KLC1	3.28E-04	135.8	109.2	234.1	244.5	218.0	240.1	212.2	262.2	221.6	444.4	338.3	323.0	343.3	339.7	218.0	338.3	1.6
212878_s_at	KLC1	5.41E-03	190.7	154.4	203.1	222.8	192.8	213.6	202.6	244.2	170.5	264.6	257.2	295.8	309.4	274.4	202.6	264.6	1.3
208961_s_at	KLF6	9.38E-03	1108.6	736.8	756.1	842.3	792.1	673.8	761.9	1023.8	1066.0	1425.9	929.5	1557.1	1448.6	1383.5	761.9	1383.5	1.8
224606_at	KLF6	6.89E-03	1437.8	961.9	1012.2	1013.6	1209.0	1069.6	981.1	1530.6	1443.6	2146.4	1304.7	1552.5	1395.0	1580.4	1013.6	1530.6	1.5
243982_at	KLHL28	4.92E-04	51.7	51.6	54.9	49.9	49.7	56.7	49.5	61.7	90.5	108.2	88.2	87.7	80.7	91.9	51.6	88.2	1.7
226001_at	KLHL5	3.45E-03	43.0	45.5	56.8	65.4	73.6	46.2	79.6	82.4	60.4	114.1	128.7	94.4	64.9	89.3	56.8	89.3	1.6
220239_at	KLHL7	6.53E-03	116.2	118.7	154.1	130.9	130.7	137.5	157.4	153.1	147.7	188.8	168.1	156.5	159.1	191.9	130.9	159.1	1.2
214470_at	KLRB1	2.82E-03	69.9	105.6	57.5	70.9	162.9	120.4	84.2	145.1	138.5	165.5	260.4	229.3	182.6	356.2	84.2	182.6	2.2
205306_x_at	KMO	3.04E-03	1294.1	1096.5	2225.8	1659.6	2281.3	2213.0	2094.5	2039.3	2248.5	4317.4	2489.4	2763.4	2808.6	2575.8	2094.5	2575.8	1.2
211138_s_at	KMO	1.69E-03	1475.3	1182.6	2314.4	1785.0	2426.9	2244.3	2150.9	2137.3	2355.3	3544.8	2646.2	2961.6	3073.6	2811.8	2150.9	2811.8	1.3
209653_at	KPNA4	9.30E-03	186.5	192.8	217.5	203.0	251.1	238.4	267.0	285.6	219.4	395.4	302.9	338.4	264.8	303.9	217.5	302.9	1.4
208974_x_at	KPNB1	8.21E-03	5739.3	5230.5	5032.1	5094.9	5337.0	5399.2	5893.0	6235.3	6686.1	7350.1	6768.2	6148.0	7147.9	7161.1	5337.0	6768.2	1.3
213507_s_at	KPNB1	2.68E-03	3335.5	3591.8	2775.3	2978.6	3293.7	3111.9	3173.8	4152.1	4273.0	4307.0	4073.1	4220.8	3922.0	4623.4	3173.8	4220.8	1.3
217027_x_at	KPNB1	9.53E-03	208.3	164.5	320.9	331.0	305.7	299.2	381.5	271.2	359.6	527.1	403.9	358.3	396.5	452.8	305.7	396.5	1.3
218963_s_at	KRT23	7.90E-04	61.6	76.4	45.3	42.0	66.6	53.6	37.0	76.4	182.8	177.7	74.6	160.1	196.0	149.5	53.6	160.1	3.0
204385_at	KYNU	8.18E-04	1316.2	646.4	1282.1	1364.4	2239.5	910.7	2209.3	2197.2	3332.4	5397.6	3227.9	3641.9	3389.6	4265.2	1316.2	3389.6	2.6
210662_at	KYNU	2.78E-05	65.8	26.5	52.9	55.5	45.2	45.8	79.0	195.9	89.5	299.1	165.0	104.8	214.1	219.0	52.9	195.9	3.7
210663_s_at	KYNU	5.67E-04	1831.0	702.7	1399.9	1484.8	2554.5	958.0	2455.0	3068.0	4028.5	6012.9	3871.8	4690.9	4028.6	5169.6	1484.8	4028.6	2.7
217388_s_at	KYNU	6.89E-04	2619.4	1379.1	2190.0	2304.7	4143.8	1643.2	4024.0	4426.1	5710.0	7471.9	5362.9	6222.0	5653.0	7064.3	2304.7	5710.0	2.5
241305_at	KYNU	1.32E-04	24.6	31.2	33.0	35.1	44.6	29.4	50.5	50.1	59.2	122.8	120.8	94.7	93.3	93.0	33.0	93.3	2.8
1552485_at	LACTB	6.12E-04	219.0	221.2	346.3	363.3	392.6	271.7	380.8	383.9	458.2	966.8	597.1	476.5	497.0	781.8	346.3	497.0	1.4
216840_s_at	LAMA2	9.02E-04	57.3	47.8	55.2	54.9	55.7	49.7	64.7	87.8	68.7	115.2	98.8	65.5	91.0	99.7	55.2	91.0	1.6
201505_at	LAMB1	3.91E-05	489.8	1501.2	1208.6	1022.9	945.5	1064.5	808.3	1101.5	2268.1	2715.9	2263.6	1844.8	2209.2	2020.9	1022.9	2209.2	2.2
211651_s_at	LAMB1	2.05E-04	655.6	1525.2	918.1	873.1	789.9	959.4	697.2	1032.1	2049.4	2199.6	1840.2	1834.2	2121.5	1745.3	873.1	1840.2	2.1
209270_at	LAMB3	7.62E-05	77.1	57.6	70.7	71.6	98.9	59.8	80.3	200.3	187.3	331.9	133.3	404.4	368.4	399.7	71.6	331.9	4.6

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
205569_at	LAMP3	3.20E-05	42.4	46.0	23.1	46.9	90.7	58.1	60.2	257.0	400.7	514.6	410.2	370.7	250.1	496.7	46.9	400.7	8.5
218219_s_at	LANCL2	5.79E-03	458.8	436.7	390.6	475.4	539.0	409.2	445.1	520.4	545.1	669.1	564.0	668.5	602.7	628.8	445.1	602.7	1.4
217933_s_at	LAP3	1.02E-04	1573.7	2009.0	1962.5	2013.4	1942.2	1669.2	2145.2	3206.5	3140.7	3938.1	3065.0	3094.4	3259.4	3536.6	1962.5	3206.5	1.6
226750_at	LARP1B	5.84E-03	67.8	87.0	117.1	90.2	140.3	117.8	146.7	125.0	110.0	237.3	147.4	152.1	150.1	190.4	117.1	150.1	1.3
231011_at	LARP2	6.95E-03	54.6	49.2	106.2	96.0	102.2	90.4	92.1	94.3	100.6	170.3	111.4	111.8	112.1	129.6	92.1	111.8	1.2
213261_at	LBA1	7.96E-04	115.6	105.6	163.0	160.3	129.0	131.8	136.5	162.0	143.0	210.3	226.8	245.5	228.0	227.1	131.8	226.8	1.7
221011_s_at	LBH	1.95E-03	40.6	51.4	43.0	67.5	81.2	53.0	39.9	66.7	88.2	125.8	191.8	91.5	81.1	89.3	51.4	89.3	1.7
205269_at	LCP2	7.47E-03	841.5	746.0	1069.8	1158.5	1391.0	1224.4	1387.0	1174.2	1520.4	2355.2	1293.3	1928.9	1346.2	2165.8	1158.5	1520.4	1.3
205270_s_at	LCP2	2.72E-03	2255.2	1732.7	2074.6	2227.1	2471.0	1951.3	2227.2	2816.4	2978.6	3586.3	2276.3	4051.0	3134.4	4008.1	2227.1	3134.4	1.4
244556_at	LCP2	3.64E-05	72.6	53.7	98.4	76.5	96.2	96.2	101.3	142.4	134.4	338.6	146.6	280.0	205.7	236.1	96.2	205.7	2.1
244578_at	LCP2	1.18E-04	38.7	39.3	62.4	58.1	73.5	54.0	70.2	93.0	83.0	218.5	87.3	185.5	108.1	156.5	58.1	108.1	1.9
202067_s_at	LDLR	1.16E-03	71.0	40.2	33.9	33.8	73.1	37.5	56.2	81.4	58.1	84.8	58.1	159.0	85.8	97.0	40.2	84.8	2.1
202068_s_at	LDLR	1.05E-03	410.8	183.9	124.6	151.9	466.5	171.7	394.4	557.6	617.6	760.9	313.5	968.0	728.1	919.0	183.9	728.1	4.0
217173_s_at	LDLR	1.69E-03	463.0	260.2	159.7	195.1	376.1	164.0	379.4	575.3	539.0	544.0	267.9	979.1	649.8	818.6	260.2	575.3	2.2
217183_at	LDLR	2.95E-04	246.0	172.6	111.0	129.8	239.8	139.7	220.5	354.5	306.4	319.0	199.8	586.8	353.7	493.3	172.6	353.7	2.0
208450_at	LGALS2	2.45E-03	135.6	80.2	76.4	78.1	135.8	106.5	80.9	176.2	112.0	87.5	109.8	216.0	218.0	130.6	80.9	130.6	1.6
212658_at	LHFPL2	2.08E-03	4130.4	2778.7	1805.6	2559.3	2917.6	1698.4	3013.8	4676.6	4051.9	3463.9	4042.4	3879.7	3661.7	4661.5	2778.7	4042.4	1.5
206235_at	LIG4	6.81E-03	357.5	290.5	424.1	387.4	420.0	431.1	422.6	440.4	418.3	619.6	489.6	432.1	563.7	565.7	420.0	489.6	1.2
207872_s_at	LILRA1	9.33E-04	42.4	49.7	46.3	38.5	41.5	46.0	46.1	132.4	64.1	135.1	81.8	276.9	113.2	218.0	46.0	132.4	2.9
210660_at	LILRA1	6.92E-05	88.9	71.8	89.3	68.1	89.4	96.5	74.9	325.8	157.0	296.0	236.7	605.2	273.6	489.4	88.9	296.0	3.3
206881_s_at	LILRA3	2.86E-03	92.3	98.4	75.9	68.7	78.3	55.9	72.6	150.6	111.1	205.2	160.8	312.8	198.3	563.1	75.9	198.3	2.6
1555634_a_at	LILRA5	4.68E-03	89.5	48.2	55.8	53.7	64.1	63.5	49.2	86.8	77.2	176.5	100.7	118.6	98.0	153.1	55.8	100.7	1.8
1555643_s_at	LILRA5	1.38E-03	195.2	119.6	192.8	195.3	234.1	204.2	136.4	339.4	172.2	297.4	295.3	599.1	534.1	506.3	195.2	339.4	1.7
215838_at	LILRA5	8.28E-04	300.4	211.5	252.0	267.4	326.1	298.2	179.4	597.4	331.6	437.9	429.0	844.0	789.0	792.0	267.4	597.4	2.2
215839_at	LILRA5	1.22E-03	163.8	130.6	183.7	186.2	219.9	209.2	152.0	310.2	173.7	300.0	276.9	458.5	507.6	533.0	183.7	310.2	1.7
207104_x_at	LILRB1	4.40E-03	1001.0	725.5	1056.4	1079.1	981.4	659.4	1094.0	1131.7	1046.7	1694.5	1316.2	2298.4	1733.9	1936.8	1001.0	1694.5	1.7
211336_x_at	LILRB1	2.68E-03	961.7	634.1	996.9	994.9	844.3	598.3	1010.5	1219.8	1025.0	1579.1	1291.8	2449.4	1678.4	1843.3	961.7	1579.1	1.6
229937_x_at	LILRB1	4.79E-05	3026.6	2866.5	3464.8	3823.0	3658.8	3133.7	3170.0	4966.5	5479.4	6157.6	5834.8	5966.7	5701.9	5650.9	3170.0	5701.9	1.8
207697_x_at	LILRB2	6.59E-04	1386.2	1245.2	1687.9	1753.2	1633.0	1446.4	1328.5	2174.8	1870.8	2763.7	2964.1	4225.5	4155.4	4028.0	1446.4	2964.1	2.0
210146_x_at	LILRB2	3.83E-04	627.8	564.4	988.3	973.0	926.1	918.4	686.6	969.4	1110.3	1708.9	1825.0	1785.5	2175.0	2535.7	918.4	1785.5	1.9
1569504_at	LILRB4	1.53E-03	59.3	69.9	60.9	54.8	69.3	53.6	61.5	106.6	74.8	119.7	86.9	105.0	83.6	90.3	60.9	90.3	1.5
210152_at	LILRB4	7.96E-03	371.9	221.6	463.6	299.0	319.8	150.9	730.8	381.3	361.8	796.2	447.3	933.2	690.0	1253.9	319.8	690.0	2.2
202193_at	LIMK2	2.84E-04	2040.2	1726.3	1831.0	1823.1	3069.8	1819.6	3126.7	3640.0	4294.4	5624.4	4213.2	4288.0	4423.2	5259.4	1831.0	4294.4	2.3
210582_s_at	LIMK2	6.92E-05	339.5	225.9	306.0	291.8	617.4	338.5	596.9	750.4	887.5	1245.7	929.1	1141.3	1206.0	1326.9	338.5	1141.3	3.4
217475_s_at	LIMK2	1.46E-04	66.3	59.6	113.0	113.2	128.4	90.6	150.7	133.6	123.5	265.2	186.4	276.0	338.0	293.3	113.0	265.2	2.3
236156_at	LIPA	4.55E-05	63.9	72.6	79.9	76.6	57.6	44.2	50.5	156.3	208.4	456.5	185.0	156.1	161.7	241.9	63.9	185.0	2.9
203276_at	LMNB1	8.26E-04	68.3	68.4	79.5	79.7	69.7	59.6	76.9	85.9	92.5	191.8	145.9	119.0	99.7	156.4	69.7	119.0	1.7
209204_at	LMO4	7.77E-03	176.3	136.8	156.1	184.2	195.1	158.8	201.1	228.0	155.4	261.6	228.4	240.1	348.3	288.3	176.3	240.1	1.4
209205_s_at	LMO4	3.41E-03	533.8	447.5	631.7	503.9	720.7	618.0	799.7	754.0	707.3	1205.2	999.8	814.2	904.5	949.9	618.0	904.5	1.5
227155_at	LMO4	6.74E-03	143.0	118.2	153.2	154.3	172.5	181.9	205.1	194.7	164.7	212.9	234.1	184.2	236.1	230.5	154.3	212.9	1.4
1556643_at	LOC100128718	2.39E-03	434.8	595.0	658.9	510.1	465.3	543.5	528.9	621.8	884.2	1299.6	805.6	576.9	617.2	831.6	528.9	805.6	1.5
1555392_at	LOC100128868	7.44E-03	68.0	44.4	52.2	79.2	68.3	59.6	54.8	74.1	60.7	119.1	153.9	86.7	77.5	77.2	59.6	77.5	1.3
226526_s_at	LOC100130905	8.91E-04	87.8	82.5	65.1	96.0	60.3	50.8	75.8	133.9	106.0	169.9	150.7	153.4	152.5	189.7	75.8	152.5	2.0
244659_at	LOC100131015	6.32E-03	47.0	44.9	59.8	55.0	54.1	44.7	49.8	58.2	50.8	67.2	79.0	69.3	61.8	78.3	49.8	67.2	1.4
228675_at	LOC100131733	7.78E-03	102.7	116.9	112.9	97.6	82.9	111.6	102.7	130.6	113.4	160.1	145.1	165.8	155.5	152.3	102.7	152.3	1.5
212707_s_at	LOC100132214 /// RASA4 /// RASA4B /// RASA4P	8.52E-04	231.5	313.9	324.9	362.6	380.5	333.3	325.9	286.3	532.4	533.6	545.9	543.7	655.8	444.2	325.9	533.6	1.6
1559125_at	LOC100133019	3.17E-04	66.7	57.0	78.5	63.8	86.7	66.0	68.3	101.0	114.9	230.5	113.3	135.9	113.1	127.0	66.7	114.9	1.7
226407_at	LOC100190939	5.83E-04	147.4	119.0	199.5	181.7	170.8	131.2	183.2	222.4	209.5	511.8	294.3	247.3	203.8	283.5	170.8	247.3	1.4
227709_at	LOC100190939	5.12E-04	219.0	218.2	376.1	317.0	324.8	240.3	371.6	426.1	335.1	834.8	495.7	456.9	437.7	500.4	317.0	456.9	1.4
227710_s_at	LOC100190939	4.35E-03	151.7	101.9	184.3	190.1	196.7	162.6	203.8	196.5	148.9	314.2	227.5	231.2	244.5	245.9	184.3	231.2	1.3
228913_at	LOC100190939	5.77E-03	99.4	142.6	240.7	221.3	195.8	201.7	229.6	189.5	204.4	615.7	349.0	244.5	232.4	300.5	201.7	244.5	1.2
229424_s_at	LOC100288194 /// LOC100293513	2.91E-03	194.3	187.2	250.3	280.1	239.6	213.5	195.4	247.0	268.8	328.3	312.5	395.1	398.6	347.1	213.5	328.3	1.5
214084_x_at	LOC100289727 /// NCF1 /// NCF1B /// NCF1C	3.76E-05	674.0	268.0	537.5	598.5	600.2	336.6	399.3	1782.1	1853.5	2975.3	2013.5	2346.5	3155.0	1619.4	537.5	2013.5	3.7

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
236898_at	LOC100290882	1.49E-03	34.9	42.4	74.7	68.3	80.3	71.5	94.5	68.7	62.6	225.2	75.0	167.7	148.5	178.8	71.5	148.5	2.1
201205_at	LOC100292328	6.13E-03	461.9	388.7	372.9	377.4	375.1	372.7	386.9	515.8	448.6	572.2	451.3	534.7	509.1	516.0	377.4	515.8	1.4
1567440_at	LOC100293538	2.66E-04	251.7	190.1	294.3	286.6	310.9	252.5	270.1	330.1	294.0	531.7	492.5	447.6	471.2	503.2	270.1	471.2	1.7
231387_at	LOC100293912	1.43E-03	552.0	469.0	459.2	435.7	552.8	363.0	567.3	691.5	806.3	915.5	603.2	740.6	724.0	796.6	469.0	740.6	1.6
1568768_s_at	LOC100302650 /// RBKS	3.84E-04	43.0	34.2	60.6	46.3	64.3	29.0	45.2	65.5	88.0	196.7	75.0	232.6	78.7	205.3	45.2	88.0	1.9
1554115_at	LOC133874	6.45E-04	131.8	104.9	164.1	170.7	146.2	131.4	137.4	211.5	206.1	478.5	222.9	308.6	207.4	260.7	137.4	222.9	1.6
238654_at	LOC147645	5.25E-03	82.6	88.0	121.2	87.7	83.6	55.3	75.6	106.3	99.3	144.6	111.7	105.6	76.4	116.9	83.6	106.3	1.3
1557049_at	LOC149478	3.42E-04	117.3	89.3	127.2	131.5	174.8	77.4	178.4	219.2	174.9	443.5	259.5	268.5	229.7	319.7	127.2	259.5	2.0
238102_s_at	LOC149478	6.66E-04	79.6	41.1	84.3	75.2	75.5	51.5	105.4	111.5	124.9	292.2	213.9	167.6	231.7	165.3	75.5	167.6	2.2
238058_at	LOC150381	4.87E-03	341.5	271.4	361.2	289.1	346.2	355.5	353.2	374.7	384.6	487.8	371.9	431.7	467.7	437.9	346.2	431.7	1.2
227868_at	LOC154761	9.27E-04	50.8	51.8	40.8	47.6	47.4	47.1	34.7	72.5	78.7	64.5	86.2	68.7	54.2	58.6	47.4	68.7	1.5
211012_s_at	LOC161527 /// PML	2.00E-05	315.7	197.3	279.8	317.4	275.4	237.3	294.8	676.6	725.9	1178.9	737.6	917.2	934.7	1212.3	279.8	917.2	3.3
211014_s_at	LOC161527 /// PML	7.51E-05	52.9	42.6	76.3	90.0	62.7	53.1	78.9	101.7	99.7	191.5	139.3	144.9	162.6	157.3	62.7	144.9	2.3
1563745_a_at	LOC283050	1.04E-03	92.6	50.3	71.1	62.9	117.4	32.2	82.3	126.7	102.6	155.5	90.0	199.7	94.0	123.8	71.1	123.8	1.7
1556854_at	LOC283501	8.68E-03	56.6	44.9	66.7	67.0	52.8	55.3	88.3	69.2	71.8	81.9	79.6	69.5	77.4	95.2	56.6	77.4	1.4
227415_at	LOC283508	1.19E-03	123.4	137.4	172.7	103.8	223.2	155.4	193.3	211.3	244.7	488.0	247.9	242.5	296.9	355.0	155.4	247.9	1.6
237032_x_at	LOC283567	1.07E-03	57.2	66.5	47.5	74.5	81.7	54.7	71.3	88.7	139.9	273.5	191.0	148.0	110.4	289.9	66.5	148.0	2.2
230353_at	LOC284112	3.37E-03	208.2	178.9	185.2	232.2	255.0	186.2	221.5	228.3	214.9	314.8	300.4	403.1	280.5	349.6	208.2	300.4	1.4
1555847_a_at	LOC284454	8.12E-03	3067.1	2212.1	1659.8	1724.2	1718.8	1256.9	1542.6	2826.6	2917.0	2560.2	2274.2	3435.0	2767.3	3206.5	1718.8	2826.6	1.6
235317_at	LOC284454	1.64E-03	86.7	71.3	62.6	61.1	64.9	53.1	65.8	97.4	99.0	93.1	83.8	99.9	99.8	109.9	64.9	99.0	1.5
232504_at	LOC285628	1.51E-04	156.5	106.7	327.2	132.4	533.0	113.5	308.5	556.2	760.7	1607.5	693.0	1051.1	981.4	788.0	156.5	788.0	5.0
243601_at	LOC285957	6.50E-05	99.7	76.4	116.5	114.4	173.5	152.1	156.7	284.4	159.0	497.9	302.7	320.3	587.3	439.1	116.5	320.3	2.7
238893_at	LOC338758	1.02E-03	48.1	54.0	82.3	86.5	71.8	86.1	82.3	91.5	92.6	210.9	106.0	131.8	123.2	129.5	82.3	123.2	1.5
238790_at	LOC374443	5.42E-03	33.1	50.9	24.5	35.3	23.1	25.0	27.7	56.5	59.3	154.6	61.7	42.9	58.6	59.4	27.7	59.3	2.1
228786_at	LOC387647	3.42E-04	176.2	143.1	186.0	133.9	159.2	125.6	111.3	245.1	215.0	388.9	196.7	236.4	230.8	188.8	143.1	230.8	1.6
1560058_at	LOC399900	1.57E-04	51.6	80.4	102.1	71.6	63.7	70.5	66.6	136.7	152.8	344.7	142.8	127.5	118.0	119.8	70.5	136.7	1.9
226582_at	LOC400043	5.94E-04	100.0	118.1	142.9	80.8	151.1	194.7	145.8	162.3	265.2	375.8	109.5	212.9	476.4	311.0	142.9	265.2	1.9
227885_at	LOC400236	1.58E-03	52.4	41.4	60.1	67.9	78.8	77.0	72.3	77.3	55.0	95.6	108.5	101.6	95.7	91.0	67.9	95.6	1.4
227887_at	LOC400236	2.90E-03	46.8	41.0	51.0	61.2	51.4	63.4	57.3	55.0	51.9	69.8	83.6	88.0	87.6	72.5	51.4	72.5	1.4
1560520_at	LOC401312	3.05E-04	30.3	42.3	29.6	20.6	29.5	26.9	28.3	50.9	82.1	107.4	66.1	47.2	62.1	96.2	29.5	66.1	2.2
232001_at	LOC439949	4.34E-03	40.9	38.4	55.9	106.4	54.2	63.9	56.4	53.3	60.8	110.3	115.6	96.9	78.7	81.4	55.9	81.4	1.5
1556378_a_at	LOC440896	4.54E-06	40.0	28.1	45.3	39.4	71.3	34.0	56.4	360.9	705.0	1309.2	353.6	729.2	487.6	874.2	40.0	705.0	17.6
1556883_a_at	LOC440896	4.15E-03	41.6	48.1	34.5	30.8	31.6	32.5	34.8	44.5	75.8	216.2	57.8	109.9	71.6	133.7	34.5	75.8	2.2
1570388_a_at	LOC440896	1.15E-05	26.5	38.4	36.5	15.6	30.2	19.8	24.2	127.0	349.3	911.2	174.7	197.1	171.5	293.7	26.5	197.1	7.4
232253_at	LOC441108	4.22E-03	78.1	91.3	72.0	56.8	89.6	73.7	61.6	103.5	128.8	177.3	137.7	111.0	91.8	117.0	73.7	117.0	1.6
1562749_at	LOC644090	6.02E-04	64.4	52.4	43.4	32.1	54.9	32.5	49.8	106.5	72.4	108.7	144.9	171.9	117.2	119.1	49.8	117.2	2.4
238319_at	LOC644090	5.44E-03	85.1	78.6	50.6	65.0	40.2	39.1	72.9	113.2	80.1	95.8	118.7	105.8	77.6	93.8	65.0	95.8	1.5
229566_at	LOC645638	8.85E-03	314.0	440.1	143.6	232.8	152.7	204.2	252.8	379.3	538.7	172.9	275.6	190.6	342.7	314.4	232.8	314.4	1.4
211588_s_at	LOC652346 /// PML	5.69E-05	60.4	54.3	73.1	69.3	67.8	75.9	68.0	115.3	79.6	163.4	156.7	172.9	165.0	136.1	68.0	156.7	2.3
201239_s_at	LOC653566 /// SPCS2	6.50E-03	1527.6	1508.4	1478.2	1449.6	1477.3	1476.8	1534.5	1776.6	1850.3	2067.8	1960.9	1711.1	1851.6	1875.0	1478.2	1851.6	1.3
227384_s_at	LOC727820	4.41E-03	508.8	468.2	517.1	445.6	460.5	518.9	420.6	590.7	562.3	825.4	660.6	543.4	676.3	643.0	468.2	643.0	1.4
231247_s_at	LOC727820	9.11E-03	508.2	501.2	566.3	424.7	536.2	559.6	478.7	688.3	557.8	809.2	781.0	599.7	675.5	670.7	508.2	675.5	1.3
229678_at	LOC728431	1.02E-03	57.7	45.6	65.3	55.9	59.3	43.7	69.6	81.8	77.1	131.4	93.1	87.1	113.2	92.6	57.7	92.6	1.6
229200_at	LOC729810	6.92E-04	708.4	691.7	896.7	587.4	567.4	467.2	651.2	859.4	1090.4	1395.9	904.0	840.3	942.8	1268.1	651.2	942.8	1.4
1559777_at	LOC731424	4.92E-05	127.0	59.3	106.9	62.5	206.3	116.8	316.7	442.0	424.6	965.5	291.3	550.3	958.3	1087.3	116.8	550.3	4.7
1569095_at	LOC731424	2.98E-04	1546.5	488.7	679.2	1006.6	1767.6	539.4	1601.7	3357.7	4456.5	5748.7	3266.0	4602.0	5107.0	5728.0	1006.6	4602.0	4.6
226038_at	LONRF1	4.54E-03	691.5	379.2	752.0	758.8	939.7	525.1	1106.7	861.6	885.2	1555.5	1267.3	1018.7	1043.1	1427.7	752.0	1043.1	1.4
236556_s_at	LONRF1	5.22E-03	114.6	86.8	101.2	105.5	120.3	102.4	128.2	130.5	114.3	175.2	129.9	151.5	141.6	165.1	105.5	141.6	1.3
204036_at	LPAR1	5.16E-03	82.1	82.7	75.3	156.5	183.2	96.7	265.9	174.2	131.8	250.5	336.1	207.3	280.9	294.7	96.7	250.5	2.6
204037_at	LPAR1	5.31E-03	1130.9	863.8	556.6	956.3	1411.5	881.5	1513.5	1716.1	1370.7	1470.5	1961.2	1422.7	1875.6	1896.6	956.3	1716.1	1.8
204038_s_at	LPAR1	8.10E-04	98.2	74.6	76.8	131.7	166.9	90.4	202.3	197.6	163.8	239.3	311.7	222.2	314.7	297.2	98.2	239.3	2.4
1555058_a_at	LPGAT1	9.31E-03	205.3	221.0	227.4	243.0	257.9	284.8	261.3	275.7	238.3	376.2	297.0	301.9	356.8	354.5	243.0	301.9	1.2
230996_at	LPP	3.37E-03	110.7	86.1	134.1	146.7	155.4	150.4	130.4	144.6	132.2	192.4	165.3	190.2	209.2	167.8	134.1	167.8	1.3
219631_at	LRP12	1.66E-03	68.4	61.1	75.6	74.8	85.0	84.4	100.0	138.5	98.7	172.3	96.5	123.5	102.6	171.3	75.6	123.5	1.6
220254_at	LRP12	1.20E-03	102.4	102.1	123.7	123.2	167.0	123.4	156.0	189.5	146.9	275.6	155.1	216.8	214.1	251.8	123.4	214.1	1.7
1553940_a_at	LRRC28	3.10E-03	101.7	116.0	161.4	166.5	165.4	137.5	117.6	162.2	153.9	279.0	197.7	204.3	168.5	190.5	137.5	190.5	1.4
215084_s_at	LRRC42	3.79E-03	194.1	146.8	280.0	262.8	271.8	221.0	254.1	283.1	268.8	349.2	306.6	369.1	295.1	325.3	254.1	306.6	1.2

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
222068_s_at	LRRC50	2.14E-05	102.8	109.7	89.0	76.7	83.0	87.0	93.9	321.7	514.6	936.1	458.9	546.5	786.8	1256.0	89.0	546.5	6.1
222231_s_at	LRRC59	7.19E-03	572.4	608.2	547.1	664.0	685.8	606.5	720.3	839.9	733.9	903.6	778.2	781.8	819.9	879.0	608.2	819.9	1.3
202245_at	LSS	2.47E-05	219.0	137.0	152.8	235.4	270.1	139.3	242.3	465.3	516.2	709.4	586.1	711.3	504.4	719.7	219.0	586.1	2.7
211018_at	LSS	4.69E-05	65.3	72.1	74.9	66.4	144.2	65.6	121.1	146.1	133.2	246.0	165.7	263.6	186.6	262.0	72.1	186.6	2.6
211019_s_at	LSS	1.41E-03	69.7	48.9	35.0	43.8	53.1	36.8	56.2	78.2	73.3	132.6	97.6	136.6	100.8	128.2	48.9	100.8	2.1
206975_at	LTA	2.04E-03	45.2	17.0	39.2	51.9	38.3	40.6	42.3	50.0	39.6	62.8	77.8	55.8	68.7	64.7	40.6	62.8	1.5
202625_at	LYN	1.00E-03	1527.7	1095.6	1821.0	1910.4	2227.9	1790.3	2807.1	2390.4	2949.6	4103.1	3340.1	3020.7	3248.6	3781.1	1821.0	3248.6	1.8
202626_s_at	LYN	7.17E-05	1575.8	1138.0	1412.0	1569.3	2077.9	1309.3	2237.5	3019.9	2903.3	3793.7	3212.1	3549.6	3485.4	3771.3	1569.3	3485.4	2.2
210754_s_at	LYN	1.08E-04	1638.3	1050.0	1340.1	1509.8	1717.7	1137.7	1803.4	2661.6	2784.5	3427.9	2682.1	3211.9	3080.9	3256.7	1509.8	3080.9	2.0
218561_s_at	LYRM4	1.91E-03	756.1	552.5	657.7	630.5	733.4	713.1	851.6	910.3	1036.4	2098.6	1004.8	1122.2	1241.9	1489.6	713.1	1122.2	1.6
226748_at	LYSMD2	3.84E-04	353.1	335.0	380.9	467.8	518.7	491.1	504.8	614.2	665.1	621.3	795.6	690.5	665.2	776.9	467.8	665.2	1.4
218559_s_at	MAFB	4.28E-04	5460.9	4726.6	4076.5	3549.6	5270.0	2784.0	3834.1	7028.3	8001.7	8362.3	7001.2	7933.7	7097.5	7741.1	4076.5	7741.1	1.9
222670_s_at	MAFB	1.12E-03	2120.9	1593.6	1351.8	1106.2	1535.8	816.7	1161.6	2276.1	2808.4	3495.4	2321.5	2875.9	2597.4	2628.9	1351.8	2628.9	1.9
220302_at	MAK	1.74E-04	56.3	87.8	70.2	70.0	86.4	61.7	69.7	93.8	190.7	225.2	136.2	135.0	160.7	190.4	70.0	160.7	2.3
235106_at	MAML2	5.96E-04	74.2	79.3	104.9	85.2	147.8	138.6	139.8	158.8	153.7	339.6	211.7	205.5	248.9	210.2	104.9	210.2	2.0
235457_at	MAML2	5.71E-04	173.3	262.9	317.2	291.4	377.9	399.2	339.9	481.1	603.5	939.0	621.0	548.1	568.7	574.2	317.2	574.2	1.8
205088_at	MAMLD1	2.39E-04	35.0	24.9	32.9	34.5	49.3	32.2	43.9	51.4	50.5	94.8	92.8	95.9	52.3	121.7	34.5	92.8	2.7
202655_at	MANF	1.66E-03	1294.0	1126.5	917.8	1163.1	1013.8	791.5	1112.7	1544.2	1442.3	1429.5	1737.5	1452.2	1469.5	1521.7	1112.7	1469.5	1.3
224378_x_at	MAP1LC3A	8.07E-03	69.7	44.4	64.2	65.4	60.3	63.8	67.8	88.0	59.6	139.7	71.5	136.4	147.8	82.7	64.2	88.0	1.4
227219_x_at	MAP1LC3A	2.79E-03	59.1	49.9	48.6	56.5	65.0	57.8	67.7	81.2	60.8	108.2	82.9	129.2	89.0	84.9	57.8	84.9	1.5
207667_s_at	MAP2K3	2.98E-04	104.4	76.7	143.3	148.4	153.3	124.0	157.2	149.8	123.8	249.1	190.4	251.6	236.7	256.4	143.3	236.7	1.7
215498_s_at	MAP2K3	1.00E-03	1878.1	1961.9	2341.2	1828.5	2488.8	2177.9	2869.6	2792.5	3015.7	3819.9	3215.1	3144.7	3190.9	3494.8	2177.9	3190.9	1.5
215499_at	MAP2K3	1.12E-03	949.9	880.4	1129.1	1059.5	1414.7	1159.6	1592.2	1355.0	1728.3	2077.1	1629.3	1619.2	1864.0	2342.3	1129.1	1728.3	1.5
210284_s_at	MAP3K7IP2	2.10E-03	116.0	126.7	199.6	164.5	207.3	161.8	191.4	190.7	159.6	334.9	243.7	248.9	201.4	268.9	164.5	243.7	1.5
205027_s_at	MAP3K8	3.10E-03	205.6	206.4	291.0	353.3	367.0	369.6	417.5	290.0	607.5	1141.1	608.1	549.7	542.6	697.5	353.3	607.5	1.7
235421_at	MAP3K8	9.77E-04	826.0	603.3	744.8	742.1	680.7	554.3	782.0	957.7	1434.8	2069.6	1188.2	1114.6	1247.7	1506.0	742.1	1247.7	1.7
206571_s_at	MAP4K4	1.30E-03	452.7	321.6	508.4	438.4	607.8	405.5	483.3	549.6	660.8	930.9	605.7	792.3	663.7	841.9	452.7	663.7	1.5
202889_x_at	MAP7	1.79E-03	51.2	53.2	77.1	92.5	72.6	84.3	50.3	66.9	82.8	125.9	113.5	86.8	128.2	88.4	72.6	88.4	1.2
212497_at	MAPK1IP1L	6.05E-03	86.6	87.0	117.8	112.8	129.8	121.9	133.2	136.5	91.4	176.3	148.3	155.8	186.3	166.5	117.8	155.8	1.3
229845_at	MAPKAP1	4.24E-03	301.6	201.2	284.8	301.6	308.8	258.8	290.3	309.1	501.6	622.2	422.7	399.9	485.2	537.0	290.3	485.2	1.7
213256_at	MARCH3	1.72E-03	146.5	114.5	116.9	108.0	192.8	101.9	151.6	228.1	143.0	253.4	209.0	227.9	156.5	263.0	116.9	227.9	1.9
218582_at	MARCH5	2.65E-03	148.4	194.4	221.0	208.6	219.7	232.6	239.3	264.2	260.4	367.6	276.1	272.3	274.4	343.7	219.7	274.4	1.2
230001_at	MARCH9	9.34E-03	46.9	53.1	44.9	46.6	47.9	38.3	32.8	54.0	68.6	124.7	63.3	59.4	59.5	77.6	46.6	63.3	1.4
201668_x_at	MARCKS	4.22E-04	154.6	78.9	98.8	137.8	231.2	53.7	219.8	330.1	487.3	800.8	640.6	474.9	584.6	669.2	137.8	584.6	4.2
201669_s_at	MARCKS	9.14E-04	685.5	140.7	540.6	628.4	1702.6	257.9	2067.2	2294.5	3079.0	5324.5	4363.3	3673.4	3563.6	4509.5	628.4	3673.4	5.8
201670_s_at	MARCKS	2.68E-03	3647.7	655.7	1810.5	2448.7	5600.4	966.4	5812.7	6921.2	8280.1	11332.8	9624.9	8759.8	9926.6	10789.2	2448.7	9624.9	3.9
213002_at	MARCKS	3.37E-03	7168.1	1906.4	4007.0	5059.9	10109.4	1839.5	10510.8	12333.8	14986.3	17460.5	15470.8	15254.0	15647.6	16045.2	5059.9	15470.8	3.1
225897_at	MARCKS	1.58E-04	174.6	46.5	117.5	125.6	414.2	53.6	423.5	835.5	862.1	1723.4	1287.5	1202.3	1110.3	1616.0	125.6	1202.3	9.6
200644_at	MARCKSL1	2.83E-05	72.9	72.5	39.8	50.3	120.0	60.0	85.1	257.0	138.1	160.4	214.3	401.8	245.1	493.6	72.5	245.1	3.4
228468_at	MASTL	3.41E-05	51.5	53.4	81.0	82.4	99.0	82.0	100.4	183.6	260.2	612.2	253.2	295.2	208.8	406.2	82.0	260.2	3.2
209331_s_at	MAX	3.95E-03	1553.6	1461.7	1667.1	1286.6	1340.7	1417.0	1332.0	1739.2	2042.2	2024.9	1713.7	1814.0	1780.0	2008.1	1417.0	1814.0	1.3
214108_at	MAX	8.51E-03	114.4	84.3	141.4	138.1	152.7	116.2	153.6	118.1	124.1	265.1	202.9	187.2	145.4	200.5	138.1	187.2	1.4
1558111_at	MBNL1	1.45E-03	285.2	271.7	364.7	384.0	305.1	297.0	297.1	345.4	418.3	602.8	501.9	392.1	477.1	408.3	297.1	418.3	1.4
200796_s_at	MCL1	5.44E-03	308.7	261.3	233.5	320.9	235.0	340.3	245.2	324.9	311.8	420.9	402.9	419.0	522.0	458.4	261.3	419.0	1.6
200798_x_at	MCL1	5.70E-03	405.1	525.5	585.5	493.2	528.9	641.7	610.6	617.4	799.0	1154.9	793.6	639.0	648.1	846.8	528.9	793.6	1.5
214056_at	MCL1	7.67E-03	2822.4	2902.2	2512.7	2636.8	2413.5	2745.4	2611.2	2852.1	3720.7	4140.7	3558.0	3428.1	3268.6	3961.3	2636.8	3558.0	1.3
1555465_at	MCOLN2	3.16E-04	143.2	136.7	59.2	104.4	114.2	59.5	113.9	194.5	296.1	290.6	341.4	334.4	262.7	495.0	113.9	296.1	2.6
230110_at	MCOLN2	1.24E-05	137.9	88.6	79.9	155.7	300.9	91.3	261.8	498.8	602.0	674.2	777.3	924.6	691.8	1235.4	137.9	691.8	5.0
1554730_at	MCTP1	1.02E-03	65.3	52.8	78.3	86.5	136.7	45.2	97.4	126.4	109.4	245.3	206.8	157.9	158.6	172.8	78.3	158.6	2.0
220122_at	MCTP1	5.14E-03	329.4	264.1	435.7	536.2	665.6	445.7	640.7	625.7	667.3	1479.9	964.9	643.6	782.0	885.2	445.7	782.0	1.8
229021_at	MCTP2	1.69E-03	45.5	51.2	27.8	16.9	21.5	28.2	23.3	48.2	83.7	105.5	62.2	60.6	98.0	131.7	27.8	83.7	3.0
217599_s_at	MDFIC	8.47E-03	323.4	259.7	339.7	283.1	383.8	367.0	333.1	379.0	513.6	789.0	455.7	450.5	480.0	404.1	333.1	455.7	1.4
239172_x_at	MDFIC	6.39E-03	169.0	207.7	191.6	179.9	224.1	216.1	187.0	257.4	225.9	334.0	298.5	303.4	258.1	222.3	191.6	258.1	1.3
223780_s_at	MED13	3.59E-03	249.7	233.5	238.5	248.8	358.6	323.5	323.4	384.0	259.8	445.3	356.2	497.1	397.0	443.1	249.7	397.0	1.6
1553993_s_at	MED25	7.44E-03	101.7	127.4	139.5	121.1	137.9	151.6	124.7	176.8	163.6	203.8	155.6	198.1	153.5	157.7	127.4	163.6	1.3
221598_s_at	MED27	9.38E-03	176.6	186.5	236.5	220.9	235.1	216.3	253.2	316.3	175.2	363.1	267.4	373.0	324.9	327.6	220.9	324.9	1.5
51176_at	MED27	5.73E-03	312.9	324.9	353.7	331.8	395.9	346.6	404.4	495.3	338.0	552.6	379.3	540.2	554.7	554.8	346.6	540.2	1.6
209199_s_at	MEF2C	7.46E-03	88.3	66.8	112.9	108.7	98.8	95.1	109.5	113.2	107.8	192.8	157.2	145.1	88.7	232.4	98.8	145.1	1.5
230011_at	MEI1	4.68E-03	52.9	67.7	42.9	56.5	75.9	61.9	64.1	95.5	72.1	71.1	101.3	81.8	96.1	100.5	61.9	95.5	1.5
223264_at	MESDC1	6.52E-04	337.5	291.2	412.9	406.0	509.0	470.7	570.5	536.5	757.7	1181.6	673.3	708.1	796.5	1057.2	412.9	757.7	1.8
204027_s_at	METTL1	8.55E-04	89.0	46.7	125.2	128.2	120.5	97.7	164.2	172.9	156.7	302.4	200.2	195.5	169.2	237.1	120.5	195.5	1.6
207098_s_at	MFN1	1.06E-03	85.9	114.7	188.2	228.5	151.9	166.0	184.9	192.4	351.4	689.0	423.9	194.0	254.0	413.4	166.0	351.4	2.1
211801_x_at	MFN1	1.16E-03	115.1	124.7	143.1	207.2	128.1	132.9	147.2	146.1	307.8	484.1	307.8	224.5	246.1	328.1	132.9	307.8	2.3
217043_s_at	MFN1	5.27E-04	90.7	96.2	129.7	148.4	102.8	99.0	102.0	138.6	248.0	386.8	232.0	152.0	193.1	253.1	102.0	232.0	2.3
1553386_at	MFSD2	4.76E-03	72.1	50.0	62.2	59.6	61.7	59.5	71.4	70.6	81.6	110.5	81.9	83.3	91.0	99.9	61.7	83.3	1.3
225316_at	MFSD2	4.17E-04	372.7	114.3	344.2	300.3	512.0	197.9	625.4	758.0	1084.0	1799.5	1012.4	1496.8	1906.2	1571.2	344.2	1496.8	4.3

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
206522_at	MGAM	1.84E-04	32.3	29.8	20.0	37.4	36.1	43.4	30.8	75.7	133.6	231.4	121.6	123.3	119.7	153.5	32.3	123.3	3.8
223974_at	MGC11082	1.22E-03	54.4	33.3	44.0	38.1	44.7	36.0	40.7	77.5	45.2	64.8	52.2	78.7	75.2	98.3	40.7	75.2	1.8
224507_s_at	MGC12916	8.08E-05	76.3	86.1	58.9	42.9	78.5	35.7	64.9	189.8	160.8	325.5	204.3	255.2	116.1	329.8	64.9	204.3	3.1
224508_at	MGC12916	2.18E-05	33.9	21.1	38.4	37.4	73.4	37.4	40.6	179.2	111.5	344.0	183.5	214.6	113.3	282.7	37.4	183.5	4.9
210484_s_at	MGC31957 /// TNFRSF10C	7.64E-03	48.8	26.2	51.6	48.8	49.5	52.4	36.9	44.8	50.8	91.9	56.6	79.5	88.4	82.7	48.8	79.5	1.6
239104_at	MGC42157	2.59E-03	117.2	143.5	172.7	183.4	189.5	133.6	180.7	177.1	168.5	291.2	260.0	234.3	180.9	231.8	172.7	231.8	1.3
1565162_s_at	MGST1	4.11E-03	58.8	50.6	203.8	105.3	219.6	90.2	184.1	142.4	70.5	412.7	178.2	263.4	164.3	202.7	105.3	178.2	1.7
224918_x_at	MGST1	8.91E-03	798.2	518.0	1235.4	707.6	1323.4	540.1	1180.2	920.4	613.8	2403.3	988.0	1880.7	1059.6	1325.1	798.2	1059.6	1.3
231736_x_at	MGST1	7.98E-03	665.2	376.2	971.8	511.0	1031.7	447.5	844.2	816.4	397.2	1859.8	701.2	1468.1	833.7	1034.5	665.2	833.7	1.3
1569057_s_at	MIA3	2.34E-03	97.3	100.3	153.6	130.6	139.0	152.3	140.5	167.8	119.9	236.5	196.4	221.7	192.9	168.0	139.0	192.9	1.4
212305_s_at	MIA3	3.37E-03	196.7	199.5	244.6	244.6	242.0	247.5	218.0	316.5	223.6	332.7	283.7	385.1	343.5	359.6	242.0	332.7	1.4
227168_at	MIAT	5.27E-03	117.1	67.9	97.6	143.1	88.1	75.7	77.1	117.5	94.0	130.3	181.3	133.1	106.3	117.7	88.1	117.7	1.3
205905_s_at	MICA /// MICB	4.63E-03	189.1	153.3	229.3	186.3	230.5	265.5	171.3	248.1	162.5	305.7	244.5	384.4	350.3	242.5	189.1	248.1	1.3
221779_at	MICALL1	4.07E-05	180.5	130.7	156.5	209.7	241.7	162.2	274.2	425.4	541.1	747.5	427.1	654.7	615.3	819.8	180.5	615.3	3.4
55081_at	MICALL1	1.15E-05	91.8	119.4	157.2	176.8	202.8	144.5	247.4	436.9	492.0	731.4	400.8	660.2	577.8	740.1	157.2	577.8	3.7
206860_s_at	MIOS	3.84E-03	283.3	279.0	387.5	346.7	400.1	306.3	418.7	456.8	363.3	510.6	508.8	497.0	451.7	454.2	346.7	456.8	1.3
229437_at	MIR155HG	1.77E-04	171.5	81.2	198.4	192.2	258.5	144.2	252.9	416.8	535.0	1441.0	574.0	513.5	549.7	867.8	192.2	549.7	2.9
224784_at	MLLT6	1.96E-04	291.9	271.8	357.5	364.0	422.5	354.5	453.5	427.7	466.6	602.6	552.6	616.9	493.2	703.4	357.5	552.6	1.5
225628_s_at	MLLT6	2.47E-04	101.2	69.8	138.3	138.6	132.8	113.3	139.9	148.4	106.1	277.2	189.9	249.1	210.5	230.4	132.8	210.5	1.6
236347_at	MMAA	9.97E-04	427.9	476.6	507.8	544.6	566.4	462.6	526.0	621.9	724.9	1029.2	784.0	666.1	759.7	866.4	507.8	759.7	1.5
239852_at	MMAA	4.01E-03	41.8	68.7	79.5	54.4	75.1	69.1	68.9	87.1	86.8	129.8	99.9	84.4	94.2	90.8	68.9	90.8	1.3
205680_at	MMP10	2.45E-04	69.5	101.7	24.8	52.8	52.1	30.8	47.2	315.4	278.7	297.2	118.0	170.7	133.0	386.6	52.1	278.7	5.3
160020_at	MMP14	5.84E-04	182.3	126.5	162.8	225.2	159.4	126.1	223.2	227.0	263.6	451.7	365.0	337.4	402.5	492.7	162.8	365.0	2.2
202827_s_at	MMP14	1.53E-03	106.0	89.1	68.1	107.0	78.8	70.5	105.8	120.2	124.5	192.2	189.9	194.9	184.0	214.2	89.1	189.9	2.1
202828_s_at	MMP14	1.95E-04	98.1	62.6	106.1	132.9	109.5	70.7	145.7	151.0	131.8	308.2	235.5	227.2	236.7	302.2	106.1	235.5	2.2
204575_s_at	MMP19	1.60E-03	522.8	501.6	448.6	513.8	578.2	495.4	594.9	781.4	674.2	648.0	642.3	764.1	639.2	747.3	513.8	674.2	1.3
204259_at	MMP7	4.14E-03	49.2	34.2	56.1	37.3	43.6	43.3	55.5	81.0	268.5	492.6	76.7	90.8	74.3	126.2	43.6	90.8	2.1
224277_at	MOP-1	8.00E-03	144.8	143.8	187.8	137.2	205.5	125.2	164.3	221.6	300.2	749.1	384.6	201.9	178.8	262.7	144.8	262.7	1.8
223849_s_at	MOV10	2.43E-04	232.8	249.6	323.1	309.4	230.7	261.3	240.8	335.4	445.6	590.2	435.6	518.2	528.0	552.5	249.6	518.2	2.1
233917_s_at	MOV10	6.84E-04	85.1	85.9	127.3	139.8	89.6	108.4	109.0	127.1	163.4	230.3	175.1	254.6	235.8	211.7	108.4	211.7	2.0
210087_s_at	MPZL1	9.33E-04	137.0	138.0	174.8	145.8	161.5	134.1	142.7	240.5	171.0	255.7	222.7	215.7	195.4	194.4	142.7	215.7	1.5
206538_at	MRAS	5.57E-04	317.6	201.1	327.4	265.9	234.8	180.5	216.0	390.2	354.8	582.5	369.4	445.2	400.6	401.6	234.8	400.6	1.7
225185_at	MRAS	1.53E-03	542.0	352.9	568.1	504.7	508.3	331.0	477.7	690.0	593.6	937.5	642.4	676.4	665.3	688.3	504.7	676.4	1.3
219648_at	MREG	4.68E-04	615.2	235.7	403.8	458.4	836.7	187.6	930.9	1353.5	1314.1	2324.3	1967.8	1902.9	1927.4	1953.7	458.4	1927.4	4.2
232682_at	MREG	1.18E-04	23.8	21.6	19.1	25.1	34.3	11.8	35.0	79.9	54.1	132.0	93.8	92.4	76.3	79.7	23.8	79.9	3.4
225201_s_at	MRPL14	2.93E-04	391.9	309.7	347.7	351.0	432.5	290.0	397.3	563.3	558.9	679.2	497.5	658.5	653.0	720.5	351.0	653.0	1.9
222216_s_at	MRPL17	2.46E-03	566.1	446.7	456.6	471.0	427.8	456.4	406.4	688.7	647.0	618.3	528.7	702.9	680.9	608.4	456.4	647.0	1.4
216336_x_at	MT1E /// MT1H /// MT1M	5.58E-03	254.9	235.1	968.3	738.9	561.6	760.2	443.3	475.6	757.5	1513.8	859.5	966.9	856.0	1100.8	561.6	859.5	1.5
205322_s_at	MTF1	2.20E-04	294.5	147.5	277.1	274.3	362.1	247.5	406.5	477.5	483.9	675.3	580.6	602.8	779.0	776.2	277.1	602.8	2.2
205323_s_at	MTF1	6.72E-05	765.8	466.7	560.6	551.5	833.6	547.6	850.4	1228.6	1134.3	1389.5	1360.8	1409.3	1482.5	1733.5	560.6	1389.5	2.5
227150_at	MTF1	2.42E-04	657.4	499.0	668.5	751.2	1196.8	682.7	1063.9	1306.3	1411.6	1724.5	1897.2	1665.1	1835.2	1723.2	682.7	1723.2	2.5
201761_at	MTHFD2	4.59E-03	1433.3	968.6	1281.5	1382.8	1765.7	973.4	2382.3	1824.8	2451.2	3964.0	2649.5	2173.2	2428.0	2876.2	1382.8	2451.2	1.8
1556034_s_at	MTMR11	2.70E-03	445.9	505.0	496.0	389.0	646.4	537.9	528.3	550.6	629.0	684.2	488.6	781.2	753.4	736.6	505.0	684.2	1.4
205076_s_at	MTMR11	5.33E-03	131.3	194.1	193.2	138.6	239.1	208.6	206.8	165.5	246.9	320.5	195.4	294.0	248.7	246.1	194.1	246.9	1.3
203037_s_at	MTSS1	4.00E-03	37.9	34.7	46.8	52.6	47.0	53.2	43.5	64.0	61.8	70.3	69.7	106.5	52.3	74.6	46.8	69.7	1.5
226856_at	MUSTN1	2.25E-03	126.5	115.3	143.8	147.5	120.8	134.0	120.6	171.3	168.8	275.5	165.8	265.0	209.2	275.8	126.5	209.2	1.7
202086_at	MX1	9.12E-05	1551.8	1868.9	956.5	1101.8	899.1	691.2	955.1	2969.0	4121.4	4489.1	3893.0	4540.8	3707.1	5051.1	956.5	4121.4	4.3
204994_at	MX2	7.57E-06	295.3	360.7	303.0	275.7	330.4	281.1	238.1	818.3	1104.7	1419.4	922.2	1143.8	895.2	1236.9	295.3	1104.7	3.7
206877_at	MXD1	6.44E-05	137.1	124.0	121.7	183.4	190.6	120.4	180.4	321.8	406.1	564.4	335.1	658.8	559.7	821.7	137.1	559.7	4.1
226275_at	MXD1	1.07E-04	526.7	561.3	415.7	730.2	744.9	463.6	768.9	862.9	1372.5	1462.7	1343.8	1507.0	1256.0	2148.4	561.3	1372.5	2.4
228846_at	MXD1	5.69E-05	537.3	687.7	493.1	697.8	895.1	586.3	844.9	1074.7	2377.6	2784.9	1954.1	2101.9	1974.7	3013.5	687.7	2101.9	3.1
202431_s_at	MYC	3.13E-03	300.7	173.8	322.0	279.6	219.3	217.0	325.6	569.3	246.3	318.7	503.3	600.8	385.9	587.8	279.6	503.3	1.8
201976_s_at	MYO10	1.18E-04	15.8	40.8	66.8	58.7	49.0	26.2	34.1	53.2	63.7	206.4	119.3	133.6	50.3	99.4	40.8	99.4	2.4
216222_s_at	MYO10	3.28E-03	53.2	44.5	73.3	73.5	60.6	30.0	51.0	61.1	66.8	123.9	81.8	103.0	55.9	73.0	53.2	73.0	1.4
227799_at	MYO1G	1.10E-03	75.3	49.8	90.7	118.7	93.5	75.5	108.5	124.0	98.4	193.2	159.7	262.2	344.5	237.3	90.7	193.2	2.1
244654_at	MYO1G	5.96E-04	583.7	336.6	397.7	682.8	604.3	459.6	581.8	753.6	742.0	1154.6	1009.0	1078.4	1028.3	1418.6	581.8	1028.3	1.8
216662_at	MYO7B	9.57E-04	61.1	60.4	73.3	64.8	80.0	82.0	79.2	84.6	85.6	120.1	133.6	102.4	121.8	117.6	73.3	117.6	1.6
201798_s_at	MYOF	4.68E-03	1550.1	1356.5	1618.6	1566.0	1486.4	1647.2	1857.4	2042.5	2109.1	2417.3	1944.2	1756.4	1924.4	2328.6	1566.0	2042.5	1.3
211864_s_at	MYOF	1.53E-03	1386.3	1040.1	1239.9	1145.3	1088.5	1172.2	1306.8	1705.0	1616.9	1753.9	1465.7	1460.6	1501.3	1855.2	1172.2	1616.9	1.4
204601_at	N4BP1	1.92E-04	594.5	363.5	659.7	578.7	765.1	659.9	703.3	934.9	968.5	1424.0	852.2	1313.8	1266.1	1457.0	659.7	1266.1	1.9
32069_at	N4BP1	5.71E-04	163.2	158.2	375.5	290.4	460.3	435.5	439.6	500.7	439.1	1007.6	618.0	704.6	600.6	761.9	375.5	618.0	1.6
214887_at	N4BP2L1	5.49E-03	38.4	41.5	78.0	60.0	60.4	60.7	50.7	50.2	54.9	117.9	94.3	71.0	64.1	78.5	60.0	71.0	1.2
229718_at	N4BP2L1	6.72E-04	105.9	112.8	141.6	124.7	111.9	128.0	111.1	138.5	195.8	360.8	194.7	164.9	236.9	244.4	112.8	195.8	1.7

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
208047_s_at	NAB1	8.02E-03	51.8	42.5	85.3	91.5	99.7	89.0	97.6	107.0	69.1	157.6	127.4	118.6	101.8	109.3	89.0	109.3	1.2
209272_at	NAB1	7.45E-03	640.3	727.9	982.0	859.5	1145.2	1083.8	1017.9	1016.7	1036.5	1520.6	1284.7	1251.9	1127.7	1343.0	982.0	1251.9	1.3
211139_s_at	NAB1	3.26E-04	451.1	359.3	398.7	425.9	483.2	376.6	419.1	625.7	512.5	684.9	594.8	734.4	710.8	706.3	419.1	684.9	1.6
208917_x_at	NADK	1.69E-03	144.2	122.1	180.5	164.8	149.7	113.6	165.7	180.8	179.9	272.4	203.6	282.2	237.4	248.8	149.7	237.4	1.6
208918_s_at	NADK	1.84E-04	1604.9	1562.2	1533.0	1604.0	1938.2	1269.6	1588.5	2112.7	3249.3	3456.0	2787.5	3219.2	2730.4	3426.9	1588.5	3219.2	2.0
213607_x_at	NADK	3.10E-03	292.2	215.2	259.4	238.1	231.6	174.2	251.0	278.5	348.8	500.8	355.9	511.1	469.1	530.0	238.1	469.1	2.0
213613_s_at	NADK	2.98E-04	223.5	192.9	190.0	195.6	222.5	163.0	197.4	272.8	322.8	451.0	361.6	469.0	357.8	420.6	195.6	361.6	1.8
215159_s_at	NADK	2.70E-03	122.7	92.6	152.3	121.8	117.0	98.7	134.3	160.9	116.0	203.7	170.7	250.1	214.8	208.1	121.8	203.7	1.7
1555167_s_at	NAMPT	1.81E-04	2254.9	1509.2	1566.2	1813.8	3077.8	1860.5	3281.3	3737.0	5043.2	6382.9	4355.9	6155.7	5930.9	6460.8	1860.5	5930.9	3.2
217738_at	NAMPT	8.15E-04	1169.4	808.3	1307.8	1216.1	1939.8	1419.5	2366.1	1865.6	2831.7	4074.5	2687.3	2940.8	2938.8	3618.6	1307.8	2938.8	2.2
217739_s_at	NAMPT	3.14E-03	3339.4	2630.1	3566.4	3663.4	5245.9	4064.1	6100.5	4269.9	6565.8	8539.1	6188.0	6360.2	7327.9	8025.3	3663.4	6565.8	1.8
243296_at	NAMPT	1.46E-04	96.2	64.2	110.5	68.1	144.1	98.4	92.2	161.0	275.7	741.2	186.4	432.3	320.3	308.3	96.2	308.3	3.2
202905_x_at	NBN	7.13E-05	1860.2	1129.3	1561.8	1533.1	2539.1	1365.2	2300.3	4036.2	5990.0	8306.0	4551.8	5632.8	5335.1	6789.6	1561.8	5632.8	3.6
202906_s_at	NBN	6.44E-05	768.7	513.7	826.6	796.2	1219.9	698.9	1309.6	2115.0	3355.4	5762.9	2632.5	3122.9	2943.5	3725.4	796.2	3122.9	3.9
202907_s_at	NBN	6.71E-04	1461.7	1063.1	1868.7	1638.6	2606.5	1768.1	3420.8	2718.5	4653.7	7230.5	4760.5	4059.7	4297.1	5578.4	1768.1	4653.7	2.6
217299_s_at	NBN	1.37E-04	546.2	304.1	591.7	567.2	839.2	491.6	913.0	1376.5	2388.7	4271.0	1846.1	2036.1	2098.2	2643.0	567.2	2098.2	3.7
40640_at	NCAPH2	2.44E-03	591.4	531.3	578.5	603.1	694.6	457.8	620.4	831.8	608.3	699.6	892.6	1178.0	863.4	957.8	591.4	863.4	1.5
204961_s_at	NCF1 /// NCF1B /// NCF1C	2.57E-05	566.0	278.8	447.2	463.3	413.4	277.3	357.3	1598.0	1397.7	2378.7	1671.7	2274.9	2720.1	1265.6	413.4	1671.7	4.0
203315_at	NCK2	1.94E-03	277.0	269.0	303.3	380.2	451.7	225.5	374.5	606.3	493.1	972.2	538.0	540.0	430.8	602.0	303.3	540.0	1.8
209060_x_at	NCOA3	9.61E-03	309.0	245.0	377.0	389.1	305.2	353.1	399.8	377.9	441.7	536.9	502.5	364.9	387.2	502.4	353.1	441.7	1.3
209062_x_at	NCOA3	3.70E-04	102.2	93.7	118.3	108.1	107.6	89.5	117.3	148.5	125.9	235.5	157.8	168.5	150.6	181.4	107.6	157.8	1.5
225344_at	NCOA7	1.68E-04	230.0	242.3	418.3	357.4	401.2	453.6	416.6	635.1	1115.0	1930.3	898.9	954.6	710.9	1277.7	401.2	954.6	2.4
232093_at	NCRNA00085	1.70E-03	43.6	54.8	54.6	34.6	46.7	44.1	45.2	73.8	67.2	111.7	72.5	71.6	58.3	61.1	45.2	71.6	1.6
231303_at	NCRNA00158	2.66E-03	59.4	49.6	25.2	24.8	34.0	27.0	40.8	68.1	126.6	228.5	68.1	78.0	60.1	152.2	34.0	78.0	2.3
1553607_at	NCRNA00189	2.64E-04	27.4	12.5	36.0	42.8	69.0	35.3	38.3	62.2	35.5	151.9	151.1	97.4	122.7	78.6	36.0	97.4	2.7
1553608_a_at	NCRNA00189	5.52E-05	140.7	56.0	143.1	169.1	253.2	155.0	208.8	380.6	184.7	625.7	445.4	586.9	657.6	395.0	155.0	445.4	2.9
208093_s_at	NDEL1	3.61E-03	433.3	404.7	511.6	485.4	563.0	435.9	555.7	558.3	611.4	737.3	650.9	623.5	590.1	681.1	485.4	623.5	1.3
206022_at	NDP	2.88E-05	62.8	33.1	30.4	36.2	86.4	22.3	74.3	302.1	176.7	520.7	457.5	332.1	236.8	453.1	36.2	332.1	9.2
1559701_s_at	NDST2	2.46E-03	52.7	54.3	62.7	76.3	94.3	88.2	66.7	100.0	65.7	140.2	98.8	129.7	129.0	145.0	66.7	129.0	1.9
203916_at	NDST2	1.08E-03	109.8	108.9	161.8	178.1	202.3	178.4	157.6	197.2	132.8	278.2	228.6	318.7	249.0	237.7	161.8	237.7	1.5
208969_at	NDUFA9	3.30E-03	1435.9	1372.7	1282.4	1295.0	1339.3	1227.3	1193.5	1739.7	1636.5	1775.2	1647.8	1689.0	1578.5	1690.4	1295.0	1689.0	1.3
202150_s_at	NEDD9	6.82E-03	141.6	114.2	145.1	156.8	153.2	142.3	148.7	209.8	124.0	158.2	215.9	203.9	190.3	216.1	145.1	203.9	1.4
218888_s_at	NETO2	3.37E-03	46.8	58.2	62.7	38.2	65.0	37.1	61.1	68.1	65.5	87.1	66.7	75.3	54.5	90.1	58.2	68.1	1.2
232593_at	NEURL3	2.21E-05	67.7	45.9	50.3	46.0	42.8	37.9	59.8	146.0	135.8	285.4	149.7	148.2	132.3	183.7	46.0	148.2	3.2
1552309_a_at	NEXN	6.17E-06	218.4	200.1	252.8	215.9	166.9	135.8	174.6	768.7	1780.5	2596.4	1347.5	1112.6	1023.5	1831.9	200.1	1347.5	6.7
226103_at	NEXN	2.42E-06	245.5	245.3	286.1	225.2	194.6	198.4	215.7	1153.1	1985.4	2743.7	1530.1	1511.7	1239.1	2310.5	225.2	1530.1	6.8
204323_x_at	NF1	4.15E-03	110.8	84.3	122.0	112.9	164.7	144.7	158.1	185.9	148.8	198.2	181.0	186.8	180.4	179.9	122.0	181.0	1.5
204325_s_at	NF1	1.05E-03	88.8	80.0	122.1	112.2	140.3	129.9	135.6	177.9	121.6	176.1	187.1	168.8	186.1	196.5	122.1	177.9	1.5
211914_x_at	NF1	6.53E-03	128.1	105.7	156.1	152.4	208.5	170.6	194.2	172.9	159.0	216.4	215.6	204.7	220.5	259.3	156.1	215.6	1.4
208003_s_at	NFAT5	6.07E-04	96.5	108.1	139.0	126.5	174.8	133.2	172.9	172.2	177.7	407.7	272.6	215.3	253.6	346.3	133.2	253.6	1.9
215092_s_at	NFAT5	8.55E-05	152.9	131.2	169.6	176.1	278.9	162.8	248.9	305.4	294.6	541.0	356.7	440.5	431.0	511.5	169.6	431.0	2.5
224984_at	NFAT5	5.56E-04	112.4	102.5	132.5	133.9	215.1	134.5	174.8	182.3	179.8	421.7	226.5	320.4	234.1	345.7	133.9	234.1	1.7
201146_at	NFE2L2	6.69E-03	712.7	798.9	1086.1	986.8	1258.4	865.7	1343.9	1164.9	1167.6	1785.8	1462.7	1266.4	1290.4	1492.8	986.8	1290.4	1.3
204702_s_at	NFE2L3	1.37E-05	92.1	68.5	118.4	194.5	115.1	74.9	115.1	283.8	142.3	408.1	466.6	252.6	231.0	354.1	115.1	283.8	2.5
236471_at	NFE2L3	7.13E-04	49.0	41.6	72.9	99.8	49.0	49.0	56.4	75.5	47.0	141.9	171.6	78.0	79.8	108.4	49.0	79.8	1.6
209807_s_at	NFIX	8.92E-03	140.7	114.2	117.1	105.8	128.5	101.9	111.5	149.6	138.7	157.5	117.1	189.3	155.7	180.9	114.2	155.7	1.4
209239_at	NFKB1	2.52E-05	658.9	346.5	479.8	565.5	940.1	421.8	873.4	1599.3	1895.5	2889.2	2106.1	2995.4	2647.5	2959.0	565.5	2647.5	4.7
207535_s_at	NFKB2	4.54E-05	40.6	22.9	44.6	42.4	86.0	28.0	88.9	112.0	99.4	287.6	162.4	214.0	181.5	259.9	42.4	181.5	4.3
209636_at	NFKB2	8.55E-04	52.8	43.9	50.2	69.3	83.7	46.5	84.6	79.9	80.9	152.4	117.2	169.7	213.8	193.4	52.8	152.4	2.9
201502_s_at	NFKBIA	5.66E-05	3048.0	2435.4	2358.1	2338.7	4113.8	2104.8	3631.1	5759.0	6347.1	7559.4	6121.2	7809.7	8091.0	8572.4	2435.4	7559.4	3.1
228388_at	NFKBIB	4.44E-03	133.5	95.8	148.8	124.3	131.7	97.2	137.7	164.6	151.6	229.7	151.7	152.8	202.8	202.6	131.7	164.6	1.2
203927_at	NFKBIE	1.46E-04	342.8	222.6	307.4	297.7	421.5	243.2	391.4	524.4	438.7	665.3	559.5	814.0	748.5	712.3	307.4	665.3	2.2
223217_s_at	NFKBIZ	1.53E-04	1040.1	701.2	820.1	999.7	961.3	623.0	1070.2	1582.3	2248.1	2955.1	1927.2	2414.1	2400.7	2968.6	961.3	2400.7	2.5
223218_s_at	NFKBIZ	1.18E-04	423.4	393.7	702.8	824.7	873.4	710.9	1077.1	956.0	1654.1	2609.9	1705.3	1749.0	1643.6	2230.5	710.9	1705.3	2.4
203045_at	NINJ1	9.97E-05	258.3	75.0	117.3	150.2	432.1	129.7	299.1	697.4	535.4	1045.0	595.9	1713.3	1657.9	1022.1	150.2	1022.1	6.8
209706_at	NKX3-1	9.17E-04	95.4	51.3	112.1	88.0	115.5	89.9	110.4	186.8	89.4	336.8	180.1	167.2	113.1	217.4	95.4	180.1	1.9
225943_at	NLN	4.07E-04	100.0	70.2	92.4	113.2	158.3	110.9	163.9	157.6	142.6	275.2	187.7	233.7	261.8	290.0	110.9	233.7	2.1
226474_at	NLRC5	6.17E-06	133.1	137.5	214.0	241.6	217.5	132.7	240.1	306.5	335.9	636.8	557.2	465.3	352.5	609.5	214.0	465.3	2.2
207075_at	NLRP3	2.78E-05	51.7	33.1	64.4	80.5	83.1	56.5	66.6	129.5	184.0	304.3	202.6	362.0	194.6	409.4	64.4	202.6	3.1
203964_at	NMI	2.08E-04	1465.2	1421.8	1549.8	1514.7	1677.9	1300.9	1500.3	1909.3	2767.3	3532.0	2759.4	2691.4	2435.7	2675.5	1500.3	2691.4	1.8
205895_s_at	NOLC1	3.84E-03	197.1	147.7	202.6	232.8	209.4	211.2	226.6	215.5	192.2	339.5	301.2	281.1	289.0	310.9	209.4	289.0	1.4

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
214011_s_at	NOP16	9.13E-03	424.6	292.0	428.1	410.5	417.9	393.3	493.8	504.8	370.5	585.9	544.3	462.7	596.5	555.4	417.9	544.3	1.3
213462_at	NPAS2	7.74E-04	39.6	54.0	37.0	48.3	37.2	46.1	58.1	48.4	81.4	83.3	72.2	71.3	74.2	97.7	46.1	74.2	1.6
210519_s_at	NQO1	2.50E-03	121.8	208.1	90.1	166.3	163.7	135.7	167.0	140.4	336.5	153.2	221.5	206.1	185.6	231.3	163.7	206.1	1.3
203920_at	NR1H3	4.91E-03	1972.8	1192.8	1349.1	1518.0	1707.4	952.3	1657.0	2289.3	1617.3	2324.0	2241.6	2707.3	2267.7	1954.9	1518.0	2267.7	1.5
202340_x_at	NR4A1	2.51E-04	52.9	37.6	62.0	62.8	74.9	66.6	74.3	75.3	59.7	88.8	87.8	116.2	101.4	105.2	62.8	88.8	1.4
204622_x_at	NR4A2	1.65E-03	39.7	39.9	37.4	46.3	46.8	47.1	40.1	54.3	60.9	87.4	72.6	58.8	71.5	58.1	40.1	60.9	1.5
207978_s_at	NR4A3	6.44E-05	18.3	31.2	36.5	22.4	34.5	24.9	22.6	50.6	52.9	142.3	54.2	73.1	74.5	74.9	24.9	73.1	2.9
209959_at	NR4A3	6.48E-05	108.5	79.6	92.3	68.9	134.1	89.0	91.2	188.4	268.6	432.5	184.8	343.0	242.9	352.3	91.2	268.6	2.9
202647_s_at	NRAS	6.78E-03	459.8	401.7	574.1	678.1	633.3	592.2	700.4	625.3	720.0	1129.0	900.9	672.6	722.0	966.3	592.2	722.0	1.2
204652_s_at	NRF1	8.36E-03	281.1	245.0	263.2	291.5	317.3	284.3	297.9	315.4	328.4	477.0	339.8	357.1	426.0	469.7	284.3	357.1	1.3
219557_s_at	NRIP3	1.27E-03	59.3	53.6	40.5	35.4	53.0	39.1	57.4	70.9	72.5	104.8	84.6	92.5	85.1	99.5	53.0	85.1	1.6
222900_at	NRIP3	2.43E-05	168.5	81.4	97.4	114.7	202.2	93.8	203.7	366.7	266.6	443.9	379.4	428.2	317.2	662.7	114.7	379.4	3.3
223298_s_at	NT5C3	4.31E-06	652.2	826.0	880.4	689.9	625.1	676.8	519.1	2363.7	4016.6	5745.8	3458.0	3271.4	2892.2	4136.7	676.8	3458.0	5.1
233072_at	NTNG2	1.71E-03	39.0	36.5	50.2	41.9	44.3	35.2	35.6	48.2	49.1	126.1	75.0	80.9	62.9	109.1	39.0	75.0	1.9
1557071_s_at	NUB1	7.94E-04	105.8	109.0	132.6	101.1	158.9	141.0	126.3	159.7	224.1	336.7	226.6	220.6	190.2	312.6	126.3	224.1	1.8
1569030_s_at	NUB1	9.26E-04	232.4	195.3	219.0	266.3	222.2	189.2	234.1	314.3	563.1	881.7	550.0	332.1	391.0	654.3	222.2	550.0	2.5
222512_at	NUB1	2.23E-04	2773.1	2737.4	2676.7	2142.9	2828.9	2539.5	2272.6	4148.8	3862.2	4374.8	3699.6	3986.6	3998.5	4290.3	2676.7	3998.5	1.5
234332_at	NUB1	1.12E-04	391.1	420.2	534.2	463.7	497.1	486.0	493.6	697.2	997.3	1580.9	1226.1	812.4	835.7	1230.6	486.0	997.3	2.1
225439_at	NUDCD1	2.76E-04	73.0	83.9	125.3	115.0	135.6	117.5	139.1	180.1	159.7	278.0	190.1	221.7	164.5	227.8	117.5	190.1	1.6
230462_at	NUMB	1.65E-03	70.0	62.2	75.9	69.9	88.9	82.6	83.0	94.0	84.8	125.9	90.0	119.5	112.1	102.8	75.9	102.8	1.4
212691_at	NUP188	5.84E-04	167.1	137.2	173.5	189.7	201.7	159.5	229.1	243.1	206.9	336.6	238.4	317.6	309.6	349.4	173.5	309.6	1.8
217601_at	NUP188	1.66E-04	92.1	99.6	129.0	131.7	117.4	127.0	156.7	164.1	141.0	292.9	211.0	203.1	222.9	252.5	127.0	211.0	1.7
212247_at	NUP205	7.15E-04	222.3	237.9	252.8	261.5	284.2	257.9	293.5	345.5	336.7	436.1	344.9	362.3	394.4	412.1	257.9	362.3	1.4
222382_x_at	NUP205	7.95E-03	67.8	57.7	58.1	57.2	58.1	51.5	60.0	78.9	68.6	73.9	63.6	73.1	73.1	83.4	58.1	73.1	1.3
202153_s_at	NUP62	6.56E-05	429.9	378.2	528.0	503.1	673.9	435.0	608.8	937.8	670.0	997.2	892.7	1027.0	888.3	986.6	503.1	937.8	1.9
207740_s_at	NUP62	4.03E-03	133.4	85.8	100.4	124.1	124.8	94.5	128.7	155.3	116.9	176.1	150.1	292.0	231.2	211.5	124.1	176.1	1.4
236505_at	NUP62	5.34E-04	59.6	39.5	75.3	87.1	94.5	58.4	78.4	118.9	78.4	220.4	169.6	120.1	136.8	120.9	75.3	120.9	1.6
203194_s_at	NUP98	3.97E-03	219.1	174.7	220.5	244.9	266.6	229.3	286.0	346.9	238.4	348.7	326.2	376.1	309.0	292.7	229.3	326.2	1.4
210793_s_at	NUP98	6.75E-03	172.8	180.3	272.3	259.8	359.0	269.7	368.2	313.1	272.4	671.8	432.3	362.4	355.8	485.0	269.7	362.4	1.3
202869_at	OAS1	4.29E-04	1133.6	594.7	1061.0	981.2	1067.3	488.2	441.7	1559.0	992.1	2271.4	1549.6	1876.1	747.6	1094.6	981.2	1549.6	1.6
205552_s_at	OAS1	2.23E-04	2532.3	2443.3	2024.3	2019.4	1986.7	1453.2	1450.9	3563.7	4523.1	4445.2	3456.9	4016.5	3656.4	4251.4	2019.4	4016.5	2.0
204972_at	OAS2	2.40E-04	1324.4	1658.9	1372.7	1318.8	1004.8	911.4	1177.1	1813.7	2981.5	3688.4	2700.5	2031.7	2394.5	3608.2	1318.8	2700.5	2.0
206553_at	OAS2	6.65E-05	263.8	278.8	211.5	213.6	162.6	191.7	184.5	429.2	569.5	761.8	554.8	468.8	498.0	608.4	211.5	554.8	2.6
228607_at	OAS2	1.02E-04	319.2	431.4	260.8	367.9	359.9	420.5	189.1	673.0	671.2	718.2	740.7	729.1	957.0	623.3	359.9	718.2	2.0
218400_at	OAS3	1.08E-04	1502.7	1608.5	1292.7	1266.5	994.7	831.0	906.5	2561.7	3684.3	4269.3	3110.4	2731.1	3079.1	4449.7	1266.5	3110.4	2.5
232666_at	OAS3	2.67E-04	45.1	35.5	35.5	45.2	34.8	35.5	39.7	60.1	67.4	101.0	77.6	93.8	81.1	96.1	35.5	81.1	2.3
205660_at	OASL	1.99E-04	847.8	1235.6	405.5	495.7	570.2	569.2	606.8	1599.4	2314.7	2734.7	1652.7	2317.2	2011.7	2453.1	570.2	2314.7	4.1
210797_s_at	OASL	2.90E-04	588.9	783.2	292.8	431.1	339.1	359.3	400.9	1035.5	1658.2	2034.2	1186.9	1757.1	2062.6	1878.5	400.9	1757.1	4.4
201364_s_at	OAZ2	6.58E-05	222.3	201.4	223.0	221.9	283.0	184.1	291.3	411.2	385.6	636.3	427.2	492.0	489.5	582.2	222.3	489.5	2.2
201365_at	OAZ2	5.90E-04	1008.5	849.7	919.1	752.9	1054.0	829.9	1187.5	1408.2	1125.0	1352.7	1233.6	1557.7	1392.9	1539.7	919.1	1392.9	1.5
219334_s_at	OBFC2A	2.93E-03	95.0	126.0	202.1	203.2	205.7	188.8	246.8	163.3	158.8	467.8	307.5	315.1	253.0	300.9	202.1	300.9	1.5
222872_x_at	OBFC2A	9.86E-03	498.2	714.4	1009.9	1004.3	1159.1	1167.1	1259.5	792.1	1220.7	1794.9	1351.7	1205.2	1309.3	1534.6	1009.9	1309.3	1.3
233085_s_at	OBFC2A	8.14E-03	1641.7	1966.1	2191.1	2254.0	2402.0	2412.6	2664.7	2017.0	2913.1	3743.7	2869.2	2713.2	2884.0	3234.7	2254.0	2884.0	1.3
230926_s_at	ODF2L	1.71E-03	46.6	35.5	75.2	62.7	55.8	59.6	56.0	86.1	66.8	96.3	90.1	76.6	76.3	76.2	56.0	76.6	1.4
219582_at	OGFRL1	1.06E-03	363.7	589.9	530.4	519.9	689.2	596.7	516.3	863.7	903.7	1384.3	770.6	1151.8	758.1	938.1	530.4	903.7	1.7
228170_at	OLIG1	9.39E-05	15.5	17.5	8.6	9.2	5.8	7.9	13.0	78.7	51.1	78.7	50.0	129.4	44.3	68.9	9.2	68.9	7.5
213825_at	OLIG2	2.19E-04	57.3	40.1	29.0	40.1	33.3	31.9	32.3	76.4	70.4	50.7	58.8	70.4	57.8	58.7	33.3	58.8	1.8
229944_at	OPRK1	7.96E-04	35.3	37.3	21.0	16.9	94.5	50.4	66.8	91.0	95.2	106.8	97.4	137.8	170.5	118.9	37.3	106.8	2.9
202073_at	OPTN	1.11E-04	256.2	188.8	596.2	385.1	305.2	210.7	443.7	546.2	689.0	1620.2	1001.5	543.9	695.1	770.1	305.2	695.1	2.3
202074_s_at	OPTN	3.94E-04	2986.5	1134.7	2091.3	1592.4	2467.1	992.0	2596.1	4312.6	5166.3	7250.3	4566.2	4966.8	4996.9	6397.7	2091.3	4996.9	2.4
230170_at	OSM	5.93E-05	91.4	53.3	128.9	83.6	167.8	80.6	146.7	241.9	513.6	1278.5	243.6	831.8	469.1	1026.4	91.4	513.6	5.6
238998_x_at	OTUD1	8.56E-03	71.0	52.8	75.8	84.3	92.6	53.5	89.6	91.7	65.5	119.4	82.3	148.7	118.0	141.3	75.8	118.0	1.6
203479_s_at	OTUD4	1.51E-03	875.2	697.2	762.3	758.0	839.3	637.5	912.7	1207.7	947.8	1308.5	873.3	1269.4	1072.7	1249.9	762.3	1207.7	1.6
238848_at	OTUD4	4.41E-03	653.7	539.0	602.1	580.1	671.9	607.4	645.9	769.0	786.7	1134.6	828.4	800.5	764.7	880.9	607.4	800.5	1.3
204088_at	P2RX4	4.59E-04	528.1	432.5	436.0	557.2	639.9	489.5	665.4	854.0	612.9	977.6	832.1	1485.6	1283.2	1137.7	528.1	977.6	1.9
207091_at	P2RX7	9.77E-04	290.3	188.1	229.6	267.1	345.0	181.0	371.3	398.8	387.5	689.9	456.6	1034.1	938.2	842.8	267.1	689.9	2.6
206277_at	P2RY2	8.01E-05	29.7	14.2	25.4	21.2	33.8	22.5	45.5	50.0	31.7	62.4	47.4	140.6	60.7	128.9	25.4	60.7	2.4
208373_s_at	P2RY6	4.85E-03	77.4	62.8	65.2	57.6	76.3	56.9	74.9	103.5	61.5	101.5	89.2	108.6	75.5	124.0	65.2	101.5	1.6
202760_s_at	PALM2-AKAP2	9.43E-05	362.7	107.6	128.0	175.2	239.6	339.1	1457.7	1309.0	1832.6	2672.1	1227.3	1443.4	2569.3	5097.7	239.6	1832.6	7.6
202336_s_at	PAM	4.05E-03	431.2	443.0	596.4	574.2	571.1	438.4	639.9	667.3	721.2	854.5	735.1	645.4	607.4	738.9	571.1	721.2	1.3
228965_s_at	PANK2	5.27E-04	95.5	117.6	147.8	145.9	153.1	158.5	137.3	158.6	160.3	235.2	230.1	210.5	207.7	192.7	145.9	207.7	1.4
238856_s_at	PANK2	5.58E-03	104.1	96.1	162.2	156.0	147.8	186.2	172.7	178.5	179.6	352.7	243.5	189.4	186.1	228.9	156.0	189.4	1.2
204715_at	PANX1	4.79E-05	232.6	217.8	213.5	228.9	262.0	226.6	285.4	425.5	757.5	830.4	497.4	597.0	622.5	811.9	228.9	622.5	2.7
226843_s_at	PAPD5	3.69E-04	244.9	310.3	370.0	336.6	312.4	360.6	309.1	387.4	444.2	623.7	438.1	511.3	513.8	570.5	312.4	511.3	1.6
228669_x_at	PARP10	2.36E-03	76.7	54.3	96.8	97.5	79.6	80.5	81.0	91.6	83.1	142.7	112.3	161.3	140.7	133.7	80.5	133.7	1.7

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
229350_x_at	PARP10	2.05E-04	349.7	384.3	423.6	438.2	422.4	362.0	417.9	504.5	647.5	819.2	634.0	633.2	676.9	835.8	417.9	647.5	1.5
220315_at	PARP11	1.15E-03	188.8	203.2	171.6	203.7	178.3	197.9	168.6	280.7	302.8	485.3	307.4	344.7	269.4	329.9	188.8	307.4	1.6
229138_at	PARP11	4.93E-03	239.6	283.0	351.3	336.9	293.3	307.7	367.7	310.4	432.7	593.2	540.8	340.6	367.6	434.3	307.7	432.7	1.4
218543_s_at	PARP12	5.57E-04	1732.3	1872.7	1631.7	1585.0	1671.9	1576.8	1695.7	2410.4	2395.1	2804.8	2136.4	2512.1	2454.9	2655.9	1671.9	2454.9	1.5
224701_at	PARP14	5.15E-04	3310.8	3491.2	3139.5	2843.7	2906.0	2490.3	2933.8	4227.8	5318.6	7131.0	4788.0	4619.6	5493.8	6253.3	2933.8	5318.6	1.8
232610_at	PARP14	8.61E-06	226.6	255.2	209.0	240.3	267.7	182.3	236.2	520.6	723.0	914.3	861.0	799.8	645.8	948.2	236.2	799.8	3.4
223220_s_at	PARP9	2.11E-04	2431.7	2914.5	2365.4	2139.4	1926.4	2062.4	2208.7	3249.5	4297.8	4844.2	4001.9	3278.3	3734.0	4461.5	2208.7	4001.9	1.8
227807_at	PARP9	3.32E-04	179.2	167.8	179.7	179.6	171.8	147.5	155.1	259.3	213.4	357.2	304.5	288.0	260.9	309.6	171.8	288.0	1.7
225466_at	PATL1	3.10E-03	227.1	256.3	285.9	285.4	306.2	240.7	325.8	385.3	311.4	459.9	378.4	350.5	378.1	424.4	285.4	378.4	1.3
225468_at	PATL1	9.56E-03	345.6	398.8	688.6	627.8	561.6	549.9	835.7	612.8	786.7	1315.0	803.2	650.1	635.0	942.5	561.6	786.7	1.4
235234_at	PATL1	4.65E-03	1226.4	880.8	1056.1	1210.2	978.3	797.5	1098.6	1333.7	1368.7	1778.0	1405.9	1298.8	1563.3	1693.8	1056.1	1405.9	1.3
235235_s_at	PATL1	1.49E-03	1332.5	1123.4	1145.9	1043.5	994.8	818.2	1094.7	1493.7	1626.4	1946.2	1381.2	1700.9	1599.6	1866.8	1094.7	1626.4	1.5
244342_at	PATL1	2.47E-04	170.7	195.2	270.2	202.3	201.8	228.0	228.4	268.5	363.8	582.5	322.4	305.2	315.0	401.9	202.3	322.4	1.6
230536_at	PBX4	9.05E-03	77.3	61.5	71.0	85.8	73.9	80.5	74.8	84.4	95.2	96.4	113.6	89.0	89.2	102.8	74.8	95.2	1.3
229194_at	PCGF5	4.52E-03	294.2	430.5	607.6	517.6	568.7	653.1	587.4	542.4	781.1	1371.6	838.4	721.3	646.9	873.6	568.7	781.1	1.4
229996_s_at	PCGF5	2.95E-04	367.0	356.2	426.5	416.1	391.7	341.1	316.2	594.2	512.8	728.3	583.8	573.3	528.8	635.7	367.0	583.8	1.6
213159_at	PCNX	2.89E-04	570.1	405.5	435.9	396.9	662.8	513.3	525.4	746.5	740.4	984.0	658.4	1082.1	1209.0	1112.9	513.3	984.0	1.9
206474_at	PCTK2	6.56E-03	183.4	148.6	213.5	229.5	210.2	190.8	215.7	211.6	218.0	323.7	272.0	255.7	243.3	259.7	210.2	255.7	1.2
219275_at	PDCD5	3.92E-03	1035.8	672.1	669.0	790.7	907.5	716.8	907.5	1112.6	1134.1	1172.0	1059.3	1054.5	1258.4	1570.3	790.7	1134.1	1.4
203708_at	PDE4B	7.13E-05	152.2	157.9	305.4	197.7	464.1	187.1	358.8	441.4	932.1	1781.0	864.0	855.7	972.3	1187.2	197.7	932.1	4.7
211302_s_at	PDE4B	2.27E-05	136.5	120.5	222.0	166.9	296.2	151.7	229.6	358.4	721.9	1345.0	613.7	770.9	714.3	918.4	166.9	721.9	4.3
204491_at	PDE4D	4.49E-03	40.7	41.4	35.1	52.3	41.8	42.9	43.6	46.4	46.5	79.4	94.7	69.4	78.5	131.1	41.8	78.5	1.9
205872_x_at	PDE4DIP	6.95E-03	3954.1	4032.3	2083.7	3337.0	4474.0	1374.7	2740.9	3951.1	5418.3	3354.3	4578.0	5702.5	2858.3	4365.5	3337.0	4365.5	1.3
210305_at	PDE4DIP	8.95E-04	106.8	68.3	245.5	57.2	276.4	144.5	117.1	185.5	83.6	619.6	103.7	393.5	305.1	194.2	117.1	194.2	1.7
212390_at	PDE4DIP	1.64E-03	202.0	186.4	133.8	165.6	279.2	124.4	207.6	267.0	278.7	350.9	294.3	369.6	251.5	309.0	186.4	294.3	1.6
214099_s_at	PDE4DIP	9.80E-03	146.3	202.9	122.2	138.1	211.0	110.6	152.0	188.9	225.2	262.7	183.5	233.2	181.8	223.3	146.3	223.3	1.5
214129_at	PDE4DIP	9.51E-03	1636.1	1757.0	1201.8	1334.2	2079.9	1185.5	1559.7	1917.3	1961.4	2118.4	1929.1	2281.9	1776.5	2093.0	1559.7	1961.4	1.3
214130_s_at	PDE4DIP	2.15E-03	360.0	382.3	312.1	347.3	486.5	292.1	355.6	558.9	409.2	492.6	486.4	700.8	481.1	470.9	355.6	486.4	1.4
232509_at	PDE4DIP	1.69E-03	66.7	67.0	65.9	62.2	98.2	67.7	69.7	87.3	86.3	115.7	98.9	125.1	85.7	107.8	67.0	98.9	1.5
205463_s_at	PDGFA	1.53E-03	97.1	82.5	65.9	79.1	97.1	60.6	80.2	161.0	111.8	113.6	116.6	293.9	91.8	202.8	80.2	116.6	1.5
205226_at	PDGFRL	4.47E-06	40.7	35.3	40.5	22.2	25.4	36.1	38.2	222.4	462.0	534.5	309.1	414.3	237.9	461.5	36.1	414.3	11.5
203242_s_at	PDLIM5	8.43E-04	289.2	256.3	308.1	297.1	330.8	274.3	351.2	471.1	381.6	717.8	437.0	506.5	479.6	449.7	297.1	471.1	1.6
211681_s_at	PDLIM5	3.24E-03	456.6	280.9	347.1	384.2	474.5	367.5	492.5	524.1	435.5	662.2	524.4	625.9	834.9	710.5	384.2	625.9	1.6
213684_s_at	PDLIM5	9.83E-04	26.7	18.5	34.2	39.4	73.2	46.9	53.3	60.9	30.6	88.0	99.2	105.9	84.8	65.3	39.4	84.8	2.2
216804_s_at	PDLIM5	6.11E-04	382.4	334.1	377.2	378.8	485.5	347.4	446.6	659.1	590.5	1037.2	620.5	652.1	687.5	677.6	378.8	659.1	1.7
1569150_x_at	PDLIM7	7.41E-04	73.5	43.1	58.3	63.7	85.1	53.9	69.2	127.5	65.8	93.5	129.2	114.5	111.2	87.9	63.7	111.2	1.7
214121_x_at	PDLIM7	7.32E-03	99.6	75.5	84.0	87.4	96.7	86.1	129.4	120.0	107.5	109.7	124.8	190.5	165.6	134.9	87.4	124.8	1.4
220865_s_at	PDSS1	1.02E-04	180.5	181.2	269.6	249.4	287.1	245.7	300.9	393.6	280.0	494.0	381.8	472.2	410.0	574.4	249.4	410.0	1.6
218018_at	PDXK	6.13E-03	1598.1	1325.6	1273.4	1236.4	1274.1	928.1	1568.3	1670.6	1779.3	1986.4	1719.5	1765.6	1721.2	1886.2	1274.1	1765.6	1.4
200787_s_at	PEA15	5.15E-04	927.9	800.4	778.7	904.8	1093.3	589.7	815.5	1338.8	1051.0	1278.3	1315.5	1716.0	1239.8	1464.0	815.5	1315.5	1.6
218319_at	PELI1	5.41E-04	153.7	189.8	201.4	191.2	196.9	210.5	166.6	236.3	609.2	1308.7	378.4	462.4	692.9	748.6	191.2	609.2	3.2
232213_at	PELI1	3.61E-03	44.5	53.4	33.9	36.7	29.1	43.5	41.5	49.6	107.0	187.4	56.7	79.1	88.9	97.2	41.5	88.9	2.1
232304_at	PELI1	3.16E-04	54.4	63.7	81.5	60.7	67.1	67.7	54.3	95.9	200.3	495.4	112.9	185.9	165.8	198.4	63.7	185.9	2.9
202464_s_at	PFKFB3	5.36E-04	1584.0	2002.6	2479.0	2010.7	2588.4	2058.0	2939.6	2167.1	3857.8	4307.5	2673.8	3627.5	3136.4	5087.5	2058.0	3627.5	1.8
201037_at	PFKP	1.43E-03	1694.5	1179.0	932.0	1062.7	653.2	631.0	647.1	2056.5	1463.4	1955.7	1614.2	1261.1	1331.4	1407.7	932.0	1463.4	1.6
204604_at	PFTK1	2.29E-03	587.1	597.2	865.0	755.6	751.9	859.5	920.7	940.8	990.5	1254.1	1075.1	953.0	1008.9	1142.5	755.6	1008.9	1.3
211502_s_at	PFTK1	6.80E-04	356.3	287.9	390.1	399.6	364.7	408.6	425.1	538.2	496.7	777.4	580.9	465.9	562.3	671.9	390.1	562.3	1.4
243761_at	PFTK1	1.50E-03	30.5	12.8	30.5	24.6	48.7	30.5	97.7	62.4	51.1	285.5	82.5	78.3	90.8	180.8	30.5	82.5	2.7
244321_at	PGAP1	1.61E-03	48.9	50.0	35.8	37.5	44.2	27.1	37.1	67.4	55.3	76.2	97.0	73.1	62.7	81.5	37.5	73.1	2.0
204047_s_at	PHACTR2	2.33E-04	254.3	255.9	333.6	328.5	352.4	315.2	326.3	405.3	426.2	674.5	469.4	549.4	447.5	526.0	326.3	469.4	1.4
204048_s_at	PHACTR2	8.28E-04	244.0	327.7	412.3	401.4	425.0	411.6	419.7	587.0	539.9	844.3	729.0	555.9	558.3	651.5	411.6	587.0	1.4
204049_s_at	PHACTR2	4.68E-03	143.5	190.7	256.1	265.7	289.4	292.0	297.7	281.0	345.7	536.2	421.9	320.2	317.5	434.6	265.7	345.7	1.3
244774_at	PHACTR2	9.60E-03	97.8	124.5	262.4	229.4	229.2	220.9	217.8	183.1	229.8	600.4	280.2	220.1	302.3	299.9	220.9	280.2	1.3
219235_s_at	PHACTR4	6.24E-04	84.6	88.5	111.3	73.6	114.4	94.7	105.7	160.3	123.2	281.3	146.0	159.5	138.9	199.9	94.7	159.5	1.7
226823_at	PHACTR4	1.02E-03	403.9	377.0	468.8	503.2	523.3	351.9	492.9	627.8	707.3	1175.8	762.8	683.2	488.3	908.5	468.8	707.3	1.5
221816_s_at	PHF11	2.64E-04	793.4	708.6	890.7	821.7	887.3	816.3	796.4	1101.9	1270.8	2087.0	1651.8	1389.9	1243.6	1532.0	816.3	1389.9	1.7
212660_at	PHF15	4.69E-03	219.5	272.7	324.7	248.3	289.2	325.6	204.3	393.0	323.7	421.7	397.0	360.0	381.8	376.6	272.7	381.8	1.4
232279_at	PHF15	6.02E-04	86.5	88.4	75.8	65.0	73.7	61.2	60.2	140.8	113.2	148.5	109.5	113.4	124.2	157.2	73.7	124.2	1.7
204866_at	PHF16	6.35E-03	57.5	58.1	59.9	54.0	79.6	58.1	71.8	90.0	79.4	138.4	76.4	84.2	88.7	91.3	58.1	88.7	1.5
1554472_a_at	PHF20L1	2.05E-03	35.3	46.0	55.5	43.8	55.1	38.4	43.8	50.3	61.5	80.0	67.1	59.7	57.8	60.1	43.8	60.1	1.4
209802_at	PHLDA2	5.08E-03	113.0	106.4	114.4	122.8	116.7	103.0	110.6	152.4	136.7	151.4	132.7	236.7	162.7	160.0	113.0	152.4	1.3
209803_s_at	PHLDA2	1.46E-04	63.1	63.0	65.2	42.4	86.6	39.4	69.8	102.7	153.0	261.5	174.3	182.0	132.8	169.8	63.1	169.8	2.7
229494_s_at	PHLDA2	8.98E-06	25.6	22.0	30.1	30.1	46.0	29.6	30.1	56.8	77.5	134.0	95.0	133.6	91.4	91.4	30.1	91.4	3.0
215285_s_at	PHTF1	7.13E-03	115.8	117.0	155.0	142.3	129.2	141.2	137.6	173.8	148.4	230.4	206.5	142.9	152.1	183.5	137.6	173.8	1.3
203691_at	PI3	1.81E-04	72.6	46.9	54.4	77.6	104.6	55.1	62.4	227.0	482.5	1725.5	285.5	1023.8	805.2	1878.1	62.4	805.2	12.9
41469_at	PI3	9.31E-05	45.2	20.6	24.9	30.1	58.8	24.4	29.2	159.1	315.7	1367.7	231.3	812.1	509.0	1356.2	29.2	509.0	17.4

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
222631_at	PI4K2B	2.97E-05	1121.8	1097.2	1107.9	1080.1	1420.6	1206.9	1528.7	2280.1	2904.3	4145.2	3011.5	2768.7	2900.8	3682.4	1121.8	2904.3	2.6
219093_at	PID1	1.39E-04	21.1	27.7	15.5	17.3	41.2	10.4	26.8	62.1	45.9	109.1	77.6	163.5	44.0	186.9	21.1	77.6	3.7
237867_s_at	PID1	5.75E-03	51.3	61.8	40.5	44.6	38.6	38.9	44.9	63.5	61.8	68.5	55.7	71.0	69.2	77.3	44.6	68.5	1.5
205077_s_at	PIGF	3.29E-03	1349.9	1328.0	1470.6	1406.3	1746.6	1441.7	1540.7	1850.7	1727.6	2064.8	1814.9	1975.6	1899.8	1924.6	1441.7	1899.8	1.3
219238_at	PIGV	3.46E-04	149.9	168.4	219.3	203.5	268.5	250.9	243.1	359.8	300.4	499.6	339.0	359.5	473.1	371.7	219.3	359.8	1.6
51146_at	PIGV	2.30E-03	69.3	74.1	100.9	83.7	137.9	129.8	121.7	148.5	100.6	227.6	181.6	167.5	203.7	157.6	100.9	167.5	1.7
1554508_at	PIK3AP1	8.59E-05	431.2	298.2	416.9	563.7	597.5	345.7	720.5	854.0	919.2	1342.3	1102.4	1207.3	1154.7	1369.5	431.2	1154.7	2.7
226459_at	PIK3AP1	1.20E-03	3238.9	2403.4	3342.7	3238.5	3926.1	2893.8	4187.1	4205.5	5127.5	6161.4	5018.1	4949.4	5135.1	5912.1	3238.9	5127.5	1.6
220566_at	PIK3R5	2.46E-03	429.8	208.2	329.8	344.8	370.1	271.9	406.3	445.1	426.4	620.9	476.8	643.3	632.7	620.6	344.8	620.6	1.8
227553_at	PIK3R5	3.09E-04	981.1	697.7	738.5	773.6	1148.6	671.7	968.5	1395.3	1253.0	1482.7	1135.6	1597.2	1324.4	1606.8	773.6	1395.3	1.8
227645_at	PIK3R5	5.16E-03	2389.2	1507.3	1549.4	1568.0	2297.8	1331.9	1873.3	2451.1	2492.7	2957.6	2329.5	2638.6	2772.8	3036.2	1568.0	2638.6	1.7
219788_at	PILRA	1.45E-03	1622.9	1680.1	1275.7	1658.0	1887.7	1251.6	1506.3	2434.9	1991.1	2315.5	2167.3	3216.7	2651.0	2259.7	1622.9	2315.5	1.4
204269_at	PIM2	4.60E-04	71.2	61.8	82.3	89.2	77.2	83.3	72.4	112.8	160.5	298.6	189.8	114.9	194.3	270.4	77.2	189.8	2.5
224739_at	PIM3	2.09E-03	563.3	328.0	616.8	585.1	775.2	421.5	917.5	797.8	1182.5	1386.1	895.4	1098.8	1151.2	1450.0	585.1	1151.2	2.0
207391_s_at	PIP5K1A	4.34E-03	195.5	193.2	275.1	227.9	255.3	255.0	269.6	274.3	323.2	409.2	324.7	276.7	300.6	358.5	255.0	323.2	1.3
210256_s_at	PIP5K1A	6.63E-03	207.7	191.4	219.2	213.7	269.9	292.0	270.0	300.3	231.6	382.5	337.0	393.4	293.0	350.1	219.2	337.0	1.5
211205_x_at	PIP5K1A	2.46E-03	169.9	162.9	206.3	202.3	252.4	239.9	241.8	298.4	221.6	329.1	296.9	308.6	287.6	312.8	206.3	298.4	1.4
207469_s_at	PIR	1.39E-03	128.9	103.5	115.8	157.8	164.8	95.0	162.1	230.0	150.1	298.4	206.6	244.7	191.1	228.8	128.9	228.8	1.8
201190_s_at	PITPNA	2.12E-03	629.0	674.2	585.5	639.8	801.9	680.5	824.5	933.8	831.6	1041.7	988.6	1032.9	883.6	1046.8	674.2	988.6	1.5
201191_at	PITPNA	8.12E-03	491.1	546.9	417.6	472.7	557.5	456.5	563.3	754.1	504.7	649.5	659.1	702.9	761.0	797.7	491.1	702.9	1.4
201192_s_at	PITPNA	1.05E-03	1097.9	952.1	714.3	823.5	851.3	659.4	805.6	1201.7	1660.4	1579.1	1349.9	1613.4	1771.7	1883.9	823.5	1613.4	2.0
219584_at	PLA1A	2.53E-04	212.6	274.6	180.8	171.7	184.0	188.2	279.7	359.0	611.3	528.3	420.6	278.5	317.6	499.4	188.2	420.6	2.2
210145_at	PLA2G4A	1.08E-05	452.9	629.2	697.9	765.4	1057.0	982.0	984.9	1540.3	3601.8	6235.1	3718.6	3468.4	4663.0	4631.6	765.4	3718.6	4.9
206214_at	PLA2G7	4.59E-04	502.5	196.2	366.6	350.7	379.3	88.0	1000.7	1050.0	1106.8	3337.8	1918.0	1149.7	1179.7	2372.3	366.6	1179.7	3.2
219014_at	PLAC8	5.68E-04	701.1	248.5	2843.8	446.5	370.8	3363.9	2474.1	2329.3	1039.9	6479.2	2284.5	1433.7	4729.0	4542.1	701.1	2329.3	3.3
202924_s_at	PLAGL2	6.17E-06	181.6	115.6	177.3	138.8	213.7	143.6	210.3	407.1	371.7	548.8	396.6	588.1	544.0	581.8	177.3	544.0	3.1
202925_s_at	PLAGL2	2.00E-05	132.3	85.0	193.8	150.7	227.1	120.3	224.6	319.6	334.2	609.2	418.8	474.0	448.5	551.2	150.7	448.5	3.0
210845_s_at	PLAUR	1.51E-04	4561.7	3686.9	4849.3	4979.2	5938.5	4501.3	6396.3	6712.9	7572.5	9588.9	8150.6	9121.3	7956.2	9757.9	4849.3	8150.6	1.7
211924_s_at	PLAUR	2.26E-03	2337.4	1333.5	1859.6	2321.5	1982.1	1445.2	2625.0	2524.2	3090.6	3937.1	3049.3	4362.1	4337.4	4754.0	1982.1	3937.1	2.0
214866_at	PLAUR	2.86E-04	766.1	595.2	757.3	831.6	959.0	763.8	1181.7	1172.1	1000.1	1356.7	1153.0	1457.8	1345.8	1590.3	766.1	1345.8	1.8
177_at	PLD1	8.06E-03	189.5	160.8	209.8	216.5	237.6	202.6	245.0	258.9	171.5	342.7	259.6	346.4	232.5	343.0	209.8	259.6	1.2
205203_at	PLD1	1.49E-03	365.6	309.3	437.7	375.9	448.0	358.3	517.5	470.8	434.6	705.1	476.7	596.8	467.3	693.4	375.9	476.7	1.3
203470_s_at	PLEK	7.60E-04	1926.1	1033.6	1697.5	1608.8	2761.5	1377.1	2330.4	2620.0	2682.1	5282.0	2971.1	3968.3	2911.9	4274.9	1697.5	2971.1	1.8
203471_s_at	PLEK	6.95E-04	1637.0	1336.0	1957.1	1919.2	2964.9	1736.2	2569.0	2850.4	3249.9	5583.0	3734.3	3708.6	3308.3	4008.9	1919.2	3708.6	1.9
219011_at	PLEKHA4	1.16E-04	35.8	32.4	54.6	54.8	52.1	48.1	56.9	74.5	71.6	204.1	85.0	119.2	146.9	156.8	52.1	119.2	2.3
218640_s_at	PLEKHF2	4.40E-03	316.6	297.7	480.8	424.9	530.0	442.5	537.3	426.8	563.4	992.3	664.7	582.1	544.2	764.1	442.5	582.1	1.3
222699_s_at	PLEKHF2	1.18E-03	183.9	206.5	287.3	248.3	337.6	257.5	320.8	256.9	376.7	665.0	455.9	444.1	331.6	533.8	257.5	444.1	1.7
233986_s_at	PLEKHG2	4.50E-03	70.3	56.5	55.6	54.1	57.4	38.5	68.6	81.4	62.8	106.4	82.3	123.6	102.8	112.8	56.5	102.8	1.8
218223_s_at	PLEKHO1	1.61E-04	202.3	159.1	148.3	215.8	213.3	110.3	165.8	350.7	312.5	414.0	468.9	600.9	514.6	573.9	165.8	468.9	2.8
204958_at	PLK3	8.02E-04	61.7	45.8	60.9	70.7	67.5	57.0	88.6	107.1	74.8	182.2	95.4	169.4	166.8	146.7	61.7	146.7	2.4
215462_at	PLK3	3.39E-03	106.6	72.4	118.2	99.7	120.7	101.7	111.0	124.0	141.6	299.7	154.4	148.9	144.1	221.4	106.6	148.9	1.4
229825_at	PLK3	1.19E-03	71.4	60.1	64.4	69.0	84.1	62.4	94.4	103.2	84.5	178.9	113.5	142.8	174.7	154.4	69.0	142.8	2.1
202430_s_at	PLSCR1	3.06E-03	444.4	412.5	689.8	801.6	781.4	675.5	1044.2	669.9	932.0	2008.0	1460.8	980.9	966.6	1378.5	689.8	980.9	1.4
202446_s_at	PLSCR1	2.89E-04	2611.0	2278.1	2545.4	2645.8	2928.3	1967.8	2937.1	3559.5	4511.1	5856.1	4740.0	4209.0	4251.3	5195.2	2611.0	4511.1	1.7
1558140_at	PLXNA1	8.82E-03	101.7	76.9	111.0	107.8	116.1	72.6	126.2	115.2	98.6	194.1	126.4	175.9	179.2	172.5	107.8	172.5	1.6
221537_at	PLXNA1	6.76E-04	184.2	124.1	185.1	177.6	229.0	114.5	209.2	269.8	284.2	430.4	266.1	330.6	322.9	374.0	184.2	322.9	1.8
206470_at	PLXNC1	7.41E-03	55.6	46.3	35.2	43.2	51.5	45.5	43.2	69.2	50.7	81.4	57.5	94.5	57.2	93.0	45.5	69.2	1.5
206471_s_at	PLXNC1	2.14E-05	19.4	17.2	29.7	42.0	30.9	25.0	23.3	45.9	38.6	69.3	71.6	59.8	57.1	63.2	25.0	59.8	2.4
213241_at	PLXNC1	1.59E-04	36.8	37.2	46.1	49.2	64.0	49.0	49.5	75.1	72.3	143.6	89.5	113.8	79.4	133.6	49.0	89.5	1.8
204285_s_at	PMAIP1	1.32E-04	108.2	76.3	104.7	93.6	93.8	87.1	112.8	172.7	228.6	487.2	196.1	286.9	229.5	297.2	93.8	229.5	2.4
206503_x_at	PML	6.65E-05	152.2	114.2	149.9	157.8	142.8	124.4	163.3	264.0	246.2	451.2	274.9	329.1	373.8	381.4	149.9	329.1	2.2
209640_at	PML	1.45E-05	32.4	32.9	40.9	40.3	44.8	42.1	40.8	66.0	98.1	135.2	98.3	97.5	99.8	125.1	40.8	98.3	2.4
210362_x_at	PML	1.89E-03	55.5	27.5	50.0	63.6	49.9	38.1	57.6	62.8	63.3	96.8	79.7	114.1	102.4	106.0	50.0	96.8	1.9
211013_x_at	PML	5.69E-05	143.7	96.7	144.2	153.7	141.4	125.3	156.7	248.7	252.3	443.2	274.6	287.9	330.0	361.8	143.7	287.9	2.0
235508_at	PML	1.60E-04	330.6	265.5	277.2	284.8	296.5	294.7	271.7	494.4	775.5	1299.8	654.5	819.9	818.9	1053.7	284.8	818.9	2.9
239582_at	PML	2.95E-04	61.9	59.5	49.8	58.0	60.9	68.0	66.9	114.8	85.6	168.2	102.9	133.2	134.4	142.9	60.9	133.2	2.2
233177_s_at	PNKD	4.91E-04	53.3	41.3	65.9	39.2	53.6	25.6	64.4	85.5	61.7	96.8	62.2	118.4	56.9	93.1	53.3	85.5	1.6
1553364_at	PNPLA1	8.45E-04	23.3	21.4	29.4	42.1	73.9	27.5	61.6	77.4	54.1	166.6	165.5	96.9	123.5	107.9	29.4	107.9	3.7
223309_x_at	PNPLA8	2.66E-03	491.6	608.7	676.0	581.6	731.5	608.5	698.7	670.9	736.5	936.5	821.2	864.5	804.9	891.1	608.7	821.2	1.3
225291_at	PNPT1	1.03E-05	342.8	273.6	296.3	305.1	262.0	267.1	295.5	947.5	1737.4	2327.6	1208.6	1566.1	1399.0	1939.6	295.5	1566.1	5.3
209034_at	PNRC1	2.31E-03	616.6	497.6	807.0	667.2	1124.7	641.7	1050.5	1000.1	1050.9	1565.1	1164.9	1223.4	1303.8	1282.4	667.2	1223.4	1.8
222406_s_at	PNRC2	7.00E-04	445.8	470.0	462.9	599.5	543.0	467.7	537.5	577.2	794.8	1148.3	864.2	980.6	845.8	833.4	470.0	845.8	1.8
201578_at	PODXL	5.73E-03	69.4	91.8	91.7	114.8	79.6	89.7	71.5	91.0	115.7	119.5	125.0	106.2	124.7	85.6	89.7	115.7	1.3
204441_s_at	POLA2	3.61E-03	158.0	142.2	157.4	143.4	153.7	130.8	132.9	212.1	163.0	192.1	189.5	200.1	205.6	175.0	143.4	192.1	1.3
202466_at	POLS	2.02E-03	488.4	477.5	532.2	546.8	539.9	481.2	476.8	636.1	867.6	990.2	664.8	689.1	699.3	929.7	488.4	699.3	1.4

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
204148_s_at	POMZP3 /// ZP3	2.86E-04	126.7	138.2	211.6	120.5	342.1	108.4	403.9	560.0	212.3	1048.2	660.9	1379.9	241.0	1008.0	138.2	660.9	4.8
211771_s_at	POU2F2	2.12E-04	105.9	66.5	72.3	80.7	102.4	81.1	83.3	141.3	110.9	146.8	155.0	172.2	198.2	164.7	81.1	155.0	1.9
228343_at	POU2F2	3.41E-05	43.1	32.0	43.5	49.2	50.3	56.8	52.0	81.1	67.1	153.0	157.2	131.3	161.8	113.2	49.2	131.3	2.7
229750_at	POU2F2	8.85E-04	141.9	148.1	138.7	132.3	123.0	109.9	124.3	236.4	172.3	248.6	266.8	293.7	330.3	337.7	132.3	266.8	2.0
217848_s_at	PPA1	1.08E-03	1924.7	2037.3	1751.5	1795.5	1615.4	1846.4	858.1	2332.0	3289.3	3231.6	2531.0	2691.1	2934.8	2059.3	1795.5	2691.1	1.5
223568_s_at	PPAPDC1B	3.64E-03	176.0	156.3	201.7	226.7	222.4	167.3	199.2	254.7	201.7	273.2	266.3	269.2	220.8	245.5	199.2	254.7	1.3
242218_at	PPARD	8.43E-03	211.0	128.3	179.2	229.3	181.1	169.7	278.2	278.3	155.0	320.2	226.7	265.4	279.3	368.7	181.1	278.3	1.5
214146_s_at	PPBP	1.58E-03	256.8	42.5	17.2	31.1	38.7	24.0	104.1	335.9	50.1	53.6	77.0	74.6	54.2	295.7	38.7	74.6	1.9
201489_at	PPIF	2.55E-05	1772.6	1042.2	1625.1	1460.5	2228.9	1414.6	2217.8	3208.5	3018.6	4141.9	2779.2	4814.2	3716.4	4901.3	1625.1	3716.4	2.3
201490_s_at	PPIF	1.14E-04	693.6	402.5	620.4	541.8	708.7	426.1	728.9	1168.1	1009.0	1693.4	996.4	2595.6	1585.2	1812.8	620.4	1585.2	2.6
235061_at	PPM1K	2.80E-03	40.5	64.6	138.5	84.5	73.9	91.7	94.7	95.9	125.5	261.0	131.8	133.0	86.4	153.3	84.5	131.8	1.6
244011_at	PPM1K	6.23E-03	57.6	66.2	66.7	57.2	48.3	54.0	52.0	68.8	102.4	116.7	61.6	73.8	63.0	78.6	57.2	73.8	1.3
202014_at	PPP1R15A	3.93E-03	185.1	107.4	193.3	213.9	198.1	142.5	199.2	209.7	197.4	448.0	239.0	533.1	510.3	464.3	193.3	448.0	2.3
37028_at	PPP1R15A	3.27E-03	214.2	125.5	224.4	244.5	196.1	149.7	228.0	255.6	277.1	543.0	273.8	546.8	598.4	491.4	214.2	491.4	2.3
212750_at	PPP1R16B	4.76E-04	43.1	33.5	33.5	58.8	57.1	35.1	32.6	75.3	59.8	55.2	147.2	69.1	68.5	69.2	35.1	69.1	2.0
41577_at	PPP1R16B	1.48E-03	37.9	38.4	37.9	50.4	45.1	40.6	49.3	48.9	49.9	53.0	103.5	69.5	64.1	68.1	40.6	64.1	1.6
202313_at	PPP2R2A	2.98E-04	274.3	311.3	376.9	350.0	410.0	396.1	419.7	499.3	684.0	816.9	584.4	569.5	556.1	753.3	376.9	584.4	1.6
236492_at	PPP2R2A	6.44E-03	72.4	91.2	77.8	87.8	74.3	72.6	81.1	88.9	131.0	144.1	105.0	88.0	89.4	112.1	77.8	105.0	1.4
237636_at	PPP2R2A	3.37E-03	133.6	123.9	147.5	145.0	126.4	141.2	142.9	157.1	185.4	303.9	263.2	192.5	154.8	238.9	141.2	192.5	1.4
207000_s_at	PPP3CC	1.11E-03	372.8	302.8	334.9	333.0	397.5	327.9	369.8	431.0	487.8	664.4	440.5	613.1	581.3	662.8	334.9	581.3	1.7
32540_at	PPP3CC	1.22E-03	185.3	237.0	259.7	258.6	305.2	281.9	309.6	311.0	373.9	642.8	446.7	374.7	401.3	480.4	259.7	401.3	1.5
32541_at	PPP3CC	7.37E-04	259.6	235.3	262.5	269.1	310.1	270.8	282.4	349.5	384.5	549.9	372.4	432.3	396.9	485.2	269.1	396.9	1.5
225519_at	PPP4R2	6.76E-04	668.6	627.0	941.8	837.8	971.5	935.2	1009.8	934.3	1321.8	2475.1	1372.5	1378.2	1518.3	1724.1	935.2	1378.2	1.5
212527_at	PPPDE2	6.56E-04	1366.7	1402.9	1155.7	1293.4	1265.0	1115.6	1199.4	1718.1	1873.8	2141.9	1873.2	1999.4	2006.5	1970.5	1265.0	1970.5	1.6
203737_s_at	PPRC1	6.86E-03	313.4	248.3	357.1	361.6	362.8	320.7	400.7	462.7	300.6	447.4	421.8	546.4	440.0	441.8	357.1	441.8	1.2
217192_s_at	PRDM1	2.95E-04	59.9	76.8	69.5	71.7	74.2	62.2	73.3	107.5	105.3	155.3	104.9	171.8	153.9	150.4	71.7	150.4	2.1
228964_at	PRDM1	1.47E-04	51.1	47.2	58.1	37.9	48.3	40.5	41.3	100.7	119.1	243.3	168.3	134.5	83.0	225.6	47.2	134.5	2.9
235668_at	PRDM1	2.39E-04	49.3	70.0	58.5	49.7	43.8	33.8	38.1	73.0	116.0	167.6	139.9	92.4	69.9	120.8	49.3	116.0	2.4
224232_s_at	PRELID1	1.81E-03	421.5	347.4	360.7	356.7	448.7	413.2	506.0	604.2	431.9	463.4	510.8	657.0	569.0	602.4	413.2	569.0	1.4
214617_at	PRF1	2.25E-05	57.6	61.7	82.2	86.3	78.5	122.9	106.4	147.9	123.1	241.3	276.7	183.1	305.8	424.1	82.2	241.3	2.9
228230_at	PRIC285	2.52E-05	71.3	61.7	61.1	52.7	66.3	55.7	67.4	146.4	142.1	280.9	175.6	209.5	198.6	252.6	61.7	198.6	3.2
232517_s_at	PRIC285	8.43E-03	80.7	81.0	58.6	60.0	56.0	65.6	66.2	85.9	87.7	156.7	77.5	137.0	126.4	138.5	65.6	126.4	1.9
232518_at	PRIC285	6.95E-03	55.9	44.5	56.3	71.1	55.0	51.1	71.2	64.2	56.8	110.1	77.3	92.0	100.8	98.6	55.9	92.0	1.6
232787_at	PRIC285	5.12E-04	75.4	55.4	77.7	65.0	63.1	48.3	93.9	120.1	82.7	250.3	146.4	239.2	167.3	192.6	65.0	167.3	2.6
209799_at	PRKAA1	9.01E-03	244.8	193.4	205.2	222.2	249.9	261.4	244.2	289.0	248.6	284.5	338.3	284.4	324.4	275.6	244.2	284.5	1.2
218292_s_at	PRKAG2	2.14E-04	142.9	142.1	134.2	144.7	143.9	135.8	133.9	228.2	216.2	307.9	239.0	231.2	203.7	255.4	142.1	231.2	1.6
222582_at	PRKAG2	2.98E-04	462.9	435.5	475.3	412.9	481.4	411.4	391.3	656.3	778.5	890.2	686.4	647.5	700.4	852.1	435.5	700.4	1.6
233748_x_at	PRKAG2	5.49E-04	141.7	133.7	106.2	133.5	133.7	136.7	110.0	199.3	207.6	262.0	205.6	244.7	200.8	230.0	133.7	207.6	1.6
209685_s_at	PRKCB	1.23E-04	41.3	49.9	57.7	63.9	45.3	38.3	45.2	94.3	109.7	142.1	124.2	157.2	84.1	217.2	45.3	124.2	2.7
38269_at	PRKD2	3.77E-03	128.5	123.5	160.8	181.7	160.9	156.9	165.1	166.6	143.0	201.3	221.3	229.3	259.3	270.9	160.8	221.3	1.4
228725_x_at	PRMT2	2.65E-03	514.7	361.7	392.6	423.8	406.5	397.2	366.5	529.8	552.2	698.9	532.5	716.6	697.0	657.8	397.2	657.8	1.7
232629_at	PROK2	3.60E-04	22.8	10.4	11.6	32.2	30.2	12.9	11.3	69.8	512.5	948.2	156.0	325.2	538.6	666.6	12.9	512.5	39.6
202251_at	PRPF3	1.64E-04	789.6	690.4	825.8	722.7	865.5	650.7	834.7	1078.8	1345.4	1792.2	1230.0	1321.2	1211.0	1572.3	789.6	1321.2	1.7
202126_at	PRPF4B	7.89E-03	641.7	736.3	826.9	823.0	745.5	730.9	773.2	753.3	1022.2	1394.4	1099.7	837.4	867.3	989.5	745.5	989.5	1.3
211090_s_at	PRPF4B	4.78E-03	63.7	67.3	141.6	125.4	126.8	128.3	116.7	154.7	112.2	244.9	181.1	139.5	170.1	152.9	125.4	154.7	1.2
227192_at	PRRT2	4.35E-03	67.0	56.0	91.7	76.6	89.0	64.2	77.1	94.9	115.7	130.5	90.6	102.1	113.3	107.1	76.6	107.1	1.4
226695_at	PRRX1	2.57E-03	41.5	39.7	33.3	32.6	15.7	29.3	24.6	52.9	69.6	130.4	48.8	71.7	57.8	89.5	32.6	69.6	2.1
203354_s_at	PSD3	2.38E-03	470.5	550.2	401.0	622.3	984.0	425.6	1010.4	837.7	924.7	1380.2	1276.8	1155.5	1033.4	1417.1	550.2	1155.5	2.1
203355_s_at	PSD3	5.94E-03	764.9	850.8	740.9	1133.0	1593.2	813.4	2108.1	1212.2	1558.1	2300.1	2136.7	1726.5	1701.4	2367.0	850.8	1726.5	2.0
1567443_x_at	PSEN1	3.50E-03	304.1	202.5	252.1	261.3	296.2	252.2	245.2	306.5	264.5	464.7	425.7	412.1	479.0	442.9	252.2	425.7	1.7
203460_s_at	PSEN1	5.49E-03	915.8	949.1	1102.3	1048.8	1226.9	1035.3	1274.5	1052.4	1456.0	1852.7	1352.1	1396.1	1356.9	1678.1	1048.8	1396.1	1.3
201316_at	PSMA2	3.63E-03	246.5	338.7	314.3	316.3	333.0	309.7	300.7	445.4	506.1	585.4	475.8	347.2	380.9	451.2	314.3	451.2	1.4
201317_s_at	PSMA2	1.23E-03	1543.8	1609.2	1746.1	1785.8	1649.2	1706.9	1957.5	2061.3	2762.1	3786.3	2752.8	2210.9	2240.6	3035.1	1706.9	2752.8	1.6
201532_at	PSMA3	1.33E-03	1403.0	1134.9	1089.4	1353.1	1229.6	1007.6	1393.1	1749.3	1828.7	2381.0	1941.3	1702.2	1699.1	1969.2	1229.6	1828.7	1.5
203396_at	PSMA4	3.03E-04	1305.4	1581.2	1542.5	1420.3	1369.0	1286.5	1618.3	1782.7	2351.3	2885.6	2274.8	1899.0	1977.8	2588.5	1420.3	2274.8	1.6
201274_at	PSMA5	3.98E-03	1740.9	1477.3	1341.7	1528.7	1469.1	1349.4	1496.7	1928.3	1883.5	2149.5	1967.4	1842.5	1955.5	2056.2	1477.3	1955.5	1.3
208805_at	PSMA6	6.33E-04	4551.7	4762.1	4506.8	4551.1	4989.9	4157.3	5313.3	6001.1	6323.6	7198.7	6477.1	6757.2	6142.8	7475.5	4551.7	6477.1	1.4
204279_at	PSMB9	1.69E-03	3933.4	4041.1	3794.9	3400.0	3417.4	2818.2	3123.5	4698.8	4905.0	5327.0	5414.4	4862.8	4662.9	5487.8	3417.4	4905.0	1.4
208777_s_at	PSMD11	6.74E-03	485.1	510.3	442.4	555.5	524.7	443.8	493.9	757.4	532.4	740.2	743.3	607.5	606.0	670.9	493.9	670.9	1.4
226724_s_at	PSPC1	3.60E-03	205.8	135.8	241.7	235.3	245.5	242.6	267.6	261.3	206.3	293.7	287.6	342.0	349.6	313.9	241.7	293.7	1.2
219938_s_at	PSTPIP2	2.01E-04	194.9	69.9	257.9	204.9	515.2	146.1	494.2	785.4	886.6	2144.0	1114.5	1198.5	1171.8	1235.2	204.9	1171.8	5.7
206631_at	PTGER2	2.38E-03	42.4	30.9	58.4	50.5	45.0	36.7	34.9	58.5	38.8	74.6	60.8	64.3	60.4	46.0	42.4	60.4	1.4
204896_s_at	PTGER4	9.88E-05	95.9	73.8	119.6	118.8	129.7	111.6	128.6	159.9	133.8	340.6	286.1	328.3	403.0	282.0	118.8	286.1	2.4
204897_at	PTGER4	5.15E-04	1318.7	1149.4	1334.3	1297.7	1772.9	1511.6	1697.4	2164.7	2436.3	3808.0	2886.2	2437.7	2595.6	2663.1	1334.3	2595.6	1.9
1554997_a_at	PTGS2	1.49E-05	47.7	48.9	49.8	62.4	171.7	68.2	128.2	290.5	1682.0	2689.6	813.8	2032.0	1894.9	2874.1	62.4	1894.9	30.4

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
204748_at	PTGS2	1.12E-05	81.8	78.0	112.9	89.1	333.6	149.8	235.3	502.0	2703.2	4162.3	1355.5	3097.3	3134.8	4582.2	112.9	3097.3	27.4
204935_at	PTPN2	8.13E-04	16.3	16.9	41.8	46.0	54.4	38.6	61.4	46.1	49.1	124.7	88.4	76.8	70.7	85.1	41.8	76.8	1.8
213137_s_at	PTPN2	2.30E-03	2671.3	2156.9	2199.3	2778.6	3328.0	2379.2	3102.0	3414.9	3323.2	3689.8	3435.4	4136.8	4139.1	4035.4	2671.3	3689.8	1.4
241622_at	PTPN2	4.01E-03	135.4	107.1	175.3	158.1	171.1	137.5	191.6	171.9	168.5	287.4	193.7	223.7	182.6	218.6	158.1	193.7	1.2
241623_at	PTPN2	8.05E-04	268.5	213.9	356.3	305.5	357.4	262.6	362.0	339.0	329.5	592.2	447.1	458.8	369.3	523.2	305.5	447.1	1.5
241983_at	PTPN2	7.73E-03	220.6	176.4	343.9	258.9	270.0	256.9	302.7	294.0	280.6	372.8	323.0	321.5	336.7	381.5	258.9	323.0	1.2
221840_at	PTPRE	9.39E-04	352.0	264.5	496.3	435.3	709.5	555.0	775.5	782.3	574.6	1162.7	939.1	1016.0	811.2	957.5	496.3	939.1	1.9
210173_at	PTPRJ	7.13E-05	136.8	97.2	139.8	196.3	207.2	140.3	197.6	245.8	213.6	484.0	380.3	404.8	343.3	416.7	140.3	380.3	2.7
214137_at	PTPRJ	3.89E-05	101.1	60.9	92.6	94.2	123.9	73.0	109.4	184.2	110.8	249.3	200.1	247.0	198.6	215.1	94.2	200.1	2.1
227396_at	PTPRJ	2.55E-04	1548.9	1144.2	1392.3	1508.0	1870.3	1149.4	1866.3	2344.3	2288.8	2985.4	2716.7	2655.4	2739.7	2978.9	1508.0	2716.7	1.8
206157_at	PTX3	4.32E-05	152.3	54.0	210.2	180.9	569.5	224.7	763.4	1866.8	5198.1	6968.5	4964.1	4222.2	4401.2	5999.7	210.2	4964.1	23.6
212662_at	PVR	8.54E-03	794.6	521.2	731.4	659.5	492.7	583.8	864.2	929.7	914.8	1778.1	771.6	649.7	1256.4	1061.9	659.5	929.7	1.4
203149_at	PVRL2	7.13E-05	138.5	99.0	125.1	246.9	138.2	87.3	145.7	238.2	197.8	420.3	622.1	368.7	343.8	399.1	138.2	368.7	2.7
225418_at	PVRL2	1.97E-04	117.5	150.2	115.8	112.1	126.8	80.7	115.9	190.2	239.1	329.6	186.4	259.6	211.9	261.3	115.9	239.1	2.1
232078_at	PVRL2	5.94E-05	56.8	38.4	50.5	67.7	61.4	42.3	75.0	110.6	85.4	163.5	125.8	174.7	133.0	148.3	56.8	133.0	2.3
232079_s_at	PVRL2	6.11E-06	120.1	84.0	149.7	161.6	172.1	99.3	159.1	315.7	309.7	445.3	392.9	494.1	363.9	503.3	149.7	392.9	2.6
201087_at	PXN	4.22E-03	45.2	55.7	48.3	50.6	50.3	46.8	48.4	66.1	62.1	86.5	58.0	111.8	73.4	103.4	48.4	73.4	1.5
205174_s_at	QPCT	2.03E-03	94.9	78.0	74.0	82.5	85.7	48.6	82.8	118.0	95.3	154.9	111.0	151.8	102.4	176.5	82.5	118.0	1.4
204155_s_at	QSK	1.19E-04	112.1	100.4	151.5	163.1	189.9	146.9	190.5	191.4	173.7	321.2	274.8	261.1	298.7	343.9	151.5	274.8	1.8
204156_at	QSK	2.93E-04	181.3	160.0	253.6	244.4	293.9	204.7	282.6	286.7	402.8	579.6	477.9	383.0	418.3	514.0	244.4	418.3	1.7
204157_s_at	QSK	8.92E-05	110.5	105.0	150.8	118.0	222.6	126.1	163.8	224.8	300.4	707.6	373.6	386.3	397.3	466.2	126.1	386.3	3.1
213034_at	QSK	9.88E-05	213.2	162.5	226.4	257.9	325.4	218.4	290.3	351.5	374.5	540.8	436.2	505.9	517.6	616.7	226.4	505.9	2.2
206039_at	RAB33A	5.76E-04	42.4	54.4	26.1	30.9	38.4	20.3	36.0	70.4	76.3	78.6	100.5	76.4	70.2	69.6	36.0	76.3	2.1
1554800_at	RAB39	4.79E-04	263.1	228.7	211.1	216.8	248.4	241.9	276.7	345.0	391.6	468.9	406.0	333.8	442.1	469.6	241.9	406.0	1.7
225001_at	RAB3D	8.99E-03	71.1	59.7	74.1	101.8	79.1	62.5	74.9	91.6	92.6	146.7	87.0	132.5	97.3	149.5	74.1	97.3	1.3
206113_s_at	RAB5A	1.09E-03	698.2	530.0	589.1	562.6	633.7	640.3	631.8	900.8	744.1	897.9	686.8	911.5	894.7	861.1	631.8	894.7	1.4
240990_at	RAB5A	3.86E-03	39.0	52.9	53.4	52.9	54.2	63.9	52.9	49.8	57.8	113.8	89.9	71.5	93.3	89.1	52.9	89.1	1.7
218700_s_at	RAB7L1	5.20E-03	114.0	147.1	205.0	212.7	207.6	193.7	188.5	246.8	207.7	698.3	326.0	242.0	326.8	266.7	193.7	266.7	1.4
219210_s_at	RAB8B	8.91E-05	1136.0	1123.6	982.5	1008.3	1220.5	1126.0	1277.3	1694.2	2279.8	2583.3	1792.6	2206.1	2270.4	2545.5	1126.0	2270.4	2.0
222846_at	RAB8B	8.93E-04	1517.1	1633.4	1601.5	1581.1	1657.3	1761.3	1755.5	1832.3	2574.5	3167.3	2415.0	2342.5	2506.6	2937.5	1633.4	2506.6	1.5
226633_at	RAB8B	1.80E-03	973.0	1108.6	1255.2	1352.2	1344.8	1471.4	1635.0	1255.5	1956.9	2605.2	2063.7	1725.6	1917.4	2362.2	1344.8	1956.9	1.5
203020_at	RABGAP1L	9.39E-05	143.6	297.4	247.0	227.7	244.7	259.5	192.0	373.8	635.8	859.1	531.0	460.7	436.4	613.3	244.7	531.0	2.2
213982_s_at	RABGAP1L	5.76E-05	571.2	569.4	688.0	622.3	567.0	681.5	429.8	1157.8	2107.2	2520.0	1533.8	1521.7	1442.6	1931.4	571.2	1533.8	2.7
215342_s_at	RABGAP1L	8.13E-04	200.2	222.7	186.1	173.6	182.5	179.6	152.0	252.3	397.4	523.8	304.8	340.0	281.0	394.4	182.5	340.0	1.9
226089_at	RABL3	1.92E-03	149.0	97.7	166.2	172.0	210.7	148.6	158.4	195.1	151.3	295.1	242.8	266.9	186.8	206.7	158.4	206.7	1.3
214435_x_at	RALA	6.91E-03	151.1	142.5	247.7	245.7	315.9	241.9	332.7	271.7	295.7	478.1	372.1	327.4	283.6	424.8	245.7	327.4	1.3
203096_s_at	RAPGEF2	1.84E-04	236.8	174.8	262.4	312.5	324.6	295.3	392.4	510.6	400.8	569.4	498.5	517.0	510.6	573.8	295.3	510.6	1.7
203097_s_at	RAPGEF2	2.53E-03	341.0	377.1	728.8	597.1	834.4	681.0	881.0	677.2	811.3	1623.0	1084.9	983.6	859.7	1155.3	681.0	983.6	1.4
215987_at	RAPGEF2	9.12E-05	394.9	282.2	345.9	391.8	422.4	386.4	501.5	615.7	585.6	738.7	691.9	777.6	762.6	735.2	391.8	735.2	1.9
215992_s_at	RAPGEF2	9.40E-04	320.1	350.0	625.7	504.7	565.1	539.5	710.9	661.4	724.0	1198.0	821.3	749.9	787.8	899.4	539.5	787.8	1.5
206391_at	RARRES1	2.67E-04	80.1	48.6	109.2	89.0	124.4	54.7	90.2	166.0	113.2	535.4	179.9	223.4	119.3	217.7	89.0	179.9	2.0
206392_s_at	RARRES1	1.08E-04	93.4	38.4	129.1	80.7	156.3	57.5	129.9	186.7	133.7	784.9	284.5	364.7	147.4	343.2	93.4	284.5	3.0
221872_at	RARRES1	7.21E-05	76.7	40.9	133.2	68.1	158.0	38.6	109.6	165.5	139.2	879.2	308.6	355.0	145.9	361.9	76.7	308.6	4.0
206636_at	RASA2	7.77E-03	216.5	168.9	253.9	240.3	274.8	287.8	272.2	282.4	231.3	353.9	309.9	295.1	330.4	342.7	253.9	309.9	1.2
1553785_at	RASGEF1B	1.74E-04	725.7	485.6	546.8	640.8	759.5	618.0	750.2	1074.5	1194.9	1747.3	1251.5	1408.1	1309.8	1441.4	640.8	1309.8	2.0
1554999_at	RASGEF1B	4.16E-04	111.5	91.6	163.5	113.3	167.8	133.7	187.5	262.8	262.9	552.8	328.3	239.6	216.1	346.2	133.7	262.9	2.0
205590_at	RASGRP1	3.26E-04	130.0	78.2	210.6	183.7	434.5	98.6	401.5	489.3	434.0	892.4	1035.9	754.2	847.5	814.5	183.7	814.5	4.4
205801_s_at	RASGRP3	2.76E-04	244.9	200.4	206.0	176.7	111.7	106.1	157.6	337.4	337.7	628.2	324.3	268.5	257.9	393.0	176.7	337.4	1.9
203185_at	RASSF2	1.15E-04	84.7	57.9	61.9	82.0	86.6	39.4	60.9	163.1	153.7	246.8	203.4	284.3	194.9	386.8	61.9	203.4	3.3
211540_s_at	RB1	9.30E-03	100.9	101.3	98.7	102.1	138.3	122.2	133.9	133.8	135.3	148.3	149.1	153.3	131.5	161.9	102.1	148.3	1.5
223802_s_at	RBBP6	7.63E-03	125.9	158.2	187.4	149.8	163.4	152.1	187.1	191.9	191.7	308.8	194.3	177.4	183.4	239.5	158.2	191.9	1.2
227635_at	RBBP6	3.53E-03	381.1	409.2	425.5	402.9	416.3	340.0	431.8	479.0	525.2	699.9	432.7	594.1	534.6	632.9	409.2	534.6	1.3
207713_s_at	RBCK1	1.32E-03	313.3	305.1	292.4	294.9	283.0	323.0	262.1	427.9	389.9	450.0	350.6	417.9	449.1	417.5	294.9	417.9	1.4
221827_at	RBCK1	2.76E-04	628.6	523.2	560.5	446.1	633.2	453.4	508.3	825.1	959.3	1216.1	742.9	1044.8	745.0	1132.9	523.2	959.3	1.8
218593_at	RBM28	8.66E-03	334.2	232.0	302.2	289.6	334.0	249.0	328.1	382.5	309.0	518.4	440.1	350.3	343.7	412.2	302.2	382.5	1.3
214943_s_at	RBM34	8.79E-03	293.4	440.1	564.7	506.3	519.1	593.6	534.8	687.5	682.4	987.0	619.3	636.3	659.9	706.8	519.1	682.4	1.3
243038_at	RBM43	5.44E-03	42.2	58.2	98.7	80.5	96.9	115.3	86.9	133.7	80.5	185.1	158.0	122.2	131.9	143.1	86.9	133.7	1.5
229421_s_at	RBM47	4.13E-03	272.0	263.5	318.7	332.7	411.9	326.5	424.3	414.7	402.1	601.2	460.5	459.0	493.4	481.8	326.5	460.5	1.4
203748_x_at	RBMS1	6.21E-03	1430.0	1205.4	1255.4	1362.0	1504.3	1235.0	1486.2	1731.3	1551.3	1877.1	1525.6	1773.5	1791.2	1906.1	1362.0	1773.5	1.3
207266_x_at	RBMS1	7.16E-03	1550.7	1175.6	1228.4	1421.5	1539.9	1267.9	1468.9	1695.0	1585.0	1859.1	1616.5	1900.5	1690.4	1977.7	1421.5	1695.0	1.2
230133_at	RC3H2	8.11E-03	73.7	92.8	123.0	100.3	101.8	114.0	109.0	131.9	94.7	162.2	129.5	177.5	142.4	146.6	101.8	142.4	1.4
203498_at	RCAN2	4.15E-04	163.9	65.6	70.2	89.0	162.9	33.8	238.9	387.5	221.0	472.4	537.9	415.8	310.9	472.8	89.0	415.8	4.7
201063_at	RCN1	4.51E-04	433.6	396.1	611.6	520.1	522.7	433.9	556.5	586.5	614.4	1083.3	772.9	678.9	645.7	856.6	520.1	678.9	1.3
204969_s_at	RDX	7.09E-03	178.4	152.8	195.1	211.6	188.9	163.1	214.5	257.5	189.1	354.1	227.8	235.9	210.7	293.2	188.9	235.9	1.2
218599_at	REC8	8.10E-03	124.3	92.1	182.3	159.2	130.9	102.5	202.1	135.2	135.0	258.1	184.3	223.1	205.8	245.8	130.9	205.8	1.6
206035_at	REL	3.58E-03	178.6	219.7	409.2	295.0	405.8	392.2	426.8	266.3	391.9	815.7	447.6	424.9	512.3	596.4	392.2	447.6	1.1

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
206036_s_at	REL	5.15E-04	134.7	149.0	260.5	210.7	252.4	250.1	231.7	230.6	201.6	487.4	263.5	383.6	427.6	414.7	231.7	383.6	1.7
201783_s_at	RELA	2.50E-04	577.9	481.3	677.2	640.1	901.3	604.0	810.4	848.2	1197.4	1498.9	1068.0	1351.6	1179.9	1413.0	640.1	1197.4	1.9
209878_s_at	RELA	4.91E-03	40.5	28.1	40.1	48.8	50.1	40.3	54.8	46.1	43.4	70.2	61.6	92.7	60.7	61.5	40.5	61.5	1.5
230202_at	RELA	9.75E-04	661.0	454.7	583.7	629.8	819.1	573.8	761.5	850.8	1133.0	1384.3	885.6	1219.3	1159.5	1375.6	629.8	1159.5	1.8
205205_at	RELB	7.19E-04	107.2	61.6	73.3	94.5	147.0	72.3	135.0	143.0	125.8	215.9	171.5	273.9	218.2	210.6	94.5	210.6	2.2
227060_at	RELT	6.66E-03	140.5	120.4	190.5	205.4	210.5	170.6	217.4	193.6	137.2	263.0	274.0	263.2	296.4	245.5	190.5	263.0	1.4
200939_s_at	RERE	1.11E-03	32.2	33.1	39.9	44.1	49.6	46.5	30.3	70.1	49.2	89.8	61.0	72.5	60.4	54.7	39.9	61.0	1.5
212646_at	RFTN1	1.39E-04	92.9	91.7	157.0	127.3	232.5	125.2	170.3	216.6	155.1	321.3	239.7	336.1	230.8	266.9	127.3	239.7	1.9
209568_s_at	RGL1	6.64E-06	138.7	63.9	112.3	75.1	107.8	63.8	103.1	635.5	1196.3	1551.4	684.3	841.5	573.7	1323.2	103.1	841.5	8.2
202988_s_at	RGS1	9.16E-05	88.2	73.1	133.7	101.3	106.5	88.7	86.4	183.5	223.0	264.7	324.0	196.6	160.5	177.8	88.7	196.6	2.2
209325_s_at	RGS16	6.30E-03	52.2	35.7	44.9	44.0	46.7	40.0	43.9	59.9	42.9	52.7	75.1	107.4	60.7	76.9	44.0	60.7	1.4
202388_at	RGS2	7.96E-04	123.4	167.3	178.5	101.4	273.4	137.7	144.0	152.7	724.5	952.4	205.8	1228.6	539.8	1142.9	144.0	724.5	5.0
219202_at	RHBDF2	2.96E-04	106.8	80.8	140.7	139.1	121.7	115.3	157.6	164.5	120.1	210.7	197.3	231.9	244.9	264.5	121.7	210.7	1.7
219045_at	RHOF	8.91E-03	102.0	62.5	107.2	98.7	98.8	57.7	97.1	157.6	60.5	122.4	133.7	163.2	119.2	178.2	98.7	133.7	1.4
204951_at	RHOH	1.05E-04	158.6	158.5	204.0	215.8	234.8	185.4	315.2	305.7	824.4	1421.4	526.0	759.2	801.2	1200.9	204.0	801.2	3.9
212117_at	RHOQ	7.31E-03	2997.5	2815.1	3023.6	3231.1	3546.7	3073.3	3445.7	3562.6	3620.1	4445.9	3909.4	4121.2	4017.8	4042.4	3073.3	4017.8	1.3
223169_s_at	RHOU	2.51E-03	478.9	414.7	484.7	559.5	638.7	549.8	562.1	589.4	806.6	905.2	640.2	894.5	810.9	1039.9	549.8	810.9	1.5
226310_at	RICTOR	1.26E-03	146.1	134.3	209.2	181.6	211.2	210.5	191.9	196.4	206.0	405.1	281.8	256.8	282.4	341.0	191.9	281.8	1.5
226312_at	RICTOR	5.44E-03	728.4	611.7	953.9	827.1	965.9	947.0	976.6	874.2	1231.6	1958.8	1252.0	1112.7	1143.0	1495.1	947.0	1231.6	1.3
228248_at	RICTOR	1.08E-03	102.3	109.9	217.5	196.2	208.2	199.1	198.0	197.6	190.0	480.1	382.6	247.1	256.0	336.4	198.0	256.0	1.3
227983_at	RILPL2	6.24E-03	1495.1	1259.4	1501.5	1481.9	1854.1	1392.3	1888.3	2096.4	1699.3	2157.6	1954.1	1875.3	2076.1	2305.2	1495.1	2076.1	1.4
225978_at	RIMKLB	6.79E-03	743.0	911.9	1004.9	988.4	883.0	973.6	952.4	852.1	1475.6	1835.7	1437.7	1054.5	1057.2	1601.3	952.4	1437.7	1.5
225999_at	RIMKLB	2.80E-03	142.9	113.9	141.0	138.8	145.8	136.8	123.7	176.5	189.6	269.4	186.5	168.8	188.5	218.2	138.8	188.5	1.4
229344_x_at	RIMKLB	7.19E-03	437.0	546.3	689.1	576.5	541.4	453.6	580.8	509.8	915.7	1140.3	752.5	578.1	573.7	813.4	546.3	752.5	1.4
209684_at	RIN2	5.43E-03	3124.7	2572.6	3702.4	3738.5	4418.8	4571.2	4301.3	4124.5	5169.8	6202.5	4890.9	5391.0	5024.8	6603.9	3738.5	5169.8	1.4
233811_at	RIN2	1.11E-03	91.3	60.5	69.4	61.9	58.9	63.4	76.9	126.0	78.8	111.8	100.2	159.5	122.5	135.9	63.4	122.5	1.9
202129_s_at	RIOK3	6.93E-03	293.1	267.6	307.0	347.8	316.9	311.2	327.9	394.0	324.3	440.0	402.5	425.9	369.1	379.6	311.2	394.0	1.3
209941_at	RIPK1	4.98E-03	374.6	432.3	486.5	497.2	513.7	495.6	555.9	508.8	626.6	943.0	649.9	566.8	625.5	775.0	495.6	626.6	1.3
209544_at	RIPK2	5.74E-04	31.2	45.6	86.4	72.4	84.1	92.5	118.6	108.6	117.1	352.4	167.5	181.1	142.9	176.7	84.1	167.5	2.0
209545_s_at	RIPK2	8.61E-06	897.7	606.4	790.5	657.5	984.1	733.9	896.8	1993.0	2089.1	3144.6	1716.6	2746.2	2101.8	2687.2	790.5	2101.8	2.7
206111_at	RNASE2	6.26E-03	33.2	44.6	43.0	41.8	27.9	30.8	42.9	59.1	58.2	56.0	52.9	84.1	40.5	78.4	41.8	58.2	1.4
218497_s_at	RNASEH1	1.74E-03	533.9	499.9	491.5	501.1	460.6	450.4	487.0	597.6	733.7	940.1	785.5	592.4	738.0	882.1	491.5	738.0	1.5
212724_at	RND3	3.07E-03	911.9	412.7	436.6	612.3	935.0	207.5	1104.6	1073.5	2526.2	4264.9	1906.5	1702.2	1675.7	2530.0	612.3	1906.5	3.1
200868_s_at	RNF114	2.87E-03	420.3	451.8	510.6	412.0	536.6	503.7	444.8	566.2	597.5	937.4	573.6	645.1	619.1	653.2	451.8	619.1	1.4
212742_at	RNF115	3.29E-03	611.6	633.6	726.3	702.1	822.5	797.9	592.3	929.2	1093.6	1581.0	934.4	943.8	1012.8	888.8	702.1	943.8	1.3
228153_at	RNF144B	1.14E-03	2926.0	2058.7	3595.6	2336.0	4305.4	3061.6	4577.7	4639.8	5631.1	7909.2	5288.7	5179.8	5558.6	6687.5	3061.6	5558.6	1.8
235549_at	RNF144B	1.35E-04	244.6	161.8	402.8	235.8	576.6	358.0	600.6	744.9	860.3	1266.0	807.5	957.6	998.4	1290.6	358.0	957.6	2.7
239012_at	RNF144B	8.67E-05	2235.0	1573.8	2677.0	1583.2	3466.1	2104.8	3619.9	3935.4	4708.6	6707.8	4547.5	5706.2	5651.1	7197.1	2235.0	5651.1	2.5
239704_at	RNF144B	5.51E-05	428.4	217.3	400.6	245.5	449.1	306.1	495.5	733.6	704.4	1378.2	658.7	1164.4	1443.0	1543.4	400.6	1164.4	2.9
236465_at	RNF175	7.66E-05	144.5	100.3	97.0	117.7	149.3	91.9	124.9	228.5	160.5	217.9	229.1	330.2	175.5	311.8	117.7	228.5	1.9
220483_s_at	RNF19A	2.76E-04	682.2	584.0	553.2	589.7	775.3	567.6	628.2	858.1	969.7	1160.3	1094.9	1200.8	1048.0	1157.2	589.7	1094.9	1.9
223085_at	RNF19A	1.67E-03	506.0	423.4	574.8	640.2	791.0	617.5	643.9	658.6	894.5	1330.4	1137.6	1020.3	841.7	1009.6	617.5	1009.6	1.6
213038_at	RNF19B	1.91E-05	547.3	251.3	305.8	284.7	601.6	269.5	539.9	1390.7	1461.8	2129.8	1253.3	2118.0	1782.7	2066.2	305.8	1782.7	5.8
36564_at	RNF19B	9.06E-06	524.0	316.4	364.9	371.0	728.8	337.5	611.2	1595.3	1856.0	2651.2	1534.8	2600.2	2169.5	2734.2	371.0	2169.5	5.8
1569078_at	RNF213	4.11E-03	42.2	33.9	37.2	41.3	36.5	34.9	23.4	50.0	45.1	128.1	73.3	88.1	58.6	96.2	36.5	73.3	2.0
225929_s_at	RNF213	4.06E-04	1171.0	1291.5	574.4	1259.6	1091.3	994.6	1073.4	1610.4	1959.9	1457.3	2304.5	2060.1	2353.0	2995.8	1091.3	2060.1	1.9
225931_s_at	RNF213	8.16E-04	1065.2	1173.0	502.9	943.9	995.0	967.7	838.9	1420.4	1692.1	1317.1	2021.5	1593.2	1888.6	2358.7	967.7	1692.1	1.7
230000_at	RNF213	4.97E-05	189.3	159.4	111.7	147.6	129.6	133.5	124.1	331.5	323.8	382.1	382.4	334.8	388.1	451.0	133.5	382.1	2.9
233880_at	RNF213	4.93E-03	297.0	288.6	151.2	329.5	247.4	230.6	188.0	352.9	339.5	340.5	486.1	350.1	474.7	516.8	247.4	352.9	1.4
241480_at	RNF213	2.92E-03	201.8	185.8	187.4	258.5	191.5	184.2	211.9	300.3	197.0	400.8	373.0	503.4	562.5	555.2	191.5	400.8	2.1
231635_x_at	RNF31	8.85E-03	697.7	647.6	589.9	577.1	633.8	543.4	662.1	754.9	711.5	759.0	756.8	856.3	802.0	858.4	633.8	759.0	1.2
222279_at	RP3-377H14.5	1.15E-03	431.0	385.9	639.3	615.1	561.0	479.4	570.0	593.5	653.2	1084.4	884.0	720.5	586.6	839.1	561.0	720.5	1.3
218499_at	RP6-213H19.1	2.14E-05	84.1	65.1	144.5	174.7	102.9	79.7	178.3	318.0	633.2	2132.0	719.8	512.7	539.5	1269.0	102.9	633.2	6.2
224407_s_at	RP6-213H19.1	3.32E-04	48.4	75.7	51.1	50.7	37.6	29.5	39.1	109.7	119.2	387.7	179.4	182.3	171.2	266.6	48.4	179.4	3.7
221143_at	RPA4	1.86E-03	39.7	22.8	43.5	43.5	62.8	40.5	42.6	58.4	44.6	88.7	81.3	61.4	90.8	83.9	42.6	81.3	1.9
218909_at	RPS6KC1	6.07E-04	244.4	193.3	228.2	269.5	263.8	220.2	248.9	308.5	426.7	688.5	531.8	413.8	415.1	482.6	244.4	426.7	1.7
213903_s_at	RQCD1	5.00E-03	131.5	131.3	189.8	168.8	205.1	148.5	199.1	222.7	165.2	227.6	252.3	244.1	209.2	235.5	168.8	227.6	1.3
218088_s_at	RRAGC	9.69E-03	2300.6	2013.2	1715.9	1855.5	2120.6	1810.3	1991.7	2372.6	2819.1	2982.6	2110.1	2537.6	2714.8	3043.2	1991.7	2714.8	1.4
222514_at	RRAGC	7.62E-03	530.0	603.1	743.4	836.0	855.7	698.7	804.8	819.4	993.1	1453.1	901.6	954.5	905.2	1106.7	743.4	954.5	1.3
201204_s_at	RRBP1	9.51E-03	463.2	391.0	382.5	427.8	419.4	412.0	412.5	475.1	564.8	664.8	466.0	528.0	653.7	634.3	412.5	564.8	1.4
213495_s_at	RRBP1	8.28E-03	458.4	398.1	534.1	612.7	556.7	575.8	577.7	646.1	538.6	757.2	566.5	772.0	891.2	792.5	556.7	757.2	1.4
33307_at	RRP7A	4.80E-03	227.5	201.5	247.8	309.7	241.4	197.0	375.3	286.8	229.8	383.0	377.7	330.9	290.0	450.1	241.4	330.9	1.4
213797_at	RSAD2	1.43E-05	2517.9	1357.4	1011.9	697.0	687.4	566.7	716.0	7651.4	11857.6	12784.2	9193.9	8412.0	7825.7	11269.1	716.0	9193.9	12.8

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
242625_at	RSAD2	6.17E-06	427.9	245.9	248.4	154.4	220.8	158.8	163.9	2082.1	3893.3	4937.4	3168.7	2964.0	2363.8	4113.6	220.8	3168.7	14.4
34408_at	RTN2	7.29E-03	112.3	116.4	113.8	143.9	111.9	123.6	122.5	156.8	133.8	132.0	161.8	163.4	214.4	172.2	116.4	161.8	1.4
219684_at	RTP4	2.76E-05	268.2	297.7	267.4	239.3	236.9	239.2	193.9	517.4	609.2	720.4	426.8	559.1	501.0	537.0	239.3	537.0	2.2
203724_s_at	RUFY3	2.95E-04	213.7	217.1	282.4	196.1	303.2	201.8	247.7	371.0	421.9	717.9	450.8	399.0	337.9	446.7	217.1	421.9	1.9
210251_s_at	RUFY3	2.90E-04	536.5	399.0	451.5	468.1	617.8	459.6	577.6	860.4	929.3	1466.6	820.6	1035.9	997.9	993.5	468.1	993.5	2.1
213430_at	RUFY3	4.65E-03	22.7	28.9	52.2	49.1	80.9	45.9	67.5	56.1	46.8	173.6	95.0	93.2	83.5	78.5	49.1	83.5	1.7
213437_at	RUFY3	1.49E-04	463.2	367.1	393.7	420.3	508.2	366.8	442.2	681.4	792.8	1128.6	747.6	900.1	868.9	886.3	420.3	868.9	2.1
213939_s_at	RUFY3	9.01E-05	53.3	58.4	87.9	70.9	84.2	70.0	79.3	108.8	114.1	269.8	172.3	155.9	122.5	139.2	70.9	139.2	2.0
227802_at	RUFY3	4.05E-03	133.0	169.6	339.9	307.9	367.1	322.0	437.6	315.0	323.9	859.7	559.4	415.2	423.2	545.1	322.0	423.2	1.3
229334_at	RUFY3	4.94E-05	401.8	481.2	580.3	535.0	756.2	514.8	718.0	846.2	1014.3	1505.0	1055.1	1237.8	1161.9	1201.1	535.0	1161.9	2.2
236859_at	RUNX2	1.57E-03	66.1	84.9	54.2	60.4	73.1	59.6	52.9	91.7	109.2	135.8	96.3	98.1	119.4	103.6	60.4	103.6	1.7
204197_s_at	RUNX3	4.69E-05	118.9	69.2	93.6	65.1	117.3	80.7	100.8	206.4	121.5	203.8	169.1	235.6	152.7	264.6	93.6	203.8	2.2
204198_s_at	RUNX3	2.62E-04	137.1	93.2	96.1	73.5	108.5	63.0	115.7	237.7	131.7	222.4	148.6	309.2	193.2	364.0	96.1	222.4	2.3
206949_s_at	RUSC1	6.93E-04	94.8	99.5	128.7	105.4	134.5	135.4	126.9	146.1	161.2	215.0	194.8	181.8	169.5	177.6	126.9	177.6	1.4
201844_s_at	RYBP	3.09E-03	233.3	264.9	384.7	310.8	360.0	330.7	387.7	374.9	329.7	586.1	411.0	447.6	391.5	510.7	330.7	411.0	1.2
201845_s_at	RYBP	9.96E-03	265.2	277.1	333.2	335.1	360.6	302.8	324.0	339.0	383.5	540.0	385.4	399.1	344.6	446.0	324.0	385.4	1.2
201846_s_at	RYBP	1.54E-03	313.8	281.9	288.5	309.5	302.6	281.0	298.8	424.8	356.6	473.0	363.0	522.0	428.6	521.6	298.8	428.6	1.4
205863_at	S100A12	1.15E-05	38.8	30.9	31.2	25.4	47.8	33.5	39.8	256.5	383.5	668.6	175.6	891.8	656.0	1490.9	33.5	656.0	19.6
202917_s_at	S100A8	4.85E-03	4987.9	3865.7	3932.6	5863.0	6615.5	5579.6	5267.3	5556.7	6533.7	6552.6	6419.0	8658.1	8362.6	8935.8	5267.3	6552.6	1.2
214370_at	S100A8	1.63E-03	2592.7	2052.3	1936.7	2802.8	3639.6	3119.9	2910.4	3091.5	3398.9	3698.8	3574.8	4959.0	4642.7	5160.5	2802.8	3698.8	1.3
204351_at	S100P	1.15E-03	252.7	129.4	249.5	360.8	303.8	214.5	329.5	353.3	280.9	682.9	400.3	700.9	544.5	790.7	252.7	544.5	2.2
208537_at	S1PR2	9.09E-03	44.8	55.3	55.1	63.4	60.6	54.6	58.3	71.0	60.7	87.4	74.5	65.5	93.8	81.7	55.3	74.5	1.3
227684_at	S1PR2	8.59E-05	262.4	204.5	221.7	208.4	190.4	166.5	230.0	373.9	466.2	581.0	402.4	412.5	443.7	599.1	208.4	443.7	2.1
208607_s_at	SAA1 /// SAA2	4.07E-05	114.1	140.8	154.5	100.7	154.4	119.9	99.9	233.9	250.8	260.0	203.9	267.3	210.5	159.4	119.9	233.9	2.0
214456_x_at	SAA1 /// SAA2	2.47E-04	165.4	220.2	198.0	110.6	177.1	149.4	114.2	318.8	385.6	263.4	229.5	265.8	304.4	185.1	165.4	265.8	1.6
212845_at	SAMD4A	4.19E-03	441.5	636.4	694.6	581.6	493.5	613.8	570.7	581.8	830.7	1254.3	753.2	626.6	709.2	799.0	581.6	753.2	1.3
215495_s_at	SAMD4A	6.72E-05	184.2	208.8	183.6	156.3	151.9	139.2	161.1	284.5	513.1	706.4	398.2	478.6	447.1	536.7	161.1	478.6	3.0
219691_at	SAMD9	6.17E-06	80.7	89.3	140.1	111.2	128.9	125.6	114.4	241.4	328.5	587.4	322.4	346.9	333.6	432.0	114.4	333.6	2.9
228531_at	SAMD9	1.24E-04	2138.6	2593.4	2512.4	2214.9	2265.6	2876.6	2528.8	3212.8	4717.6	5254.5	4052.1	4067.0	4085.6	5191.0	2512.4	4085.6	1.6
226603_at	SAMD9L	3.71E-05	1758.1	2284.3	1865.6	1646.7	1448.9	1492.6	1371.3	3230.6	4615.4	5305.7	3974.5	3523.7	3306.5	4808.2	1646.7	3974.5	2.4
230036_at	SAMD9L	8.20E-04	1100.6	1442.5	1145.2	964.8	1001.7	904.3	784.1	1750.4	1879.0	2495.3	1752.4	1402.3	1449.7	1905.0	1001.7	1752.4	1.7
235643_at	SAMD9L	1.65E-04	1741.1	2001.6	1686.6	1604.7	1392.6	1436.4	1273.6	2664.4	3421.3	4058.1	3067.6	3071.6	3012.7	4083.0	1604.7	3071.6	1.9
1555638_a_at	SAMSN1	5.80E-05	118.9	101.2	194.9	214.4	463.8	207.0	386.4	317.4	413.6	885.3	622.6	830.7	581.1	974.5	207.0	622.6	3.0
220330_s_at	SAMSN1	3.54E-04	104.5	81.8	224.9	256.3	589.5	253.5	487.6	379.5	422.2	1033.5	732.3	900.2	599.0	986.1	253.5	732.3	2.9
201543_s_at	SAR1A	1.38E-03	1287.1	1134.1	1107.2	1282.4	1327.3	1283.1	1223.2	1535.1	1610.8	2065.0	1747.5	1940.7	1904.0	1704.7	1282.4	1747.5	1.4
213236_at	SASH1	2.77E-05	170.8	110.6	156.7	127.8	177.9	122.5	193.2	286.6	248.3	359.0	233.8	348.0	259.4	343.8	156.7	286.6	1.8
226022_at	SASH1	2.38E-03	556.9	553.1	633.6	439.6	596.9	601.6	858.9	710.9	1151.0	1702.4	902.5	829.6	759.3	1399.8	596.9	902.5	1.5
41644_at	SASH1	6.44E-05	242.1	192.9	214.4	174.0	239.9	213.0	305.2	441.3	393.3	522.0	337.3	388.4	355.8	530.1	214.4	393.3	1.8
203455_s_at	SAT1	4.29E-03	4522.5	4402.1	5434.8	4955.2	5796.5	5880.8	5890.0	5581.9	7692.9	9161.3	7137.2	6725.6	7383.1	7411.3	5434.8	7383.1	1.4
210592_s_at	SAT1	2.86E-03	6520.0	6664.4	6648.3	6458.5	7502.9	7162.6	6948.6	7830.5	9539.8	11817.6	9175.1	8921.6	9626.4	9425.6	6664.4	9425.6	1.4
213988_s_at	SAT1	1.02E-04	5041.8	2868.9	2540.5	2542.8	4855.4	3860.3	2605.5	7176.7	5749.5	6825.7	4985.7	9373.1	8830.4	6615.1	2868.9	6825.7	2.4
222573_s_at	SAV1	2.38E-03	451.4	357.1	489.9	491.0	615.3	493.5	547.8	595.2	610.6	916.2	556.2	824.7	739.5	766.4	491.0	739.5	1.5
1555021_a_at	SCARF1	5.41E-04	179.0	125.0	139.3	161.8	152.4	159.8	192.2	215.8	214.8	299.9	299.8	338.0	245.1	449.7	159.8	299.8	1.9
206995_x_at	SCARF1	2.95E-04	80.8	74.6	105.9	102.4	88.1	114.0	140.2	123.0	155.0	271.2	175.0	141.7	168.8	248.2	102.4	168.8	1.6
219196_at	SCG3	2.19E-03	48.7	42.7	51.6	48.2	43.0	35.8	31.4	54.5	68.4	90.0	108.4	68.6	50.5	43.2	43.0	68.4	1.6
218793_s_at	SCML1	6.86E-04	106.2	174.2	237.6	219.1	284.9	197.8	287.1	284.2	380.7	871.5	406.2	430.6	323.9	472.2	219.1	406.2	1.9
222747_s_at	SCML1	3.28E-04	214.1	237.9	231.4	210.5	294.6	217.2	243.6	401.3	462.4	870.4	400.9	496.4	369.7	579.3	231.4	462.4	2.0
206147_x_at	SCML2	8.50E-03	215.8	182.8	225.0	206.7	241.7	222.0	281.6	254.8	285.5	298.8	290.4	296.8	230.6	376.2	222.0	290.4	1.3
205508_at	SCN1B	3.09E-03	41.6	34.1	41.7	30.2	38.2	35.3	46.8	47.6	40.5	91.2	52.0	96.8	61.2	74.5	38.2	61.2	1.6
205241_at	SCO2	3.53E-03	696.8	542.5	637.0	641.4	763.0	470.6	722.2	760.4	720.0	937.6	974.5	1337.5	1093.9	1060.0	641.4	974.5	1.5
219197_s_at	SCUBE2	5.55E-03	75.5	62.7	52.0	51.4	73.5	54.5	45.1	81.1	107.1	119.9	79.2	96.3	75.4	122.9	54.5	96.3	1.8
202071_at	SDC4	2.00E-03	916.5	273.6	774.4	759.1	1283.9	502.0	1437.2	1747.1	1325.5	3082.6	1502.5	2106.1	1961.6	1832.0	774.4	1832.0	2.4
218681_s_at	SDF2L1	5.19E-03	251.5	209.1	216.8	243.2	248.0	220.0	245.6	303.7	236.4	284.1	308.5	365.0	351.6	304.2	243.2	304.2	1.3
202083_s_at	SEC14L1	7.53E-03	77.0	80.0	107.1	93.7	89.4	94.1	89.0	97.6	84.0	148.0	118.7	131.8	113.0	116.1	89.4	116.1	1.3
216392_s_at	SEC23IP	8.46E-03	602.0	500.1	585.6	561.4	610.8	546.5	644.0	721.2	609.4	781.5	691.7	715.3	807.0	732.9	585.6	721.2	1.2
212902_at	SEC24A	4.55E-03	208.3	220.0	222.8	263.9	320.7	239.0	305.5	283.5	349.7	515.3	361.2	349.8	347.1	442.9	239.0	349.8	1.5
202375_at	SEC24D	9.61E-03	46.2	77.5	130.4	144.3	142.1	118.7	148.5	144.2	141.3	309.1	246.3	159.9	144.4	171.6	130.4	159.9	1.2
222385_x_at	SEC61A1	3.98E-04	386.5	287.2	332.9	398.2	327.7	309.0	366.9	510.1	444.3	618.6	536.3	576.0	560.9	569.1	332.9	560.9	1.7
203133_at	SEC61B	1.42E-03	720.1	750.4	816.0	714.6	871.2	788.5	921.4	1386.0	958.3	1431.9	1165.1	1307.9	975.2	1230.6	788.5	1230.6	1.6
244700_at	SEC61B	2.80E-03	112.6	110.5	140.9	124.8	108.4	86.8	128.6	144.8	116.5	220.0	170.7	155.9	136.5	196.9	112.6	155.9	1.4
203484_at	SEC61G	4.55E-03	2610.5	2736.8	2364.9	2493.8	2911.4	2693.4	2943.6	3522.5	3257.8	3703.9	3626.6	3458.9	3380.2	3535.7	2693.4	3522.5	1.3
1555274_a_at	SELI	4.57E-03	362.4	281.8	440.8	387.0	465.9	396.0	615.1	572.4	836.0	1471.1	803.3	528.7	518.4	991.1	396.0	803.3	2.0
204563_at	SELL	1.01E-04	35.7	46.7	34.9	36.1	24.9	40.3	35.7	92.4	159.7	352.0	185.1	294.6	183.2	414.2	35.7	185.1	5.2
223209_s_at	SELS	4.13E-03	2251.1	2172.3	1839.1	2086.1	2135.4	1744.2	1876.0	2618.8	2716.4	2699.8	2576.3	2533.4	2525.5	2643.5	2086.1	2618.8	1.3

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203788_s_at	SEMA3C	3.37E-03	372.5	314.7	454.8	340.2	449.9	488.9	509.7	423.3	436.1	697.5	446.8	583.7	624.9	644.0	449.9	583.7	1.3
219259_at	SEMA4A	1.04E-03	72.6	72.9	108.3	117.1	133.6	97.2	94.3	127.4	84.7	160.4	184.2	189.8	142.5	180.4	97.2	160.4	1.6
234072_at	SEMA4A	9.69E-04	43.8	43.1	34.5	31.4	34.7	38.4	29.5	57.7	57.9	54.0	74.4	54.5	67.1	64.0	34.7	57.9	1.7
203528_at	SEMA4D	2.57E-05	3306.6	3015.1	3010.2	2512.2	3152.1	2450.7	3697.1	5822.9	7479.2	8508.1	6788.6	6058.7	6627.6	8211.2	3015.1	6788.6	2.3
228891_at	SEMA4D	9.19E-04	120.1	164.4	214.7	163.6	165.1	147.7	139.9	239.9	203.0	292.2	278.8	225.5	259.9	233.4	163.6	239.9	1.5
57703_at	SENP5	9.78E-03	548.3	638.1	597.6	569.6	568.1	604.8	576.9	650.6	686.3	735.1	709.4	719.8	776.4	736.4	576.9	719.8	1.2
239213_at	SERPINB1	5.32E-03	172.2	152.8	159.4	113.4	165.1	119.7	151.2	173.6	210.3	230.5	140.6	252.1	161.8	244.6	152.8	210.3	1.4
204614_at	SERPINB2	1.73E-03	26.6	45.2	5.9	29.5	45.0	9.1	16.2	53.6	145.5	166.6	94.7	136.8	129.8	86.0	26.6	129.8	4.9
206034_at	SERPINB8	1.28E-03	413.2	316.7	299.1	497.2	519.8	288.3	442.4	523.5	641.1	773.6	703.2	752.5	765.2	928.7	413.2	752.5	1.8
209722_s_at	SERPINB9	8.17E-05	69.7	52.6	45.5	43.2	44.8	27.7	46.7	200.1	112.8	195.9	202.3	397.8	189.5	313.8	45.5	200.1	4.4
209723_at	SERPINB9	2.46E-06	38.0	38.1	45.6	35.3	68.0	15.1	91.8	268.2	540.3	1080.7	446.1	920.0	353.0	1257.3	38.1	540.3	14.2
242814_at	SERPINB9	1.99E-04	62.9	44.7	38.3	30.5	36.5	26.6	33.5	127.7	96.5	258.4	197.4	242.2	120.9	316.9	36.5	197.4	5.4
202628_s_at	SERPINE1	9.53E-03	76.7	54.7	67.8	46.6	52.6	41.2	37.4	98.5	61.0	120.6	51.2	77.8	89.2	97.8	52.6	89.2	1.7
223394_at	SERTAD1	6.82E-03	342.7	255.8	287.7	317.7	325.4	274.1	353.6	360.9	323.7	443.2	365.4	574.8	458.9	491.4	317.7	443.2	1.4
226763_at	SESTD1	7.10E-03	718.3	808.9	776.3	820.7	996.4	676.2	776.1	858.4	967.3	1288.7	961.8	1156.5	1044.0	1086.3	776.3	1044.0	1.3
1569105_at	SETD5	8.84E-03	58.7	41.9	68.5	78.1	72.5	64.3	73.1	84.3	52.7	93.5	89.9	75.9	90.7	91.9	68.5	89.9	1.3
226898_s_at	SFPQ	1.91E-03	300.3	225.2	309.3	360.2	356.5	329.0	415.7	420.4	370.1	555.0	432.6	461.2	508.4	526.4	329.0	461.2	1.4
222310_at	SFRS15	8.37E-03	74.2	67.7	86.5	81.6	65.7	61.8	66.1	86.3	116.5	110.0	118.3	93.2	64.8	85.2	67.7	93.2	1.4
241245_at	SFRS4	5.20E-03	136.4	124.9	184.4	186.7	215.0	189.1	237.3	197.3	148.4	314.8	227.5	262.9	236.2	306.7	186.7	236.2	1.3
214838_at	SFT2D2	4.28E-04	538.1	561.0	570.4	757.6	658.9	684.3	769.7	820.2	1164.8	1579.7	1178.2	1049.7	1057.7	1551.3	658.9	1164.8	1.8
201739_at	SGK1	9.94E-03	5604.3	4348.4	6068.3	4716.9	4988.0	3484.7	5853.4	6434.5	5479.5	7621.2	6278.0	5682.8	5311.6	6718.3	4988.0	6278.0	1.3
220008_at	SGK269	5.12E-04	50.6	62.9	70.0	59.9	94.3	62.2	64.1	98.8	92.9	141.6	85.5	138.2	83.7	109.2	62.9	98.8	1.6
225913_at	SGK269	5.62E-03	214.2	181.4	243.9	229.4	328.8	220.8	268.8	247.1	262.7	451.4	312.2	374.5	285.2	372.1	229.4	312.2	1.4
212989_at	SGMS1	2.12E-03	60.0	66.6	133.9	155.5	192.3	154.9	197.6	149.8	162.8	371.9	302.7	231.6	230.5	256.9	154.9	231.6	1.5
238567_at	SGPP2	6.54E-04	29.8	31.5	24.8	18.2	32.6	15.8	29.4	86.3	50.4	362.6	97.8	111.9	80.5	111.5	29.4	97.8	3.3
228745_at	SGTB	1.04E-03	114.6	139.2	180.2	214.7	335.6	194.1	381.9	274.5	198.8	510.0	354.5	466.0	460.1	580.0	194.1	460.1	2.4
232084_at	SGTB	2.68E-03	29.5	33.5	37.8	33.7	68.8	21.3	75.0	59.0	42.1	111.5	83.6	94.5	79.2	110.9	33.7	83.6	2.5
222169_x_at	SH2D3A	1.64E-03	89.2	67.5	109.8	95.5	94.7	99.9	116.7	108.4	113.7	161.5	121.9	127.2	152.8	152.8	95.5	127.2	1.3
209091_s_at	SH3GLB1	2.93E-03	1097.4	917.4	1029.9	1145.7	1179.5	1059.7	1138.4	1366.7	1718.9	2170.7	1497.6	1471.9	1471.5	1727.5	1097.4	1497.6	1.4
210101_x_at	SH3GLB1	4.01E-03	1949.7	1439.4	1631.7	1749.0	1869.6	1630.9	1747.8	2082.1	2668.7	2961.5	2259.5	2362.9	2409.7	2699.7	1747.8	2409.7	1.4
231823_s_at	SH3PXD2B	6.81E-03	232.8	111.4	142.4	190.4	138.4	89.6	421.6	344.8	187.1	267.6	304.7	189.4	351.3	499.8	142.4	304.7	2.1
209339_at	SIAH2	3.44E-04	137.9	121.9	125.3	148.0	154.1	132.1	149.9	193.3	201.9	275.5	218.5	224.4	218.2	269.0	137.9	218.5	1.6
219519_s_at	SIGLEC1	7.05E-03	1967.6	2820.6	2362.2	2615.8	2056.2	1342.4	1142.4	2410.8	3311.6	3724.6	3573.1	2781.1	2723.4	3140.4	2056.2	3140.4	1.5
1552807_a_at	SIGLEC10 /// SIGLEC12	1.78E-03	173.3	125.8	207.8	125.3	195.8	126.0	137.0	355.7	173.7	246.3	190.7	410.1	184.7	328.3	137.0	246.3	1.8
208078_s_at	SIK1	2.36E-03	43.5	49.1	25.6	35.2	34.3	18.0	30.1	44.3	63.2	58.5	66.7	69.8	43.0	65.9	34.3	63.2	1.8
202255_s_at	SIPA1L1	4.90E-04	115.1	140.4	142.2	184.3	185.7	120.1	159.8	162.5	205.5	287.3	245.3	278.2	217.2	289.3	142.2	245.3	1.7
202896_s_at	SIRPA	1.02E-03	917.7	674.9	902.2	993.4	932.2	828.5	969.2	1221.5	1052.9	1400.3	1175.1	1595.2	1511.1	1385.2	917.7	1385.2	1.5
215889_at	SKIL	5.24E-04	397.6	339.2	413.1	405.4	391.0	347.6	446.2	494.2	479.7	668.7	740.8	653.6	694.1	686.8	397.6	668.7	1.7
217591_at	SKIL	1.09E-03	331.6	358.5	438.4	535.0	368.2	344.7	409.1	423.4	473.5	687.3	671.5	571.4	600.7	598.6	368.2	598.6	1.6
1555626_a_at	SLAMF1	6.38E-05	59.3	42.6	47.1	43.6	66.6	27.4	59.5	131.9	157.5	429.6	190.7	339.5	244.1	465.7	47.1	244.1	5.2
206181_at	SLAMF1	6.17E-06	35.8	32.0	35.0	41.7	51.1	30.8	53.3	142.5	170.1	363.1	186.0	273.2	198.0	432.0	35.8	198.0	5.5
219159_s_at	SLAMF7	1.03E-04	1597.1	299.8	630.5	367.5	1675.9	145.0	977.7	6087.8	7693.2	9371.7	6422.2	7654.9	5988.1	8523.6	630.5	7654.9	12.1
222838_at	SLAMF7	2.52E-05	305.6	77.1	214.0	130.1	631.5	54.1	376.5	2596.2	3552.4	4776.7	3108.6	3738.3	2277.9	4335.3	214.0	3552.4	16.6
234306_s_at	SLAMF7	7.38E-06	225.9	62.4	130.5	84.1	317.1	43.5	167.7	1567.1	1609.2	2597.0	1573.3	2459.5	1261.7	2213.7	130.5	1609.2	12.3
203123_s_at	SLC11A2	4.05E-03	1946.2	957.1	1500.7	1586.4	1676.3	1115.4	1866.9	2051.7	1661.3	3173.0	2353.0	2077.2	2142.3	2669.7	1586.4	2142.3	1.4
203124_s_at	SLC11A2	1.78E-03	684.3	335.4	744.3	734.4	916.7	558.1	885.9	971.5	680.7	1610.5	1213.7	992.0	986.1	1315.3	734.4	992.0	1.4
203125_x_at	SLC11A2	6.93E-04	303.3	245.8	211.6	214.5	275.6	184.1	250.3	390.0	392.6	494.9	371.2	382.8	325.9	407.8	245.8	390.0	1.6
237106_at	SLC11A2	2.11E-03	75.9	63.7	94.8	119.9	104.8	88.8	124.8	93.2	120.3	250.7	203.9	138.1	129.6	203.3	94.8	138.1	1.5
207057_at	SLC16A7	2.47E-04	22.9	15.4	36.7	28.0	20.0	26.6	40.4	54.6	23.0	77.3	67.1	72.6	44.1	103.8	26.6	67.1	2.5
210807_s_at	SLC16A7	9.28E-04	30.4	30.4	61.0	49.1	48.2	43.3	64.4	68.9	52.9	86.8	59.8	123.7	75.8	118.1	48.2	75.8	1.6
208389_s_at	SLC1A2	1.93E-04	48.9	58.3	49.1	43.9	47.3	47.1	55.2	77.0	97.6	186.4	126.7	133.6	138.2	202.0	48.9	133.6	2.7
225491_at	SLC1A2	1.83E-03	34.7	31.5	26.2	33.2	34.1	27.9	36.5	45.9	57.9	145.6	95.8	50.7	87.7	132.7	33.2	87.7	2.6
1569054_at	SLC1A3	5.79E-04	34.5	37.1	58.3	66.2	61.1	40.8	70.8	68.0	86.2	199.6	119.7	87.9	76.7	111.0	58.3	87.9	1.5
202800_at	SLC1A3	2.09E-03	2014.3	915.6	1563.6	1952.0	2569.4	1108.5	2841.7	3667.2	3741.8	4914.7	3752.5	3546.9	4304.5	3860.6	1952.0	3752.5	1.9
209610_s_at	SLC1A4	1.39E-03	278.0	167.2	199.0	245.2	207.6	244.7	242.0	425.4	287.1	396.6	341.1	307.4	286.1	340.3	242.0	340.3	1.4
212810_s_at	SLC1A4	9.59E-04	401.1	263.5	282.3	345.6	245.4	246.6	371.2	588.4	421.5	532.6	396.3	355.0	465.8	601.5	282.3	465.8	1.6
212811_x_at	SLC1A4	1.09E-03	297.9	209.2	182.7	201.1	183.5	213.4	193.5	393.0	304.7	369.5	270.7	272.8	289.0	298.8	201.1	298.8	1.5
205896_at	SLC22A4	3.76E-05	49.4	68.4	60.0	71.0	76.1	49.3	73.1	97.2	120.8	135.6	137.5	135.0	104.5	116.1	68.4	120.8	1.8
221432_s_at	SLC25A28	2.03E-05	316.7	323.7	397.6	334.2	372.0	297.9	362.4	621.4	628.9	931.6	630.8	974.7	803.7	936.1	334.2	803.7	2.4
223192_at	SLC25A28	3.37E-05	841.5	696.7	696.8	678.3	707.5	653.2	688.1	1350.5	1588.8	1895.6	1369.3	1699.4	1586.3	1920.9	696.7	1588.8	2.3
223296_at	SLC25A33	9.76E-04	197.4	121.2	204.9	170.6	201.7	166.8	232.2	294.7	212.6	438.9	261.7	254.3	270.8	308.3	197.4	270.8	1.4
218136_s_at	SLC25A37	1.21E-05	155.1	168.4	234.2	197.8	244.4	192.9	292.3	335.2	546.7	698.1	390.9	627.3	531.8	865.5	197.8	546.7	2.8
221920_s_at	SLC25A37	1.03E-04	32.5	32.1	70.9	68.6	53.8	73.9	68.9	73.2	75.7	157.7	91.3	137.0	145.1	164.9	68.6	137.0	2.0
222528_s_at	SLC25A37	4.32E-05	82.9	79.0	99.5	82.4	101.8	96.7	84.9	160.2	176.0	309.3	145.4	270.5	226.5	266.1	84.9	226.5	2.7
222529_at	SLC25A37	5.52E-04	140.7	96.7	104.0	91.2	110.0	104.9	103.0	161.0	211.6	271.3	159.6	221.8	198.2	256.3	104.0	211.6	2.0

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
226179_at	SLC25A37	1.88E-05	267.9	315.2	379.4	278.1	383.4	325.3	347.5	571.1	679.2	844.3	546.5	996.4	604.8	973.3	325.3	679.2	2.1
226928_x_at	SLC25A37	9.31E-05	73.2	60.3	100.2	74.9	82.1	74.4	109.8	112.9	149.3	239.5	123.1	234.8	183.4	261.4	74.9	183.4	2.4
228527_s_at	SLC25A37	1.30E-04	37.6	42.3	63.1	53.4	70.0	51.7	65.4	71.4	63.9	147.9	78.9	128.6	105.4	145.0	53.4	105.4	2.0
242335_at	SLC25A37	8.77E-05	37.8	57.5	104.2	97.9	113.4	83.2	104.4	131.2	173.6	329.4	168.1	231.4	160.5	322.2	97.9	173.6	1.8
220091_at	SLC2A6	2.48E-04	568.1	249.1	403.0	532.0	838.2	317.4	791.1	1130.6	1237.9	1729.1	1355.5	1896.3	2053.6	1876.4	532.0	1729.1	3.2
207362_at	SLC30A4	1.37E-03	36.0	37.4	32.0	37.4	50.8	27.1	43.6	61.8	42.0	147.2	111.2	104.4	85.1	122.7	37.4	104.4	2.8
239596_at	SLC30A7	1.89E-03	222.4	195.2	210.8	245.9	248.9	222.9	250.4	256.5	289.1	450.4	377.6	346.3	322.6	379.8	222.9	346.3	1.6
224626_at	SLC35A4	5.93E-03	340.8	378.3	321.2	347.5	347.7	350.2	381.0	514.3	394.5	436.2	454.8	494.6	457.6	461.0	347.7	457.6	1.3
225277_at	SLC39A13	7.22E-03	168.7	119.0	158.3	159.4	144.3	137.5	161.5	242.4	140.4	172.3	194.9	230.9	212.0	199.3	158.3	199.3	1.3
209267_s_at	SLC39A8	8.13E-04	1024.5	119.7	408.6	465.7	1417.8	125.2	1321.9	2568.3	2355.2	4108.3	4170.4	3408.9	2909.0	4166.0	465.7	3408.9	7.3
216504_s_at	SLC39A8	2.19E-04	374.9	66.1	190.1	252.7	642.6	68.6	595.9	1303.9	1246.9	2650.5	2425.1	2068.2	1551.4	2347.3	252.7	2068.2	8.2
219869_s_at	SLC39A8	2.77E-04	624.8	36.6	195.2	256.9	717.4	80.7	633.7	2203.7	1574.7	3079.4	2600.5	3013.7	2157.5	3087.5	256.9	2600.5	10.1
222935_x_at	SLC39A8	7.92E-04	76.8	80.2	112.1	87.7	109.5	74.4	107.3	153.1	96.8	181.7	162.8	215.1	172.8	149.5	87.7	162.8	1.9
228945_s_at	SLC39A8	6.92E-05	633.2	127.7	209.1	336.8	740.6	110.4	629.0	2315.6	1606.6	2868.3	2667.7	2754.9	2118.5	3173.6	336.8	2667.7	7.9
223798_at	SLC41A2	2.77E-05	248.3	186.4	273.7	321.9	368.1	228.6	300.1	639.9	761.0	1399.5	1022.0	788.6	1052.1	952.0	273.7	952.0	3.5
235299_at	SLC41A2	1.03E-04	386.4	224.7	410.2	484.0	664.7	342.7	531.8	739.2	761.4	1531.2	1226.1	1095.4	1126.5	1310.3	410.2	1126.5	2.7
243894_at	SLC41A2	1.15E-04	406.9	260.1	360.3	429.4	609.7	325.7	453.2	834.5	1109.4	1845.6	1247.8	1153.0	1393.9	1260.7	406.9	1247.8	3.1
226629_at	SLC43A2	4.22E-03	117.1	82.7	121.6	161.1	150.8	149.6	154.3	165.5	135.8	213.8	185.1	158.3	236.7	263.6	149.6	185.1	1.2
210692_s_at	SLC43A3	1.78E-04	1061.2	507.0	595.6	634.4	943.6	467.5	945.1	1690.3	1506.7	2320.1	1374.6	2344.6	2089.4	2178.6	634.4	2089.4	3.3
213113_s_at	SLC43A3	4.25E-04	3696.4	2410.9	2169.8	2485.9	3536.4	1541.1	3277.5	5629.3	5879.5	7002.7	4381.5	6538.3	5846.0	6652.4	2485.9	5879.5	2.4
234976_x_at	SLC4A5	1.86E-03	1108.2	399.0	643.6	757.5	842.2	456.8	1191.7	1428.9	1242.1	1868.8	1411.6	1346.2	1577.2	1721.6	757.5	1428.9	1.9
211030_s_at	SLC6A6	5.11E-04	58.6	35.4	65.0	72.5	71.7	80.9	75.6	74.0	56.3	110.9	99.0	107.6	121.9	109.2	71.7	107.6	1.5
212290_at	SLC7A1	4.49E-04	1200.1	469.1	673.6	756.2	1134.6	728.2	1230.1	1638.5	1072.5	1795.6	1368.6	1692.0	1784.9	2154.1	756.2	1692.0	2.2
212292_at	SLC7A1	9.61E-04	68.4	43.8	63.1	55.3	85.9	47.1	85.3	104.7	56.2	140.5	100.2	133.4	114.8	124.1	63.1	114.8	1.8
212295_s_at	SLC7A1	1.19E-03	670.1	301.4	532.5	535.6	795.5	500.6	1010.6	903.5	667.9	1391.6	995.5	1024.2	1113.9	1493.1	535.6	1024.2	1.9
201195_s_at	SLC7A5	8.66E-05	69.7	69.5	47.5	56.4	65.9	53.0	70.3	172.2	156.7	208.3	161.7	497.5	201.6	346.2	65.9	201.6	3.1
210542_s_at	SLCO3A1	2.07E-04	100.1	75.7	122.3	143.0	103.2	85.9	104.1	150.0	120.5	242.8	221.1	150.1	161.8	156.9	103.2	156.9	1.5
219229_at	SLCO3A1	2.85E-04	710.2	286.4	375.0	597.4	639.7	428.6	562.8	1040.7	992.6	1398.8	1246.5	1321.3	1498.5	1212.2	562.8	1246.5	2.2
227367_at	SLCO3A1	9.83E-04	272.7	141.3	250.3	343.4	345.5	290.6	360.6	463.1	477.1	700.5	580.4	515.0	614.1	526.4	290.6	526.4	1.8
229776_at	SLCO3A1	5.18E-04	103.2	60.6	69.0	105.9	111.6	68.4	94.8	142.0	139.3	218.3	214.1	188.2	244.3	195.3	94.8	195.3	2.1
219911_s_at	SLCO4A1	1.03E-03	35.1	36.6	39.9	42.7	28.2	23.6	33.1	64.3	52.0	62.7	51.8	65.5	49.2	83.5	35.1	62.7	1.8
219885_at	SLFN12	1.71E-04	94.1	165.2	188.4	205.3	196.6	152.9	221.2	220.8	341.7	480.5	364.9	328.3	252.6	331.0	188.4	331.0	1.8
1553055_a_at	SLFN5	7.73E-05	624.1	386.0	745.5	896.4	788.6	646.3	664.8	1087.4	727.2	2117.7	2097.0	1391.0	1726.2	1995.1	664.8	1726.2	2.6
1557078_at	SLFN5	4.93E-05	349.2	180.7	402.0	453.4	422.7	367.2	344.6	704.3	293.5	1057.9	1078.8	874.5	1000.1	1055.1	367.2	1000.1	2.7
238430_x_at	SLFN5	1.52E-04	407.5	291.7	579.3	738.7	646.0	559.6	594.5	629.7	413.4	1064.1	1305.2	1008.0	1083.4	1256.0	579.3	1064.1	1.8
243999_at	SLFN5	8.92E-05	240.4	150.3	257.9	289.8	287.1	218.0	237.0	448.1	233.9	669.1	670.5	532.1	555.3	688.1	240.4	555.3	2.3
205397_x_at	SMAD3	1.90E-03	60.6	54.7	40.2	38.7	44.9	35.1	29.8	80.7	67.3	82.6	63.6	119.5	80.8	99.4	40.2	80.8	2.0
205398_s_at	SMAD3	3.55E-05	36.5	19.6	23.1	22.3	25.1	32.0	22.4	80.2	55.6	99.5	103.3	124.9	81.3	111.6	23.1	99.5	4.3
218284_at	SMAD3	1.91E-05	147.7	120.6	89.7	138.4	90.1	121.8	85.7	372.0	461.7	345.8	486.1	476.8	405.7	600.9	120.6	461.7	3.8
202303_x_at	SMARCA5	2.28E-03	1177.3	1101.1	1435.6	1298.3	1290.9	1374.6	1393.1	1467.9	2037.9	2542.8	1820.9	1667.0	1661.8	2181.8	1298.3	1820.9	1.4
213859_x_at	SMARCA5	9.70E-03	881.8	752.4	1015.5	862.3	884.8	837.7	918.1	936.0	1354.8	1623.0	1118.3	967.9	1060.9	1461.5	881.8	1118.3	1.3
1558747_at	SMCHD1	2.48E-04	246.3	287.8	387.0	401.5	391.4	441.2	422.4	491.8	537.5	962.4	618.6	584.3	664.5	791.4	391.4	618.6	1.6
212569_at	SMCHD1	6.30E-03	216.8	213.0	377.8	341.7	355.8	326.4	392.7	317.3	485.2	1001.8	499.9	389.9	425.7	565.7	341.7	485.2	1.4
212577_at	SMCHD1	7.56E-04	116.5	130.0	186.1	193.7	218.5	221.4	230.4	240.2	293.2	623.7	368.7	309.2	312.7	428.1	193.7	312.7	1.6
241621_at	SMCHD1	5.70E-03	58.8	64.6	82.2	90.1	80.4	87.2	81.6	70.7	124.6	191.9	130.2	101.2	99.6	139.6	81.6	124.6	1.5
222270_at	SMEK2	4.88E-03	191.1	283.0	321.9	350.4	372.6	321.5	343.0	339.1	331.2	579.8	426.0	544.1	377.2	470.9	321.9	426.0	1.3
201793_x_at	SMG7	5.32E-03	575.3	515.2	521.0	551.6	540.6	535.9	497.0	707.5	670.8	678.8	573.2	823.1	778.5	743.5	535.9	707.5	1.3
217189_s_at	SMG7	8.01E-03	89.3	127.1	147.7	127.4	139.9	144.4	141.6	145.4	129.6	190.8	179.0	180.4	191.2	174.7	139.9	179.0	1.3
205622_at	SMPD2	9.33E-04	141.7	72.1	139.8	127.2	139.0	109.9	147.6	191.4	128.2	246.0	160.7	244.0	256.9	220.0	139.0	220.0	1.6
213624_at	SMPDL3A	2.02E-03	211.8	119.1	160.1	170.6	227.7	74.0	110.4	308.9	136.8	266.0	302.7	506.8	212.4	334.4	160.1	302.7	1.9
202043_s_at	SMS	1.00E-03	2772.3	2101.7	3013.6	2553.4	2994.0	2617.7	3037.1	3432.3	3738.6	4943.5	4038.0	3607.7	4359.9	4677.5	2772.3	4038.0	1.5
218393_s_at	SMU1	8.58E-03	573.1	541.5	554.2	626.5	600.0	557.1	616.6	631.6	700.6	819.5	718.2	704.6	787.5	796.7	573.1	718.2	1.3
242790_at	SNF8	9.35E-03	93.6	74.6	109.2	115.9	107.1	124.6	122.2	100.2	112.1	130.1	143.8	130.1	161.6	158.6	109.2	130.1	1.2
219409_at	SNIP1	8.66E-03	125.9	100.2	168.2	164.4	150.5	141.4	173.5	169.5	128.1	227.4	170.1	176.7	196.0	220.4	150.5	176.7	1.2
218032_at	SNN	1.17E-03	498.9	384.6	921.2	875.8	1047.6	658.7	960.4	722.2	1620.8	2787.5	1307.2	1714.5	1668.9	2228.3	875.8	1668.9	1.9
218033_s_at	SNN	3.11E-04	52.6	44.5	66.4	64.9	70.9	54.6	74.3	70.7	89.2	163.6	92.4	158.8	116.8	147.1	64.9	116.8	1.8
208821_at	SNRPB	9.64E-03	253.4	206.0	271.6	291.5	277.9	250.2	310.9	331.7	303.2	332.5	313.6	356.0	356.7	346.5	271.6	332.5	1.2
1559343_at	SNRPN	2.05E-03	323.1	378.3	470.3	450.7	535.8	455.5	551.7	488.7	545.1	866.6	561.6	640.7	661.7	737.1	455.5	640.7	1.4
1555388_s_at	SNX25	1.37E-03	145.1	170.2	222.4	196.6	218.1	188.0	152.2	219.3	243.0	445.5	258.8	273.4	300.3	320.3	188.0	273.4	1.5
217789_at	SNX6	3.79E-03	1240.0	1030.6	1092.8	1105.0	1000.1	1011.6	998.2	1313.3	1475.0	1549.0	1377.8	1303.2	1495.9	1557.9	1030.6	1475.0	1.4
223027_at	SNX9	9.14E-03	267.1	301.3	375.0	371.8	389.6	375.2	411.1	366.0	387.8	667.6	407.7	423.3	537.9	549.6	375.0	423.3	1.1
223028_s_at	SNX9	4.54E-04	680.1	579.6	634.3	656.7	710.4	611.7	682.8	837.0	942.3	1163.8	923.4	1127.6	1142.0	1176.8	656.7	1127.6	1.7
210001_s_at	SOCS1	3.51E-05	54.5	52.5	91.3	80.9	71.2	65.8	49.7	128.8	121.8	407.4	191.9	240.7	202.2	233.7	65.8	202.2	3.1
213337_s_at	SOCS1	3.41E-05	67.9	90.5	143.6	128.9	112.0	92.4	75.6	168.6	210.5	579.1	274.5	330.3	297.0	344.9	92.4	297.0	3.2
206359_at	SOCS3	8.28E-04	173.6	76.9	96.2	79.6	135.9	81.0	112.4	174.5	272.5	370.2	179.0	535.8	306.4	520.8	96.2	306.4	3.2
206360_s_at	SOCS3	4.47E-04	80.7	33.1	90.4	96.8	100.5	57.8	102.5	123.2	187.2	444.6	169.0	420.9	362.6	453.5	90.4	362.6	4.0

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
227697_at	SOCS3	9.09E-04	1043.1	414.1	1349.8	1192.6	1894.3	521.9	1994.4	2077.4	3443.6	6086.4	2548.4	3941.3	3365.4	4599.6	1192.6	3443.6	2.9
1566342_at	SOD2	5.50E-03	6122.7	3207.7	5200.3	6326.2	9135.7	3771.3	9150.5	9268.3	9408.3	10834.3	10549.7	10568.1	9892.9	10171.6	6122.7	10171.6	1.7
215078_at	SOD2	6.73E-05	147.2	50.2	290.6	172.5	420.0	87.4	388.8	848.9	1758.3	3278.5	1357.3	1723.8	1505.6	2447.0	172.5	1723.8	10.0
215223_s_at	SOD2	7.14E-04	4218.9	906.2	2207.7	2925.5	5900.2	1364.4	5922.3	10226.3	9649.6	11595.2	10678.1	12031.8	11467.8	12572.6	2925.5	11467.8	3.9
216841_s_at	SOD2	1.69E-03	2734.6	632.9	1933.2	2359.1	3878.9	1150.4	4163.2	4990.1	6103.9	8726.3	7258.2	6477.9	6082.5	7696.3	2359.1	6477.9	2.7
221477_s_at	SOD2	6.72E-04	2031.1	637.6	1443.9	1493.0	1553.2	493.5	1743.4	3316.4	3599.2	5432.8	4135.9	3320.9	3148.3	3536.5	1493.0	3536.5	2.4
230295_at	SOLH	5.10E-03	52.0	21.3	47.3	70.2	52.5	40.2	60.2	91.6	29.2	59.7	78.5	73.4	56.2	71.8	52.0	71.8	1.4
212777_at	SOS1	1.87E-04	233.1	240.1	258.4	310.5	274.1	272.2	245.8	351.4	372.1	502.1	559.5	403.1	392.6	403.6	258.4	403.1	1.6
212780_at	SOS1	1.33E-03	68.1	100.4	162.0	164.1	167.4	168.7	157.5	197.1	197.6	404.2	290.4	232.3	221.2	243.1	162.0	232.3	1.4
202863_at	SP100	5.98E-04	356.6	349.8	469.9	478.7	526.7	465.5	528.7	628.4	699.2	1046.1	733.1	692.7	664.3	817.5	469.9	699.2	1.5
202864_s_at	SP100	3.25E-04	1047.7	969.8	896.0	1067.8	1158.4	1028.8	1003.1	1465.6	1533.1	1913.2	1536.8	1790.7	1659.5	1647.5	1028.8	1647.5	1.6
210218_s_at	SP100	6.59E-04	1151.2	864.4	842.2	933.5	808.0	674.0	691.4	1305.9	1417.2	1497.5	1476.7	1397.5	1224.4	1478.3	842.2	1417.2	1.7
210985_s_at	SP100	1.37E-03	87.5	75.2	107.7	128.6	108.0	119.2	135.2	134.3	154.9	210.5	232.5	162.4	150.8	164.4	108.0	162.4	1.5
237426_at	SP100	1.73E-03	35.2	51.2	42.2	41.2	43.6	42.9	31.5	87.9	68.0	88.3	71.0	63.0	52.9	52.9	42.2	68.0	1.6
208012_x_at	SP110	7.13E-05	1995.0	1715.4	1692.2	1606.3	1492.7	1377.7	685.1	3110.1	3945.3	4461.5	3670.7	3417.7	2929.7	2356.4	1606.3	3417.7	2.1
208392_x_at	SP110	9.01E-05	273.3	269.0	279.5	227.9	228.5	205.5	135.9	382.8	532.5	735.3	504.6	505.6	489.3	373.6	228.5	504.6	2.2
209761_s_at	SP110	2.14E-05	833.1	664.0	754.2	659.5	663.4	745.5	344.0	1683.6	1511.8	2319.8	1625.0	1851.3	1545.5	1178.5	664.0	1625.0	2.4
209762_x_at	SP110	7.73E-05	1920.6	1912.2	1568.4	1541.2	1353.9	1242.2	704.9	2903.5	4074.4	4423.7	3804.2	3050.5	3026.2	2379.8	1541.2	3050.5	2.0
223980_s_at	SP110	2.15E-04	727.6	814.3	735.7	594.1	618.1	576.1	319.9	981.0	1662.1	2035.4	1130.4	1310.8	1382.2	994.5	618.1	1310.8	2.1
207777_s_at	SP140	5.78E-04	329.3	319.8	243.1	293.2	275.1	261.5	163.6	447.6	510.8	576.2	504.4	382.1	421.9	279.0	275.1	447.6	1.6
214791_at	SP140L	5.86E-04	1005.1	630.1	1065.1	951.0	564.5	831.9	914.0	1145.6	1094.2	2266.6	1490.3	1002.3	1648.1	1866.4	914.0	1490.3	1.6
210117_at	SPAG1	4.34E-04	57.8	78.6	61.6	97.9	121.2	93.8	117.4	149.4	158.3	414.3	297.0	252.1	219.4	247.5	93.8	247.5	2.6
206748_s_at	SPAG9	4.97E-03	581.9	467.2	517.5	490.9	546.5	499.1	571.9	576.1	743.4	814.4	620.2	794.0	731.4	780.1	517.5	743.4	1.4
222154_s_at	SPATS2L	3.97E-03	1299.3	1437.9	1280.4	1109.4	1242.0	1286.0	1107.4	1578.5	1762.9	1904.5	1594.7	1465.8	1561.1	1586.7	1280.4	1586.7	1.2
216965_x_at	SPG20	4.54E-03	48.4	51.8	57.2	56.7	52.3	44.7	56.9	58.5	61.7	90.6	101.3	66.4	56.4	75.7	52.3	66.4	1.3
219257_s_at	SPHK1	1.02E-05	60.5	25.1	44.1	70.1	104.6	25.2	90.4	316.9	243.0	456.4	358.5	835.1	507.0	643.9	60.5	456.4	7.5
1553973_a_at	SPINK6	3.18E-03	121.3	73.6	62.2	56.1	143.8	83.2	142.0	140.8	153.4	376.3	143.8	242.5	206.6	281.1	83.2	206.6	2.5
1562415_a_at	SPOCD1	8.13E-03	115.4	58.4	131.7	144.8	128.0	71.7	215.1	176.7	100.7	242.8	178.9	141.6	130.0	224.4	128.0	176.7	1.4
226353_at	SPPL2A	1.73E-03	2476.9	2797.1	2625.4	2639.6	3082.4	1949.4	2866.9	3195.7	3802.2	4811.2	3984.8	3597.7	3136.1	4136.3	2639.6	3802.2	1.4
219677_at	SPSB1	3.86E-03	45.3	49.7	47.1	51.4	42.6	35.2	50.0	57.9	64.5	125.4	58.5	81.3	72.7	90.0	47.1	72.7	1.5
226075_at	SPSB1	1.86E-03	22.6	38.7	49.6	57.1	38.1	36.4	47.0	40.3	58.8	86.9	61.2	72.7	52.6	112.0	38.7	61.2	1.6
203127_s_at	SPTLC2	2.93E-04	448.6	308.6	408.5	488.8	375.7	414.5	377.4	708.5	885.7	1047.9	693.4	694.0	815.0	899.3	408.5	815.0	2.0
216202_s_at	SPTLC2	5.40E-04	98.9	88.0	96.9	120.4	126.4	144.7	89.2	297.8	150.4	235.9	208.7	249.3	189.7	160.4	98.9	208.7	2.1
209218_at	SQLE	4.70E-03	269.2	225.7	107.1	115.9	263.3	161.3	204.5	361.3	265.9	253.7	221.8	319.0	237.3	304.2	204.5	265.9	1.3
213562_s_at	SQLE	2.85E-03	98.9	56.7	54.6	49.4	107.2	56.2	91.8	135.3	77.9	104.1	86.4	118.2	106.8	122.2	56.7	106.8	1.9
217995_at	SQRDL	1.43E-03	6047.8	4269.9	4261.9	5557.6	5580.3	3754.6	6822.7	7822.7	6671.2	7199.5	7937.2	7967.9	7574.8	8405.6	5557.6	7822.7	1.4
1558211_s_at	SRC	4.22E-03	85.7	72.5	91.1	73.7	83.6	73.2	85.8	98.1	87.0	126.9	122.0	152.7	172.9	126.5	83.6	126.5	1.5
213324_at	SRC	1.91E-05	156.0	119.4	211.3	226.8	267.4	245.5	279.4	354.5	234.8	541.4	454.8	492.4	530.8	516.0	226.8	492.4	2.2
221284_s_at	SRC	7.18E-04	55.5	30.1	71.9	74.0	67.5	59.5	78.8	78.5	48.2	128.9	106.2	120.1	142.4	107.8	67.5	107.8	1.6
202401_s_at	SRF	6.39E-03	1064.0	881.1	889.3	972.6	1026.8	919.7	1028.7	1115.6	1139.8	1229.7	1216.5	1253.2	1424.0	1588.4	972.6	1229.7	1.3
1556202_at	SRGAP2	3.68E-03	66.6	42.5	66.2	65.4	63.6	57.1	65.4	68.2	56.8	121.5	116.0	90.0	79.9	125.5	65.4	90.0	1.4
213329_at	SRGAP2	1.43E-04	181.7	130.0	139.2	187.6	159.4	150.9	133.5	291.0	243.4	306.3	299.4	296.0	296.8	382.0	150.9	296.8	2.0
227649_s_at	SRGAP2	3.08E-05	176.4	170.5	240.6	220.0	232.5	204.6	207.6	361.6	356.4	504.0	387.3	396.4	341.7	460.1	207.6	387.3	1.9
1568955_at	SRGAP2P1	3.93E-03	57.9	43.5	65.2	94.7	90.0	117.6	92.1	112.8	82.9	213.9	216.6	132.1	109.8	181.9	90.0	132.1	1.5
1568957_x_at	SRGAP2P1	3.03E-03	65.8	63.2	76.3	105.2	103.5	110.2	103.5	118.3	76.9	194.1	186.1	152.9	125.7	197.9	103.5	152.9	1.5
228628_at	SRGAP2P1	2.88E-03	131.0	101.0	177.0	196.0	185.4	183.1	204.6	248.9	172.5	341.3	256.7	227.2	217.7	287.6	183.1	248.9	1.4
229067_at	SRGAP2P1	5.56E-03	257.6	409.2	429.3	570.7	421.0	562.7	570.7	485.4	665.3	1031.4	815.4	520.1	591.3	845.1	429.3	665.3	1.5
1554676_at	SRGN	1.42E-05	31.9	55.0	65.9	43.0	55.6	62.5	66.7	96.2	161.7	416.1	184.4	205.5	169.5	243.0	55.6	184.4	3.3
201858_s_at	SRGN	3.57E-03	9012.0	9878.5	8794.8	10560.2	11150.0	9177.8	10846.0	10671.1	13097.9	13000.5	12828.5	13505.1	12461.7	14227.8	9878.5	13000.5	1.3
201859_at	SRGN	5.68E-03	1198.4	1381.1	1812.8	2062.5	2342.9	2007.4	2247.4	1801.4	2550.6	2768.1	2826.8	2584.2	2235.6	3069.5	2007.4	2584.2	1.3
208921_s_at	SRI	1.74E-03	4005.0	3576.7	3337.9	3840.4	4233.1	3152.4	4247.6	4732.8	5108.0	5989.0	5755.4	5311.6	5502.8	5953.8	3840.4	5502.8	1.4
202816_s_at	SS18	2.99E-03	530.8	389.6	499.2	476.6	533.0	499.1	542.0	650.2	592.3	903.8	601.8	661.0	704.9	705.2	499.2	661.0	1.3
209954_x_at	SS18	5.44E-03	421.7	346.4	390.1	363.3	385.4	334.6	358.5	433.6	411.0	541.1	503.0	537.0	532.6	537.9	363.3	532.6	1.5
217051_s_at	SS18	1.32E-03	203.2	173.6	248.5	217.0	248.3	208.6	249.3	307.4	238.0	358.7	291.2	312.1	286.3	307.0	217.0	307.0	1.4
201138_s_at	SSB	2.62E-03	3210.0	2878.8	2789.9	3046.5	2722.6	2948.5	2731.1	3549.7	4452.8	4847.0	4143.3	3654.8	3838.3	4629.9	2878.8	4143.3	1.4
201139_s_at	SSB	9.20E-03	5923.3	5546.6	5369.1	5665.7	4748.0	5009.2	4975.5	5640.1	7706.7	7986.3	7047.4	6290.3	6726.9	7550.6	5369.1	7047.4	1.3
229744_at	SSFA2	5.40E-03	105.7	110.0	190.1	146.5	161.2	151.1	183.4	156.1	154.1	334.8	274.8	190.9	187.4	205.3	151.1	190.9	1.3
236207_at	SSFA2	6.88E-03	436.7	401.1	537.5	494.6	595.5	607.8	600.9	587.8	646.3	885.0	759.2	646.8	692.8	728.8	537.5	692.8	1.3
203759_at	ST3GAL4	6.30E-03	38.2	29.9	39.6	43.4	43.7	41.1	53.0	52.1	33.1	69.8	54.4	70.3	82.5	62.1	41.1	62.1	1.5
203217_s_at	ST3GAL5	4.56E-03	884.4	931.3	1080.4	1371.6	681.4	751.5	650.4	1307.2	1255.8	1339.0	1576.6	925.0	912.5	1156.9	884.4	1255.8	1.4
206925_at	ST8SIA4	1.03E-03	66.7	64.3	39.3	48.3	68.8	49.1	33.4	109.2	77.6	75.6	93.5	122.0	74.5	93.6	49.1	93.5	1.9
230261_at	ST8SIA4	6.75E-03	44.0	44.0	29.6	38.5	42.9	22.2	34.8	53.2	44.0	96.2	132.6	62.7	51.0	97.8	38.5	62.7	1.6
230836_at	ST8SIA4	8.02E-04	32.4	27.8	28.0	46.0	56.5	27.8	41.7	65.4	35.2	62.7	102.3	81.9	42.6	66.5	32.4	65.4	2.0
242943_at	ST8SIA4	2.64E-03	43.6	39.1	22.6	41.3	25.7	25.4	26.1	48.9	50.0	59.7	70.0	60.6	41.3	60.1	26.1	59.7	2.3
38487_at	STAB1	9.97E-03	99.7	68.3	65.6	72.3	61.1	56.2	72.4	91.5	89.3	100.0	98.8	150.7	91.2	151.8	68.3	98.8	1.4
1554343_a_at	STAP1	2.00E-05	64.4	97.0	321.2	586.1	187.4	48.0	304.5	318.3	1090.2	2107.7	1857.6	902.0	195.2	1299.1	187.4	1090.2	5.8

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
220059_at	STAP1	7.30E-05	57.3	72.6	145.1	245.4	102.7	43.1	123.3	149.9	513.3	927.0	916.1	363.9	92.7	545.9	102.7	513.3	5.0
226390_at	STARD4	1.55E-05	186.5	200.7	183.5	155.6	216.2	142.9	232.1	436.4	488.2	699.3	377.3	470.9	340.7	676.9	186.5	470.9	2.5
206868_at	STARD8	9.31E-03	115.4	102.1	134.4	150.0	147.0	101.8	137.9	152.9	110.9	177.9	165.6	198.7	169.1	176.2	134.4	169.1	1.3
200887_s_at	STAT1	5.96E-04	849.5	1056.3	1488.6	1021.7	1098.3	972.8	1275.7	1285.0	1630.7	2555.6	2040.0	1418.6	1320.4	1981.5	1056.3	1630.7	1.5
209969_s_at	STAT1	1.05E-04	369.8	567.7	445.5	361.5	398.6	247.2	321.6	691.0	866.2	1132.0	983.7	822.7	729.8	992.1	369.8	866.2	2.3
205170_at	STAT2	8.89E-06	241.0	280.6	386.3	344.3	314.6	263.9	365.3	465.7	695.1	1050.1	779.5	664.3	599.8	898.9	314.6	695.1	2.2
217199_s_at	STAT2	6.92E-04	36.6	37.5	54.2	59.5	60.6	38.9	46.8	63.4	49.5	92.6	89.2	87.6	93.9	98.6	46.8	89.2	1.9
225636_at	STAT2	2.76E-04	3657.0	4126.6	4149.4	3864.2	3648.8	3427.9	3936.5	5164.7	6174.1	7566.3	5985.7	5118.4	5024.1	6881.4	3864.2	5985.7	1.5
208992_s_at	STAT3	3.48E-03	1538.0	1320.1	1185.6	1364.0	1504.2	1110.2	1447.0	1746.2	1709.0	2182.0	1815.6	1974.8	2149.4	2228.3	1364.0	1974.8	1.4
225289_at	STAT3	7.96E-03	469.3	392.8	487.0	551.5	613.7	535.5	716.8	649.9	559.9	757.3	624.8	692.6	706.0	821.3	535.5	692.6	1.3
243213_at	STAT3	7.77E-03	48.5	52.6	71.3	71.3	66.5	60.5	65.1	63.3	55.3	151.2	91.2	81.7	106.8	125.3	65.1	91.2	1.4
206118_at	STAT4	1.16E-05	57.3	55.0	57.7	79.6	94.2	42.4	45.9	267.0	507.7	1299.0	573.1	717.2	597.4	736.1	57.3	597.4	10.4
203986_at	STBD1	2.83E-05	108.8	84.7	125.3	88.5	102.6	109.1	141.8	189.1	167.6	363.5	190.0	208.1	255.9	304.0	108.8	208.1	1.9
220187_at	STEAP4	1.55E-04	7.0	18.2	12.3	22.6	10.8	19.7	22.6	35.3	61.0	197.2	52.2	116.2	111.7	139.5	18.2	111.7	6.1
225987_at	STEAP4	1.46E-04	71.1	87.8	39.3	61.6	63.3	37.2	56.5	212.9	421.2	686.7	187.4	436.3	512.0	645.6	61.6	436.3	7.1
202693_s_at	STK17A	4.38E-03	70.3	76.6	119.3	109.5	175.4	109.5	160.5	147.0	132.0	321.3	241.3	191.3	178.6	181.4	109.5	181.4	1.7
202695_s_at	STK17A	8.58E-03	97.6	110.0	129.7	105.4	154.9	133.2	157.3	128.2	127.3	229.7	192.9	201.7	150.3	193.6	129.7	192.9	1.5
205214_at	STK17B	6.08E-03	286.3	350.0	385.3	409.3	460.2	634.2	540.5	546.1	446.5	797.9	617.0	621.5	666.4	718.5	409.3	621.5	1.5
204068_at	STK3	8.72E-03	328.2	312.3	421.2	482.0	534.6	474.1	568.3	463.5	679.9	1044.5	653.8	556.2	622.8	798.2	474.1	653.8	1.4
211078_s_at	STK3	6.00E-03	39.8	48.6	62.1	59.8	80.3	76.3	69.6	94.3	74.9	150.4	93.0	93.4	89.8	93.2	62.1	93.2	1.5
223852_s_at	STK40	2.51E-03	857.5	754.8	671.1	755.0	682.3	651.1	789.8	983.1	1024.0	1116.1	929.9	1322.4	1254.8	1236.4	754.8	1116.1	1.5
225015_s_at	STK40	2.16E-03	121.1	85.9	134.0	138.7	116.9	118.3	135.7	149.2	126.4	218.9	155.3	212.8	229.6	213.9	121.1	212.8	1.8
201061_s_at	STOM	4.37E-03	4735.5	4103.4	4607.0	3391.0	4769.9	3852.2	5272.8	6128.6	4745.3	5951.7	5117.3	5845.8	5974.3	6410.1	4607.0	5951.7	1.3
204701_s_at	STOML1	3.26E-03	78.7	69.3	82.2	79.1	80.8	70.1	72.0	81.4	101.1	137.0	97.4	122.0	113.8	112.4	78.7	112.4	1.4
33736_at	STOML1	4.25E-04	258.5	294.5	313.7	293.9	326.6	309.4	278.6	337.1	451.2	530.4	406.5	455.0	465.3	427.4	294.5	451.2	1.5
218666_s_at	STX17	4.76E-04	157.5	182.5	250.7	231.9	251.8	265.1	248.1	268.1	313.0	527.9	360.7	352.8	346.2	387.9	248.1	352.8	1.4
222708_s_at	STX17	1.40E-03	139.8	159.2	218.9	173.5	200.6	207.8	183.7	222.4	268.3	429.8	260.7	231.0	266.2	314.9	183.7	266.2	1.4
209238_at	STX3	6.81E-03	237.6	220.2	343.6	278.5	351.0	275.2	342.8	308.1	353.7	582.3	321.9	407.4	329.3	450.5	278.5	353.7	1.3
214512_s_at	SUB1	2.35E-03	1090.3	1025.7	1156.2	1256.9	1162.3	1204.0	1172.5	1367.9	1594.6	2178.9	1602.0	1614.9	1498.1	1663.1	1162.3	1602.0	1.4
224724_at	SULF2	4.54E-03	39.7	42.0	26.8	27.0	35.1	29.4	24.4	87.9	56.3	65.3	52.0	178.5	35.3	129.9	29.4	65.3	2.2
222978_at	SURF4	8.29E-03	1246.2	1064.5	1021.8	1073.2	1057.9	983.2	1043.9	1418.9	1198.7	1340.1	1244.8	1451.5	1541.6	1390.3	1057.9	1390.3	1.3
222979_s_at	SURF4	3.87E-03	260.7	297.9	278.1	271.1	280.6	274.6	304.4	369.5	342.7	476.4	446.3	335.8	364.0	390.4	278.1	369.5	1.3
226264_at	SUSD1	2.96E-03	1561.2	1251.9	899.4	1213.3	1750.9	839.9	1839.2	2198.6	2164.6	2960.0	2049.9	2674.3	2161.3	2258.5	1251.9	2198.6	1.8
1560879_a_at	SYT15	9.60E-03	49.6	48.2	49.1	46.1	50.9	53.0	55.6	51.7	54.7	71.4	54.5	77.1	72.7	78.3	49.6	71.4	1.4
242109_at	SYTL3	4.38E-04	69.5	79.5	106.8	85.5	82.3	89.0	78.4	143.2	117.1	278.2	130.1	120.8	150.7	165.9	82.3	143.2	1.7
1552541_at	TAGAP	2.28E-04	128.8	80.3	116.7	104.0	109.3	90.4	118.1	166.9	195.4	475.9	254.8	281.8	277.9	354.5	109.3	277.9	2.5
1552542_s_at	TAGAP	1.58E-04	87.6	52.2	69.5	78.7	89.9	64.9	70.8	187.3	114.2	430.4	203.9	213.0	221.5	313.3	70.8	213.0	3.0
229723_at	TAGAP	3.86E-04	165.4	139.4	198.4	250.4	290.0	185.2	310.6	335.2	470.2	1211.4	648.0	556.1	361.8	801.1	198.4	556.1	2.8
207616_s_at	TANK	5.18E-04	1098.2	907.8	1037.4	945.9	1217.5	996.8	1286.4	1399.2	1894.6	2236.9	1469.1	1818.2	1647.6	2146.4	1037.4	1818.2	1.8
209451_at	TANK	4.36E-03	94.6	87.2	160.2	143.9	168.8	175.0	217.3	148.2	204.8	469.1	248.0	203.0	219.2	309.5	160.2	219.2	1.4
210458_s_at	TANK	4.15E-04	520.9	394.6	516.5	500.8	603.7	564.4	681.5	738.4	895.6	1182.8	807.1	876.6	914.9	1175.9	520.9	895.6	1.7
202307_s_at	TAP1	1.84E-05	862.1	806.3	869.5	832.6	998.3	532.9	918.4	1760.3	2154.3	2718.9	1986.4	2218.2	1979.5	2697.2	862.1	2154.3	2.5
204769_s_at	TAP2	3.93E-03	93.3	157.4	173.1	135.0	180.3	122.7	183.7	146.5	176.2	321.6	170.6	212.8	216.6	293.5	157.4	212.8	1.4
204770_at	TAP2	7.26E-04	147.2	150.5	167.0	199.6	164.4	152.6	140.9	277.2	169.5	359.6	431.4	261.0	247.2	269.0	152.6	269.0	1.8
208428_at	TAP2	1.44E-03	88.8	41.9	43.9	40.3	41.6	41.8	89.9	126.7	51.1	69.9	80.3	51.6	71.2	141.9	41.9	71.2	1.7
225973_at	TAP2	2.72E-04	221.0	373.0	496.5	606.1	375.9	326.8	368.0	411.5	487.2	1012.2	1086.7	530.0	588.9	700.0	373.0	588.9	1.6
210294_at	TAPBP	1.64E-04	82.5	76.7	110.2	111.2	122.8	80.2	130.9	151.2	135.4	260.5	195.6	168.5	151.7	214.6	110.2	168.5	1.5
212350_at	TBC1D1	6.21E-03	689.5	459.7	610.8	570.6	672.7	434.1	605.7	749.3	595.5	851.2	637.6	926.5	664.2	833.6	605.7	749.3	1.2
214013_s_at	TBC1D1	1.16E-03	72.1	63.6	68.7	74.4	79.6	62.7	85.6	103.9	81.0	118.1	110.6	129.7	103.3	100.9	72.1	103.9	1.4
1554701_a_at	TBC1D16	4.20E-03	77.9	77.6	90.2	81.1	91.2	60.2	81.7	100.2	87.8	132.0	129.9	117.2	134.1	128.4	81.1	128.4	1.6
222116_s_at	TBC1D16	4.17E-03	169.9	191.2	146.7	194.0	194.7	131.0	182.0	232.0	214.7	314.5	288.6	233.6	257.3	290.0	182.0	257.3	1.4
216549_s_at	TBC1D22B	2.82E-03	36.7	41.1	63.4	56.6	63.5	68.4	67.9	81.8	46.4	104.4	83.6	130.7	86.1	103.6	63.4	86.1	1.4
223375_at	TBC1D22B	1.24E-03	256.6	241.6	278.6	226.0	305.7	290.3	354.3	334.5	384.4	565.8	348.4	390.9	425.2	489.2	278.6	390.9	1.4
212956_at	TBC1D9	1.11E-03	1393.3	1450.7	2055.4	1731.3	2210.7	1766.9	2517.5	2052.8	2884.3	5254.9	3804.2	2880.3	2938.4	3476.7	1766.9	2938.4	1.7
212960_at	TBC1D9	4.07E-05	168.9	151.1	183.9	187.8	219.1	190.6	233.3	355.8	293.2	613.8	397.3	546.4	559.9	453.4	187.8	453.4	2.4
218520_at	TBK1	8.13E-04	331.3	437.6	575.7	590.5	594.4	508.0	696.8	612.2	810.3	1304.1	937.5	721.1	833.2	980.1	575.7	833.2	1.4
220684_at	TBX21	2.06E-03	64.3	69.0	66.2	66.1	56.2	66.1	54.8	88.8	91.1	99.5	173.0	81.2	103.8	85.1	66.1	91.1	1.4
203753_at	TCF4	2.42E-06	94.6	63.1	98.1	93.3	89.1	59.2	100.1	356.1	324.6	677.4	455.7	463.5	303.7	685.3	93.3	455.7	4.9
212382_at	TCF4	7.57E-06	330.2	182.8	309.3	281.4	212.6	192.8	270.6	1005.0	1364.3	2136.2	1300.4	1265.3	1082.1	2394.9	270.6	1300.4	4.8
212385_at	TCF4	2.43E-05	20.2	22.4	28.7	23.9	16.2	16.8	28.4	47.7	51.3	130.1	114.2	68.3	65.1	140.2	22.4	68.3	3.1
212386_at	TCF4	7.65E-06	28.0	40.0	53.9	49.8	40.1	46.0	66.0	114.3	123.6	400.2	228.1	144.2	184.1	363.6	46.0	184.1	4.0
212387_at	TCF4	1.12E-05	132.7	107.7	140.3	156.2	107.2	100.9	143.7	348.3	397.9	855.1	494.5	380.2	413.8	732.0	132.7	413.8	3.1
213891_s_at	TCF4	4.69E-05	175.9	126.6	156.8	141.9	109.8	112.7	125.7	359.2	511.9	882.8	517.5	424.9	374.0	914.7	126.6	511.9	4.0
222146_s_at	TCF4	1.16E-05	108.8	97.7	128.6	127.8	101.1	81.4	105.1	310.4	293.0	579.9	396.2	406.2	353.6	679.8	105.1	396.2	3.8
221016_s_at	TCF7L1	3.06E-03	83.9	84.7	176.7	103.8	90.9	106.8	93.8	119.3	140.4	213.0	136.4	134.3	119.6	135.9	93.8	135.9	1.4
232692_at	TDRD6	4.28E-05	112.7	57.2	65.8	56.5	89.3	56.1	131.8	216.7	165.5	306.6	232.0	227.8	158.4	354.6	65.8	227.8	3.5

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
213361_at	TDRD7	1.46E-04	1646.0	1742.7	1254.8	1297.4	1391.0	1525.6	1506.8	2302.7	3516.5	4054.0	2728.8	2946.7	3464.4	3649.6	1506.8	3464.4	2.3
229790_at	TERF2	2.02E-03	70.4	76.6	100.8	102.0	95.4	82.9	96.6	110.6	106.4	159.3	126.2	117.1	110.8	122.8	95.4	117.1	1.2
202719_s_at	TES	8.23E-03	571.7	440.8	303.6	416.7	445.7	264.9	266.5	609.1	503.9	507.6	542.1	628.6	595.9	469.2	416.7	542.1	1.3
1569385_s_at	TET2	2.20E-03	381.3	315.4	390.9	359.4	415.7	396.1	327.9	456.7	397.2	594.0	467.6	601.7	532.2	576.5	381.3	532.2	1.4
204147_s_at	TFDP1	9.28E-03	163.0	160.7	182.1	175.2	188.5	160.6	166.2	259.4	169.3	213.2	210.2	243.0	224.9	226.4	166.2	224.9	1.4
242939_at	TFDP1	3.68E-03	237.0	143.4	238.9	262.2	256.7	282.3	326.3	271.2	347.1	667.0	470.6	390.8	362.2	514.1	256.7	390.8	1.5
1565347_s_at	TFE3	7.13E-03	120.8	79.8	92.7	100.7	98.6	97.2	132.0	138.2	116.6	133.2	138.5	138.6	136.3	133.9	98.6	136.3	1.4
206715_at	TFEC	8.24E-04	811.9	878.7	928.8	875.7	1027.2	873.7	1030.3	1347.2	1548.5	2263.3	1548.7	1367.8	1220.7	1505.9	878.7	1505.9	1.7
217839_at	TFG	3.59E-03	634.7	601.0	672.6	717.8	739.4	655.4	818.5	795.7	993.9	1272.0	968.3	863.3	868.0	1094.1	672.6	968.3	1.4
221871_s_at	TFG	2.19E-03	364.5	331.4	339.5	351.0	375.5	342.1	403.3	491.5	523.7	667.8	545.1	424.1	467.5	572.5	351.0	523.7	1.5
209278_s_at	TFPI2	2.19E-03	35.6	40.3	20.4	25.4	24.0	24.1	29.1	55.7	97.5	156.1	56.2	66.3	34.5	113.3	25.4	66.3	2.6
226625_at	TGFBR3	9.35E-03	113.1	134.1	68.2	76.1	52.4	64.8	74.1	135.0	170.2	163.1	129.2	59.8	80.1	121.2	74.1	129.2	1.7
218724_s_at	TGIF2	3.69E-03	60.5	44.2	74.8	62.0	66.3	57.0	67.0	102.3	46.2	130.9	88.6	101.4	75.1	87.1	62.0	88.6	1.4
213191_at	TICAM1	2.74E-04	120.9	83.9	123.5	136.4	158.3	126.7	174.8	188.6	220.8	383.4	217.0	289.8	316.5	327.2	126.7	289.8	2.3
1552280_at	TIMD4	2.95E-04	35.4	116.2	46.9	27.9	44.5	31.0	23.8	79.5	219.9	93.1	42.2	63.5	83.2	64.6	35.4	79.5	2.2
201821_s_at	TIMM17A	5.16E-03	443.0	429.0	537.1	675.0	513.6	455.7	572.3	538.0	642.1	818.6	881.7	696.5	585.7	611.5	513.6	642.1	1.3
201666_at	TIMP1	3.01E-04	275.2	256.9	302.2	500.2	562.3	381.5	462.2	919.7	475.4	606.5	813.2	2621.1	1001.3	1491.7	381.5	919.7	2.4
219258_at	TIPIN	3.72E-03	68.3	66.1	107.5	87.9	80.8	79.8	108.5	101.1	85.1	165.4	108.1	105.7	92.3	135.4	80.8	105.7	1.3
1554351_a_at	TIPRL	2.70E-03	611.7	595.5	714.1	737.7	766.9	818.9	837.3	1010.9	850.1	1230.9	937.3	1048.8	950.4	1062.1	737.7	1010.9	1.4
202011_at	TJP1	3.91E-04	173.6	215.4	639.2	282.1	317.0	489.3	208.1	272.2	535.9	1191.5	462.4	444.7	910.5	549.2	282.1	535.9	1.9
214168_s_at	TJP1	1.72E-03	45.9	36.9	62.8	44.3	54.1	61.8	42.8	57.6	81.5	186.0	59.8	82.0	127.8	76.1	45.9	81.5	1.8
216997_x_at	TLE4	1.01E-03	177.9	128.9	196.6	223.8	196.7	178.5	194.4	240.3	238.5	386.4	261.4	293.9	301.7	321.0	194.4	293.9	1.5
233575_s_at	TLE4	2.70E-04	167.4	138.1	237.5	229.7	220.4	192.8	230.1	271.6	238.6	417.0	316.1	320.7	357.3	321.7	220.4	320.7	1.5
212986_s_at	TLK2	1.48E-04	133.8	128.0	179.3	204.9	180.4	169.0	187.5	240.0	240.4	362.0	283.5	284.0	293.1	289.8	179.3	284.0	1.6
212997_s_at	TLK2	1.10E-03	565.1	645.4	685.5	678.1	704.1	729.9	749.2	780.5	1062.4	1259.5	995.3	880.7	943.6	1099.9	685.5	995.3	1.5
233349_at	TLK2	2.61E-03	575.4	524.0	673.1	594.3	594.9	668.4	713.4	735.7	872.6	1164.4	798.4	693.7	864.2	1006.6	594.9	864.2	1.5
210176_at	TLR1	2.38E-03	513.2	421.3	602.8	571.7	713.6	555.7	784.8	795.1	663.3	994.6	945.1	760.4	847.5	967.4	571.7	847.5	1.5
204924_at	TLR2	1.46E-04	881.7	274.0	1055.8	952.9	1266.3	564.2	997.6	1902.3	1478.2	2727.1	2189.6	2510.6	2060.7	2475.0	952.9	2189.6	2.3
220146_at	TLR7	2.97E-03	419.5	544.5	827.1	723.8	961.0	927.9	751.3	821.2	1099.8	1778.1	1095.7	1013.1	1267.7	1074.4	751.3	1095.7	1.5
222952_s_at	TLR7	1.09E-03	273.1	197.2	306.5	263.9	310.0	319.0	271.1	341.2	413.0	573.5	362.4	408.5	545.1	489.3	273.1	413.0	1.5
209149_s_at	TM9SF1	1.96E-04	240.1	160.7	264.4	241.3	253.6	255.4	261.0	336.5	283.5	434.5	371.5	419.5	403.2	359.7	253.6	371.5	1.5
212194_s_at	TM9SF4	2.33E-04	149.5	142.1	213.3	230.4	240.4	174.4	229.1	323.1	228.2	373.1	308.8	398.9	343.9	362.5	213.3	343.9	1.6
212198_s_at	TM9SF4	2.04E-03	620.4	570.0	481.9	517.5	710.1	583.7	599.4	1036.9	631.4	640.6	741.0	972.4	928.6	837.3	583.7	837.3	1.4
1552302_at	TMEM106A	1.49E-05	213.3	164.1	265.2	207.4	242.2	184.8	245.9	428.8	595.8	972.4	576.9	612.7	694.3	732.6	213.3	612.7	2.9
1552303_a_at	TMEM106A	9.42E-05	82.7	74.6	73.6	63.4	73.7	63.1	78.4	124.6	142.7	246.7	169.0	194.4	159.3	181.0	73.7	169.0	2.3
234580_at	TMEM106A	3.03E-04	97.2	84.7	97.0	96.7	113.0	85.2	102.4	156.9	113.6	300.8	209.6	245.5	183.5	228.1	97.0	209.6	2.2
213851_at	TMEM110	2.07E-05	182.0	247.9	257.9	261.5	231.4	238.3	237.0	542.1	651.7	817.0	572.9	1028.7	585.5	934.4	238.3	651.7	2.7
227078_at	TMEM110	2.60E-04	127.3	170.9	183.2	211.9	176.9	195.6	190.0	266.3	246.8	339.4	310.1	352.1	284.0	386.7	183.2	310.1	1.7
227127_at	TMEM110	1.84E-04	99.0	110.3	130.4	117.5	99.5	113.4	102.5	169.2	166.9	237.8	183.6	214.9	215.2	269.2	110.3	214.9	1.9
223113_at	TMEM138	9.92E-03	411.2	369.2	455.0	471.2	461.1	396.8	473.8	639.2	390.4	634.5	592.7	583.4	512.6	539.8	455.0	583.4	1.3
218999_at	TMEM140	5.00E-03	1403.4	1472.3	896.2	1059.3	770.5	614.6	765.7	1571.1	1906.0	1956.2	1195.3	1430.5	1321.0	1621.0	896.2	1571.1	1.8
238063_at	TMEM154	4.66E-04	44.1	29.7	50.4	74.4	64.4	42.4	52.7	78.5	124.6	299.4	121.1	159.7	126.7	228.9	50.4	126.7	2.5
226825_s_at	TMEM165	4.76E-03	528.5	454.5	428.0	497.2	574.1	493.6	559.3	688.6	507.8	576.9	695.0	922.9	646.8	657.4	497.2	657.4	1.3
226827_at	TMEM165	3.05E-03	492.2	542.6	479.2	570.9	612.8	491.7	620.5	740.2	647.5	751.5	749.8	752.6	767.5	745.3	542.6	749.8	1.4
228505_s_at	TMEM170A	7.79E-04	265.7	267.4	372.9	377.2	411.6	392.6	406.8	373.0	416.6	685.0	509.8	560.3	515.7	615.2	377.2	515.7	1.4
230414_s_at	TMEM170A	2.19E-03	223.0	239.8	267.8	277.8	307.6	277.3	300.4	317.4	282.1	461.3	325.9	435.5	425.3	448.3	277.3	425.3	1.5
1553559_at	TMEM171	5.84E-06	44.2	47.8	40.3	46.5	42.9	42.3	45.2	253.2	378.0	661.0	235.1	333.3	354.8	426.7	44.2	354.8	8.0
240770_at	TMEM171	1.43E-05	28.1	23.9	14.6	18.2	15.6	8.0	23.5	163.7	301.2	736.2	241.7	195.3	201.5	322.3	18.2	241.7	13.3
219253_at	TMEM185B	1.57E-03	227.7	223.1	247.4	261.7	269.0	205.0	302.7	365.5	278.4	549.8	387.0	380.2	344.4	399.8	247.4	380.2	1.5
212619_at	TMEM194A	7.73E-05	110.2	97.0	146.0	119.1	145.4	173.0	147.1	196.9	191.3	364.0	224.0	239.1	284.8	253.1	145.4	239.1	1.6
212621_at	TMEM194A	1.17E-03	246.1	208.8	274.2	269.1	359.7	368.0	281.3	311.0	397.8	710.1	454.9	477.3	585.5	536.7	274.2	477.3	1.7
222736_s_at	TMEM38B	2.75E-03	369.6	362.7	529.0	405.2	499.7	362.2	579.6	517.2	505.6	971.0	504.5	684.8	644.2	675.1	405.2	644.2	1.6
222418_s_at	TMEM43	7.44E-03	383.6	396.2	344.8	316.8	375.6	376.6	397.4	464.5	409.2	455.3	471.8	485.6	479.9	556.2	376.6	471.8	1.3
218776_s_at	TMEM62	7.19E-03	464.5	343.4	512.8	528.8	467.2	633.5	533.9	604.1	618.1	736.6	688.5	564.5	685.8	693.5	512.8	685.8	1.3
229452_at	TMEM88	7.73E-05	62.2	45.9	80.0	78.1	105.6	85.5	86.1	110.4	86.7	204.4	125.2	228.3	141.0	176.7	80.0	141.0	1.8
201645_at	TNC	1.75E-05	30.0	35.1	31.4	26.8	61.0	18.2	28.3	63.4	101.1	123.6	143.6	237.7	73.4	114.7	30.0	114.7	3.8
207113_s_at	TNF	1.89E-05	296.6	154.6	306.0	277.6	573.8	257.0	503.6	1360.7	1872.7	3700.4	1473.8	2089.9	2089.8	2734.0	296.6	2089.8	7.0
202509_s_at	TNFAIP2	1.49E-04	181.7	146.9	193.2	201.3	217.3	147.3	203.3	280.7	249.2	516.8	356.5	429.4	394.6	401.9	193.2	394.6	2.0
202510_s_at	TNFAIP2	2.76E-04	3166.2	2993.3	3560.1	2871.6	3742.2	2838.7	3478.7	4219.5	4269.7	5767.1	4748.9	5628.6	5250.8	5413.6	3166.2	5250.8	1.7
202643_s_at	TNFAIP3	4.32E-05	658.9	525.0	625.6	647.7	1061.4	499.0	986.0	1567.4	2858.7	3672.6	2160.6	2549.4	2331.0	3193.7	647.7	2549.4	3.9
202644_s_at	TNFAIP3	7.39E-05	1143.3	916.1	1222.7	1296.4	2014.9	1022.3	1915.2	2881.2	4023.2	5776.5	3593.6	3702.6	3638.3	4718.4	1222.7	3702.6	3.0
206025_s_at	TNFAIP6	1.35E-03	2302.0	77.5	1031.1	1304.0	3599.4	298.4	3304.0	8828.3	9298.0	15350.0	11280.2	11326.3	10125.8	14121.5	1304.0	11280.2	8.7
206026_s_at	TNFAIP6	4.49E-03	2452.2	76.5	1531.4	2033.0	4225.8	410.9	4794.7	7187.9	7583.0	13252.7	10786.2	9103.5	8443.8	11210.0	2033.0	9103.5	4.5
208296_x_at	TNFAIP8	4.60E-04	834.2	889.7	1176.4	1100.1	1248.2	1093.2	1154.3	1197.4	1531.9	2165.2	1848.9	1693.4	1419.9	2059.3	1100.1	1693.4	1.5
210260_s_at	TNFAIP8	1.14E-04	508.7	595.6	801.6	820.2	924.4	753.1	866.5	978.9	1105.8	1635.5	1637.3	1406.6	1048.2	1645.6	801.6	1406.6	1.8
1552648_a_at	TNFRSF10A	1.17E-04	77.7	63.5	71.2	64.9	70.3	74.0	100.2	107.0	116.2	142.3	107.1	112.0	142.9	176.1	71.2	116.2	1.6

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
231775_at	TNFRSF10A	9.76E-04	230.7	220.6	257.3	216.3	188.9	264.2	341.3	336.3	455.0	563.9	306.2	279.6	338.6	678.2	230.7	338.6	1.5
209294_x_at	TNFRSF10B	9.85E-03	273.0	293.5	286.2	311.4	284.2	307.8	306.3	394.5	296.7	365.7	377.3	423.1	403.3	377.6	293.5	377.6	1.3
206222_at	TNFRSF10C	7.45E-03	89.1	57.5	86.3	62.4	90.5	75.8	67.3	92.8	151.4	240.9	68.2	163.4	118.0	209.8	75.8	151.4	2.0
203508_at	TNFRSF1B	3.04E-03	851.9	826.3	1089.6	997.5	1136.0	941.4	787.4	1478.7	1390.2	1472.1	1095.3	2846.1	1707.3	2348.5	941.4	1478.7	1.6
207536_s_at	TNFRSF9	4.39E-04	79.1	68.2	51.9	56.4	56.4	56.4	52.7	107.9	98.8	94.6	78.1	105.9	89.0	106.6	56.4	98.8	1.8
202687_s_at	TNFSF10	8.98E-06	817.2	823.4	783.7	859.4	700.8	593.3	502.0	2667.2	3910.6	4905.3	2915.0	3412.1	2540.6	4013.1	783.7	3412.1	4.4
202688_at	TNFSF10	8.78E-06	285.4	207.7	284.0	329.5	287.9	225.3	225.2	1264.6	1742.6	2603.8	1290.7	1494.8	1065.1	2140.7	284.0	1494.8	5.3
214329_x_at	TNFSF10	2.66E-05	34.2	34.8	80.1	65.9	69.0	51.3	61.9	173.0	309.8	727.1	338.6	195.7	177.7	475.8	61.9	309.8	5.0
223501_at	TNFSF13B	7.16E-04	969.7	1025.4	1374.9	1198.9	1205.5	1326.3	1233.8	1813.6	1844.9	2493.2	2191.8	1390.7	1827.7	2049.4	1205.5	1844.9	1.5
223502_s_at	TNFSF13B	1.21E-05	849.6	850.5	909.0	895.1	919.5	807.2	746.5	1836.1	1781.8	2181.3	2031.3	1765.6	1692.6	2122.1	850.5	1836.1	2.2
207907_at	TNFSF14	8.97E-03	79.7	44.4	49.8	60.6	63.2	48.8	58.4	75.5	61.5	75.2	69.3	100.8	82.5	106.0	58.4	75.5	1.3
207216_at	TNFSF8	7.81E-05	66.6	45.5	52.5	69.2	68.6	49.8	52.2	192.9	103.7	210.2	202.0	405.0	143.7	363.1	52.5	202.0	3.9
206907_at	TNFSF9	5.12E-04	86.9	70.5	133.0	90.7	124.8	135.2	95.5	167.1	379.4	927.0	214.4	373.6	240.5	403.1	95.5	373.6	3.9
211828_s_at	TNIK	2.49E-04	156.6	122.5	211.6	221.9	331.3	204.7	294.5	316.0	441.9	852.1	557.4	498.7	599.5	595.9	211.6	557.4	2.6
213107_at	TNIK	1.35E-03	560.6	324.0	522.9	520.1	751.2	458.1	646.0	767.7	882.4	1332.1	1080.2	860.9	1014.8	1166.6	522.9	1014.8	1.9
213109_at	TNIK	5.52E-04	282.4	150.9	342.8	336.0	478.0	313.4	409.8	536.4	746.1	1431.0	980.4	652.5	1032.9	941.8	336.0	941.8	2.8
239288_at	TNIK	1.25E-04	173.6	136.1	190.0	152.9	304.5	143.7	225.2	303.8	486.9	780.2	552.7	550.4	627.4	696.8	173.6	552.7	3.2
207196_s_at	TNIP1	1.22E-05	372.5	191.4	309.7	310.0	513.6	265.7	530.7	933.2	977.7	1584.2	1071.9	1810.9	1605.8	1885.0	310.0	1584.2	5.1
218335_x_at	TNIP2	8.35E-03	1575.5	1307.9	1401.2	1505.8	1334.5	1288.5	1413.7	1650.0	1615.6	1820.9	1767.0	1916.5	1904.2	1849.3	1401.2	1820.9	1.3
232160_s_at	TNIP2	5.94E-03	1604.6	1405.0	1325.4	1571.0	1368.4	1325.5	1415.5	1941.2	1683.2	1748.6	1697.1	1931.8	1980.4	1961.0	1405.0	1931.8	1.4
48531_at	TNIP2	6.65E-03	2081.8	1823.4	1637.9	1742.4	1698.7	1640.5	1694.8	2343.8	2098.4	2021.1	2114.3	2357.6	2442.3	2445.9	1698.7	2343.8	1.4
220655_at	TNIP3	2.98E-03	1115.3	158.4	848.9	874.6	2645.6	491.5	3126.2	3100.1	5278.4	5870.9	4508.5	4297.5	5197.7	6415.9	874.6	5197.7	5.9
215389_s_at	TNNT2	1.63E-03	46.4	29.0	37.2	45.5	54.3	35.3	41.9	62.3	41.7	57.9	57.2	64.2	49.6	57.9	41.9	57.9	1.4
229257_at	TNRC18	2.49E-03	123.1	104.8	91.6	114.5	103.7	106.0	103.9	145.7	164.7	165.7	174.5	131.5	137.2	137.8	104.8	145.7	1.4
208900_s_at	TOP1	2.60E-03	508.4	501.5	592.6	713.2	625.2	674.0	612.6	778.6	768.0	945.1	807.3	830.1	817.1	847.3	612.6	817.1	1.3
202348_s_at	TOR1A	4.61E-03	1129.5	1048.5	945.6	918.7	964.0	901.1	916.0	1329.2	1244.7	1242.5	1068.0	1306.1	1281.0	1291.4	945.6	1281.0	1.4
223929_s_at	TOR1AIP1	8.68E-03	60.5	52.7	70.6	68.2	68.0	69.1	58.4	89.8	65.7	104.6	72.6	89.8	75.5	86.6	68.0	86.6	1.3
209593_s_at	TOR1B	1.32E-04	1322.7	1416.4	943.5	1047.9	999.5	1065.1	960.3	1969.3	2863.4	3083.1	2127.7	2610.5	2674.1	3118.7	1047.9	2674.1	2.6
201684_s_at	TOX4	6.11E-03	627.2	539.1	596.6	562.1	613.5	617.9	648.2	767.3	674.4	877.8	636.3	732.3	778.4	882.9	613.5	767.3	1.3
203120_at	TP53BP2	1.04E-04	248.7	217.7	239.5	258.5	323.9	194.5	274.1	416.5	513.6	725.4	464.4	579.5	554.8	611.6	248.7	554.8	2.2
224836_at	TP53INP2	9.01E-04	1201.4	836.7	695.8	800.5	1385.6	582.0	1035.4	1532.5	2072.4	2906.6	2128.1	2128.8	2092.1	2561.7	836.7	2128.1	2.5
224164_at	TPM3	2.98E-03	120.9	85.5	116.8	106.0	127.5	88.2	122.6	127.0	142.1	235.6	171.8	154.8	141.6	214.7	116.8	154.8	1.3
209344_at	TPM4	4.44E-03	1243.1	917.6	830.2	1274.3	936.5	658.8	1078.9	1339.2	1273.6	1279.3	1620.4	1295.6	1369.7	1655.5	936.5	1339.2	1.4
210180_s_at	TRA2B	2.68E-03	443.9	286.2	393.5	428.4	369.7	379.6	384.9	465.7	427.6	613.6	533.4	643.8	595.7	637.6	384.9	595.7	1.5
1729_at	TRADD	8.67E-05	277.3	260.8	331.8	336.2	356.6	315.4	316.0	450.5	406.7	568.8	481.9	569.7	513.1	552.1	316.0	513.1	1.6
205641_s_at	TRADD	5.86E-04	315.6	321.0	343.5	335.3	390.1	299.9	336.1	446.7	454.3	529.4	429.3	524.9	506.1	542.1	335.3	506.1	1.5
205599_at	TRAF1	2.42E-06	90.6	64.2	89.6	94.5	130.5	89.9	118.3	441.7	350.8	625.0	447.2	924.3	787.5	962.5	90.6	625.0	6.9
235116_at	TRAF1	1.27E-05	16.6	29.4	35.0	32.9	33.0	28.5	50.0	70.2	72.6	226.3	118.8	185.1	137.2	177.1	32.9	137.2	4.2
208315_x_at	TRAF3	4.99E-03	143.7	133.7	164.0	156.6	235.9	173.8	214.0	215.2	160.6	248.1	215.0	255.4	249.6	260.5	164.0	248.1	1.5
215411_s_at	TRAF3IP2	2.53E-04	559.1	687.2	560.0	622.5	688.1	655.2	692.0	748.6	1058.0	1162.4	935.3	1154.5	1159.4	1266.9	655.2	1154.5	1.8
202837_at	TRAFD1	1.62E-03	399.0	521.1	552.0	516.9	495.0	418.5	470.9	546.6	808.2	1048.9	733.6	565.3	629.3	911.6	495.0	733.6	1.5
242497_at	TRAFD1	8.04E-03	1894.4	1710.5	1656.1	1918.1	1436.8	1415.0	1444.4	1929.8	2417.5	2862.9	2040.6	2189.3	2605.4	2821.5	1656.1	2417.5	1.5
35254_at	TRAFD1	6.14E-04	846.2	889.8	1092.7	1114.2	896.7	935.1	1029.3	1125.7	1604.9	2042.2	1561.0	1210.1	1365.4	1752.4	935.1	1561.0	1.7
1555446_s_at	TRAPPC10	2.93E-03	91.9	68.9	111.5	99.9	105.1	89.2	83.2	107.5	108.8	159.1	139.2	124.5	115.6	139.7	91.9	124.5	1.4
210915_x_at	TRBC1	5.26E-03	96.6	106.6	103.1	135.6	141.7	125.3	98.0	146.4	110.5	143.1	328.3	234.2	183.3	260.5	106.6	183.3	1.7
211796_s_at	TRBC1	1.95E-03	126.6	143.5	142.3	203.0	203.7	181.7	155.7	214.9	160.8	223.4	586.0	344.5	418.5	473.3	155.7	344.5	2.2
213193_x_at	TRBC1	2.15E-03	77.8	96.3	98.5	147.2	169.4	128.4	117.2	161.9	95.1	173.1	373.0	263.3	218.4	253.0	117.2	218.4	1.9
219748_at	TREML2	6.74E-03	53.5	43.0	47.3	50.3	44.0	47.1	47.9	54.0	55.9	93.7	59.9	75.2	70.2	87.6	47.3	70.2	1.5
202241_at	TRIB1	5.76E-04	293.3	253.9	260.0	295.0	397.5	357.1	423.0	440.9	511.1	773.1	481.6	642.4	605.4	672.9	295.0	605.4	2.1
202478_at	TRIB2	8.67E-05	46.4	43.6	63.4	77.5	41.6	50.4	50.1	117.2	143.9	294.6	197.1	107.6	83.2	175.9	50.1	143.9	2.9
202479_s_at	TRIB2	1.16E-05	66.8	65.5	80.7	85.2	49.1	44.6	73.4	149.0	132.6	254.2	204.8	116.8	99.3	208.6	66.8	149.0	2.2
204804_at	TRIM21	9.01E-04	682.3	782.7	739.3	743.0	744.5	772.1	684.2	998.9	1039.6	1116.9	985.0	1048.6	989.5	1177.5	743.0	1039.6	1.4
213293_s_at	TRIM22	4.50E-03	1828.7	2103.1	2927.3	2750.9	2344.2	2772.9	2857.5	2506.5	3383.8	4748.9	3855.2	2790.8	2967.2	3853.5	2750.9	3383.8	1.2
206911_at	TRIM25	1.97E-03	164.3	135.6	157.3	163.6	180.9	152.1	201.1	190.3	204.3	262.2	193.0	257.3	233.5	328.8	163.6	233.5	1.4
202702_at	TRIM26	3.11E-03	323.1	294.0	410.7	384.0	375.9	365.0	348.3	373.8	406.8	545.6	448.1	512.7	506.6	533.0	365.0	506.6	1.4
210159_s_at	TRIM31	1.23E-03	63.4	82.5	60.2	62.1	62.3	65.6	48.6	95.7	177.9	218.1	89.2	122.5	98.0	131.8	62.3	122.5	2.0
215444_s_at	TRIM31	5.83E-03	70.2	44.3	38.1	61.5	48.2	46.7	45.2	71.7	109.4	151.1	86.1	81.2	74.0	116.9	46.7	86.1	1.8
224175_s_at	TRIM34 /// TRIM6-TRIM34	7.20E-03	350.1	280.5	291.7	309.3	296.8	311.5	249.2	384.7	357.9	388.4	354.3	468.6	394.0	402.0	296.8	388.4	1.3
219736_at	TRIM36	1.61E-04	178.3	218.5	261.3	286.4	272.8	226.1	257.1	358.5	539.7	815.2	627.7	365.4	515.5	551.4	257.1	539.7	2.1
225868_at	TRIM47	4.89E-03	92.5	51.4	75.0	70.7	87.2	52.3	88.3	114.9	64.2	124.4	102.6	161.3	132.0	107.4	75.0	114.9	1.5
210705_s_at	TRIM5	7.69E-05	305.1	296.2	452.4	312.7	300.0	330.0	370.4	594.7	816.9	1785.1	829.0	597.0	620.5	1083.8	312.7	816.9	2.6
223830_s_at	TRIM5	3.53E-03	40.0	50.2	35.7	43.1	34.8	34.0	39.5	51.2	69.1	121.5	83.8	60.5	46.3	70.8	39.5	69.1	1.8
231876_at	TRIM56	7.06E-04	646.5	632.4	587.2	602.2	535.9	587.9	539.0	771.8	1169.5	1409.6	866.5	1011.1	1282.1	1262.1	587.9	1169.5	2.0
232464_at	TRIMP1	2.35E-04	67.8	79.0	88.8	74.5	87.4	86.9	81.8	127.2	140.4	235.5	154.9	130.5	128.2	185.4	81.8	140.4	1.7
202734_at	TRIP10	1.26E-04	118.5	76.3	146.5	150.2	163.5	124.1	188.1	244.4	266.0	707.5	298.6	404.1	665.5	614.2	146.5	404.1	2.8

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
201546_at	TRIP12	3.55E-03	3110.0	3401.9	2852.3	3093.9	3464.3	3036.1	3249.3	3720.6	4162.4	4651.2	4146.2	4197.0	4126.6	4404.6	3110.0	4162.4	1.3
203732_at	TRIP4	2.62E-03	608.4	498.6	691.3	749.8	727.9	673.1	693.2	754.9	917.8	1095.4	985.0	893.9	878.0	985.2	691.3	917.8	1.3
210954_s_at	TSC22D2	2.29E-03	40.4	37.0	38.9	35.3	56.2	47.8	45.4	53.9	48.7	72.3	52.9	70.3	64.4	58.1	40.4	58.1	1.4
215547_at	TSC22D2	1.08E-03	146.2	158.3	187.6	193.9	250.9	198.8	249.8	316.1	230.7	385.8	287.7	338.7	304.0	335.2	193.9	316.1	1.6
212656_at	TSFM	2.46E-03	230.4	198.1	196.6	275.7	272.6	253.2	268.5	311.0	243.0	344.4	372.3	375.4	326.6	341.3	253.2	341.3	1.3
223392_s_at	TSHZ3	4.45E-03	118.6	89.9	148.8	140.7	140.9	81.7	125.9	152.4	101.0	288.2	179.4	190.1	157.5	187.7	125.9	179.4	1.4
221002_s_at	TSPAN14	5.00E-03	1651.5	1515.6	1752.5	1768.0	1906.9	1795.4	1973.9	2009.7	2144.2	2706.0	1871.4	2582.0	2491.9	2536.5	1768.0	2491.9	1.4
225775_at	TSPAN33	2.00E-03	139.2	139.6	96.4	179.7	290.7	96.5	121.0	227.0	266.5	340.5	266.5	426.5	185.1	491.7	139.2	266.5	1.9
218272_at	TTC38	4.51E-03	345.2	298.0	344.9	291.3	271.7	408.9	284.9	403.8	348.7	466.0	346.5	425.4	622.0	482.6	298.0	425.4	1.4
204141_at	TUBB2A	8.22E-03	3148.6	2940.9	1518.8	2103.0	2180.7	2638.3	2963.4	3364.6	4556.8	3972.5	3563.7	2599.5	3970.2	4081.5	2638.3	3970.2	1.5
209372_x_at	TUBB2A /// TUBB2B	3.21E-03	363.0	261.6	185.2	220.1	215.7	234.0	306.8	345.3	439.5	357.5	357.5	356.8	596.9	515.8	234.0	357.5	1.5
213476_x_at	TUBB3	9.28E-03	688.6	456.4	445.2	571.3	466.0	431.0	626.5	691.2	673.6	822.8	670.0	790.0	1049.2	844.2	466.0	790.0	1.7
218965_s_at	TUT1	3.13E-03	449.9	229.9	362.8	384.0	457.6	286.1	503.6	534.5	467.7	699.7	525.0	769.8	941.0	757.2	384.0	699.7	1.8
214007_s_at	TWF1	2.61E-03	210.0	211.5	247.3	241.6	277.9	220.8	254.7	341.5	272.6	392.5	412.7	332.5	305.9	301.4	241.6	332.5	1.4
204858_s_at	TYMP	8.19E-03	67.0	62.4	84.0	85.5	73.7	86.7	90.3	90.3	71.8	119.8	95.1	119.5	194.9	122.8	84.0	119.5	1.4
217497_at	TYMP	6.81E-04	417.2	361.8	370.4	372.7	327.3	303.5	347.5	534.9	503.7	683.6	516.1	567.9	622.7	653.1	361.8	567.9	1.6
209340_at	UAP1	4.87E-03	414.9	388.7	505.7	564.5	637.1	486.7	647.9	584.8	790.8	1221.8	809.8	667.9	909.2	844.9	505.7	809.8	1.6
222600_s_at	UBA6	2.97E-04	141.7	165.0	230.3	212.3	238.0	234.2	306.2	268.2	247.6	448.9	376.1	316.0	353.2	471.6	230.3	353.2	1.5
222601_at	UBA6	9.61E-03	816.4	845.0	947.3	896.8	1022.1	1030.4	1346.3	1022.0	1338.2	1733.2	1484.7	1175.8	1120.6	1601.7	947.3	1338.2	1.4
1294_at	UBA7	6.73E-03	1062.6	1058.7	955.5	1105.1	831.5	874.8	835.1	1110.5	1461.3	1380.2	1215.9	1561.6	1484.0	1496.1	955.5	1461.3	1.5
203281_s_at	UBA7	7.33E-03	713.8	695.4	669.7	645.6	505.7	571.1	539.4	733.3	861.3	930.8	807.6	1047.8	976.0	927.5	645.6	927.5	1.4
201898_s_at	UBE2A	1.99E-03	782.0	763.1	676.8	782.6	762.9	702.8	836.6	1074.3	897.3	1154.1	993.5	1161.1	978.6	1119.4	763.1	1074.3	1.4
212519_at	UBE2E1	4.50E-03	385.5	416.8	792.4	630.5	716.4	720.9	843.3	687.2	825.9	1339.9	892.5	853.5	842.1	1026.7	716.4	853.5	1.2
238958_at	UBE2E1	2.38E-03	85.9	134.0	158.4	136.6	126.8	126.6	167.2	193.6	195.0	268.5	207.5	146.8	215.8	211.8	134.0	207.5	1.5
201649_at	UBE2L6	6.68E-04	4132.5	4834.0	4502.2	4309.3	4076.9	4069.3	4086.4	5613.4	6206.7	6663.7	5728.8	5631.1	6184.7	6179.7	4132.5	6179.7	1.5
201523_x_at	UBE2N	3.09E-04	451.8	393.1	423.1	494.3	509.6	381.0	504.6	716.8	646.9	810.4	717.2	666.8	676.3	760.4	451.8	716.8	1.6
202779_s_at	UBE2S	1.61E-03	55.7	40.5	79.5	71.4	50.7	50.4	74.6	73.0	72.7	147.9	95.3	155.3	157.1	146.7	55.7	146.7	2.6
217750_s_at	UBE2Z	3.41E-05	1290.4	1100.8	1203.6	1065.1	1360.7	1012.0	1310.7	2047.9	1902.5	2493.4	2144.9	2619.8	2197.0	2346.4	1203.6	2197.0	1.8
222395_s_at	UBE2Z	1.84E-04	353.6	291.9	368.7	315.5	326.5	312.4	388.7	479.4	518.7	791.9	529.4	509.6	601.3	650.5	326.5	529.4	1.6
236107_at	UBE2Z	6.89E-04	167.1	159.8	161.6	161.6	180.5	186.2	181.9	231.7	220.2	328.9	271.5	238.5	280.0	313.4	167.1	271.5	1.6
211285_s_at	UBE3A	5.80E-03	577.6	601.7	767.7	702.7	836.7	841.3	937.5	746.3	935.3	1436.8	974.8	944.1	967.0	1277.2	767.7	967.0	1.3
205687_at	UBFD1	5.29E-03	76.4	78.0	124.6	110.4	120.5	113.4	95.0	138.5	109.5	187.0	149.7	130.4	130.2	138.2	110.4	138.2	1.3
218082_s_at	UBP1	6.05E-03	964.8	1237.9	1495.1	1384.8	1430.4	1388.1	1653.0	1249.1	2061.7	2521.0	2063.7	1544.1	1672.7	2044.8	1388.1	2044.8	1.5
211950_at	UBR4	2.02E-03	475.9	448.4	441.0	556.3	644.2	472.9	528.6	643.7	578.8	753.4	708.7	806.3	903.4	938.8	475.9	753.4	1.6
224834_at	UBTD2	5.33E-03	145.7	86.8	165.3	210.2	221.3	134.0	282.9	275.0	210.2	561.4	295.1	278.9	299.4	308.7	165.3	295.1	1.8
235327_x_at	UBXN2A	5.06E-03	511.0	426.2	471.7	462.6	490.9	520.3	546.2	624.7	601.4	777.6	645.0	678.1	531.3	880.5	490.9	645.0	1.3
212007_at	UBXN4	3.93E-03	685.4	655.5	724.1	700.4	690.2	608.6	674.1	904.6	781.0	952.2	888.9	861.7	831.9	798.1	685.4	861.7	1.3
204881_s_at	UGCG	2.69E-03	1997.4	652.9	1442.1	1347.2	2299.0	911.4	2993.1	2755.6	3510.6	5472.0	3320.9	3469.9	3780.7	4515.3	1442.1	3510.6	2.4
221765_at	UGCG	1.21E-03	395.2	160.9	475.0	375.1	715.6	270.0	1136.9	832.2	1060.5	2365.5	1111.0	1138.5	1330.5	1804.3	395.2	1138.5	2.9
224967_at	UGCG	4.13E-03	3536.1	2056.1	3965.4	3011.0	5483.2	2543.0	6594.0	5246.5	6576.6	9673.1	6822.5	6136.0	6112.3	7863.5	3536.1	6576.6	1.9
225869_s_at	UNC93B1	5.39E-04	133.1	127.4	172.5	134.3	124.1	122.5	136.4	194.4	161.7	239.1	194.6	206.5	220.8	215.5	133.1	206.5	1.6
1558569_at	UNQ6228	7.61E-05	108.9	65.2	105.9	119.6	110.2	104.5	95.3	166.5	154.5	308.1	296.3	212.2	214.0	189.3	105.9	212.2	2.0
220507_s_at	UPB1	1.90E-03	50.2	32.3	43.4	44.8	36.1	43.9	40.6	68.5	60.6	110.1	59.9	97.0	57.0	77.7	43.4	68.5	1.6
201831_s_at	USO1	5.12E-03	891.2	849.2	845.3	843.5	986.1	908.2	988.8	1027.2	1144.6	1440.2	1162.0	1115.2	1262.1	1280.6	891.2	1162.0	1.3
201832_s_at	USO1	7.21E-03	1729.0	1827.7	1572.3	1581.0	1872.8	1655.9	1950.4	2344.9	2081.2	2395.6	2172.1	2159.2	2140.3	2254.4	1729.0	2172.1	1.3
215886_x_at	USP12	2.59E-03	174.8	139.2	185.2	165.1	224.1	153.4	192.0	245.9	228.5	591.2	236.8	300.2	288.0	312.3	174.8	288.0	1.6
205356_at	USP13	2.00E-03	154.9	100.0	176.8	191.2	291.3	160.5	283.1	262.6	193.4	333.2	308.1	318.9	336.3	353.1	176.8	318.9	1.8
227788_at	USP13	9.07E-03	191.3	113.5	215.2	168.0	341.1	185.6	338.4	359.7	153.0	347.3	350.5	342.3	343.2	362.2	191.3	347.3	1.8
201672_s_at	USP14	9.78E-03	554.0	510.9	584.1	555.2	617.0	598.7	567.6	763.7	624.2	856.4	753.0	647.5	692.0	708.6	567.6	708.6	1.2
210681_s_at	USP15	1.06E-03	723.8	814.3	813.0	861.6	867.3	742.9	695.2	906.9	1329.2	1678.4	1253.9	1151.6	1097.8	1254.0	813.0	1253.9	1.5
231990_at	USP15	7.14E-03	114.3	130.5	173.9	182.8	179.0	191.0	181.4	169.2	193.2	395.2	302.9	209.8	191.4	307.3	179.0	209.8	1.2
219211_at	USP18	6.17E-06	356.9	284.9	268.6	187.1	181.7	176.5	215.1	1292.8	2207.3	3327.4	1514.9	1749.8	1650.1	2356.6	215.1	1749.8	8.1
226172_at	USP42	1.91E-03	77.0	68.5	78.9	101.2	116.8	86.7	105.6	136.5	112.1	208.6	132.9	164.5	123.4	152.2	86.7	136.5	1.6
238164_at	USP6NL	2.64E-03	61.0	55.5	179.5	95.4	147.2	174.1	184.4	137.6	111.3	495.2	219.8	190.0	239.9	218.2	147.2	218.2	1.5
219675_s_at	UXS1	5.51E-05	492.3	558.9	513.5	548.1	601.3	453.0	572.8	883.7	994.8	1289.3	1061.9	961.3	851.3	1204.5	548.1	994.8	1.8
225583_at	UXS1	4.38E-04	1318.5	1316.3	1330.5	1339.9	1494.4	1309.2	1631.3	2057.1	2391.4	3580.5	2463.8	1996.8	2294.4	2833.8	1330.5	2391.4	1.8
216407_at	VAC14	7.35E-03	151.5	93.6	147.1	165.8	143.7	102.2	150.7	180.7	130.8	199.5	166.9	200.6	166.8	203.6	147.1	180.7	1.2
218169_at	VAC14	4.52E-03	235.6	128.7	241.7	256.5	230.0	162.2	255.5	324.2	187.2	311.8	278.5	322.0	294.1	322.5	235.6	311.8	1.3
204929_s_at	VAMP5	8.13E-04	229.3	181.4	154.2	222.3	198.2	169.0	162.2	297.0	220.8	333.9	394.3	376.4	321.1	341.2	181.4	333.9	1.8
214115_at	VAMP5	5.76E-04	148.2	129.4	152.0	181.4	146.6	119.5	117.6	231.4	146.4	334.0	364.6	327.1	232.9	236.0	146.6	236.0	1.6
206219_s_at	VAV1	2.93E-04	1274.6	1067.7	1275.6	1411.4	1290.3	1201.3	1502.9	1729.3	1756.8	2173.7	2043.6	2347.2	2647.4	2529.5	1275.6	2173.7	1.7
204619_s_at	VCAN	2.94E-04	30.1	30.8	49.2	84.1	88.1	40.8	94.3	75.1	66.6	139.8	104.4	219.7	81.1	307.7	49.2	104.4	2.1
204620_s_at	VCAN	6.37E-04	460.2	242.9	374.9	601.0	609.7	221.5	512.4	854.0	590.0	776.5	704.4	1818.0	602.7	1826.6	460.2	776.5	1.7
211571_s_at	VCAN	9.01E-04	246.2	125.9	185.0	310.2	324.0	126.4	266.2	495.3	273.0	353.9	344.2	908.3	367.9	945.6	246.2	367.9	1.5
215646_s_at	VCAN	7.16E-04	234.9	127.8	242.1	372.9	381.6	141.2	328.6	444.8	299.7	486.9	427.3	1033.7	395.7	1179.3	242.1	444.8	1.8

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
221731_x_at	VCAN	4.14E-04	264.3	157.7	279.5	407.4	426.6	161.6	366.0	492.6	386.0	584.0	493.2	1200.8	429.3	1183.0	279.5	493.2	1.8
210512_s_at	VEGFA	3.28E-04	44.0	83.8	59.5	56.2	127.5	124.2	142.9	197.3	152.2	187.7	175.1	300.0	186.5	325.3	83.8	187.7	2.2
210513_s_at	VEGFA	9.58E-04	105.6	117.2	92.1	81.8	135.2	111.6	126.1	187.5	159.1	134.3	137.7	415.2	233.7	340.1	111.6	187.5	1.7
211527_x_at	VEGFA	1.18E-04	142.1	194.0	108.1	114.0	229.4	231.5	198.9	420.5	318.7	246.0	385.4	721.4	397.8	594.1	194.0	397.8	2.1
212171_x_at	VEGFA	1.80E-03	113.3	166.0	102.7	95.6	154.6	166.7	166.0	258.1	191.8	172.4	179.5	487.4	235.4	363.2	154.6	235.4	1.5
209950_s_at	VILL	7.82E-03	80.6	50.0	79.8	78.1	92.1	59.2	99.3	106.0	77.1	145.9	104.3	142.4	143.8	97.1	79.8	106.0	1.3
1558549_s_at	VNN1	8.00E-03	84.9	104.1	188.7	79.1	97.2	82.5	78.9	122.3	146.3	231.8	152.7	123.0	109.5	83.5	84.9	123.0	1.4
205922_at	VNN2	6.86E-03	563.8	471.5	747.1	583.3	596.6	586.1	433.5	713.4	663.3	899.8	708.7	681.1	747.1	735.5	583.3	713.4	1.2
220528_at	VNN3	3.33E-05	31.1	41.4	47.1	31.0	43.4	32.2	33.4	73.2	86.2	144.9	105.7	133.1	112.7	174.3	33.4	112.7	3.4
200628_s_at	WARS	3.88E-05	1426.1	1183.4	1304.3	1226.6	1290.0	850.3	1556.6	2406.7	2737.4	3671.3	2554.9	3362.3	2795.9	3630.1	1290.0	2795.9	2.2
200629_at	WARS	2.75E-05	2645.0	2313.5	2104.2	1970.6	2374.1	1709.7	2537.9	4251.6	4082.4	4726.4	3906.0	4650.5	3669.0	5218.4	2313.5	4251.6	1.8
233559_s_at	WDFY1	3.59E-03	929.6	953.8	1001.8	1134.1	1268.4	1110.5	1096.4	1374.2	1497.4	1599.0	1343.9	1396.3	1441.5	1571.8	1096.4	1441.5	1.3
201294_s_at	WSB1	4.07E-05	1730.0	2153.3	2046.4	1362.7	1522.2	1373.5	1655.1	2682.4	3835.4	4514.9	2821.5	2885.1	2455.8	3520.7	1655.1	2885.1	1.7
201295_s_at	WSB1	1.63E-03	185.0	286.8	435.2	326.3	342.5	392.0	462.1	328.2	678.8	1155.3	722.1	520.5	432.3	728.0	342.5	678.8	2.0
201296_s_at	WSB1	1.36E-03	2612.4	2881.0	3536.3	3402.4	3626.8	3533.8	3713.1	3504.3	5049.1	6545.8	4727.3	4556.5	4741.7	5327.2	3533.8	4741.7	1.3
210561_s_at	WSB1	3.81E-04	1445.4	1749.7	1947.2	1633.0	1944.7	1922.4	2074.0	2367.7	3090.3	4274.9	2818.0	2641.2	2729.0	3203.8	1922.4	2818.0	1.5
213406_at	WSB1	8.77E-05	1015.1	986.9	1135.3	1020.9	1128.9	948.1	1087.8	1490.6	1888.9	2619.8	1698.1	1994.5	1693.6	2019.1	1020.9	1888.9	1.9
1560274_at	WTAP	1.89E-04	29.1	17.5	29.7	27.2	34.5	25.1	36.9	53.3	41.6	113.3	73.6	78.4	51.2	57.9	29.1	57.9	2.0
203137_at	WTAP	2.66E-05	596.3	526.3	694.3	624.3	999.7	643.2	829.6	1373.2	1336.9	2126.2	1523.9	1629.7	1534.6	1953.4	643.2	1534.6	2.4
210285_x_at	WTAP	2.00E-05	611.8	514.4	529.8	563.8	786.2	544.8	669.0	1162.3	1214.6	1717.2	1220.5	1734.3	1567.9	1766.3	563.8	1567.9	2.8
214759_at	WTAP	2.53E-05	68.9	63.9	96.2	81.4	117.9	86.2	119.3	156.3	117.0	293.3	187.3	298.2	211.4	224.3	86.2	211.4	2.5
229630_s_at	WTAP	1.78E-03	3776.3	3983.6	5134.9	4809.2	5552.4	4697.1	5584.5	4879.0	7555.3	9507.9	7121.8	6311.0	7055.1	8517.9	4809.2	7121.8	1.5
241626_at	WTAP	6.07E-05	79.1	76.2	95.6	86.7	90.6	65.8	85.1	132.4	115.6	213.0	161.6	169.3	119.5	149.5	85.1	149.5	1.8
206133_at	XAF1	2.16E-04	1217.9	1812.7	1467.7	1104.2	826.2	737.5	777.7	2035.2	2553.5	3585.6	2419.6	2124.3	2045.6	2470.9	1104.2	2419.6	2.2
228617_at	XAF1	2.95E-04	1009.3	1222.0	1105.8	951.5	666.8	550.3	618.6	1402.4	2124.1	3142.3	1975.9	1506.7	1534.5	2133.3	951.5	1975.9	2.1
242234_at	XAF1	1.24E-04	50.5	74.2	92.5	52.5	45.6	50.8	61.3	101.9	102.7	265.7	149.4	115.5	118.8	125.6	52.5	118.8	2.3
200670_at	XBP1	1.18E-03	180.1	126.1	136.3	119.6	209.9	151.3	235.4	253.6	224.3	355.8	282.7	311.0	257.9	308.8	151.3	282.7	1.9
206366_x_at	XCL1	6.46E-03	57.5	65.9	49.8	60.8	60.5	76.5	52.6	69.0	69.2	67.0	89.0	99.6	94.0	80.0	60.5	80.0	1.3
208453_s_at	XPNPEP1	3.99E-03	584.8	489.9	548.0	626.1	578.4	450.4	577.1	664.2	688.5	850.4	734.9	808.0	627.4	718.0	577.1	718.0	1.2
211982_x_at	XPO6	2.76E-03	486.7	467.3	528.6	531.6	478.8	417.2	549.6	625.7	559.9	714.6	680.6	790.7	830.2	855.8	486.7	714.6	1.5
214784_x_at	XPO6	1.78E-03	172.7	188.3	264.6	229.6	245.9	220.3	291.5	260.3	230.8	418.1	363.7	291.6	370.0	379.4	229.6	363.7	1.6
1555785_a_at	XRN1	2.52E-05	145.6	157.5	220.0	241.0	255.2	196.8	300.5	405.5	549.8	1073.8	623.8	542.1	542.1	863.6	220.0	549.8	2.5
1570394_at	XRN1	1.37E-04	70.7	86.9	104.9	77.2	93.9	94.6	111.4	152.2	218.7	525.7	268.7	199.0	181.0	296.4	93.9	218.7	2.3
225814_at	XRN1	2.13E-04	1050.6	1041.5	1326.2	1224.9	1368.3	1416.1	1418.9	1807.8	2706.8	4123.4	2824.4	2099.0	2377.2	3385.5	1326.2	2706.8	2.0
233632_s_at	XRN1	1.65E-04	151.1	191.0	237.0	245.3	258.7	292.7	306.7	340.8	472.0	890.0	554.2	424.0	498.1	682.9	245.3	498.1	2.0
213725_x_at	XYLT1	2.75E-03	32.5	46.5	38.1	28.9	52.6	33.7	56.8	63.4	61.5	122.8	63.5	71.0	59.9	74.9	38.1	63.5	1.7
1557047_at	YEATS2	4.54E-03	77.8	87.5	58.5	63.5	49.4	48.9	67.8	78.2	116.5	87.4	91.0	77.8	65.1	93.1	63.5	87.4	1.4
221203_s_at	YEATS2	4.37E-03	298.8	299.3	342.4	316.0	319.7	336.6	311.7	382.3	387.4	582.4	433.5	371.3	398.2	507.2	316.0	398.2	1.3
217785_s_at	YKT6	8.59E-04	194.0	150.2	192.1	199.6	198.5	178.6	225.8	287.8	203.4	372.4	266.5	300.1	295.5	297.4	194.0	295.5	1.5
218647_s_at	YRDC	8.67E-04	161.3	167.0	250.9	240.3	266.6	231.7	359.0	278.2	332.8	513.1	404.4	366.4	319.6	454.8	240.3	366.4	1.5
222703_s_at	YRDC	1.49E-04	241.0	182.3	241.1	276.6	242.5	226.3	268.0	337.2	305.6	483.8	421.6	429.7	481.7	508.8	241.1	429.7	1.8
1554821_a_at	ZBED1	1.10E-03	304.1	311.1	350.0	332.8	388.1	317.9	347.9	335.5	507.7	682.5	466.6	616.1	560.9	624.5	332.8	560.9	1.7
203043_at	ZBED1	1.35E-03	109.0	90.0	111.6	112.1	137.0	114.3	139.3	127.8	147.6	200.8	149.9	210.7	169.6	187.0	112.1	169.6	1.5
208087_s_at	ZBP1	4.69E-05	78.1	94.1	101.4	70.4	93.6	95.5	67.7	190.2	207.6	472.9	238.5	224.1	236.2	289.9	93.6	236.2	2.5
242020_s_at	ZBP1	4.31E-05	142.7	163.0	121.4	82.6	87.9	135.7	87.8	336.8	434.0	577.6	282.0	464.5	362.4	501.6	121.4	434.0	3.6
1554036_at	ZBTB24	4.59E-03	90.2	90.1	131.9	103.3	127.4	95.2	184.6	161.9	148.5	363.5	150.0	135.2	141.7	264.1	103.3	150.0	1.5
229691_at	ZBTB42	1.16E-03	144.5	131.7	190.5	173.2	186.2	175.4	159.4	247.7	192.0	268.3	193.2	290.3	260.7	269.6	173.2	260.7	1.5
204180_s_at	ZBTB43	3.48E-04	133.3	130.7	169.3	149.0	204.3	155.5	185.4	200.4	215.9	350.6	251.5	265.5	249.7	283.5	155.5	251.5	1.6
204181_s_at	ZBTB43	6.81E-03	184.8	142.4	176.4	162.1	187.5	167.0	214.9	190.5	257.5	336.8	204.9	228.3	242.0	319.5	176.4	242.0	1.4
204182_s_at	ZBTB43	1.15E-03	60.6	53.8	99.6	84.3	99.6	98.3	122.2	119.3	124.7	185.5	116.8	136.8	129.9	183.1	98.3	129.9	1.3
218810_at	ZC3H12A	2.44E-05	52.7	34.1	76.5	62.3	104.5	46.2	119.3	147.3	206.9	451.5	312.0	425.5	446.4	408.2	62.3	408.2	6.5
231899_at	ZC3H12C	3.79E-04	31.4	10.8	31.2	24.9	80.1	20.6	99.2	96.4	44.1	318.9	134.7	156.5	113.5	206.5	31.2	134.7	4.3
213323_s_at	ZC3H7B	9.11E-04	44.8	39.2	52.5	48.6	53.2	48.1	54.8	71.0	59.2	76.2	76.9	78.0	60.3	67.1	48.6	71.0	1.5
213051_at	ZC3HAV1	3.93E-03	638.5	747.7	701.9	629.3	539.0	547.0	692.2	704.3	899.7	1081.0	926.9	704.1	710.2	1002.9	638.5	899.7	1.4
220104_at	ZC3HAV1	6.18E-04	274.4	268.4	326.4	292.9	281.3	278.7	316.1	388.3	734.6	1123.5	576.8	461.8	464.6	801.0	281.3	576.8	2.1
225634_at	ZC3HAV1	8.31E-03	293.2	325.7	350.5	283.7	303.8	314.6	349.9	377.0	341.1	593.9	417.2	427.3	344.2	527.4	314.6	417.2	1.3
1559399_s_at	ZCCHC10	1.46E-04	292.5	174.7	270.4	255.4	330.5	237.6	358.9	415.6	349.8	545.0	384.5	571.5	522.6	653.7	270.4	522.6	1.9
224503_s_at	ZCCHC2	1.16E-03	166.5	153.8	159.6	112.7	164.7	134.5	115.1	222.3	242.0	266.7	176.8	192.8	183.6	165.5	153.8	192.8	1.3
219296_at	ZDHHC13	8.55E-04	179.0	195.9	223.7	222.7	199.1	171.0	221.3	253.9	255.0	337.0	292.6	271.5	248.1	288.1	199.1	271.5	1.4
217486_s_at	ZDHHC17	1.35E-03	104.3	80.7	107.5	131.3	125.2	118.7	130.4	146.9	164.5	324.2	174.3	211.1	185.1	238.3	118.7	185.1	1.6
222451_s_at	ZDHHC9	4.37E-04	62.5	80.0	152.7	119.3	152.9	138.0	161.5	185.4	166.1	368.7	260.0	224.8	215.0	248.0	138.0	224.8	1.6
233031_at	ZEB2	9.12E-04	94.0	80.9	173.8	164.8	157.3	147.7	170.7	153.2	128.6	326.9	218.7	240.5	186.9	228.9	157.3	218.7	1.4
233033_at	ZEB2	3.22E-04	158.6	106.2	213.7	177.8	206.6	192.4	191.3	220.7	169.9	383.9	259.0	300.7	275.0	275.2	191.3	275.0	1.4
235593_at	ZEB2	2.86E-03	119.3	110.0	182.5	151.8	266.8	173.3	232.5	207.3	186.9	396.7	224.7	306.6	228.6	301.7	173.3	228.6	1.3
226650_at	ZFAND2A	9.94E-03	310.1	590.8	420.2	447.7	380.1	358.9	379.6	450.7	616.7	526.5	584.9	495.1	437.7	454.6	380.1	495.1	1.3
222493_s_at	ZFAND3	3.68E-03	823.2	553.5	754.6	709.2	790.6	757.3	744.5	1052.8	756.2	998.3	786.3	985.7	1085.1	993.1	754.6	993.1	1.3

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
201531_at	ZFP36	1.80E-03	1316.2	1136.3	1411.2	1350.6	1484.8	1293.8	1354.3	1736.8	2543.7	3258.5	1562.6	2777.1	1880.5	2920.9	1350.6	2543.7	1.9
211962_s_at	ZFP36L1	4.71E-03	452.4	561.9	634.8	631.6	820.6	501.4	580.8	593.8	770.7	1179.5	1023.2	805.6	737.6	949.8	580.8	805.6	1.4
211965_at	ZFP36L1	1.72E-03	165.0	168.3	223.2	184.8	256.2	160.7	186.9	212.0	287.0	342.6	284.1	309.2	227.4	395.6	184.8	287.0	1.6
213277_at	ZFP36L1	1.26E-03	47.8	47.4	55.2	50.2	49.9	52.8	51.4	58.3	71.7	70.1	68.3	66.8	83.8	77.1	50.2	70.1	1.4
207920_x_at	ZFX	5.12E-04	270.1	254.3	389.1	349.2	490.7	327.8	422.7	413.3	520.9	978.3	501.5	670.8	634.2	783.6	349.2	634.2	1.8
217176_s_at	ZFX	9.30E-03	64.4	43.2	58.3	62.7	72.8	44.9	75.1	69.1	110.0	170.8	101.3	71.7	94.0	125.4	62.7	101.3	1.6
207247_s_at	ZFX /// ZFY	5.62E-03	125.8	145.6	222.5	209.7	293.1	214.7	255.0	259.5	194.8	523.4	278.0	322.7	297.6	378.2	214.7	297.6	1.4
203556_at	ZHX2	1.88E-03	507.7	331.5	644.9	580.2	709.3	591.0	811.8	733.4	775.2	1456.6	850.8	862.2	947.2	1175.4	591.0	862.2	1.5
54970_at	ZMIZ2	4.14E-03	1334.0	1110.8	1476.2	1388.9	1382.6	1187.1	1299.6	1834.3	1448.9	1783.4	1577.3	1844.1	1700.7	1606.3	1334.0	1700.7	1.3
202049_s_at	ZMYM4	3.79E-03	161.8	167.3	219.6	176.2	260.8	235.5	204.8	230.1	238.5	378.4	309.7	301.2	266.3	281.3	204.8	281.3	1.4
1554158_at	ZMYND11	8.91E-03	64.3	56.3	74.5	83.6	89.4	86.9	63.1	100.0	79.5	175.6	139.0	89.4	118.2	78.5	74.5	100.0	1.3
243312_at	ZNF107	6.97E-03	47.5	64.3	63.5	46.0	61.0	47.2	52.7	61.7	104.1	123.8	88.1	75.1	50.1	67.1	52.7	75.1	1.4
214706_at	ZNF200	1.91E-03	47.4	51.1	74.0	60.3	61.7	57.0	73.2	72.3	75.4	114.8	89.4	67.8	72.2	105.4	60.3	75.4	1.3
219540_at	ZNF267	1.46E-03	210.5	188.9	229.7	278.8	332.4	276.2	377.3	376.3	365.7	680.9	462.7	440.3	391.8	569.7	276.2	440.3	1.6
231704_at	ZNF498	3.35E-04	113.0	52.9	104.7	89.4	190.6	78.8	190.6	244.5	297.5	863.0	373.8	366.1	467.1	487.2	104.7	373.8	3.6
220617_s_at	ZNF532	4.65E-03	150.1	185.7	263.3	287.8	299.1	240.8	239.6	243.4	216.4	346.0	338.5	414.4	289.4	352.0	240.8	338.5	1.4
219711_at	ZNF586	4.66E-03	171.7	226.5	214.9	210.1	246.8	208.3	239.1	238.0	328.6	369.4	257.8	275.8	250.6	341.9	214.9	275.8	1.3
226590_at	ZNF618	8.70E-04	73.2	73.2	88.1	68.1	59.4	57.9	48.0	115.1	137.4	192.9	116.6	108.8	100.4	198.0	68.1	116.6	1.7
226592_at	ZNF618	2.52E-03	40.0	44.8	53.5	29.7	46.0	41.2	33.7	63.3	66.4	122.2	79.2	62.2	57.0	116.5	41.2	66.4	1.6
238444_at	ZNF618	3.42E-04	40.8	26.4	40.8	47.1	33.2	42.6	33.7	71.1	49.6	91.4	73.4	61.5	56.0	84.5	40.8	71.1	1.7
227080_at	ZNF697	1.26E-03	167.1	168.3	206.3	256.5	343.1	158.2	347.3	301.9	251.9	470.8	332.9	450.9	276.7	495.8	206.3	332.9	1.6
206557_at	ZNF702P	1.02E-04	71.0	39.9	64.6	86.2	73.3	91.3	68.9	152.4	66.9	152.8	190.4	145.1	137.0	113.5	71.0	145.1	2.0
225076_s_at	ZNFX1	1.37E-05	379.2	362.9	372.5	401.6	484.2	384.4	439.8	815.0	832.5	1355.8	926.8	1188.7	1001.1	1312.2	384.4	1001.1	2.6
223382_s_at	ZNRF1	6.61E-03	62.4	51.1	47.3	56.1	76.8	50.1	49.0	84.3	57.8	75.3	72.5	81.1	77.3	80.6	51.1	77.3	1.5
226261_at	ZNRF2	3.73E-04	386.4	403.1	435.1	474.0	513.0	514.4	467.3	598.1	667.0	804.2	695.4	721.3	670.8	743.7	467.3	695.4	1.5
1555157_at	—	8.12E-04	35.7	36.3	41.0	39.3	53.3	28.9	55.9	51.6	68.0	226.7	130.6	101.7	119.8	165.0	39.3	119.8	3.0
1555303_at	—	7.35E-03	77.1	78.8	96.6	105.1	90.3	87.1	91.2	98.2	88.7	116.2	157.7	124.0	136.9	102.9	90.3	116.2	1.3
1555853_at	—	8.77E-05	157.3	129.6	172.5	151.6	155.2	141.8	145.2	248.0	232.7	537.5	319.6	379.1	347.7	400.8	151.6	347.7	2.3
1555976_s_at	—	9.85E-03	46.7	53.4	66.9	59.1	63.3	59.3	69.5	73.0	57.1	123.4	75.5	88.8	65.4	92.0	59.3	75.5	1.3
1555977_at	—	4.03E-03	880.2	959.3	900.7	899.5	651.0	693.8	746.0	976.2	1114.4	1358.4	1226.3	1074.0	933.1	1266.9	880.2	1114.4	1.3
1556021_at	—	4.71E-03	38.8	63.2	93.7	74.4	74.5	86.8	95.1	93.0	93.1	171.2	131.0	107.0	109.1	100.6	74.5	107.0	1.4
1556153_s_at	—	3.76E-03	42.5	50.8	53.4	49.2	49.2	41.6	46.6	49.2	75.8	127.6	107.1	57.7	70.7	124.4	49.2	75.8	1.5
1556297_a_at	—	3.24E-03	53.9	54.0	42.4	51.0	51.0	39.7	53.6	59.0	81.2	130.8	94.2	82.3	69.9	83.9	51.0	82.3	1.6
1556321_a_at	—	1.74E-03	173.4	146.4	182.8	176.5	193.7	158.2	202.6	224.3	274.6	645.5	357.2	253.7	313.6	394.6	176.5	313.6	1.8
1556332_at	—	1.60E-05	76.9	43.9	52.6	46.8	107.9	44.8	93.0	245.7	198.7	423.7	235.8	292.1	252.4	438.7	52.6	252.4	4.8
1556352_at	—	6.54E-04	40.0	64.7	51.9	81.0	66.1	64.6	59.0	65.6	101.2	124.8	156.2	83.1	101.0	97.2	64.6	101.0	1.6
1556663_s_at	—	7.49E-03	47.6	40.3	41.3	40.2	63.8	52.4	53.4	70.5	53.0	54.5	77.8	74.4	82.5	56.6	47.6	70.5	1.5
1556669_a_at	—	1.28E-03	26.2	35.6	25.7	27.8	22.6	22.2	26.0	36.1	46.7	76.2	53.4	75.4	73.2	100.2	26.0	73.2	2.8
1557193_at	—	6.07E-03	112.5	75.2	153.4	136.2	163.1	126.2	164.6	142.4	130.5	219.0	173.7	177.0	188.5	198.1	136.2	177.0	1.3
1557418_at	—	5.37E-03	180.6	129.4	157.0	174.9	122.6	101.3	149.5	178.5	161.5	238.2	249.7	196.3	204.0	284.6	149.5	204.0	1.4
1558299_at	—	5.51E-03	438.0	358.3	454.9	384.8	484.0	444.3	403.9	470.6	485.5	600.5	536.2	606.1	542.8	635.9	438.0	542.8	1.2
1558783_at	—	3.37E-03	49.6	39.4	49.6	38.1	49.6	49.8	51.9	65.0	60.6	179.4	74.4	78.0	66.8	101.2	49.6	74.4	1.5
1558938_at	—	4.42E-03	310.9	563.2	516.5	458.2	379.3	428.5	427.0	490.3	643.9	928.7	734.0	543.1	456.0	622.6	428.5	622.6	1.5
1559391_s_at	—	3.70E-04	26.6	40.7	60.1	52.8	62.2	57.0	60.2	67.8	68.4	211.5	134.4	92.8	113.3	108.0	57.0	108.0	1.9
1559530_at	—	7.75E-03	790.1	681.5	956.7	684.3	887.4	708.9	626.2	838.5	895.3	1421.1	728.9	1332.7	1020.0	998.2	708.9	998.2	1.4
1559573_at	—	7.57E-06	32.9	22.2	36.5	36.3	55.0	24.8	44.0	123.2	111.7	248.5	154.9	171.2	141.3	148.1	36.3	148.1	4.1
1560034_a_at	—	1.21E-03	39.4	47.0	35.6	20.9	31.2	21.4	26.9	50.7	65.7	59.8	53.3	71.8	35.9	76.3	31.2	59.8	1.9
1560108_at	—	5.48E-03	46.2	50.9	47.7	52.7	58.3	42.5	49.8	62.9	54.6	64.9	66.2	72.8	73.4	83.7	49.8	66.2	1.3
1560109_s_at	—	1.84E-04	107.3	145.5	138.3	141.9	199.5	155.5	197.8	245.9	251.5	513.5	329.8	331.0	297.5	466.9	145.5	329.8	2.3
1560156_at	—	4.28E-05	67.0	34.7	74.2	83.3	58.6	60.1	104.1	201.9	108.0	542.0	224.0	178.3	217.4	288.4	67.0	217.4	3.2
1560622_at	—	1.01E-03	101.9	79.6	131.2	134.8	129.6	108.7	174.3	136.7	136.7	247.1	214.8	193.9	148.1	215.0	129.6	193.9	1.5
1560705_at	—	3.95E-04	106.5	117.2	130.6	129.7	152.2	106.0	118.5	200.5	209.3	405.8	217.1	220.3	183.1	265.4	118.5	217.1	1.8
1560817_at	—	8.55E-05	78.8	93.9	99.2	78.9	64.3	68.7	84.2	113.8	154.7	191.4	139.5	144.0	140.4	168.7	78.9	144.0	1.8
1560978_at	—	4.29E-03	48.6	49.8	41.1	38.3	43.2	42.5	42.7	60.2	73.7	56.3	45.3	62.1	47.6	58.3	42.7	58.3	1.4
1561056_a_at	—	6.56E-05	32.6	18.9	43.0	38.6	35.3	27.7	39.1	46.8	47.9	81.9	91.6	73.9	63.5	87.6	35.3	73.9	2.1
1561469_at	—	1.30E-03	55.4	52.2	39.3	22.8	57.1	40.7	53.5	82.0	123.8	305.7	99.4	101.2	133.3	137.4	52.2	123.8	2.4
1561654_at	—	1.40E-03	54.7	52.8	32.0	38.6	61.9	39.7	62.7	66.0	102.9	208.3	130.7	143.8	115.8	164.6	52.8	130.7	2.5
1561738_at	—	1.00E-03	58.9	56.5	39.8	27.9	49.6	25.4	34.6	102.3	120.8	412.0	166.7	107.5	86.1	139.4	39.8	120.8	3.0
1562056_at	—	3.38E-03	44.0	36.0	37.2	57.8	46.4	50.9	50.5	69.6	41.9	62.0	116.9	102.2	55.7	83.9	46.4	69.6	1.5
1562940_at	—	6.79E-03	49.8	51.7	63.7	63.7	72.8	58.7	65.1	94.9	63.1	91.8	79.2	90.5	73.1	80.2	63.7	80.2	1.3
1563010_at	—	1.69E-03	63.4	51.0	52.3	50.8	104.7	56.2	110.7	117.5	126.7	233.3	223.8	136.1	143.4	172.9	56.2	143.4	2.6
1563118_at	—	3.41E-05	37.9	34.0	24.6	24.9	97.3	39.3	39.0	127.2	139.8	396.0	182.4	443.2	275.4	285.2	37.9	275.4	7.3
1563271_at	—	1.24E-03	109.6	66.4	95.1	114.6	125.8	161.9	121.2	158.0	153.8	268.3	196.7	158.5	252.2	231.8	114.6	196.7	1.7
1563357_at	—	6.17E-06	67.4	33.5	60.0	52.5	91.1	31.2	117.4	314.2	685.0	1020.7	538.9	1037.1	449.3	1463.6	60.0	685.0	11.4
1566002_at	—	7.31E-03	83.7	48.6	73.9	66.0	66.5	66.8	71.9	88.0	59.5	96.6	109.0	126.2	84.0	105.9	66.8	96.6	1.4
1566256_s_at	—	9.92E-03	40.8	45.3	77.3	56.0	80.0	90.3	74.9	78.0	79.8	154.4	101.1	88.3	84.3	102.7	74.9	88.3	1.2

Continued

Supplementary Table S1. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1566257_at	—	6.84E-03	95.0	106.9	118.8	87.2	122.4	123.1	107.5	114.0	140.1	212.9	159.0	133.4	149.9	166.3	107.5	149.9	1.4
1566623_at	—	1.22E-03	24.7	27.0	35.8	29.6	43.2	32.7	45.2	37.2	50.9	83.2	66.9	57.3	46.1	62.6	32.7	57.3	1.8
1566709_at	—	1.49E-04	50.8	46.1	44.8	53.4	61.3	50.3	66.0	75.7	77.8	135.6	155.8	145.2	115.5	145.6	50.8	135.6	2.7
1568832_a_at	—	2.72E-03	96.4	83.4	107.4	73.7	118.5	71.9	82.5	114.4	110.0	253.7	136.6	147.2	152.1	155.1	83.4	147.2	1.8
1568941_a_at	—	4.49E-03	279.9	254.7	306.7	290.5	342.0	255.8	360.8	300.0	411.8	770.5	511.7	402.3	463.9	569.0	290.5	463.9	1.6
1569403_at	—	2.09E-03	230.9	177.6	312.0	285.1	229.1	167.1	337.7	316.1	330.5	802.1	373.8	318.8	357.3	473.3	230.9	357.3	1.5
1569672_at	—	2.71E-03	184.9	164.4	333.0	274.6	246.7	208.2	290.6	312.7	212.8	449.5	464.8	300.5	263.4	373.9	246.7	312.7	1.3
1570022_at	—	1.14E-04	23.3	24.6	33.3	38.7	28.2	25.5	28.7	48.9	65.7	149.8	142.6	45.5	77.7	87.0	28.2	77.7	2.8
1570197_at	—	5.16E-03	56.9	78.2	80.5	61.0	80.5	72.8	53.7	75.4	95.4	198.1	89.0	197.1	85.2	106.3	72.8	95.4	1.3
1570198_x_at	—	3.08E-04	70.8	107.6	75.2	65.7	89.0	75.2	84.6	102.4	169.2	155.3	105.7	186.8	104.6	169.0	75.2	155.3	2.1
1570541_s_at	—	6.17E-06	39.3	30.0	52.6	31.5	49.1	26.7	40.3	147.4	124.8	451.0	158.9	186.0	146.8	223.0	39.3	158.9	4.0
210824_at	—	3.17E-04	1616.3	1096.0	1533.2	1116.7	1455.3	1097.3	1815.0	2552.5	1885.5	2817.6	2065.1	2151.9	2652.2	2553.3	1455.3	2552.5	1.8
211388_s_at	—	1.78E-03	428.8	351.6	395.5	447.3	434.3	361.5	505.5	527.2	476.9	651.2	686.3	627.0	782.6	686.3	428.8	651.2	1.5
213294_at	—	9.36E-03	270.8	480.3	578.5	525.8	536.7	599.6	594.1	602.0	606.7	930.6	844.4	662.5	583.8	938.3	536.7	662.5	1.2
214854_at	—	9.66E-04	64.7	49.4	65.2	75.0	82.8	54.6	91.7	85.6	80.0	150.3	122.6	155.7	150.6	131.4	65.2	131.4	2.0
215062_at	—	1.47E-03	180.7	214.0	187.7	202.8	168.4	151.4	177.2	209.2	281.3	265.4	302.7	262.1	200.2	267.8	180.7	265.4	1.5
215252_at	—	5.32E-03	920.5	927.7	1165.2	1153.1	992.2	924.5	1180.5	1062.9	1217.5	1694.1	1387.3	1170.0	1176.9	1586.4	992.2	1217.5	1.2
216062_at	—	8.42E-04	291.5	196.8	272.1	379.9	346.1	326.5	337.2	295.1	566.0	704.2	758.0	814.6	740.5	745.4	326.5	740.5	2.3
216565_x_at	—	2.53E-04	192.0	127.0	207.7	183.1	97.3	148.0	86.0	354.2	280.1	515.0	340.9	352.0	323.7	408.8	148.0	352.0	2.4
216656_at	—	3.58E-03	191.0	181.5	221.8	218.0	229.3	176.9	219.4	246.5	210.3	284.0	255.8	341.1	272.4	314.6	218.0	272.4	1.2
216871_at	—	1.02E-04	55.1	56.1	85.5	72.5	95.8	81.8	88.0	101.5	130.5	231.5	156.3	160.8	125.5	177.5	81.8	156.3	1.9
217654_at	—	2.93E-04	37.3	38.6	73.9	38.6	76.0	58.4	72.3	69.2	76.1	256.0	89.5	120.7	104.3	127.6	58.4	104.3	1.8
220467_at	—	7.11E-03	41.1	32.4	45.7	37.7	55.8	48.0	50.3	46.2	52.1	114.5	70.9	66.5	58.2	82.4	45.7	66.5	1.5
220905_at	—	9.47E-03	56.5	47.7	61.9	68.4	69.0	64.2	64.9	70.7	56.4	76.8	82.9	75.1	91.0	82.8	64.2	76.8	1.2
221155_x_at	—	5.18E-04	166.1	142.5	160.2	207.5	177.9	203.1	218.0	226.8	237.3	399.8	324.6	361.2	322.0	341.0	177.9	324.6	1.8
221969_at	—	1.43E-04	41.3	56.7	31.8	66.7	38.0	38.5	26.5	105.9	178.8	319.3	208.5	124.3	225.6	230.4	38.5	208.5	5.4
222189_at	—	9.97E-03	146.9	171.4	196.0	182.7	186.3	177.6	159.8	201.8	227.8	230.6	216.6	228.8	199.4	189.9	177.6	216.6	1.2
222303_at	—	2.50E-04	110.1	114.7	140.9	89.9	104.1	84.9	116.5	165.4	215.5	565.3	202.6	235.4	188.9	342.5	110.1	215.5	2.0
222326_at	—	3.59E-03	26.0	24.7	22.1	23.6	28.2	24.7	21.7	38.0	61.7	219.9	66.7	66.6	37.2	61.5	24.7	61.7	2.5
226107_at	—	8.29E-03	65.2	100.7	111.8	105.2	91.6	89.6	124.5	89.3	103.9	160.7	166.1	136.8	103.5	152.2	100.7	136.8	1.4
226345_at	—	2.36E-04	189.9	287.5	276.4	242.1	349.0	274.1	298.9	376.0	543.5	1045.7	422.4	657.2	505.6	708.9	276.4	543.5	2.0
226560_at	—	4.37E-04	56.4	52.9	31.6	44.2	59.4	39.7	46.1	140.2	98.8	354.1	166.9	222.4	126.6	156.5	46.1	156.5	3.4
226725_at	—	4.39E-04	312.0	167.9	413.7	529.9	481.7	350.0	344.4	590.4	264.1	925.8	983.5	659.5	836.3	1071.5	350.0	836.3	2.4
227107_at	—	3.42E-04	127.9	131.3	146.7	167.0	162.1	175.4	251.2	250.6	261.4	414.6	274.5	232.1	276.9	457.5	162.1	274.5	1.7
227193_at	—	5.46E-05	62.4	59.4	71.4	62.4	83.0	44.9	115.9	138.4	140.4	399.3	247.1	209.4	143.7	341.0	62.4	209.4	3.4
227200_at	—	2.12E-03	463.5	617.8	750.3	714.9	910.3	771.5	891.5	845.9	991.4	1082.4	1016.5	1024.3	1027.3	1212.7	750.3	1024.3	1.4
227333_at	—	3.62E-03	178.7	117.2	181.9	189.1	297.0	174.4	390.7	252.7	294.1	585.7	282.4	343.6	344.8	604.4	181.9	343.6	1.9
227368_at	—	6.36E-03	129.4	160.0	189.0	175.9	181.0	193.7	251.2	211.9	218.7	396.7	258.6	249.7	205.2	303.8	181.0	249.7	1.4
227458_at	—	8.67E-05	1317.9	1069.1	1560.7	1756.3	2305.4	1596.9	2235.6	3211.6	4214.5	5162.0	4275.1	3896.7	3809.4	4665.5	1596.9	4214.5	2.6
227501_at	—	4.09E-04	412.0	439.3	479.2	563.6	509.5	362.3	485.1	565.3	707.6	1169.0	871.7	792.8	636.2	878.0	479.2	792.8	1.7
227571_at	—	5.15E-04	84.3	52.3	95.5	76.9	129.5	60.8	98.7	117.6	119.6	205.7	112.0	203.2	150.4	166.0	84.3	150.4	1.8
227621_at	—	2.09E-03	2918.4	2933.4	3750.2	4004.5	4448.7	3759.3	4598.3	3905.1	5412.9	7861.6	5794.6	5246.5	5219.3	6892.2	3759.3	5412.9	1.4
227749_at	—	2.52E-05	90.1	64.2	53.2	81.6	80.6	54.5	100.7	206.2	153.0	260.5	351.3	291.9	263.5	329.6	80.6	263.5	3.3
227755_at	—	5.55E-03	381.2	330.7	704.9	567.4	698.0	625.0	630.2	540.0	644.6	1220.3	861.2	705.8	772.4	883.4	625.0	772.4	1.2
227985_at	—	4.37E-04	204.3	142.5	231.3	192.5	321.7	192.3	385.7	479.5	711.3	1730.7	525.1	533.5	781.2	964.4	204.3	711.3	3.5
228478_at	—	4.75E-03	66.2	76.6	108.5	130.6	130.9	110.0	154.2	134.6	120.0	200.3	213.0	156.9	128.2	180.4	110.0	156.9	1.4
228498_at	—	3.66E-03	10907.0	8583.2	8406.7	10810.2	12246.8	8465.6	11447.0	12271.1	13266.7	15096.5	14555.0	14695.7	15599.8	15803.0	10810.2	14695.7	1.4
228589_at	—	1.96E-03	127.5	118.5	80.0	84.1	110.9	76.3	104.7	142.7	173.9	258.4	147.2	234.5	237.7	307.9	104.7	234.5	2.2
228612_at	—	7.65E-03	170.6	172.3	292.2	269.8	261.4	248.0	340.3	215.1	261.4	494.1	321.9	329.8	286.3	401.3	261.4	321.9	1.2
228657_at	—	4.44E-03	203.7	136.4	159.4	180.3	184.2	167.0	198.6	249.0	245.7	355.4	202.9	232.6	257.3	360.2	180.3	249.0	1.4
228714_at	—	6.61E-03	188.8	183.4	215.9	175.6	198.5	155.6	160.4	216.2	236.2	304.7	242.7	215.7	203.7	264.0	183.4	236.2	1.3
228812_at	—	6.50E-03	239.2	280.1	488.6	417.7	508.8	486.9	497.5	371.6	437.3	870.3	477.6	522.6	642.7	738.5	486.9	522.6	1.1
228828_at	—	4.58E-03	109.8	84.1	117.3	140.6	147.2	153.7	178.9	148.0	109.6	188.2	208.5	149.3	223.8	239.5	140.6	188.2	1.3
228910_at	—	1.01E-04	291.4	147.1	411.4	397.2	479.2	345.3	665.4	536.6	454.1	1068.4	809.2	794.3	918.2	1225.5	397.2	809.2	2.0
228918_at	—	2.57E-05	325.6	210.3	231.1	305.8	498.0	264.4	430.3	697.3	566.9	824.4	731.9	1089.8	1066.8	1244.0	305.8	824.4	2.7
229041_s_at	—	2.32E-04	81.0	90.7	69.7	96.3	109.5	61.5	65.8	146.3	138.2	128.4	134.4	222.5	90.4	135.4	81.0	135.4	1.7
229074_at	—	4.58E-03	1678.6	2021.4	1468.7	1671.8	1618.3	1450.3	1430.3	1830.9	2490.7	2070.1	2179.6	2111.6	1875.4	2176.5	1618.3	2111.6	1.3
229188_s_at	—	2.54E-03	106.3	123.4	147.8	136.5	171.9	145.9	139.5	209.1	153.3	237.3	178.6	225.0	192.7	193.8	139.5	193.8	1.4
229242_at	—	1.67E-04	56.1	29.7	33.1	31.6	82.8	33.9	70.8	120.3	95.6	324.7	177.5	315.6	85.6	331.3	33.9	177.5	5.2
229373_at	—	1.72E-03	57.1	38.0	48.1	37.1	44.5	36.6	41.6	65.3	59.9	72.3	51.7	89.2	83.0	92.5	41.6	72.3	1.7
229548_at	—	6.81E-05	67.3	59.1	78.7	65.1	63.9	71.0	59.7	106.6	153.5	308.6	173.2	233.5	190.2	216.2	65.1	190.2	2.9
229695_at	—	2.57E-04	25.0	42.3	42.7	46.5	43.0	48.3	77.1	70.7	97.6	209.8	139.0	69.3	133.0	142.8	43.0	133.0	3.1
229733_s_at	—	5.16E-04	149.2	160.7	294.5	258.8	241.3	193.3	291.6	340.8	235.3	506.0	356.4	352.2	314.2	468.4	241.3	352.2	1.5
229795_at	—	7.35E-04	147.0	155.2	193.3	152.3	168.1	106.5	172.4	204.1	190.8	332.8	268.6	274.0	227.2	262.7	155.2	262.7	1.7
229830_at	—	1.39E-04	31.2	16.9	33.2	46.4	53.3	28.8	42.1	66.8	37.9	75.3	67.8	141.0	64.5	154.3	33.2	67.8	2.0
230127_at	—	2.53E-04	37.1	25.1	39.2	41.2	49.5	12.1	63.4	77.2	83.3	326.8	128.7	134.8	79.7	167.9	39.2	128.7	3.3

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
230161_at	—	2.76E-03	444.0	616.3	279.6	315.2	285.0	274.3	298.4	568.2	839.5	548.2	407.2	347.1	404.7	548.7	298.4	548.2	1.8
230260_s_at	—	9.77E-04	34.5	29.0	57.4	48.0	70.7	40.0	57.0	61.5	43.5	105.9	65.1	95.6	60.9	71.0	48.0	65.1	1.4
230267_at	—	1.06E-03	209.6	221.8	218.1	195.9	266.7	221.4	220.5	312.0	381.2	501.1	286.2	310.5	424.9	418.9	220.5	381.2	1.7
230278_at	—	5.20E-03	60.5	64.7	128.8	122.2	136.9	110.0	157.1	124.0	105.9	231.5	194.5	162.8	139.2	169.1	122.2	162.8	1.3
230314_at	—	9.56E-04	45.9	53.5	51.3	45.5	47.3	49.2	44.0	74.6	75.2	137.9	83.4	82.8	62.9	95.9	47.3	82.8	1.8
230333_at	—	2.93E-04	3096.9	3904.9	2913.9	2284.3	3127.0	2829.4	2731.5	3982.5	5764.5	5000.0	4428.9	4949.8	4721.1	4344.5	2913.9	4721.1	1.6
230383_x_at	—	3.79E-03	116.5	77.5	142.2	181.0	145.9	121.3	126.5	148.4	96.5	305.2	321.4	168.7	219.3	308.1	126.5	219.3	1.7
230387_at	—	7.17E-03	139.9	134.7	244.7	234.2	185.9	214.4	236.1	203.7	243.8	459.6	405.7	217.1	245.6	261.0	214.4	245.6	1.1
230446_at	—	8.68E-03	92.7	81.4	89.7	92.1	94.4	99.5	101.3	140.4	105.1	166.1	96.9	144.1	109.1	142.2	92.7	140.4	1.5
230499_at	—	3.05E-04	71.1	56.3	106.1	126.0	173.4	77.1	90.2	175.5	121.2	267.5	236.3	205.1	196.1	190.8	90.2	196.1	2.2
230659_at	—	2.46E-03	3806.4	3334.2	3401.6	3538.2	3740.9	4217.2	4251.5	4350.2	4678.5	5488.7	5146.4	4679.2	5401.7	6132.3	3740.9	5146.4	1.4
230714_s_at	—	4.63E-03	157.4	115.7	107.1	117.6	121.6	124.4	116.1	160.1	166.3	238.2	148.2	216.6	194.9	241.3	117.6	194.9	1.7
230733_at	—	6.19E-03	91.0	90.6	128.5	99.0	86.8	100.3	104.2	132.4	112.2	214.5	129.4	123.2	103.4	135.5	99.0	129.4	1.3
230741_at	—	4.83E-04	1647.1	1446.8	1149.4	1231.4	2415.0	1301.8	1996.5	2703.4	2757.4	3922.9	2672.1	3362.9	3330.7	3784.4	1446.8	3330.7	2.3
230850_at	—	2.87E-03	120.6	121.5	136.2	133.7	158.2	142.2	156.6	163.0	139.0	267.8	270.3	205.3	213.3	231.3	136.2	213.3	1.6
231078_at	—	2.23E-04	63.4	57.2	81.4	70.9	68.0	75.6	82.7	88.9	169.4	319.2	135.5	187.6	187.3	201.4	70.9	187.3	2.6
231083_at	—	1.16E-05	69.7	26.0	52.1	47.4	58.2	22.4	97.6	228.8	129.8	279.6	217.6	254.4	209.0	334.5	52.1	228.8	4.4
231127_at	—	5.95E-03	76.2	85.9	125.1	121.8	120.3	122.1	135.0	115.5	107.7	150.8	204.3	159.5	141.4	161.1	121.8	150.8	1.2
231227_at	—	5.10E-03	50.3	47.3	21.5	24.5	42.1	38.1	25.0	58.5	69.3	100.5	93.0	59.8	73.0	77.2	38.1	73.0	1.9
231259_s_at	—	5.30E-03	68.0	55.9	77.2	87.0	72.7	40.6	69.2	88.2	69.6	90.5	159.2	99.2	91.7	164.7	69.2	91.7	1.3
231274_s_at	—	2.66E-05	122.0	126.5	222.6	181.6	200.3	180.2	254.9	319.1	483.3	640.8	317.4	563.0	473.3	842.7	181.6	483.3	2.7
231312_at	—	4.44E-03	162.9	126.8	209.7	193.4	208.7	201.1	200.2	232.9	197.7	280.7	303.1	202.9	322.0	279.1	200.2	279.1	1.4
231513_at	—	1.71E-05	202.0	185.6	476.7	399.7	838.9	256.4	489.3	1022.9	2617.8	5372.8	2874.4	2774.8	2945.3	4266.4	399.7	2874.4	7.2
231699_at	—	1.21E-05	123.0	98.5	106.3	93.0	176.0	79.7	158.3	317.7	345.5	474.5	361.7	542.4	487.0	508.8	106.3	474.5	4.5
231937_at	—	2.87E-03	104.5	91.8	101.8	95.2	81.2	70.1	93.1	111.2	113.2	151.2	193.3	142.8	115.8	156.1	93.1	142.8	1.5
232095_at	—	9.81E-04	138.3	131.3	165.5	220.5	194.0	182.4	218.2	249.6	185.7	331.7	288.8	278.1	238.1	385.4	182.4	278.1	1.5
232150_at	—	6.53E-04	76.2	65.5	87.8	75.7	88.6	78.8	94.4	112.5	118.3	214.3	179.4	127.3	109.9	168.8	78.8	127.3	1.6
232333_at	—	1.14E-03	129.9	93.5	74.0	74.9	87.6	83.8	77.6	155.3	128.0	192.3	157.5	178.5	135.6	174.3	83.8	157.5	1.9
232375_at	—	2.27E-05	80.9	93.8	166.2	112.6	113.3	92.2	98.9	172.5	177.6	358.2	301.9	224.5	198.5	292.0	98.9	224.5	2.3
233118_at	—	1.14E-03	29.2	32.8	28.1	26.7	32.2	25.0	30.2	44.2	46.1	87.3	106.2	52.2	76.6	72.3	29.2	72.3	2.5
233137_at	—	1.15E-04	111.6	104.8	196.3	160.5	252.1	196.2	203.9	259.5	285.7	405.7	286.8	362.7	366.5	460.3	196.2	362.7	1.8
233289_at	—	7.75E-03	36.7	32.1	77.3	55.7	56.2	43.9	30.1	64.7	54.4	124.3	64.4	57.7	52.8	46.8	43.9	57.7	1.3
233935_at	—	6.14E-03	46.1	32.3	32.0	50.4	48.8	37.8	34.9	49.4	73.9	129.9	66.4	78.7	62.1	84.5	37.8	73.9	2.0
233989_at	—	1.11E-04	115.7	69.6	152.8	121.1	126.8	74.6	123.8	224.6	316.7	810.1	266.2	308.5	273.2	370.6	121.1	308.5	2.5
234326_at	—	9.94E-04	52.6	38.1	63.6	54.7	71.4	56.3	73.8	72.7	56.0	138.0	109.5	90.0	99.1	110.9	56.3	99.1	1.8
235094_at	—	2.34E-03	479.2	282.6	339.5	495.0	353.5	245.4	352.0	503.6	618.9	1155.1	694.1	686.1	710.0	941.7	352.0	694.1	2.0
235102_x_at	—	8.93E-03	90.4	87.0	226.1	115.3	106.8	120.6	134.3	169.0	105.8	216.9	195.8	156.2	166.7	182.6	115.3	169.0	1.5
235112_at	—	7.95E-03	46.8	40.1	53.5	49.9	74.8	74.0	41.9	65.7	82.8	142.8	97.7	71.0	89.4	114.6	49.9	89.4	1.8
235157_at	—	1.24E-05	140.4	159.3	168.3	227.7	224.3	179.3	247.9	399.5	555.4	1004.0	843.0	599.9	542.7	844.2	179.3	599.9	3.3
235242_at	—	1.14E-03	193.4	272.2	384.1	283.8	471.8	402.3	399.3	388.7	340.5	798.0	448.8	611.2	594.2	658.3	384.1	594.2	1.5
235295_at	—	7.30E-04	68.8	101.3	111.6	107.6	133.3	123.0	202.5	171.4	163.0	350.5	234.6	171.6	227.6	349.1	111.6	227.6	2.0
235407_at	—	8.51E-04	108.8	97.0	150.9	124.0	149.2	150.7	154.6	156.3	177.3	203.0	173.7	192.2	215.5	229.4	149.2	192.2	1.3
235454_at	—	7.68E-03	354.4	365.5	540.6	483.9	360.6	344.7	348.3	460.4	473.0	671.6	501.5	466.7	437.2	501.7	360.6	473.0	1.3
235543_at	—	3.16E-03	71.9	65.6	96.0	87.6	94.6	108.4	98.0	140.8	93.8	179.4	117.9	121.3	124.5	138.2	94.6	124.5	1.3
235661_at	—	3.70E-04	90.3	62.0	54.2	50.4	49.2	25.2	49.7	129.6	132.8	162.3	204.2	169.9	163.3	171.4	50.4	163.3	3.2
235735_at	—	1.03E-05	58.9	41.0	55.9	104.9	76.1	34.1	69.0	253.1	173.3	268.7	286.2	456.6	212.9	524.6	58.9	268.7	4.6
235740_at	—	3.66E-03	257.1	191.0	278.8	341.5	471.8	278.8	416.0	453.3	486.2	903.6	742.5	483.1	520.8	552.5	278.8	520.8	1.9
235847_at	—	7.46E-03	59.9	38.2	52.2	54.3	59.9	46.0	52.2	57.5	49.2	75.9	94.5	78.3	65.4	78.0	52.2	75.9	1.5
235920_at	—	6.61E-03	58.8	48.1	53.5	57.9	48.5	44.2	45.0	58.0	58.8	74.8	80.7	76.4	85.6	77.3	48.5	76.4	1.6
235922_at	—	1.13E-03	93.4	70.2	84.5	93.3	83.7	57.7	86.1	105.2	139.5	280.9	188.1	140.6	111.7	201.5	84.5	140.6	1.7
235971_at	—	6.95E-03	80.4	132.5	117.0	100.2	139.1	116.9	159.1	129.4	138.5	223.6	178.9	165.7	166.7	196.7	117.0	166.7	1.4
236106_at	—	2.71E-03	163.3	159.4	162.0	145.8	159.5	182.8	135.7	245.8	315.0	449.4	227.3	251.0	199.7	354.4	159.5	251.0	1.6
236139_at	—	9.72E-03	69.5	39.8	65.2	68.8	71.3	57.0	55.9	76.4	51.4	107.9	118.5	71.9	80.1	85.3	65.2	80.1	1.2
236191_at	—	1.01E-04	47.6	43.0	49.9	64.8	46.9	71.5	39.5	136.7	337.3	557.5	230.9	184.8	195.8	201.9	47.6	201.9	4.2
236198_at	—	5.42E-04	9.0	11.2	16.8	15.4	39.1	12.5	36.8	53.5	31.2	119.5	99.1	82.3	100.2	60.6	15.4	82.3	5.4
236372_at	—	4.56E-03	52.2	47.1	50.2	40.9	54.3	47.6	58.2	64.2	83.8	108.4	61.2	71.9	51.8	93.2	50.2	71.9	1.4
236399_at	—	4.65E-03	36.7	56.9	58.9	56.9	38.4	59.1	71.7	51.3	68.4	88.6	67.1	59.5	67.7	94.4	56.9	67.7	1.2
236417_at	—	9.31E-03	77.8	117.4	118.9	113.1	84.4	94.8	90.9	85.2	185.5	324.8	250.2	95.0	123.6	151.0	94.8	151.0	1.6
236437_at	—	2.13E-03	27.3	55.1	65.4	65.3	64.5	91.6	68.0	69.4	92.8	206.3	184.0	102.8	107.3	102.8	65.3	102.8	1.6
236439_at	—	3.42E-04	71.1	87.4	94.5	79.1	138.8	58.8	125.5	116.6	203.3	369.0	133.1	255.5	139.6	251.1	87.4	203.3	2.3
236495_at	—	1.55E-04	98.0	55.9	139.2	91.7	156.1	123.3	170.7	170.5	289.6	960.6	288.6	381.5	468.0	658.1	123.3	381.5	3.1
236606_at	—	2.10E-03	63.1	52.1	99.7	109.8	97.1	91.2	112.0	87.4	109.5	303.8	178.1	126.7	157.6	165.1	97.1	157.6	1.6
236670_s_at	—	5.17E-04	50.5	31.3	38.8	38.7	57.4	19.5	31.8	71.7	51.8	83.4	163.3	140.7	58.1	105.0	38.7	83.4	2.2
236683_at	—	9.45E-03	48.9	32.6	44.0	29.8	41.7	48.9	51.2	43.1	77.0	149.9	49.9	79.4	69.8	76.9	44.0	76.9	1.7
236685_at	—	2.92E-03	40.0	32.5	47.0	51.7	62.1	47.2	53.7	66.7	50.7	77.4	59.3	76.1	70.2	66.1	47.2	66.7	1.4
236727_at	—	3.46E-04	35.5	36.1	72.2	35.5	24.9	66.5	61.5	57.2	53.7	165.4	77.0	47.6	96.5	92.4	36.1	77.0	2.1

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
237082_at	—	3.33E-03	42.3	42.3	54.5	61.6	56.7	54.9	48.8	56.8	44.4	95.4	137.6	105.5	73.9	82.5	54.5	82.5	1.5
237091_at	—	1.05E-04	191.0	118.5	171.7	174.7	180.7	145.1	194.9	278.5	262.5	444.0	312.0	390.2	387.5	375.3	174.7	375.3	2.1
237104_at	—	7.46E-03	207.5	247.5	288.7	329.2	350.9	268.5	291.3	302.3	305.3	469.8	462.4	359.8	316.3	429.7	288.7	359.8	1.2
237105_at	—	5.51E-03	85.2	82.8	133.9	118.9	109.5	125.5	122.5	131.6	104.8	325.9	201.5	185.4	126.9	181.0	118.9	181.0	1.5
237154_at	—	1.54E-03	176.2	172.7	192.7	131.6	219.3	436.2	219.7	265.1	289.8	324.2	167.2	285.2	532.0	309.6	192.7	289.8	1.5
237310_at	—	6.38E-05	50.1	44.0	50.1	47.8	29.6	66.5	43.8	78.4	118.8	166.7	120.0	106.4	157.1	110.4	47.8	118.8	2.5
237563_s_at	—	2.33E-05	105.5	86.0	98.1	103.5	154.3	102.7	129.0	273.3	230.8	311.4	186.3	331.1	252.5	275.7	103.5	273.3	2.6
237954_x_at	—	7.21E-03	112.5	113.1	83.7	93.0	112.5	85.9	100.7	143.1	140.8	112.5	96.9	152.4	133.3	126.4	100.7	133.3	1.3
238361_s_at	—	3.06E-03	59.7	44.4	48.5	44.2	83.5	35.3	46.2	82.3	55.5	95.4	207.9	144.1	88.6	116.5	46.2	95.4	2.1
238389_s_at	—	9.72E-03	59.1	55.0	57.6	46.3	59.5	48.4	71.2	65.2	63.6	104.3	52.5	84.8	88.9	98.4	57.6	84.8	1.5
238403_at	—	6.25E-05	304.8	288.9	281.8	346.2	373.0	301.4	185.2	501.4	639.8	1005.7	958.2	1039.0	964.4	720.3	301.4	958.2	3.2
238405_at	—	2.84E-05	308.9	271.2	289.7	375.3	387.9	343.3	227.7	554.7	558.6	878.0	902.5	809.3	794.8	665.2	308.9	794.8	2.6
238729_x_at	—	1.62E-03	23.0	28.6	62.1	63.0	81.6	65.7	76.1	57.5	84.8	327.3	109.5	116.1	111.5	150.3	63.0	111.5	1.8
238743_at	—	2.92E-03	330.2	400.1	406.4	267.9	235.2	252.6	292.2	398.5	423.3	682.9	483.3	386.4	475.1	633.0	292.2	475.1	1.6
238758_at	—	8.84E-03	169.0	122.5	194.7	185.6	193.6	159.6	184.2	219.1	160.1	259.4	195.8	280.2	219.1	204.9	184.2	219.1	1.2
238869_at	—	3.67E-03	83.3	84.1	67.6	79.6	69.8	62.5	50.8	98.1	96.7	117.4	142.0	106.2	136.6	136.5	69.8	117.4	1.7
238942_at	—	3.09E-03	39.9	50.4	61.9	59.2	62.3	63.7	75.2	51.3	69.7	182.2	81.2	99.5	140.5	117.4	61.9	99.5	1.6
238973_s_at	—	6.10E-05	79.6	71.0	73.2	68.3	92.7	80.7	89.5	156.4	161.6	211.0	134.3	152.4	152.1	174.6	79.6	156.4	2.0
239005_at	—	6.27E-03	59.5	59.3	69.5	72.8	43.6	68.0	58.8	66.0	68.1	91.7	92.8	65.1	85.4	87.4	59.5	85.4	1.4
239032_at	—	9.66E-03	37.6	45.0	48.2	51.0	52.1	42.9	50.6	55.7	69.6	113.5	118.9	61.1	50.9	57.3	48.2	61.1	1.3
239045_at	—	6.51E-03	31.2	44.3	61.5	63.4	64.2	66.8	61.2	64.1	57.1	108.0	93.8	71.0	80.0	81.3	61.5	80.0	1.3
239060_at	—	6.86E-04	39.6	33.6	41.8	39.0	64.2	46.3	54.3	60.2	46.2	118.4	76.8	105.1	100.5	86.5	41.8	86.5	2.1
239249_at	—	2.36E-03	116.7	87.1	93.9	96.1	121.4	115.5	121.8	131.5	179.2	320.8	141.5	225.5	267.6	200.6	115.5	200.6	1.7
239258_at	—	2.73E-03	43.3	49.8	74.8	56.3	65.6	64.3	64.5	91.0	71.3	229.0	148.5	115.8	85.2	80.0	64.3	91.0	1.4
239274_at	—	8.86E-03	69.3	79.0	82.6	79.0	75.5	78.9	79.0	77.5	79.0	122.2	125.7	105.0	104.1	122.6	79.0	105.0	1.3
239277_at	—	6.60E-03	349.4	363.3	439.7	468.7	444.3	540.1	472.8	513.3	490.7	631.0	645.9	485.5	601.4	595.4	444.3	595.4	1.3
239331_at	—	2.20E-05	43.2	38.9	57.7	52.3	63.4	48.5	73.0	112.3	93.3	204.5	114.2	169.7	115.5	138.2	52.3	115.5	2.2
239414_at	—	1.67E-04	41.5	25.4	42.9	32.5	48.1	36.2	47.9	63.3	75.7	128.1	84.6	93.9	85.8	80.6	41.5	84.6	2.0
239427_at	—	2.69E-03	52.1	48.0	33.8	28.8	35.0	35.0	34.1	57.6	59.1	117.1	74.2	90.0	77.9	127.4	35.0	77.9	2.2
239451_at	—	5.56E-03	52.3	44.8	48.9	64.4	42.5	52.9	64.8	74.6	62.1	94.1	96.8	54.2	57.3	80.3	52.3	74.6	1.4
239494_at	—	3.67E-03	61.2	59.4	62.0	65.7	68.1	84.5	67.5	77.0	77.3	109.6	91.9	81.6	102.1	98.9	65.7	91.9	1.4
239555_at	—	6.89E-04	51.8	32.5	45.8	39.3	58.4	51.5	42.7	73.6	48.0	86.5	98.3	78.7	88.5	82.7	45.8	82.7	1.8
239759_at	—	8.54E-04	157.5	162.5	157.2	134.9	122.8	147.1	160.4	212.2	200.9	352.7	237.2	259.3	256.7	259.0	157.2	256.7	1.6
239779_at	—	9.25E-03	65.8	40.1	60.0	62.8	68.0	59.8	65.5	69.7	65.1	72.4	86.7	74.3	90.1	103.7	62.8	74.3	1.2
239814_at	—	4.22E-04	47.3	31.5	56.5	57.1	61.7	36.1	51.4	80.6	67.5	115.7	82.7	80.9	89.4	102.4	51.4	82.7	1.6
239817_at	—	5.42E-03	84.8	103.7	105.2	112.7	134.3	119.6	137.1	182.3	102.9	178.6	178.9	213.3	148.9	196.6	112.7	178.9	1.6
239876_at	—	1.58E-04	32.2	28.6	37.5	37.9	45.6	33.1	48.8	60.2	49.1	165.7	102.2	100.1	102.2	124.2	37.5	102.2	2.7
239979_at	—	1.23E-04	75.6	97.8	87.1	56.8	80.9	46.1	70.9	138.1	168.8	316.7	172.2	157.6	113.5	207.5	75.6	168.8	2.2
240057_at	—	7.73E-03	92.7	69.5	103.8	103.5	124.5	99.7	88.8	113.5	83.3	119.7	152.9	138.5	146.0	141.7	99.7	138.5	1.4
240103_at	—	2.15E-04	73.5	15.2	23.3	70.0	236.4	42.5	68.9	352.6	315.0	632.5	248.8	828.1	591.4	475.3	68.9	475.3	6.9
240131_at	—	1.90E-03	1119.4	313.2	443.9	279.2	1044.4	675.7	924.6	1510.5	767.7	893.7	771.6	1419.8	1612.0	1170.4	675.7	1170.4	1.7
240137_at	—	2.25E-04	16.1	10.8	18.4	14.3	29.1	5.2	60.2	76.3	36.5	129.0	105.7	77.6	47.8	112.0	16.1	77.6	4.8
240145_at	—	1.32E-04	50.3	36.3	76.1	53.3	70.0	70.7	84.0	87.8	58.9	222.1	113.3	118.0	157.5	157.0	70.0	118.0	1.7
240165_at	—	1.71E-04	75.6	53.6	73.9	90.3	126.7	94.0	85.5	120.9	114.6	304.8	217.2	272.4	228.8	174.7	85.5	217.2	2.5
240232_at	—	4.32E-05	437.2	593.1	424.4	497.5	657.7	509.4	550.8	1219.0	1618.1	2834.8	2343.0	1545.5	2223.2	1943.6	509.4	1943.6	3.8
240421_x_at	—	4.87E-03	68.8	67.6	80.3	84.0	110.0	67.4	116.3	97.8	107.8	251.3	121.9	125.0	143.7	174.4	80.3	125.0	1.6
240536_at	—	9.12E-04	134.1	45.5	66.4	37.0	102.5	34.5	112.9	168.9	97.9	277.9	107.7	170.4	122.1	260.2	66.4	168.9	2.5
240652_at	—	4.01E-03	110.0	95.6	142.4	136.9	140.7	148.5	137.4	197.2	143.7	219.0	237.6	177.4	163.1	166.0	137.4	177.4	1.3
240796_at	—	2.37E-03	58.3	44.2	32.2	42.7	75.3	47.2	63.8	78.7	96.0	170.3	138.6	104.6	155.7	117.5	47.2	117.5	2.5
240843_at	—	9.81E-03	55.8	40.5	89.6	90.9	84.3	70.5	94.4	74.6	79.3	153.3	123.7	97.7	96.0	96.4	84.3	96.4	1.1
240866_at	—	1.83E-03	33.4	28.5	48.6	34.8	58.2	49.9	58.2	69.9	76.6	145.8	125.7	92.9	111.5	59.4	48.6	92.9	1.9
241068_at	—	5.99E-03	65.6	47.4	127.5	126.5	176.0	118.4	186.8	110.0	104.5	358.7	237.6	173.6	200.3	223.0	126.5	200.3	1.6
241254_at	—	4.73E-03	70.0	57.0	50.1	46.0	52.4	42.7	57.5	66.4	69.0	113.7	90.3	114.1	109.4	100.9	52.4	100.9	1.9
241279_at	—	7.94E-04	39.8	36.3	42.2	26.1	44.1	46.6	48.9	55.6	85.8	153.5	78.5	116.3	93.3	67.9	42.2	85.8	2.0
241292_at	—	3.04E-03	39.7	38.0	50.9	44.6	45.2	41.9	36.5	53.4	40.6	77.4	76.4	59.1	57.4	56.4	41.9	57.4	1.4
241371_at	—	7.07E-04	161.9	131.4	151.2	133.4	119.3	149.8	204.6	193.5	279.6	380.5	209.3	195.8	264.3	435.8	149.8	264.3	1.8
241462_at	—	2.53E-03	96.4	101.6	119.9	98.1	110.7	129.4	111.2	121.8	142.8	276.2	191.6	161.3	188.6	142.4	110.7	161.3	1.5
241540_at	—	8.14E-03	74.0	62.7	66.4	68.6	51.9	64.8	80.6	77.7	83.2	113.7	74.5	99.9	98.6	118.3	66.4	98.6	1.5
241615_x_at	—	4.68E-03	733.9	431.0	555.6	767.5	828.0	579.9	792.7	743.5	889.6	1696.1	1099.9	1434.8	917.2	1286.3	733.9	1099.9	1.5
241616_at	—	1.55E-03	410.7	152.0	354.4	444.2	571.0	354.5	409.0	462.2	441.3	1350.1	799.9	1166.3	691.8	775.8	409.0	775.8	1.9
241631_at	—	9.29E-03	86.6	78.7	42.5	62.7	109.2	47.0	77.5	116.0	116.3	153.4	163.1	130.0	59.4	128.5	77.5	128.5	1.7
241769_at	—	6.70E-03	28.7	47.9	40.7	38.3	64.7	35.1	47.7	54.1	59.0	68.0	84.5	78.8	44.0	56.2	40.7	59.0	1.5
241824_at	—	7.15E-04	89.5	74.4	82.1	87.6	117.4	96.5	125.3	128.2	113.0	222.0	150.3	215.5	136.2	223.2	89.5	150.3	1.7
241916_at	—	1.23E-03	28.5	16.9	46.3	38.2	40.6	41.5	61.6	67.6	46.5	145.2	93.3	100.1	73.4	60.7	40.6	73.4	1.8
241991_at	—	6.45E-04	28.0	36.5	51.4	39.9	42.2	53.7	39.7	53.3	47.5	84.5	58.7	67.0	69.2	70.6	39.9	67.0	1.7
242167_at	—	3.54E-03	47.0	46.2	66.1	70.2	58.8	61.6	71.1	93.6	50.0	88.6	98.7	100.7	102.6	91.5	61.6	93.6	1.5

Continued

Supplementary Table S1. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
242277_at	—	4.19E-03	1538.9	1981.2	1913.1	1806.2	2004.3	1997.0	1923.5	2241.4	2614.1	3125.7	2894.6	2262.8	2259.5	2654.4	1923.5	2614.1	1.4
242379_at	—	4.59E-03	101.2	74.6	135.0	105.5	128.9	103.4	131.6	143.4	108.2	310.8	260.4	142.1	133.6	230.3	105.5	143.4	1.4
242388_x_at	—	1.35E-04	36.1	27.3	53.4	54.9	72.2	50.4	63.0	119.2	87.3	280.1	161.0	113.7	124.6	162.2	53.4	124.6	2.3
242405_at	—	6.64E-05	64.5	64.3	63.8	56.3	63.2	68.4	60.5	122.6	95.0	149.5	141.0	158.5	132.5	141.4	63.8	141.0	2.2
242471_at	—	5.79E-03	41.0	36.3	42.5	52.7	47.3	43.4	42.6	63.5	53.2	71.5	89.0	74.9	41.2	52.0	42.6	63.5	1.5
242575_at	—	1.86E-03	303.5	256.6	301.0	275.8	304.4	300.7	286.2	382.0	415.1	489.6	356.7	362.1	433.5	398.2	300.7	398.2	1.3
242713_at	—	4.83E-03	52.1	48.8	65.1	67.2	68.8	63.0	71.7	68.6	66.3	153.8	113.7	86.3	89.7	87.9	65.1	87.9	1.3
242784_at	—	2.77E-04	220.5	223.4	335.0	242.2	153.2	173.3	236.5	284.7	547.4	1066.0	446.1	463.5	389.5	636.7	223.4	463.5	2.1
242827_x_at	—	3.15E-03	42.2	52.5	53.2	70.0	59.4	50.4	46.9	65.4	51.7	75.8	143.5	94.1	77.3	85.5	52.5	77.3	1.5
242853_at	—	1.26E-03	85.3	58.3	68.7	102.7	84.3	91.4	88.3	114.7	87.0	241.1	165.3	187.8	164.5	196.9	85.3	165.3	1.9
242866_x_at	—	5.51E-05	121.3	93.6	77.5	86.2	86.8	70.2	95.1	229.2	165.0	183.6	233.7	233.7	195.8	346.4	86.8	229.2	2.6
242875_at	—	2.76E-03	138.7	113.3	130.6	151.0	164.5	151.7	148.0	165.5	124.9	210.0	210.6	262.6	230.4	214.0	148.0	210.6	1.4
242898_at	—	3.54E-03	253.1	292.4	283.4	238.9	245.9	250.4	267.4	372.3	295.5	455.1	424.9	395.1	312.6	482.2	253.1	395.1	1.6
242907_at	—	6.10E-05	34.2	52.5	56.4	67.0	75.6	60.1	65.0	109.1	128.2	340.1	231.0	171.5	147.5	193.2	60.1	171.5	2.9
243015_at	—	7.49E-03	35.5	47.2	29.6	21.6	33.6	30.8	34.7	28.4	79.2	129.8	52.9	59.0	61.8	99.5	33.6	61.8	1.8
243157_at	—	5.32E-03	381.5	310.7	359.9	241.5	294.1	244.0	324.9	385.9	367.2	542.9	353.8	476.5	349.7	463.1	310.7	385.9	1.2
243158_at	—	4.92E-03	25.0	40.6	50.6	42.8	48.2	53.0	57.2	52.2	50.7	95.8	80.7	67.8	64.5	64.8	48.2	64.8	1.3
243187_at	—	9.65E-03	94.0	97.0	67.3	61.9	77.5	66.8	61.4	93.8	97.2	137.2	96.0	134.2	116.1	139.9	67.3	116.1	1.7
243271_at	—	1.25E-04	403.8	419.9	417.2	326.2	314.0	260.7	252.0	610.2	861.9	1210.8	912.5	581.9	667.6	811.4	326.2	811.4	2.5
243286_at	—	7.35E-03	46.6	52.7	93.7	76.8	97.1	71.1	95.1	79.7	85.0	170.4	126.7	97.0	92.8	107.9	76.8	97.0	1.3
243342_at	—	8.48E-03	63.4	50.5	56.9	64.4	62.9	46.2	49.6	87.1	63.6	96.2	123.1	69.1	84.3	53.4	56.9	84.3	1.5
243395_at	—	3.08E-03	69.3	75.7	94.7	82.5	86.3	62.5	62.8	91.8	86.3	236.1	121.4	129.3	106.7	101.9	75.7	106.7	1.4
243410_at	—	1.36E-03	28.8	49.1	52.5	33.7	50.4	39.0	53.0	48.5	54.1	86.4	79.9	78.9	66.8	84.8	49.1	78.9	1.6
243454_at	—	7.40E-03	47.3	41.2	49.7	32.4	40.6	40.6	39.6	60.7	40.9	78.2	86.8	71.2	68.0	56.2	40.6	68.0	1.7
243633_at	—	1.83E-03	145.5	112.9	119.1	114.8	122.3	101.5	110.5	161.6	163.0	228.5	164.2	178.1	194.6	230.8	114.8	178.1	1.6
243653_at	—	5.92E-03	99.1	61.5	101.0	76.9	177.1	89.2	112.7	134.3	126.3	175.9	219.1	225.4	209.6	116.2	99.1	175.9	1.8
243675_at	—	1.45E-03	31.1	21.3	55.8	45.4	57.2	30.2	85.3	62.2	83.2	174.3	66.4	121.9	87.6	104.0	45.4	87.6	1.9
243699_at	—	1.80E-03	104.1	109.4	118.0	89.5	90.2	127.1	102.5	150.7	191.9	488.6	151.5	162.0	195.6	220.2	104.1	191.9	1.8
243754_at	—	3.68E-03	180.5	151.3	163.8	139.5	190.7	142.5	150.6	326.7	165.6	231.4	214.8	239.7	225.3	191.2	151.3	225.3	1.5
243888_at	—	1.40E-03	65.0	83.2	144.0	109.3	120.0	108.9	131.9	139.7	137.2	373.7	273.2	173.2	125.9	231.1	109.3	173.2	1.6
243931_at	—	1.73E-04	101.7	83.1	125.9	180.6	161.2	126.7	212.1	247.8	169.8	367.3	312.2	261.0	223.4	362.3	126.7	261.0	2.1
244035_at	—	6.71E-04	61.2	64.8	72.5	57.6	57.4	52.1	75.1	92.2	74.0	119.8	94.4	87.0	80.0	118.0	61.2	92.2	1.5
244054_at	—	3.79E-03	54.8	58.6	67.8	77.4	77.5	71.4	73.8	75.5	66.6	89.4	93.8	102.5	106.1	93.2	71.4	93.2	1.3
244087_at	—	9.56E-04	85.1	61.9	57.7	49.2	77.6	50.5	68.9	118.5	86.1	128.7	151.8	118.2	110.1	165.0	61.9	118.5	1.9
244218_at	—	8.67E-03	71.7	53.3	80.0	82.4	81.6	81.3	73.5	84.1	61.0	99.5	131.7	122.3	93.8	93.3	80.0	93.8	1.2
244219_at	—	2.94E-04	52.2	53.4	85.0	76.2	74.6	70.4	86.0	76.2	132.3	246.3	152.4	126.6	111.7	181.8	74.6	132.3	1.8
244335_at	—	1.28E-03	196.1	308.8	625.6	453.4	529.4	503.4	554.3	408.9	532.7	972.0	617.3	637.4	807.6	769.0	503.4	637.4	1.3
244414_at	—	2.36E-04	40.7	58.8	60.2	43.7	56.3	52.8	53.2	81.7	92.4	133.8	133.8	104.4	83.4	96.9	53.2	96.9	1.8
244415_at	—	6.53E-03	89.5	89.9	77.8	97.1	127.7	114.7	122.1	137.0	108.8	187.0	161.3	133.1	164.5	188.2	97.1	161.3	1.7
244447_at	—	2.85E-03	110.3	129.4	218.5	213.2	152.9	167.4	167.0	218.2	167.8	378.7	310.2	241.8	175.6	261.1	167.0	241.8	1.4
244456_at	—	3.77E-03	33.0	41.6	50.1	40.4	50.9	47.2	49.6	51.3	54.0	87.9	93.7	67.6	86.3	54.3	47.2	67.6	1.4
244583_at	—	7.62E-05	133.0	92.8	152.4	156.8	195.1	139.3	190.7	245.9	208.6	441.8	339.3	294.2	355.3	420.0	152.4	339.3	2.2
244598_at	—	8.02E-03	224.0	168.3	268.7	292.5	280.9	245.9	302.0	378.4	218.0	380.7	314.3	383.4	290.3	368.8	268.7	368.8	1.4
244765_at	—	7.20E-03	253.9	209.2	304.3	294.7	351.3	329.1	274.9	302.1	445.8	639.2	347.4	389.2	532.5	425.1	294.7	425.1	1.4
244781_x_at	—	9.08E-04	70.8	59.2	62.8	68.1	79.9	63.2	81.4	86.1	141.4	188.8	126.1	132.1	112.0	144.0	68.1	132.1	1.9
244796_at	—	2.24E-04	146.8	98.9	132.2	121.5	147.2	116.2	127.4	208.5	149.9	292.5	280.1	259.7	203.7	293.3	127.4	259.7	2.0
244874_at	—	8.16E-03	47.5	43.7	36.0	43.9	40.5	36.5	36.3	47.7	57.1	98.1	66.2	101.8	51.7	116.1	40.5	66.2	1.6

Supplementary Table S2.

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
225522_at	AAK1	1.75E-03	1638.0	2460.7	2142.3	2110.2	2247.5	3623.5	2356.5	1516.6	1520.2	1063.0	1562.6	1158.2	1536.7	1108.8	2247.5	1516.6	0.7
230024_at	AARS2	6.64E-03	564.0	737.4	723.3	616.3	644.5	829.4	678.9	540.9	498.7	398.9	509.0	493.3	629.1	459.3	678.9	498.7	0.7
206527_at	ABAT	5.37E-03	188.1	193.7	260.5	213.8	243.2	232.1	217.6	184.3	124.5	108.7	157.8	171.7	151.3	97.9	217.6	151.3	0.7
209460_at	ABAT	6.43E-03	191.1	203.7	311.5	269.9	295.1	299.6	199.0	229.0	94.4	58.7	141.8	164.3	127.4	55.8	269.9	127.4	0.5
209459_s_at	ABAT	8.76E-03	122.0	145.2	230.1	163.1	262.0	231.7	167.9	172.1	50.5	52.2	123.4	105.5	72.7	38.2	167.9	72.7	0.4
242553_at	ABCC3	7.24E-03	305.7	156.9	169.6	213.7	184.2	179.9	183.1	164.9	124.0	121.3	168.8	164.2	154.5	108.5	183.1	154.5	0.8
208161_s_at	ABCC3	5.10E-03	1042.3	1143.7	993.2	1061.7	1669.6	953.0	746.8	937.7	663.2	484.4	868.4	1326.3	689.6	407.5	1042.3	689.6	0.7
226363_at	ABCC5	1.86E-03	363.5	554.0	461.1	531.7	348.9	402.4	314.8	266.6	312.0	134.8	287.5	287.7	154.6	136.3	402.4	266.6	0.7
209380_s_at	ABCC5	1.87E-03	153.9	189.1	215.3	194.5	175.8	154.5	149.6	121.0	108.1	74.6	134.5	121.4	89.9	59.4	175.8	108.1	0.6
204567_s_at	ABCG1	3.78E-03	3828.4	4212.3	4981.8	4094.4	4035.9	4617.0	5468.6	3275.6	2811.2	1748.7	3342.5	2167.3	2688.0	2132.4	4212.3	2688.0	0.6
211113_s_at	ABCG1	6.70E-03	1286.8	1415.1	1554.0	1190.7	1048.8	1139.3	1443.5	1062.6	684.4	413.0	789.5	800.7	843.4	538.0	1286.8	789.5	0.6
218633_x_at	ABHD10	2.44E-03	1098.4	1421.5	1344.5	1427.7	1213.6	1585.5	1216.4	948.4	788.9	346.9	946.7	703.5	708.3	510.0	1344.5	708.3	0.5
228123_s_at	ABHD12	5.90E-03	169.3	146.9	214.1	168.0	178.2	167.8	167.1	137.8	77.9	130.3	122.0	162.2	123.2	134.4	168.0	130.3	0.8
210006_at	ABHD14A	4.65E-03	117.8	118.7	153.3	148.1	100.7	132.2	113.0	102.6	87.5	83.5	96.4	90.0	95.9	78.1	118.7	90.0	0.8
226796_at	ABHD15	9.48E-03	372.5	444.8	439.9	469.6	412.1	499.8	361.8	423.8	215.1	176.5	323.9	319.4	321.8	169.8	439.9	319.4	0.7
221815_at	ABHD2	6.08E-03	909.5	1559.0	1651.5	1769.1	1323.3	2041.1	1870.1	925.9	890.1	527.9	1121.3	994.9	1133.8	720.7	1651.5	925.9	0.6
228490_at	ABHD2	4.77E-03	542.7	950.6	1181.0	1267.4	880.3	1418.3	1321.7	544.0	666.9	463.7	867.5	595.7	713.7	572.4	1181.0	595.7	0.5
225337_at	ABHD2	7.92E-04	1232.6	1837.6	2387.1	2549.5	1730.7	2458.9	2536.4	969.8	1235.2	896.4	1567.8	997.0	1278.2	1110.1	2387.1	1110.1	0.5
87100_at	ABHD2	4.18E-03	586.7	969.9	1233.6	1256.5	898.2	1392.0	1308.6	599.8	562.7	371.5	814.2	546.7	602.5	444.6	1233.6	562.7	0.5
63825_at	ABHD2	5.84E-03	284.6	548.7	766.9	803.9	601.2	855.0	838.3	316.5	347.6	327.6	534.6	366.3	419.2	285.0	766.9	347.6	0.5
218739_at	ABHD5	4.26E-04	1966.8	2711.3	2714.4	2084.6	2344.0	2809.5	1518.8	1484.6	1453.8	879.3	1182.1	1250.5	1200.3	819.2	2344.0	1200.3	0.5
213935_at	ABHD5	2.35E-03	218.5	318.9	387.0	360.0	366.8	448.6	311.2	209.1	198.8	124.9	200.2	163.4	114.2	114.7	360.0	163.4	0.5
213805_at	ABHD5	2.09E-03	180.7	279.2	443.3	363.0	311.8	522.0	327.0	161.6	156.2	143.6	223.3	144.6	135.2	87.1	327.0	144.6	0.4
221552_at	ABHD6	8.23E-04	224.5	228.7	208.1	253.9	231.3	262.0	190.9	187.7	126.1	85.4	145.6	162.0	152.1	97.6	228.7	145.6	0.6
45288_at	ABHD6	4.09E-03	223.4	249.7	368.1	375.6	356.1	413.1	314.5	232.1	147.4	96.9	207.5	203.2	201.4	148.2	356.1	201.4	0.6
223615_at	ABI3	7.90E-03	189.2	131.9	177.3	140.8	139.7	168.9	126.0	135.3	94.3	84.2	94.9	149.0	123.2	76.4	140.8	94.9	0.7
214274_s_at	ACAA1	9.34E-03	1066.3	1106.8	1266.1	1216.5	1105.9	1147.8	1058.9	939.2	878.5	848.3	957.4	978.1	990.1	722.5	1106.8	939.2	0.8
202003_s_at	ACAA2	1.83E-03	3844.7	4298.8	3831.9	4402.1	4243.2	3928.6	3572.6	3134.4	3283.3	2368.1	3560.3	3097.5	2912.5	2333.7	3928.6	3097.5	0.8
1552616_a_at	ACACB	5.33E-03	62.4	83.6	87.7	87.2	89.1	146.8	83.6	63.4	54.4	63.4	59.4	70.3	104.7	56.9	87.2	63.4	0.7
221928_at	ACACB	1.00E-03	471.5	544.5	656.0	500.2	530.6	1224.8	610.6	359.2	315.4	178.6	331.6	215.2	527.0	219.0	544.5	315.4	0.6
49452_at	ACACB	1.24E-03	2358.5	3211.7	3551.5	2959.4	2762.9	6463.0	2850.9	1713.8	1818.1	602.7	1526.8	1062.6	2430.5	872.5	2959.4	1526.8	0.5
43427_at	ACACB	9.77E-04	1586.0	2070.4	2319.1	2023.0	1783.4	4284.9	1852.1	1150.5	1164.9	421.1	1000.7	700.6	1597.2	574.8	2023.0	1000.7	0.5
1552472_a_at	ACAP2	8.43E-03	486.1	474.3	832.7	775.1	765.0	925.1	724.7	439.2	450.1	591.2	621.5	458.5	514.6	469.2	765.0	469.2	0.6
205412_at	ACAT1	8.72E-03	1034.9	1203.2	1097.2	1070.5	975.2	996.0	1001.6	886.1	1004.7	822.8	982.5	714.2	806.5	757.7	1034.9	822.8	0.8
225317_at	ACBD6	9.10E-03	449.2	470.9	508.0	513.0	485.9	462.4	471.3	386.9	335.4	385.7	443.8	439.9	371.8	338.6	471.3	385.7	0.8
228264_at	ACCS	4.36E-03	346.9	829.1	340.3	771.9	343.0	392.2	256.8	304.6	429.2	174.5	457.0	245.9	274.3	228.8	346.9	274.3	0.8
227463_at	ACE	3.66E-03	213.3	165.2	215.7	250.8	190.9	207.3	156.4	214.0	104.0	100.0	150.2	142.3	126.0	103.4	207.3	126.0	0.6
231321_s_at	ACER3	4.09E-03	371.2	370.2	387.3	370.9	362.6	369.1	372.9	340.8	233.5	231.2	336.7	190.9	244.0	196.8	370.9	233.5	0.6
222688_at	ACER3	4.80E-03	971.1	1439.5	1182.7	1185.8	1144.4	1447.0	1293.8	988.5	1030.0	712.9	944.9	589.8	746.2	650.8	1185.8	746.2	0.6
222687_s_at	ACER3	3.51E-03	1010.3	1192.7	874.3	862.1	942.8	1046.1	912.9	1017.4	748.5	470.4	703.5	491.2	579.0	482.4	942.8	579.0	0.6
227776_at	ACER3	3.14E-03	342.0	416.3	457.6	430.5	465.9	477.6	540.2	310.9	288.7	181.5	311.9	153.0	207.3	180.6	457.6	207.3	0.5
202982_s_at	ACOT1 /// ACOT2	6.25E-03	958.6	871.1	621.9	1174.2	902.1	1103.9	754.7	880.6	636.9	455.1	826.1	730.5	957.9	559.4	902.1	730.5	0.8
208002_s_at	ACOT7	3.45E-04	1537.6	1094.1	1053.3	1320.4	1309.2	1150.0	828.9	1140.2	533.6	477.5	695.1	858.4	789.0	413.6	1150.0	695.1	0.6
204638_at	ACP5	1.86E-03	1916.9	1979.4	2007.6	1789.0	1745.0	1568.2	1724.7	1610.7	1101.6	982.1	960.8	1486.7	1054.1	883.6	1789.0	1054.1	0.6
218795_at	ACP6	5.19E-03	215.7	337.5	376.1	303.9	371.1	447.6	272.1	242.5	183.4	160.8	213.9	230.0	239.4	107.5	337.5	213.9	0.6
224882_at	ACSS1	1.27E-03	249.0	282.9	370.9	324.1	263.4	307.1	269.3	239.3	143.7	104.4	157.3	136.0	118.4	108.8	282.9	136.0	0.5
234312_s_at	ACSS2	2.46E-03	437.3	507.8	442.1	424.9	358.5	390.5	331.4	401.2	242.6	214.7	302.5	256.9	249.3	209.4	424.9	249.3	0.6
236126_at	ACVR2B	5.51E-03	133.2	147.7	174.0	190.6	182.8	178.8	156.5	136.6	104.3	117.1	116.2	134.5	138.0	105.5	174.0	117.1	0.7
226950_at	ACVRL1	4.31E-03	2392.8	2550.1	2122.0	2268.9	2074.9	2894.7	2919.5	2007.0	1869.5	876.5	1771.4	1247.1	2217.2	1620.2	2392.8	1771.4	0.7
205260_s_at	ACYP1	3.58E-04	265.5	298.8	274.7	354.2	247.8	283.3	239.3	216.6	196.5	157.4	177.1	154.4	156.3	125.6	274.7	157.4	0.6
222486_s_at	ADAMTS1	6.89E-03	208.2	98.0	108.4	118.3	230.0	625.7	299.1	244.2	50.7	24.2	60.6	114.1	138.2	39.8	208.2	60.6	0.3
222162_s_at	ADAMTS1	5.95E-03	195.9	60.2	82.1	82.1	200.2	626.6	242.4	192.5	26.9	18.0	52.9	103.0	125.8	30.3	195.9	52.9	0.3
220578_at	ADAMTSL4	1.80E-03	399.2	418.3	503.4	505.7	323.3	481.0	293.1	322.7	299.0	245.1	318.9	241.8	293.6	223.9	418.3	293.6	0.7
226071_at	ADAMTSL4	1.90E-03	3238.5	3673.8	3864.7	4053.3	3280.9	3987.2	2887.3	2922.0	2861.7	2084.0	2891.4	1785.9	2390.3	1692.3	3673.8	2390.3	0.7
204497_at	ADCY9	5.80E-03	127.0	157.0	140.7	167.2	158.5	175.6	130.2	155.2	81.5	74.2	111.4	92.1	97.0	68.5	157.0	92.1	0.6
205882_x_at	ADD3	4.18E-03	220.1	308.6	420.4	358.1	487.5	475.4	342.9	218.6	201.4	188.9	294.5	283.9	236.1	168.3	358.1	218.6	0.6
201034_at	ADD3	2.29E-03	865.2	1086.8	1627.9	1338.8	1438.7	1582.7	1220.2	757.5	754.8	557.0	896.8	827.4	652.5	556.3	1338.8	754.8	0.6
201752_s_at	ADD3	6.32E-03	246.9	342.0	482.7	446.5	493.6	520.3	384.3	291.3	215.5	195.8	298.6	293.9	210.9	170.9	446.5	215.5	0.5
201753_s_at	ADD3	7.59E-03	46.3	65.3	142.5	122.0	130.3	150.9	120.2	55.2	40.6	60.7	92.5	59.4	50.1	48.6	122.0	55.2	0.5
208848_at	ADH5	5.87E-03	103.5	119.4	172.8	134.0	128.9	172.2	161.1	101.8	99.3	89.0	103.5	79.2	99.5	102.1	134.0	99.5	0.7
226426_at	ADNP	6.39E-03	141.6	175.7	185.4	155.5	223.2	228.9	178.2	156.3	111.0	127.0	118.9	140.5	138.5	106.6	178.2	127.0	0.7
212502_at	ADO	1.89E-03	1359.9	899.9	1031.8	1032.2	1191.2	1337.7	1092.0	1092.1	743.6	635.0	815.6	672.0	737.9	694.1	1092.0	737.9	0.7
212500_at	ADO	5.86E-03	675.3	509.7	607.8	601.2	776.5	936.0	679.8	713.4	338.6	379.6	457.1	447.4	388.0	375.3	675.3	388.0	0.6
205481_at	ADORA1	8.91E-03	176.2	164.1	202.4	151.0	166.9	227.2	169.4	138.4	99.5	40.2	102.0	140.6	112.5	62.0	169.4	102.0	0.6
206170_at	ADRB2	1.11E-03	472.1	657.7	858.4	840.7	695.8	1023.7	667.1	372.9	440.5	287.6	486.7	393.0	367.9	259.7	695.8	372.9	0.5

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
228771_at	ADRBK2	7.88E-03	285.3	399.6	413.4	388.2	487.7	525.2	516.3	320.0	281.2	205.0	303.4	295.8	293.2	245.5	413.4	293.2	0.7
201924_at	AFF1	9.48E-03	1009.3	1133.4	1333.6	1363.9	1235.0	1408.7	1170.4	847.2	1079.9	991.1	1110.2	734.3	887.4	934.8	1235.0	934.8	0.8
222126_at	AGFG2	7.22E-03	124.0	96.3	136.9	140.8	105.0	122.3	100.8	93.1	62.5	59.1	100.2	64.7	125.1	69.7	122.3	69.7	0.6
228667_at	AGPAT4	6.46E-03	1202.9	1220.1	1551.4	931.2	1156.8	1183.4	1142.2	1113.1	770.9	607.4	819.9	607.7	831.3	667.3	1183.4	770.9	0.7
225114_at	AGPS	3.15E-03	1470.2	1464.9	1824.8	2148.5	1776.8	2060.4	2340.8	1094.5	1154.5	1511.4	1771.8	988.5	1198.0	1265.0	1824.8	1198.0	0.7
225113_at	AGPS	3.17E-03	648.0	754.2	776.3	871.3	739.7	828.2	879.3	653.7	492.7	491.9	656.9	431.8	535.7	484.3	776.3	492.7	0.6
225108_at	AGPS	1.01E-03	493.7	390.0	404.2	484.1	483.3	413.7	518.6	393.7	240.8	181.5	356.7	293.3	215.5	214.6	483.3	240.8	0.5
207193_at	AGRP	9.91E-03	228.9	262.2	250.0	203.5	158.0	258.3	241.7	141.5	169.0	180.4	118.9	138.9	278.5	149.2	241.7	149.2	0.6
220841_s_at	AHI1	3.62E-03	232.4	166.6	229.8	221.4	249.8	202.3	202.7	195.0	143.7	177.3	162.7	159.0	138.5	159.0	221.4	159.0	0.7
221569_at	AHI1	4.39E-03	204.3	228.7	270.8	211.2	257.4	232.9	313.2	194.1	158.2	156.0	176.5	162.7	148.7	147.9	232.9	158.2	0.7
226665_at	AHSA2	4.85E-03	468.4	640.3	510.9	407.3	466.9	446.6	256.7	352.9	517.7	408.0	324.8	304.5	234.3	209.9	466.9	324.8	0.7
223136_at	AIG1	7.16E-03	269.6	315.2	400.9	372.9	421.8	588.7	402.8	250.1	235.1	276.5	309.5	320.1	314.0	194.8	400.9	276.5	0.7
202588_at	AK1	7.85E-03	167.2	161.5	140.7	138.8	172.6	153.5	127.7	138.5	134.5	100.1	106.3	132.8	135.1	109.8	153.5	132.8	0.9
202587_s_at	AK1	8.41E-03	904.5	1198.6	901.8	870.2	877.4	820.8	717.1	615.6	752.6	493.1	505.3	817.4	783.1	554.6	877.4	615.6	0.7
201674_s_at	AKAP1	7.30E-03	232.8	267.8	261.8	221.3	305.9	238.1	198.9	217.8	184.7	127.4	187.3	205.9	183.6	137.3	238.1	184.7	0.8
221718_s_at	AKAP13	6.25E-03	2074.8	1794.9	1803.2	2257.9	2037.9	2300.0	2041.6	1768.0	1509.1	1480.9	1669.1	1489.0	1700.0	1766.8	2041.6	1669.1	0.8
230846_at	AKAP5	9.04E-03	333.3	373.0	383.7	423.2	439.5	705.6	436.1	362.2	253.7	162.2	379.6	190.1	371.5	200.3	423.2	253.7	0.6
1555220_a_at	AKR1CL2	4.79E-03	199.3	243.6	225.9	187.8	129.3	172.4	131.4	179.8	162.4	118.9	152.6	108.1	95.7	69.5	187.8	118.9	0.6
218487_at	ALAD	7.88E-04	489.9	729.3	619.8	873.0	715.2	931.1	615.1	422.6	367.2	249.4	592.3	364.1	429.0	244.6	715.2	367.2	0.5
205633_s_at	ALAS1	8.94E-03	2126.4	2458.6	3182.3	3273.2	3058.3	3049.5	2887.7	2411.1	1661.0	1127.2	2433.1	1747.6	1768.6	1293.9	3049.5	1747.6	0.6
212224_at	ALDH1A1	7.19E-03	5370.8	5956.2	7001.6	6141.4	5445.5	5501.0	5541.1	4404.2	5206.7	5273.8	5247.6	4024.2	4670.8	3806.8	5541.1	4670.8	0.8
210544_s_at	ALDH3A2	3.63E-03	502.2	659.5	478.3	734.2	628.8	756.2	660.8	541.9	431.0	249.0	471.0	405.3	448.8	334.2	659.5	431.0	0.7
202054_s_at	ALDH3A2	6.18E-04	1858.9	2090.2	1682.0	2332.0	1959.7	2253.2	2293.5	1474.7	1294.0	809.1	1453.8	1221.4	1426.8	981.7	2090.2	1294.0	0.6
202053_s_at	ALDH3A2	1.02E-03	1656.3	1943.7	1639.1	1885.2	1798.0	2087.1	1871.6	1416.0	1356.6	825.0	1352.1	1102.1	1127.6	1061.6	1871.6	1127.6	0.6
208950_s_at	ALDH7A1	8.00E-03	343.8	306.9	394.7	283.9	321.7	324.7	336.5	280.8	222.7	232.2	277.3	272.3	209.8	195.6	324.7	232.2	0.7
219374_s_at	ALG9	3.48E-03	631.8	853.4	861.9	701.6	662.0	1003.4	937.4	618.1	541.3	539.5	540.6	465.3	600.0	473.5	853.4	540.6	0.6
213952_s_at	ALOX5	4.16E-03	1749.9	1833.6	1855.1	1885.7	1622.3	1513.4	1674.8	1507.3	1074.3	739.8	1212.1	1293.1	1159.9	901.8	1749.9	1159.9	0.7
228342_s_at	ALPK3	5.19E-03	199.8	304.2	264.6	279.1	172.6	278.0	355.2	221.5	146.7	118.1	224.7	96.9	131.3	142.5	278.0	142.5	0.5
214846_s_at	ALPK3	1.77E-03	239.7	395.8	339.3	372.5	232.5	313.5	396.8	253.9	209.2	148.6	221.7	98.9	155.6	163.9	339.3	163.9	0.5
226291_at	ALS2	9.13E-03	154.8	141.3	182.0	189.2	158.4	154.7	167.7	155.0	96.8	140.1	154.1	123.7	117.7	104.7	158.4	123.7	0.8
228094_at	AMICA1	9.05E-04	3852.1	4547.3	4447.2	4936.7	3785.8	4936.3	2818.4	2713.3	2529.6	1261.4	2442.1	2722.8	2323.3	1220.8	4447.2	2442.1	0.5
226258_at	AMN1	2.53E-03	91.4	100.9	107.8	106.4	85.7	118.6	90.9	71.3	88.6	68.5	81.1	53.5	60.5	60.5	100.9	68.5	0.7
225450_at	AMOTL1	2.35E-03	638.5	1037.4	949.0	998.8	1011.7	1290.4	916.1	649.2	516.5	427.6	690.7	637.5	630.2	455.6	998.8	630.2	0.6
204294_at	AMT	3.10E-03	105.4	120.4	206.4	161.5	153.1	165.2	124.8	105.3	82.3	85.2	93.2	105.8	85.2	67.9	153.1	85.2	0.6
208498_s_at	AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B	8.26E-03	283.6	220.7	336.2	241.8	441.1	263.5	299.8	283.1	145.7	199.9	211.9	288.7	173.9	129.9	283.6	199.9	0.7
225554_s_at	ANAPC7	5.45E-03	762.9	886.4	906.9	1000.1	860.1	889.5	832.6	781.5	618.9	510.3	703.2	615.1	670.0	560.2	886.4	618.9	0.7
213569_at	ANGEL1	2.64E-03	421.1	369.3	412.2	541.8	393.3	388.4	404.6	333.3	160.7	161.0	333.3	269.4	326.9	195.4	404.6	269.4	0.7
36865_at	ANGEL1	3.06E-03	528.6	634.1	743.0	596.7	702.7	820.6	634.9	513.2	376.1	308.1	414.1	487.4	489.3	334.6	634.9	414.1	0.7
213099_at	ANGEL1	4.23E-03	433.1	589.9	646.5	486.8	570.6	700.0	520.2	428.3	333.8	271.4	355.5	427.0	383.8	287.1	570.6	355.5	0.6
213035_at	ANKRD28	8.30E-03	162.5	165.4	188.8	227.2	236.2	177.1	204.8	174.1	135.6	105.8	162.9	136.7	114.6	94.4	188.8	135.6	0.7
220144_s_at	ANKRD5	1.64E-03	59.1	75.7	76.1	94.2	72.6	107.9	82.7	47.1	53.7	39.1	62.1	50.9	66.2	33.1	76.1	50.9	0.7
225731_at	ANKRD50	9.77E-03	129.8	188.5	277.5	273.7	283.2	330.4	244.2	167.2	118.7	141.5	196.3	157.6	152.1	117.8	273.7	152.1	0.6
227034_at	ANKRD57	8.11E-03	266.1	357.6	478.3	377.3	498.6	553.7	461.3	272.2	229.1	212.2	344.5	295.7	277.6	178.9	461.3	272.2	0.6
212747_at	ANKS1A	5.99E-04	1492.5	1572.0	1386.5	1654.9	1429.5	1602.8	1455.0	1173.4	987.1	561.9	1025.0	806.0	1022.5	718.8	1492.5	987.1	0.7
201306_s_at	ANP32B	6.22E-03	5006.9	5304.6	5457.5	4803.1	5328.5	5835.9	5379.8	4588.2	4207.2	3702.9	4255.1	3929.7	4282.9	3805.8	5328.5	4207.2	0.8
206200_s_at	ANXA11	2.87E-03	2726.5	2442.8	2163.9	2227.0	1988.5	2071.0	2010.0	1890.9	1631.1	1091.5	1454.4	1693.0	1707.5	1469.0	2163.9	1631.1	0.8
214783_s_at	ANXA11	4.15E-03	305.7	338.5	358.1	295.7	317.1	330.5	308.5	296.7	207.0	213.0	237.8	241.7	219.0	197.5	317.1	219.0	0.7
228727_at	ANXA11	4.69E-03	189.2	172.3	228.4	224.0	207.2	233.2	226.6	198.2	94.8	65.9	137.5	138.7	88.2	78.0	224.0	94.8	0.4
211712_s_at	ANXA9	8.51E-03	84.1	105.4	62.9	65.7	60.9	54.8	48.7	55.3	69.7	39.8	44.3	46.2	32.6	55.6	62.9	46.2	0.7
213215_at	AP3S2	3.01E-03	93.6	108.6	127.2	111.6	143.1	149.7	103.8	80.3	79.3	56.5	88.0	99.5	77.1	55.3	111.6	79.3	0.7
228101_at	APBA1	5.46E-03	73.9	64.6	126.1	121.1	125.1	104.2	105.4	77.6	55.1	68.3	60.0	64.2	57.8	41.2	105.4	60.0	0.6
206679_at	APBA1	1.63E-03	81.7	85.6	145.4	141.1	125.6	124.0	114.9	71.9	62.8	56.9	78.5	66.5	49.1	42.2	124.0	62.8	0.5
230925_at	APBB1IP	8.88E-04	486.6	695.4	520.0	583.2	638.3	505.7	449.8	392.1	405.9	286.5	421.0	410.8	382.8	296.6	520.0	392.1	0.8
219994_at	APBB1IP	3.14E-03	190.5	187.6	200.2	232.0	201.2	165.4	150.3	152.3	136.8	111.2	189.7	137.2	132.2	114.7	190.5	136.8	0.7
210027_s_at	APEX1	3.37E-03	2915.3	2760.4	2770.0	2781.7	2348.0	2737.7	2663.0	2454.9	1833.4	1174.4	2016.5	1789.0	1956.5	1523.7	2760.4	1833.4	0.7
226358_at	APH1B	5.69E-03	548.5	702.5	806.6	761.8	904.8	1168.4	927.5	545.3	462.1	472.9	658.5	609.4	816.2	545.3	806.6	545.3	0.7
220023_at	APOB48R	8.23E-03	557.2	471.8	515.3	610.3	389.8	456.5	499.0	367.1	240.2	194.6	325.9	342.9	447.6	341.1	499.0	341.1	0.7
224491_at	APOL4	4.60E-03	264.6	242.3	218.0	238.9	234.8	362.0	148.0	238.1	169.1	140.7	186.8	114.3	147.8	102.2	238.9	147.8	0.6
223801_s_at	APOL4	4.79E-04	732.6	855.7	550.3	687.8	859.4	1051.6	512.8	504.4	422.4	152.3	431.1	300.6	436.5	265.2	732.6	422.4	0.6
1555600_s_at	APOL4	4.53E-04	940.5	975.8	697.9	956.1	1050.3	1188.6	578.1	752.0	551.4	245.3	516.0	427.1	591.7	317.2	956.1	516.0	0.5
203747_at	AQP3	1.59E-03	294.7	274.4	307.1	444.4	249.3	328.2	280.2	261.8	220.2	182.8	250.5	153.6	220.8	171.4	294.7	220.2	0.7
39249_at	AQP3	5.77E-03	548.1	508.0	537.5	762.5	342.6	441.9	440.6	393.1	391.2	250.1	369.1	279.3	398.9	278.2	508.0	369.1	0.7
218870_at	ARHGAP15	8.69E-03	480.9	549.8	686.0	590.6	700.0	694.8	518.0	465.1	426.5	481.0	485.7	587.0	511.1	370.7	590.6	481.0	0.8
225166_at	ARHGAP18	1.19E-03	770.3	674.2	858.4	811.5	873.9	911.7	686.1	642.6	509.7	457.0	593.1	558.3	554.8	378.6	811.5	554.8	0.7
225173_at	ARHGAP18	1.62E-03	2716.2	2971.6	3105.6	2953.9	3063.0	3195.8	2521.1	2337.1	2069.5	1464.5	2245.4	1908.7	1932.8	1371.1	2971.6	1932.8	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
225171_at	ARHGAP18	3.99E-03	1581.7	1977.5	2722.0	2734.6	2376.3	2882.5	2399.7	1425.8	1717.1	1529.5	2037.6	1207.3	1456.5	1161.4	2399.7	1456.5	0.6
232543_x_at	ARHGAP9	3.39E-03	786.4	933.9	721.1	832.7	660.6	800.0	611.5	639.5	546.1	356.8	547.7	616.8	526.3	413.2	786.4	546.1	0.7
226906_s_at	ARHGAP9	2.69E-03	1139.4	1341.8	1058.0	1117.5	828.0	1029.6	892.4	903.0	779.7	517.6	663.7	784.3	682.7	542.4	1058.0	682.7	0.6
224451_x_at	ARHGAP9	2.30E-03	608.2	760.0	747.3	831.9	600.1	781.4	574.2	562.3	535.7	351.5	495.0	442.4	425.7	359.6	747.3	442.4	0.6
201288_at	ARHGDIB	6.37E-03	4643.8	4939.8	5418.0	6122.8	5235.4	6018.7	4940.4	4335.2	3998.6	3286.9	4724.5	4311.6	4299.3	3480.3	5235.4	4299.3	0.8
1555811_at	ARHGDIB	6.91E-03	146.0	173.7	181.1	185.3	157.5	168.0	214.9	102.7	150.4	138.9	164.5	137.0	117.8	149.2	173.7	138.9	0.8
213039_at	ARHGEF18	7.19E-03	903.4	1003.7	1271.2	1241.9	1165.0	1008.9	965.5	925.8	639.8	550.7	868.7	950.8	637.8	534.2	1008.9	639.8	0.6
209539_at	ARHGEF6	3.84E-03	1798.3	2434.0	2668.6	2528.7	2438.8	2759.2	1942.1	1579.1	1494.0	889.3	1859.6	1772.8	1361.3	941.3	2438.8	1494.0	0.6
203263_s_at	ARHGEF9	2.45E-03	102.5	120.2	155.0	155.4	179.4	166.7	156.7	100.1	70.4	73.5	91.2	115.8	100.8	58.9	155.4	91.2	0.6
202641_at	ARL3	6.11E-03	482.2	407.1	396.3	403.1	400.8	433.8	346.2	397.3	345.9	262.7	301.8	373.3	280.9	229.9	403.1	301.8	0.7
1554480_a_at	ARMC10	6.11E-03	1744.2	1732.6	2279.2	1962.1	2113.4	2519.3	2056.0	1478.7	1581.2	1652.9	1646.0	1247.7	1547.1	1413.3	2056.0	1547.1	0.8
1555902_at	ARMCX5	5.88E-03	59.9	50.8	67.8	55.5	59.6	76.1	56.1	56.1	39.0	51.6	39.7	45.3	38.1	36.0	59.6	39.7	0.7
230619_at	ARNT	3.46E-03	745.5	828.0	795.6	704.1	679.7	988.8	659.9	613.0	537.3	382.1	589.5	503.6	625.6	486.5	745.5	537.3	0.7
225283_at	ARRDC4	5.72E-03	823.2	886.9	1056.6	1621.0	1246.3	1101.2	1713.4	844.6	686.0	543.0	1148.1	522.3	514.1	605.8	1101.2	605.8	0.6
223695_s_at	ARSD	9.96E-03	422.9	506.7	475.5	497.9	538.3	654.8	456.0	401.0	384.2	356.1	450.0	418.5	395.0	322.8	497.9	395.0	0.8
223223_at	ARV1	1.23E-03	643.3	799.0	846.1	778.3	761.5	727.6	710.7	527.2	595.1	430.3	552.1	520.9	484.7	411.6	761.5	520.9	0.7
1555419_a_at	ASAH1	3.18E-03	6810.1	6787.4	5425.3	6389.2	6229.2	6013.5	5886.8	5702.4	5029.8	3258.9	4576.2	5201.5	4727.5	4332.8	6229.2	4727.5	0.8
218862_at	ASB13	4.78E-03	346.3	532.1	624.0	489.6	585.7	610.6	425.4	344.7	289.4	194.6	378.1	339.6	330.3	191.8	532.1	330.3	0.6
205673_s_at	ASB9	3.23E-03	67.6	89.1	67.7	83.5	77.5	96.5	66.3	62.0	67.1	36.6	66.4	44.3	55.7	31.0	77.5	55.7	0.7
213561_at	ASF1A	3.53E-03	519.7	640.9	862.5	712.7	666.2	858.1	586.8	471.8	500.2	327.1	496.3	395.7	448.8	315.6	666.2	448.8	0.7
203428_s_at	ASF1A	2.52E-03	1014.4	1329.5	1378.7	1220.1	1158.3	1551.2	1026.9	890.2	773.2	513.9	984.5	685.5	793.2	559.5	1220.1	773.2	0.6
218857_s_at	ASRGL1	1.00E-03	320.3	338.4	322.7	478.8	273.5	531.2	259.8	275.4	189.7	148.5	279.1	175.7	258.2	93.1	322.7	189.7	0.6
222764_at	ASRGL1	6.37E-03	125.4	142.8	245.9	197.4	137.8	186.9	206.8	139.4	80.7	78.5	124.6	91.4	81.2	62.7	186.9	81.2	0.4
228401_at	ATAD2	1.25E-03	91.6	72.1	116.2	117.3	101.8	95.8	116.6	59.9	56.9	71.1	85.2	39.0	50.0	53.7	101.8	56.9	0.6
226684_at	ATG2B	2.90E-03	148.5	169.1	231.4	230.5	260.1	303.0	278.9	135.2	110.5	176.2	181.6	136.1	175.6	163.7	231.4	163.7	0.7
228190_at	ATG4C /// CTR9	4.26E-03	91.5	121.7	124.3	119.2	105.4	152.6	91.2	91.4	79.6	55.2	86.1	73.2	77.1	39.7	119.2	77.1	0.6
202512_s_at	ATG5	7.81E-03	256.1	271.3	319.3	323.1	354.1	337.5	311.6	257.3	190.9	164.2	272.0	228.5	183.0	121.1	319.3	190.9	0.6
223340_at	ATL1	5.70E-03	308.4	588.6	489.8	552.9	473.6	669.3	380.6	362.7	336.0	225.9	405.1	239.9	313.7	213.7	489.8	313.7	0.6
210858_x_at	ATM	6.97E-03	513.8	564.5	582.7	527.9	565.7	631.8	525.5	452.4	469.3	378.2	476.1	428.8	464.0	364.6	564.5	452.4	0.8
212672_at	ATM	5.22E-03	161.8	189.3	234.8	227.5	330.8	331.0	282.0	174.3	104.7	139.1	187.1	167.1	171.8	127.3	234.8	167.1	0.7
208442_s_at	ATM	3.40E-03	299.2	327.1	364.6	363.8	386.4	531.7	370.1	281.2	224.8	185.4	296.1	259.5	315.8	197.9	364.6	259.5	0.7
212135_s_at	ATP2B4	5.94E-03	124.2	136.2	127.7	212.9	187.3	213.5	165.9	128.9	106.8	85.7	150.8	107.6	136.4	117.3	165.9	117.3	0.7
45828_at	ATP5SL	2.17E-03	1288.0	1163.8	1077.9	1001.9	942.9	898.3	901.1	971.3	871.6	689.7	711.6	744.8	782.3	611.3	1001.9	744.8	0.7
213587_s_at	ATP6V0E2	2.77E-03	600.0	669.5	612.4	631.9	499.7	585.6	461.5	475.6	428.3	304.4	431.8	444.8	423.9	284.3	600.0	428.3	0.7
205198_s_at	ATP7A	9.62E-03	263.9	326.7	445.7	388.8	448.4	501.3	454.6	311.6	197.5	185.7	338.9	227.5	235.9	189.6	445.7	227.5	0.5
1554704_at	ATP8B3	1.09E-03	115.7	176.9	149.4	177.9	189.4	171.9	143.4	109.5	93.6	69.5	119.3	101.1	90.4	66.9	171.9	93.6	0.5
224728_at	ATPAF1	3.47E-03	85.1	128.5	174.8	162.6	160.6	199.1	163.0	85.6	78.6	99.9	125.6	85.4	84.9	90.6	162.6	85.6	0.5
218671_s_at	ATPIF1	2.96E-03	1138.6	1370.0	1180.0	1224.5	1218.4	1349.6	1091.8	929.8	982.8	523.3	888.5	957.5	902.2	659.8	1218.4	902.2	0.7
223338_s_at	ATPIF1	1.15E-03	756.5	1021.5	1048.1	1228.5	1009.0	1379.5	1048.7	590.0	775.1	698.6	825.8	606.0	626.5	529.0	1048.1	626.5	0.6
235240_at	ATXN3	3.54E-03	445.5	497.3	543.7	691.1	559.5	621.6	475.1	445.2	367.7	288.9	428.9	369.5	433.0	312.4	543.7	369.5	0.7
205052_at	AUH	6.08E-03	145.7	202.7	326.8	255.8	286.4	307.7	226.4	166.0	117.2	129.3	194.7	148.4	105.6	89.0	255.8	129.3	0.5
218631_at	AVPI1	8.11E-04	1102.4	1233.2	1022.6	1220.3	926.9	1102.0	687.0	795.2	627.7	269.5	561.2	635.0	454.4	240.8	1102.0	561.2	0.5
214742_at	AZI1	8.16E-03	177.3	140.8	183.6	214.4	181.6	185.4	181.4	152.5	110.6	126.3	159.3	169.0	153.0	134.0	181.6	152.5	0.8
203188_at	B3GNT1	1.77E-03	207.5	288.5	325.9	262.0	270.7	326.5	198.0	179.7	184.4	110.5	177.9	141.6	167.3	109.5	270.7	167.3	0.6
1555963_x_at	B3GNT7	9.19E-03	4476.1	3512.1	3219.0	3309.1	3040.7	2559.3	2157.2	3626.4	2561.1	2038.3	2089.1	2726.9	2228.2	1850.3	3219.0	2228.2	0.7
1555962_at	B3GNT7	5.36E-03	3547.3	2910.6	2735.0	2814.1	2614.6	2209.9	1975.5	3172.8	2063.1	1735.0	1808.3	2178.2	1814.5	1560.4	2735.0	1814.5	0.7
222463_s_at	BACE1	3.29E-03	724.5	904.8	1125.1	985.2	934.7	1290.2	936.3	675.1	564.3	430.4	624.8	657.2	667.9	334.1	936.3	624.8	0.7
224335_s_at	BACE1	3.01E-03	360.1	416.5	560.0	473.6	467.9	586.3	460.0	310.0	241.4	227.2	307.6	335.5	339.9	148.2	467.9	307.6	0.7
222462_s_at	BACE1	8.32E-03	244.0	368.5	437.3	394.1	418.7	541.6	379.0	307.0	196.4	212.4	281.7	261.3	243.5	159.5	394.1	243.5	0.6
217904_s_at	BACE1	1.74E-03	652.3	905.1	909.2	941.4	861.5	1172.2	754.0	588.7	522.9	343.6	566.9	544.1	541.6	257.2	905.1	541.6	0.6
228189_at	BAG4	3.80E-03	472.3	600.2	950.3	825.0	737.5	1129.9	878.2	462.2	455.7	379.8	527.6	335.5	371.0	320.2	825.0	379.8	0.5
202985_s_at	BAG5	8.97E-03	992.0	1035.1	1256.9	1152.0	1195.1	1266.1	1172.3	944.1	912.2	926.0	935.6	883.3	892.2	876.0	1172.3	912.2	0.8
202331_at	BCKDHA	8.12E-03	99.0	87.5	164.0	121.0	151.1	139.6	119.5	103.1	48.8	81.8	93.0	115.3	92.0	85.1	121.0	92.0	0.8
222343_at	BCL2L11	8.84E-03	133.5	127.7	155.0	153.7	202.7	194.7	140.0	145.7	84.3	96.1	108.4	147.5	98.4	105.3	153.7	105.3	0.7
1553088_a_at	BCL2L11	5.64E-03	114.9	120.4	91.4	112.4	86.6	109.1	76.3	100.9	76.6	60.3	67.9	69.5	54.0	67.8	109.1	67.9	0.6
213709_at	BHLHB9	8.91E-03	61.0	61.2	88.2	75.3	88.7	86.0	75.7	65.9	48.3	45.9	59.3	55.2	49.1	36.5	75.7	49.1	0.6
201170_s_at	BHLHE40	5.44E-03	872.1	748.6	1017.8	1224.7	934.0	984.3	900.0	879.3	571.8	557.1	746.5	681.6	558.2	673.0	934.0	673.0	0.7
201032_at	BLCAP	4.84E-03	3187.4	3659.4	4151.2	4138.8	3668.7	4212.9	3241.9	3035.6	2736.5	2195.2	3107.7	2786.7	2962.2	2087.6	3668.7	2786.7	0.8
221479_s_at	BNIP3L	6.71E-03	1037.4	1148.2	1515.7	1343.7	1395.4	1685.9	1401.4	1119.2	920.4	965.1	902.5	918.5	955.3	756.7	1395.4	920.4	0.7
221478_at	BNIP3L	6.72E-04	1444.9	1579.7	2128.5	1898.6	1995.0	2341.9	1980.0	1089.4	1096.2	854.7	1267.4	1104.8	1112.3	906.6	1980.0	1096.2	0.6
205750_at	BPHL	9.02E-03	301.3	331.3	302.3	286.8	306.1	414.6	291.1	295.7	215.0	210.4	244.2	259.0	289.0	177.6	302.3	244.2	0.8
204531_s_at	BRCA1	2.64E-03	66.4	83.4	62.9	76.0	64.5	69.4	56.9	54.3	55.1	32.6	66.3	36.4	51.0	37.0	66.4	51.0	0.8
203825_at	BRD3	5.10E-03	113.9	101.4	171.3	200.5	148.2	167.1	124.5	109.7	74.8	122.3	145.9	118.2	102.8	93.8	148.2	109.7	0.7
212547_at	BRD3	3.84E-03	893.0	1080.2	1129.4	1286.4	1016.9	1045.6	946.3	909.5	658.0	486.1	836.6	742.6	618.2	526.5	1045.6	658.0	0.6

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
231810_at	BRI3BP	4.26E-03	150.0	191.3	199.0	189.6	228.8	226.2	201.0	146.5	111.3	74.6	155.3	123.5	98.1	70.1	199.0	111.3	0.6
202427_s_at	BRP44	1.34E-03	2090.9	1940.4	1855.3	1535.4	1527.1	1779.8	1621.8	1517.1	1632.9	1166.0	1229.5	1027.3	1223.0	1102.3	1779.8	1223.0	0.7
227775_at	BRUNOL6	9.61E-03	100.5	133.9	140.8	91.8	113.3	124.4	121.1	96.2	92.4	84.4	78.7	98.5	89.9	74.5	121.1	89.9	0.7
204167_at	BTD	4.26E-03	267.7	265.6	341.6	350.4	288.7	347.1	275.8	265.3	174.6	180.7	241.9	209.2	262.8	173.6	288.7	209.2	0.7
209846_s_at	BTN3A2	8.83E-04	703.1	1116.3	1050.3	581.3	892.7	873.8	836.1	626.1	596.2	522.2	380.2	580.6	535.6	498.8	873.8	535.6	0.6
204820_s_at	BTN3A2 /// BTN3A3	5.01E-03	1046.9	1869.9	1927.5	1348.0	1698.1	1658.0	1686.6	1017.9	1302.4	1105.9	1163.2	954.9	786.1	1018.3	1686.6	1018.3	0.6
201456_s_at	BUB3	8.15E-03	821.3	881.6	1015.8	871.5	828.8	937.0	824.9	701.3	626.1	869.3	820.2	546.0	688.0	596.2	871.5	688.0	0.8
201458_s_at	BUB3	9.86E-03	1363.0	1706.9	1944.8	1927.2	1941.6	1972.3	1786.9	1267.7	1440.7	1427.7	1763.3	1355.0	1210.1	1174.7	1927.2	1355.0	0.7
1561890_at	C10orf128	5.71E-03	82.2	136.9	198.6	231.6	110.0	213.2	107.4	80.5	78.7	35.7	151.9	53.1	47.2	38.1	136.9	53.1	0.4
228372_at	C10orf128	2.01E-03	2045.9	2925.5	3963.6	4957.2	3155.9	4546.8	2413.2	1834.2	1488.4	477.3	2206.9	842.1	1084.5	587.2	3155.9	1084.5	0.3
231530_s_at	C11orf1	4.50E-03	564.8	663.6	694.8	623.4	643.7	757.3	565.1	565.6	443.2	403.7	442.9	495.8	544.4	372.1	643.7	443.2	0.7
1553787_at	C11orf45	9.01E-04	476.5	584.1	649.5	529.9	533.4	661.6	532.9	388.8	280.9	222.1	256.9	362.6	302.7	173.3	533.4	280.9	0.5
223009_at	C11orf59	3.42E-03	2160.7	2231.4	2634.5	2678.5	2570.3	3357.1	2943.5	2060.4	1419.6	1384.3	2009.0	1876.2	1777.9	1343.5	2634.5	1777.9	0.7
221599_at	C11orf67	4.00E-03	2118.1	2917.8	3097.4	2737.4	2973.2	3218.2	2781.1	1733.7	2730.0	2294.3	1985.7	2213.3	2197.5	1918.2	2917.8	2197.5	0.8
228249_at	C11orf74	6.95E-03	152.8	179.9	235.2	193.3	212.9	223.4	208.1	151.9	137.7	164.9	153.5	163.9	133.5	125.3	208.1	151.9	0.7
228281_at	C11orf82	2.09E-03	326.3	427.9	559.2	523.4	508.5	631.1	403.2	305.3	217.4	88.8	250.2	184.0	154.0	92.3	508.5	184.0	0.4
218220_at	C12orf10	7.85E-03	358.8	315.2	429.9	462.7	346.8	409.9	384.9	300.2	241.4	199.0	349.6	287.0	333.1	217.3	384.9	287.0	0.7
222613_at	C12orf4	6.37E-03	946.2	932.7	984.8	956.3	1001.3	839.4	930.7	828.9	807.6	750.9	829.7	721.8	591.8	636.7	946.2	750.9	0.8
219817_at	C12orf47	6.85E-03	180.1	198.0	220.3	219.7	169.7	227.4	198.3	164.4	125.7	131.5	199.4	124.9	117.4	83.9	198.3	125.7	0.6
225772_s_at	C12orf62	2.64E-03	1489.0	1854.5	1662.5	1553.4	1742.0	2016.0	1559.0	1400.8	1154.0	786.0	1150.1	1243.2	1207.7	861.5	1662.5	1154.0	0.7
218723_s_at	C13orf15	2.30E-03	3231.0	2897.3	2188.3	2529.1	1819.0	2256.6	1906.0	2363.7	1997.7	1455.4	1542.9	1068.8	1936.9	1610.0	2256.6	1610.0	0.7
206500_s_at	C14orf106	1.02E-03	1655.5	1942.6	2109.1	2095.6	1808.2	2222.1	1493.0	1303.0	977.9	658.7	1362.1	1103.9	936.5	551.5	1942.6	977.9	0.5
223060_at	C14orf119	3.11E-03	2605.6	2705.4	2544.1	2729.9	2731.0	2340.1	2129.7	2356.1	1989.5	1685.1	2079.9	2049.4	1838.5	1549.6	2605.6	1989.5	0.8
214264_s_at	C14orf143	5.64E-03	104.5	149.8	159.4	174.2	177.2	168.5	116.4	117.2	97.0	106.5	120.7	104.0	89.1	72.3	159.4	104.0	0.7
233859_at	C14orf145	5.12E-03	89.5	78.1	74.2	75.2	76.9	57.9	72.5	61.1	64.6	58.2	55.0	53.8	49.8	63.0	75.2	58.2	0.8
213508_at	C14orf147	5.43E-03	238.6	372.4	378.9	384.9	374.1	407.5	299.1	266.4	256.6	160.4	258.9	223.2	209.7	157.8	374.1	223.2	0.6
225980_at	C14orf43	7.99E-03	177.7	197.7	236.0	248.6	281.0	286.6	251.1	188.7	132.0	111.7	207.7	179.3	166.8	164.5	248.6	166.8	0.7
224804_s_at	C15orf17	1.08E-03	1367.2	1564.5	1346.2	1321.2	1231.6	1334.5	1173.4	981.0	1003.4	567.9	907.4	863.5	952.2	711.4	1334.5	907.4	0.7
225300_at	C15orf23	2.20E-03	174.3	107.8	223.0	164.8	199.1	186.5	137.8	163.3	77.3	113.0	114.2	134.4	99.9	73.9	174.3	113.0	0.6
1552400_a_at	C15orf27	1.17E-03	77.4	112.3	92.2	89.0	92.9	55.7	81.0	48.6	76.9	60.5	70.6	79.4	36.6	48.7	89.0	60.5	0.7
228666_at	C15orf38	9.01E-03	319.9	370.8	436.7	388.6	260.5	212.7	248.0	288.3	186.8	156.1	223.8	229.6	174.7	141.0	319.9	186.8	0.6
227272_at	C15orf52	1.14E-03	726.4	679.7	1033.8	782.7	708.2	700.0	637.2	558.8	291.2	219.0	392.5	409.3	323.0	205.9	708.2	323.0	0.5
1569065_s_at	C15orf62	8.32E-03	170.9	136.2	136.3	135.5	154.4	146.3	131.2	151.0	115.5	76.5	100.0	117.1	116.3	106.6	136.3	115.5	0.8
1569064_at	C15orf62	5.88E-03	123.0	86.0	136.4	129.9	129.8	118.3	106.6	107.8	56.5	66.9	95.7	101.6	93.8	81.7	123.0	93.8	0.8
231878_at	C16orf53	4.75E-03	574.8	511.1	499.4	474.6	540.7	536.2	420.3	421.2	387.7	258.7	416.4	375.2	389.7	345.8	511.1	387.7	0.8
218300_at	C16orf53	1.49E-03	423.2	343.0	357.3	393.5	308.1	377.0	318.6	306.0	219.6	196.3	252.8	229.8	328.7	218.8	357.3	229.8	0.6
213235_at	C16orf88	7.22E-03	193.9	195.6	164.7	189.9	154.0	161.3	148.4	138.6	114.6	98.3	145.8	151.1	129.8	114.9	164.7	129.8	0.8
64438_at	C17orf101	7.20E-03	144.0	133.6	129.8	126.1	119.7	96.3	105.4	113.1	103.1	87.5	110.7	74.1	86.4	83.3	126.1	87.5	0.7
226657_at	C17orf103	2.45E-03	193.8	220.7	271.1	244.5	285.5	253.8	126.0	198.1	101.2	91.6	137.8	182.0	133.6	57.3	244.5	133.6	0.5
218464_s_at	C17orf63	2.64E-03	559.3	667.2	760.4	680.0	649.6	781.9	665.2	528.5	425.1	403.4	541.3	420.9	485.0	348.6	667.2	425.1	0.6
229889_at	C17orf76	5.23E-03	227.9	434.6	313.9	455.4	353.3	440.3	333.4	262.0	226.0	86.8	295.3	174.5	214.9	110.3	353.3	214.9	0.6
236981_at	C17orf99	5.27E-04	182.1	179.3	230.5	277.6	229.0	360.6	187.5	133.9	84.2	111.5	176.5	156.7	241.1	120.2	229.0	133.9	0.6
227352_at	C19orf39	3.41E-03	107.3	92.9	100.4	102.6	121.3	116.3	90.6	89.3	70.8	83.6	80.2	71.9	86.6	64.9	102.6	80.2	0.8
235568_at	C19orf59	8.97E-03	13037.6	13791.1	12009.8	13553.5	12911.5	13432.1	13460.5	12803.6	11013.0	7388.7	11624.0	8014.0	10418.7	8867.3	13432.1	10418.7	0.8
51200_at	C19orf60	5.25E-03	1488.9	1592.4	1497.4	1633.4	973.2	1391.7	1335.1	1203.0	1112.4	764.3	1084.8	824.2	1224.1	886.5	1488.9	1084.8	0.7
228532_at	C1orf162	9.56E-03	3629.7	4238.7	4413.1	3917.3	3947.8	4672.8	3959.9	3774.3	2674.7	2274.0	3389.0	3124.9	2687.2	2163.3	3959.9	2687.2	0.7
229382_at	C1orf183	3.46E-03	128.7	160.4	151.8	158.8	140.5	161.8	135.0	122.5	93.0	71.1	120.8	97.5	110.7	81.6	151.8	97.5	0.6
1558693_s_at	C1orf85	2.64E-03	471.9	420.9	426.5	482.9	403.1	349.5	379.2	337.0	239.9	180.9	320.1	346.6	261.2	242.8	420.9	261.2	0.6
225401_at	C1orf85	7.18E-03	456.5	423.3	459.8	509.3	454.1	421.8	441.4	415.0	273.2	209.5	361.0	437.3	246.7	252.8	454.1	273.2	0.6
1558692_at	C1orf85	5.99E-03	92.9	114.4	256.5	204.6	175.9	193.5	168.4	108.1	74.1	93.8	147.2	67.4	75.9	67.9	175.9	75.9	0.4
1555145_at	C1orf96	5.17E-03	57.9	57.0	90.5	87.8	75.1	95.6	54.9	56.6	38.3	59.9	68.7	48.2	51.3	43.1	75.1	51.3	0.7
225904_at	C1orf96	3.98E-03	609.8	903.6	980.5	872.0	786.2	1004.2	642.0	627.7	531.3	381.0	679.5	424.3	490.5	272.2	872.0	490.5	0.6
224693_at	C20orf108	7.05E-03	244.4	314.8	363.8	361.4	403.3	477.6	320.3	275.3	241.4	205.6	251.3	234.0	267.0	157.9	361.4	241.4	0.7
200855_at	C20orf191 /// LOC100131704 /// NCOR1	8.30E-03	231.4	286.2	308.7	313.9	361.6	408.4	307.3	252.5	191.2	207.4	246.3	224.8	217.0	218.2	308.7	218.2	0.7
226607_at	C20orf194	5.70E-03	319.0	343.4	436.0	361.9	391.1	420.9	393.7	288.4	268.9	259.1	289.0	327.5	295.8	238.4	391.1	288.4	0.7
225825_at	C20orf194	8.14E-03	332.1	341.2	370.4	351.3	375.9	384.7	319.5	335.5	229.7	245.4	250.2	329.6	277.3	225.8	351.3	250.2	0.7
218081_at	C20orf27	1.28E-04	239.3	248.6	245.9	263.8	261.5	266.2	199.1	160.5	158.7	114.4	148.8	166.5	156.8	99.0	248.6	156.8	0.6
206656_s_at	C20orf3	2.75E-03	4157.8	4120.3	4217.2	4117.3	3911.4	4496.6	4134.6	3330.9	3156.4	1890.6	3033.2	2898.4	3031.5	2385.0	4134.6	3031.5	0.7
219958_at	C20orf46	3.90E-04	445.3	420.3	416.8	514.3	369.2	612.1	375.5	259.1	185.1	104.8	221.3	179.6	419.6	167.4	420.3	185.1	0.4
225890_at	C20orf72	5.69E-03	391.8	307.3	417.6	379.8	383.0	428.1	317.4	394.0	193.1	172.8	292.3	270.5	256.2	150.9	383.0	256.2	0.7
225499_at	C20orf74	3.79E-03	240.8	227.7	246.2	276.9	294.3	300.0	251.0	232.6	150.7	155.0	219.1	218.4	214.1	163.8	251.0	214.1	0.9
202217_at	C21orf33 /// PWP2	3.55E-03	3158.1	3071.2	2910.5	2817.7	3039.6	3184.9	3092.9	2535.2	2393.7	1618.0	2395.1	2305.5	2372.1	1980.0	3071.2	2372.1	0.8
217118_s_at	C22orf9	7.54E-03	1444.8	1177.0	1277.1	1509.9	1129.1	736.5	1235.1	1051.3	889.7	651.3	848.5	908.8	751.8	720.2	1235.1	848.5	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
212421_at	C22orf9	1.23E-03	246.1	200.6	229.0	236.6	234.7	176.8	251.2	214.5	113.1	126.7	161.6	158.4	127.1	129.4	234.7	129.4	0.6
227144_at	C22orf9	1.70E-03	220.0	152.4	218.5	249.7	218.6	153.0	232.1	175.1	114.0	99.8	152.2	128.8	116.9	108.6	218.6	116.9	0.5
212875_s_at	C2CD2	4.74E-03	317.5	287.0	425.4	457.4	307.5	350.4	378.2	313.4	206.9	242.5	294.9	253.6	236.8	240.6	350.4	242.5	0.7
1556312_at	C2orf71	1.84E-03	71.1	111.6	78.9	111.7	71.9	73.8	64.8	67.3	60.9	44.4	69.6	48.9	39.5	47.2	73.8	48.9	0.7
1568658_at	C2orf74	1.32E-03	663.5	484.5	841.6	943.1	764.5	992.0	680.6	505.6	340.0	307.2	668.4	439.6	431.4	300.6	764.5	431.4	0.6
219114_at	C3orf18	2.64E-03	67.7	56.4	90.7	80.9	95.2	69.8	83.0	46.9	41.1	56.5	71.4	54.6	58.7	51.2	80.9	54.6	0.7
226891_at	C3orf21	6.76E-03	142.0	135.7	131.7	157.3	138.8	142.0	137.1	121.9	86.3	79.7	124.8	103.5	112.0	124.1	138.8	112.0	0.8
209285_s_at	C3orf63	3.29E-03	547.7	729.1	718.7	659.8	934.7	847.5	753.1	550.2	549.2	405.5	470.4	534.4	490.7	458.1	729.1	490.7	0.7
223157_at	C4orf14	2.40E-03	458.3	571.5	726.2	724.3	729.5	736.4	655.0	446.5	404.5	379.0	488.1	488.0	445.3	360.8	724.3	445.3	0.6
48030_i_at	C5orf4	2.44E-03	470.6	617.8	476.1	390.1	497.2	601.8	325.6	359.9	422.2	147.7	270.3	316.5	317.3	183.6	476.1	316.5	0.7
48031_r_at	C5orf4	7.19E-03	40.4	69.0	74.1	70.6	98.2	146.9	58.2	46.4	35.2	16.8	48.7	46.2	27.1	15.8	70.6	35.2	0.5
241874_at	C5orf53	9.57E-03	148.1	136.5	129.8	121.8	149.2	122.7	122.3	126.7	116.6	89.6	96.2	132.6	99.7	96.1	129.8	99.7	0.8
226977_at	C5orf53	6.45E-03	235.1	320.5	304.1	281.4	357.1	349.3	293.8	241.5	203.6	149.4	236.2	243.2	223.5	155.8	304.1	223.5	0.7
236178_at	C6orf162	6.10E-03	222.7	266.4	179.9	157.7	159.0	190.1	161.4	171.1	134.2	102.4	153.0	131.6	132.8	94.4	179.9	132.8	0.7
218453_s_at	C6orf35	8.48E-03	119.3	122.5	140.6	149.7	125.6	140.8	140.2	109.8	97.1	86.7	117.4	110.5	93.9	75.0	140.2	97.1	0.7
225729_at	C6orf89	8.87E-03	471.5	516.2	498.0	591.1	570.8	633.8	519.9	507.4	339.5	254.8	404.8	442.9	454.4	359.4	519.9	404.8	0.8
220581_at	C6orf97	2.64E-03	180.9	172.3	336.6	269.4	220.5	327.2	253.4	125.2	145.3	95.6	162.2	126.1	176.6	98.5	253.4	126.1	0.5
225419_at	C7orf11	5.70E-03	443.4	500.6	518.2	527.5	538.6	603.6	532.0	424.2	389.4	390.9	426.8	370.8	426.5	402.9	527.5	402.9	0.8
224688_at	C7orf42	8.12E-03	1766.0	1619.0	1409.9	1476.8	1526.5	1656.7	1406.1	1462.4	1254.5	890.9	1291.3	1353.5	1259.4	1086.8	1526.5	1259.4	0.8
226781_at	C7orf55	5.53E-03	239.9	290.9	298.9	303.1	283.5	332.1	246.4	226.3	179.5	169.8	229.3	223.1	257.1	124.5	290.9	223.1	0.8
226780_s_at	C7orf55	8.13E-03	346.2	422.1	400.8	375.6	390.1	445.4	323.4	363.9	243.3	195.7	294.4	315.9	256.3	150.5	390.1	256.3	0.7
218507_at	C7orf68	9.33E-03	273.7	421.9	326.7	371.9	317.5	442.5	256.7	307.3	278.7	159.7	297.1	225.0	254.3	140.6	326.7	254.3	0.8
225534_at	C8orf40	8.08E-03	1393.9	990.5	1385.3	1565.1	1427.7	1524.7	1426.7	1213.7	876.2	993.3	1308.2	1166.6	1182.0	1058.5	1426.7	1166.6	0.8
227672_at	C8orf73	1.29E-03	386.8	387.6	587.1	568.4	467.0	433.2	463.3	279.8	222.7	157.8	276.8	268.5	289.0	180.4	463.3	268.5	0.6
224879_at	C9orf123	3.39E-03	1508.4	1518.1	1466.4	1267.4	1317.9	1607.0	1503.8	1304.8	1017.8	773.7	1015.1	1020.5	1183.5	863.1	1503.8	1017.8	0.7
222781_s_at	C9orf40	1.01E-03	325.7	402.2	360.3	384.4	253.0	346.3	297.2	269.8	280.9	229.9	292.4	142.6	235.6	201.5	346.3	235.6	0.7
223007_s_at	C9orf5	8.10E-03	452.6	556.0	435.0	417.5	533.4	562.7	434.0	493.8	391.2	246.4	328.4	358.7	336.7	207.5	452.6	336.7	0.7
223008_s_at	C9orf5	1.67E-03	934.7	1126.3	1180.9	1181.2	1383.3	1468.8	1245.8	838.0	795.8	803.4	885.1	819.7	852.8	684.2	1181.2	819.7	0.7
218168_s_at	CABC1	5.83E-03	745.2	1158.3	1390.7	1138.5	1009.4	1121.6	755.3	663.0	581.3	229.5	658.6	713.0	452.3	257.3	1121.6	581.3	0.5
225531_at	CABLES1	3.32E-03	122.5	178.7	199.0	171.2	144.0	143.0	137.2	121.1	96.8	64.0	82.9	105.6	77.0	68.9	144.0	82.9	0.6
225532_at	CABLES1	2.30E-03	1202.9	1784.3	1632.5	1326.7	1231.5	1201.8	915.7	729.0	911.1	221.0	699.2	742.0	460.8	317.6	1231.5	699.2	0.6
1555993_at	CACNA1D	4.55E-04	401.6	252.5	417.5	363.3	380.6	256.4	225.0	293.5	129.4	97.2	168.0	171.9	111.2	76.2	363.3	129.4	0.4
210691_s_at	CACYBP	2.69E-03	949.7	1157.7	1250.9	1185.6	1049.9	1157.1	1101.7	820.6	792.9	535.1	882.3	683.4	753.3	504.5	1157.1	753.3	0.7
211761_s_at	CACYBP	1.69E-03	577.4	724.5	800.0	701.4	738.8	780.6	643.9	499.1	501.2	326.1	506.7	423.7	397.4	310.8	724.5	423.7	0.6
201381_x_at	CACYBP	3.58E-04	1143.3	1223.9	1268.1	1246.9	1101.4	1212.7	1090.5	852.1	853.8	637.9	847.1	702.1	707.9	587.9	1212.7	707.9	0.6
209002_s_at	CALCOCO1	2.00E-03	407.1	471.4	513.3	516.6	490.6	517.6	513.8	391.6	260.9	286.5	355.4	346.3	336.8	284.5	513.3	336.8	0.7
226959_at	CAMK1D /// LOC283070	2.12E-03	483.9	352.3	372.9	644.8	372.8	367.0	301.6	372.9	220.7	191.0	334.4	287.5	312.7	189.8	372.8	287.5	0.8
226382_at	CAMK1D /// LOC283070	6.87E-03	195.1	199.5	248.1	367.2	249.2	251.9	184.5	234.2	108.1	126.5	231.2	137.3	176.6	109.6	248.1	137.3	0.6
212757_s_at	CAMK2G	4.36E-03	116.7	124.0	163.6	145.0	163.2	169.3	122.6	118.0	86.1	68.2	103.9	95.1	97.3	75.8	145.0	95.1	0.7
223460_at	CAMKK1	9.20E-03	144.0	103.8	173.5	169.9	134.4	154.1	128.1	127.9	93.8	73.0	124.1	91.8	93.5	92.5	144.0	93.5	0.6
220410_s_at	CAMSAP1	4.65E-03	607.4	498.8	629.9	650.5	623.5	617.9	655.9	517.4	418.3	419.7	534.3	374.6	484.6	479.2	623.5	479.2	0.8
220409_at	CAMSAP1	2.68E-03	496.2	447.4	525.4	584.5	494.5	535.9	513.5	437.0	339.7	331.2	406.7	361.7	421.1	390.2	513.5	390.2	0.8
212711_at	CAMSAP1	3.10E-03	671.2	691.9	672.1	777.6	737.7	788.7	740.7	628.5	549.0	462.1	550.3	420.0	534.8	507.8	737.7	534.8	0.7
212710_at	CAMSAP1	4.65E-03	94.0	82.5	117.5	105.9	127.0	165.0	135.7	86.4	58.3	64.5	94.8	74.9	91.2	62.1	117.5	74.9	0.6
213268_at	CAMTA1	6.60E-04	393.5	493.5	391.9	436.7	479.5	552.3	471.0	279.3	377.6	203.8	289.6	239.4	368.5	222.8	471.0	279.3	0.6
214475_x_at	CAPN3	1.82E-03	433.2	367.8	411.1	472.3	373.1	363.6	317.0	351.3	243.2	251.6	339.4	317.8	265.4	222.6	373.1	265.4	0.7
218456_at	CAPRIN2	2.58E-03	427.7	561.5	589.0	516.1	521.3	566.4	408.1	377.7	415.2	309.5	407.3	367.7	353.6	261.5	521.3	367.7	0.7
224910_at	CARHSP1	6.30E-03	106.9	97.6	108.7	106.8	121.8	110.0	98.6	98.6	69.2	75.0	88.3	92.0	86.1	81.2	106.9	86.1	0.8
218153_at	CARS2	5.07E-03	1073.3	1125.9	793.7	966.3	910.3	816.1	969.0	828.3	670.8	476.7	626.9	800.9	761.1	640.0	966.3	670.8	0.7
211922_s_at	CAT	2.39E-03	2505.3	3058.4	2541.1	3007.8	2706.9	2898.1	2296.4	1981.9	1970.7	1137.5	1893.6	2218.4	2160.4	1402.3	2706.9	1970.7	0.7
225234_at	CBL	8.26E-03	541.9	541.7	534.1	609.7	600.7	607.0	558.2	486.6	342.7	283.3	469.4	425.3	527.8	457.3	558.2	457.3	0.8
243475_at	CBL	3.55E-03	1065.2	1176.6	1400.0	1376.4	1298.5	1592.5	1395.6	1008.2	870.0	814.3	1057.9	911.8	1059.7	1011.2	1376.4	1008.2	0.7
225231_at	CBL	6.07E-03	482.3	557.1	738.5	720.9	754.2	984.8	901.5	482.9	425.8	434.6	594.5	450.0	476.3	498.0	738.5	476.3	0.6
229010_at	CBL	6.24E-03	284.5	327.4	440.8	412.5	419.5	533.7	462.7	270.3	255.4	269.5	371.6	265.0	314.6	276.4	419.5	270.3	0.6
1553972_a_at	CBS	7.59E-03	203.1	104.4	258.5	337.6	305.6	311.5	146.2	146.8	98.7	87.3	175.9	227.8	189.0	101.7	258.5	146.8	0.6
201518_at	CBX1	5.94E-03	980.5	1109.1	1220.3	1046.5	1083.1	1093.7	960.1	951.8	952.8	691.6	788.6	666.1	646.5	673.6	1083.1	691.6	0.6
226085_at	CBX5	3.68E-03	220.0	178.2	224.3	260.1	279.9	311.3	355.9	187.4	119.4	115.4	219.3	199.4	130.5	187.2	260.1	187.2	0.7
212914_at	CBX7	2.33E-04	399.1	387.5	491.7	434.3	492.5	453.6	383.7	302.1	189.0	191.0	211.0	291.5	259.5	173.3	434.3	211.0	0.5
227157_at	CCDC111	9.86E-03	188.8	266.0	355.8	232.7	300.3	345.1	263.1	195.9	207.5	218.2	204.0	154.1	163.0	127.7	266.0	195.9	0.7
1553542_at	CCDC125	3.23E-03	299.5	378.3	406.5	431.2	376.7	472.6	430.9	311.2	214.6	151.4	280.1	222.4	249.7	167.4	406.5	222.4	0.5
225017_at	CCDC14	3.79E-03	211.8	275.4	410.1	403.0	398.3	431.9	310.1	198.9	192.1	188.1	300.5	151.5	138.2	123.9	398.3	188.1	0.5
209479_at	CCDC28A	2.31E-03	886.5	948.3	1069.1	1026.7	1130.6	1103.2	841.1	843.6	646.3	614.5	726.9	834.8	657.3	499.8	1026.7	657.3	0.6
218628_at	CCDC53	6.21E-03	904.7	930.6	987.8	1059.0	1059.5	1099.9	927.6	843.6	746.4	763.5	803.0	784.9	816.9	761.6	987.8	784.9	0.8
1559893_at	CCDC75	2.00E-03	463.5	630.0	523.8	505.5	482.6	606.2	472.7	404.8	404.8	203.9	372.9	260.5	263.0	180.0	505.5	263.0	0.5

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
228495_at	CCDC75	5.43E-03	177.7	285.4	322.3	318.7	288.8	387.7	300.0	216.6	146.2	124.9	227.1	138.9	166.1	115.3	300.0	146.2	0.5
222809_x_at	CCDC85C	1.16E-03	592.1	767.8	728.3	691.7	638.7	822.6	502.0	460.4	405.5	167.1	377.3	327.7	360.6	154.6	691.7	360.6	0.5
37424_at	CCHCR1	5.84E-03	190.3	184.2	202.1	204.5	199.9	195.2	187.2	158.7	135.3	142.3	146.0	172.4	161.6	159.1	195.2	158.7	0.8
209698_at	CCHCR1	4.69E-03	141.6	120.1	153.4	158.0	127.5	130.5	147.7	112.7	89.5	119.8	118.3	117.6	102.4	104.0	141.6	112.7	0.8
42361_g_at	CCHCR1	8.12E-03	135.4	122.1	157.1	157.9	156.0	134.2	166.7	117.1	115.2	100.8	104.5	119.9	112.1	107.8	156.0	112.1	0.7
201700_at	CCND3	3.37E-03	3195.0	3486.1	3115.4	3548.1	3116.4	4546.9	3781.7	2983.6	2571.9	1158.7	2362.1	1568.9	2817.3	1664.7	3486.1	2362.1	0.7
202769_at	CCNG2	4.39E-03	499.7	821.9	1242.9	1222.0	863.9	1435.4	830.0	496.4	506.2	319.5	783.0	496.2	493.6	310.0	863.9	496.2	0.6
211559_s_at	CCNG2	9.27E-03	145.5	229.7	367.9	338.2	238.6	416.3	212.0	172.6	114.5	92.0	224.0	164.2	122.2	82.1	238.6	122.2	0.5
202770_s_at	CCNG2	5.80E-03	97.1	195.5	276.4	247.8	195.5	308.0	173.1	117.2	82.8	80.7	164.0	114.3	96.1	55.7	195.5	96.1	0.5
204093_at	CCNH	2.36E-03	550.3	622.0	723.7	855.0	778.1	898.3	795.4	499.9	478.3	513.1	632.7	545.9	545.9	498.1	778.1	513.1	0.7
221511_x_at	CCPG1	8.50E-03	557.5	742.6	704.6	639.1	726.2	718.2	673.1	519.0	557.4	516.6	601.6	394.5	466.4	418.2	704.6	516.6	0.7
222156_x_at	CCPG1	5.22E-03	418.5	472.1	640.9	594.6	601.3	697.0	631.1	361.4	395.5	458.8	479.2	336.5	328.5	323.0	601.3	361.4	0.6
205271_s_at	CCRK	6.45E-03	132.7	133.2	172.9	141.8	165.6	192.6	173.2	132.9	93.5	95.3	121.1	103.0	135.4	114.6	165.6	114.6	0.7
226545_at	CD109	4.69E-03	989.6	1217.4	1083.3	1060.5	1082.0	1454.8	1656.5	798.4	974.2	703.4	1010.9	593.6	809.7	945.2	1083.3	809.7	0.7
206206_at	CD180	2.01E-03	106.7	104.2	96.0	123.9	112.5	128.9	74.0	80.0	66.3	42.6	84.5	92.1	76.9	53.7	106.7	76.9	0.7
38521_at	CD22	5.03E-03	359.9	352.2	419.4	269.0	311.6	300.2	261.2	289.0	233.4	238.0	236.9	257.8	188.7	208.1	311.6	236.9	0.8
204581_at	CD22	8.50E-03	320.0	354.7	398.9	291.1	319.2	315.2	278.4	268.8	237.1	234.3	212.9	256.0	304.9	211.7	319.2	237.1	0.7
217422_s_at	CD22	8.54E-03	234.5	118.0	187.1	169.4	118.7	145.9	155.7	130.5	47.0	77.4	123.8	132.3	104.7	95.6	155.7	104.7	0.7
202256_at	CD2BP2	8.83E-03	650.5	549.6	525.2	588.3	549.2	524.3	492.2	512.6	428.6	387.9	403.8	463.8	510.7	368.7	549.2	428.6	0.8
209933_s_at	CD300A	7.59E-03	695.3	1154.5	770.9	684.0	737.5	441.6	883.4	557.1	687.3	308.0	312.5	669.6	334.7	662.9	737.5	557.1	0.8
1553043_a_at	CD300LF	2.99E-03	1094.1	1510.5	1596.9	1559.3	1533.1	2019.6	1542.0	1134.4	915.1	432.2	772.5	788.6	831.0	456.3	1542.0	788.6	0.5
206120_at	CD33	9.33E-03	591.9	671.4	804.7	866.5	983.7	1016.3	838.4	686.4	435.7	371.7	638.5	692.2	601.7	465.8	838.4	601.7	0.7
207549_x_at	CD46	7.63E-03	4155.2	4479.5	3961.6	4224.8	4344.8	4578.7	4070.7	3728.7	3711.6	2819.7	3615.1	3505.0	3596.3	2998.2	4224.8	3596.3	0.9
213958_at	CD6	1.85E-03	150.3	146.8	136.4	159.0	111.4	144.5	128.6	124.5	103.4	84.3	107.5	96.6	84.3	78.2	144.5	96.6	0.7
211190_x_at	CD84	7.33E-03	279.2	286.9	287.0	325.5	313.7	269.5	235.2	250.2	149.1	123.4	241.8	310.9	130.1	123.3	286.9	149.1	0.5
205988_at	CD84	3.23E-03	350.1	326.8	460.9	576.1	484.3	446.0	445.7	291.6	177.8	194.8	382.1	448.0	222.0	219.7	446.0	222.0	0.5
212899_at	CDC2L6	9.35E-03	407.7	464.1	418.9	376.0	449.5	518.8	325.2	414.5	306.7	296.5	321.0	325.9	246.5	186.7	418.9	306.7	0.7
212897_at	CDC2L6	5.95E-03	166.5	169.3	232.5	212.0	246.1	239.0	174.2	173.7	128.3	141.2	162.9	147.9	122.3	109.5	212.0	141.2	0.7
203376_at	CDC40	9.10E-03	630.2	649.1	769.1	763.5	772.1	794.3	689.6	606.2	505.2	469.5	696.7	541.0	578.3	472.2	763.5	541.0	0.7
218062_x_at	CDC42EP4	4.32E-03	444.5	383.4	429.1	614.4	467.8	429.6	524.1	385.8	320.1	243.5	363.7	328.5	357.7	358.8	444.5	357.7	0.8
225081_s_at	CDCA7L	2.93E-03	762.6	585.1	1478.9	927.0	831.0	1274.9	873.5	710.6	356.5	440.1	599.9	501.7	572.0	411.8	873.5	501.7	0.6
1554110_at	CDCP1	5.66E-03	1378.9	1265.2	1364.0	999.1	1087.7	989.2	876.9	1323.4	1003.8	950.8	780.5	831.5	749.0	611.0	1087.7	831.5	0.8
218451_at	CDCP1	9.88E-03	714.3	886.7	692.9	679.2	693.7	816.5	723.4	768.6	627.9	384.1	544.8	508.2	576.6	404.0	714.3	544.8	0.8
201253_s_at	CDIPT	5.51E-03	214.3	236.7	370.7	382.5	317.6	360.9	364.6	226.0	164.5	231.4	274.8	221.2	233.3	184.1	360.9	226.0	0.6
203468_at	CDK10	9.46E-03	458.9	304.2	413.7	450.3	348.5	409.0	417.5	367.8	246.3	363.3	380.2	277.2	351.9	324.4	413.7	351.9	0.9
204247_s_at	CDK5	4.26E-03	100.6	74.5	116.9	142.3	106.8	121.4	91.3	78.2	53.7	52.7	98.3	90.0	87.7	66.0	106.8	78.2	0.7
218315_s_at	CDK5RAP1	1.80E-03	597.2	623.7	700.8	632.6	549.8	626.4	549.3	452.9	419.3	394.0	495.2	449.8	470.6	362.2	623.7	449.8	0.7
218740_s_at	CDK5RAP3	7.35E-03	3147.6	2868.8	2998.3	2852.3	2503.1	2580.6	2155.4	2480.5	1960.7	1825.2	2200.3	2293.1	2233.7	1666.2	2852.3	2200.3	0.8
214907_at	CEACAM21	3.28E-03	272.8	157.5	337.9	397.2	175.1	362.5	278.6	210.7	96.8	122.9	187.5	163.5	215.8	115.9	278.6	163.5	0.6
239317_at	CEACAM21	8.59E-03	56.5	127.6	175.4	197.4	116.7	224.7	105.2	61.7	82.2	33.3	133.6	59.3	63.4	25.9	127.6	61.7	0.5
216605_s_at	CEACAM21	7.75E-03	280.2	176.7	422.2	418.1	209.0	421.6	330.4	270.8	141.6	149.8	248.2	145.2	265.1	124.0	330.4	149.8	0.5
204039_at	CEBPA	2.52E-03	474.0	433.3	563.7	677.4	464.5	584.6	521.0	289.3	206.7	100.2	329.2	315.2	339.1	124.7	521.0	289.3	0.6
225527_at	CEBPG	9.56E-03	1602.5	1454.9	1390.1	1458.9	1397.1	1373.9	1361.3	1405.2	1233.6	1065.7	1164.3	1034.3	1194.1	1129.9	1397.1	1164.3	0.8
223728_at	CENPBD1	5.31E-03	1273.4	1157.6	1001.4	1069.1	1379.1	1297.8	1047.2	1072.0	1019.4	687.2	788.5	1054.5	1094.9	773.1	1157.6	1019.4	0.9
230436_s_at	CENPV	6.86E-04	112.7	100.4	109.4	118.0	127.3	139.9	138.6	97.5	57.6	52.7	65.2	81.8	89.2	65.9	118.0	65.9	0.6
226610_at	CENPV	6.14E-04	480.4	479.2	546.0	488.1	505.9	602.5	547.7	326.1	324.1	163.1	260.5	221.9	335.0	203.1	505.9	260.5	0.5
226611_s_at	CENPV	1.23E-03	376.6	340.2	430.4	412.5	458.1	552.8	472.7	331.0	180.0	128.0	224.8	216.4	261.5	135.7	430.4	216.4	0.5
218827_s_at	CEP192	3.02E-03	307.1	311.4	381.4	404.5	421.4	427.5	373.8	294.8	220.8	234.7	316.0	284.2	291.2	225.6	381.4	284.2	0.7
203166_at	CFDP1	2.61E-03	2603.3	2665.1	2977.0	2651.9	2569.8	2679.6	2253.7	2309.0	2213.9	1818.1	1810.5	1780.2	1971.9	1550.7	2651.9	1818.1	0.7
234681_s_at	CHD6	5.36E-03	177.2	143.4	209.5	188.9	233.2	202.8	184.0	154.3	108.6	146.7	171.0	168.6	136.1	145.6	188.9	146.7	0.8
226123_at	CHD7	8.20E-03	286.2	331.9	346.3	364.3	377.1	409.1	280.0	264.8	189.7	224.9	278.5	349.1	302.1	197.0	346.3	264.8	0.8
218829_s_at	CHD7	1.67E-03	640.0	833.3	942.0	913.1	1104.4	1141.2	785.1	545.3	541.8	538.2	778.2	635.6	726.6	491.2	913.1	545.3	0.6
231994_at	CHDH	1.57E-03	251.1	207.4	386.9	338.5	248.6	235.9	268.9	206.1	151.1	154.0	169.7	159.7	156.2	126.2	251.1	156.2	0.6
1559591_s_at	CHDH	4.45E-04	455.5	431.4	602.9	473.5	452.2	370.2	430.0	343.4	251.3	230.3	246.0	273.4	228.6	184.2	452.2	246.0	0.5
229954_at	CHDH	8.47E-04	609.0	619.7	746.2	736.8	720.2	642.0	621.0	577.5	269.0	279.0	357.2	376.3	324.0	220.2	642.0	324.0	0.5
1559590_at	CHDH	8.69E-03	51.5	61.8	89.8	90.0	79.2	71.3	83.5	64.2	25.8	38.4	49.5	56.6	35.1	21.9	79.2	38.4	0.5
210416_s_at	CHEK2	4.69E-03	169.8	164.9	196.4	187.6	198.9	180.4	144.8	170.0	92.5	91.7	164.3	105.8	102.3	87.2	180.4	102.3	0.6
221675_s_at	CHPT1	6.11E-03	5364.0	5577.2	5762.9	5746.5	5277.7	7110.1	5364.2	4771.2	5065.9	4422.8	4316.3	3483.1	4515.5	4030.2	5577.2	4422.8	0.8
1553705_a_at	CHRM3	2.14E-03	116.4	138.1	166.6	106.3	119.0	177.6	126.9	103.5	81.6	96.3	79.1	70.2	66.6	69.7	126.9	79.1	0.6
210221_at	CHRNA3	9.30E-03	70.5	135.1	205.4	94.7	113.5	38.3	48.5	71.5	56.0	60.4	49.7	43.0	41.3	18.3	94.7	49.7	0.5
226314_at	CHST14	3.05E-03	236.0	263.6	300.6	305.4	311.1	375.1	294.6	228.2	149.7	118.1	213.3	203.7	232.9	145.1	300.6	203.7	0.7
226736_at	CHURC1	7.19E-03	857.2	331.4	447.3	439.0	432.4	450.9	437.9	810.8	278.0	317.2	336.7	331.9	358.8	323.5	439.0	331.9	0.8
205101_at	CIITA	3.17E-04	1360.6	1471.2	1531.6	1474.8	1282.5	1570.8	1277.6	1028.7	732.4	525.9	928.1	592.4	696.5	622.0	1471.2	696.5	0.5
212801_at	CIT	7.37E-03	127.3	99.5	89.0	94.2	81.5	69.6	87.7	78.8	99.6	67.8	56.9	52.2	47.3	76.7	89.0	67.8	0.8
221058_s_at	CKLF	2.96E-03	3334.6	3535.1	2678.8	3086.6	2353.9	2696.5	2827.0	2875.0	2508.4	1121.4	2071.5	1695.5	1870.2	1637.3	2827.0	1870.2	0.7
223451_s_at	CKLF	5.82E-03	1360.6	1524.1	1254.9	1368.6	1166.0	1331.5	1403.0	1309.1	1027.9	544.7	1066.0	835.0	872.8	665.7	1360.6	872.8	0.6

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
219161_s_at	CKLF	4.65E-03	612.0	816.2	811.0	995.3	753.6	1012.7	997.9	653.7	623.2	386.1	600.2	425.7	406.1	426.6	816.2	426.6	0.5
201735_s_at	CLCN3	5.59E-03	599.2	562.8	622.5	599.5	652.9	648.9	666.8	569.3	385.2	466.0	531.8	439.7	439.1	431.3	622.5	439.7	0.7
201734_at	CLCN3	2.93E-03	1381.9	1394.0	1794.9	1748.3	1712.9	2127.6	2024.0	1172.2	1150.0	1065.5	1430.7	1165.7	1224.1	1208.4	1748.3	1172.2	0.7
205148_s_at	CLCN4	8.12E-03	76.2	107.4	137.4	83.9	115.3	116.7	89.8	83.1	54.2	77.4	73.0	74.6	48.9	46.4	107.4	73.0	0.7
214769_at	CLCN4	4.90E-03	209.2	278.4	356.2	237.7	321.3	408.1	267.5	213.3	166.9	138.0	183.7	187.5	161.0	92.9	278.4	166.9	0.6
221132_at	CLDN18	6.97E-03	82.6	66.0	80.7	79.3	61.3	65.6	65.1	58.9	55.6	36.3	55.0	49.5	49.7	51.4	66.0	51.4	0.8
202790_at	CLDN7	5.30E-03	170.8	185.1	259.0	234.7	153.6	323.3	167.8	181.1	129.2	133.0	163.2	104.9	180.8	75.5	185.1	133.0	0.7
1552398_a_at	CLEC12A /// CLEC12B	6.09E-03	1232.8	1663.1	1778.9	1624.9	2294.9	1903.0	1660.7	1251.5	1284.0	1182.5	1267.5	1592.7	1074.8	1077.0	1663.1	1251.5	0.8
1556209_at	CLEC2B	5.99E-04	508.1	391.6	605.6	496.7	428.6	409.9	360.4	375.4	248.6	240.9	325.2	262.3	191.7	149.1	428.6	248.6	0.6
221724_s_at	CLEC4A	5.83E-03	538.1	619.0	1084.0	851.6	1041.2	1152.8	732.3	526.8	479.2	654.4	569.5	643.3	623.2	611.1	851.6	611.1	0.7
241098_at	CLEC7A	6.56E-03	103.9	114.2	207.2	148.6	121.0	144.5	114.2	93.0	104.7	120.4	114.2	88.7	82.2	77.3	121.0	93.0	0.8
1554406_a_at	CLEC7A	7.85E-03	1331.7	1406.1	1920.2	1793.1	1451.3	1648.3	1369.5	1302.8	1099.2	1045.2	1134.2	1190.3	971.6	1067.2	1451.3	1099.2	0.8
1555213_a_at	CLEC7A	5.25E-03	2213.5	2480.6	1555.5	1190.1	1664.6	1157.9	1406.7	1507.5	1667.0	729.8	796.6	1583.3	774.2	1152.6	1555.5	1152.6	0.7
1555756_a_at	CLEC7A	4.43E-03	1235.1	1237.1	1743.4	1793.2	1437.4	1790.7	1427.6	1121.9	904.5	1000.3	1197.8	1209.0	827.6	876.9	1437.4	1000.3	0.7
221698_s_at	CLEC7A	1.40E-03	2437.9	2695.6	4027.7	3577.5	3065.6	3776.5	2816.2	1861.3	2201.5	1974.0	2374.6	1587.4	1520.0	1587.6	3065.6	1861.3	0.6
1555214_a_at	CLEC7A	4.18E-03	391.9	424.7	774.9	622.2	487.4	733.8	521.3	364.4	283.5	275.9	345.9	389.4	285.5	211.5	521.3	285.5	0.5
219944_at	CLIP4	2.68E-03	807.0	994.7	997.6	1072.6	887.9	916.0	805.7	745.7	721.4	680.2	696.1	675.1	679.6	587.2	916.0	680.2	0.7
226425_at	CLIP4	9.66E-04	3605.4	4944.8	5279.7	5340.2	5061.9	5514.0	5171.8	2831.2	3651.5	2627.1	3905.1	2904.4	2865.3	2459.8	5171.8	2865.3	0.6
213839_at	CLMN	4.71E-03	105.5	108.7	136.8	125.3	209.5	134.9	157.1	97.3	65.2	51.1	113.4	113.7	72.0	66.7	134.9	72.0	0.5
209143_s_at	CLNS1A	9.29E-03	946.5	1070.3	1330.7	1110.0	1250.0	1363.0	1158.8	959.3	849.0	882.0	963.4	876.0	922.7	733.1	1158.8	882.0	0.8
226017_at	CMTM7	8.55E-03	466.3	588.1	615.3	548.5	591.5	580.1	499.9	514.5	356.6	297.0	367.9	499.2	349.5	272.2	580.1	356.6	0.6
227731_at	CNBP	3.97E-03	497.0	633.0	773.6	656.6	786.1	886.6	682.6	516.0	425.9	424.2	503.4	474.7	485.1	410.4	682.6	474.7	0.7
228437_at	CNIH4	5.51E-03	159.1	182.8	263.6	181.0	204.4	236.9	176.1	151.9	151.3	128.1	122.1	140.6	169.5	110.3	182.8	140.6	0.8
1554523_a_at	CNNM2	7.18E-03	160.9	168.1	190.3	185.6	181.1	173.0	140.8	129.5	140.2	112.9	150.2	122.9	136.8	124.5	173.0	129.5	0.7
225053_at	CNOT7	6.07E-03	1023.5	1088.3	1158.9	1229.5	1229.2	1374.0	1416.3	952.7	898.0	853.4	1012.2	914.1	978.3	896.7	1229.2	914.1	0.7
226751_at	CNRIP1	3.71E-03	255.0	235.0	489.8	387.4	373.2	214.1	329.5	202.3	155.2	287.4	338.5	271.7	143.0	143.3	329.5	202.3	0.6
226277_at	COL4A3BP	6.30E-03	3257.9	3575.4	4645.1	4531.8	5202.3	5335.1	4681.1	3273.7	2927.1	3150.6	3435.8	2987.9	2770.1	2800.7	4645.1	2987.9	0.6
52651_at	COL8A2	2.38E-03	363.7	393.8	398.1	345.1	304.2	300.8	283.0	300.2	259.0	206.0	242.0	241.2	230.0	195.9	345.1	241.2	0.7
221900_at	COL8A2	4.83E-04	442.1	477.5	557.5	515.1	411.0	405.5	365.5	340.0	312.1	262.0	294.8	254.5	285.9	221.8	442.1	285.9	0.6
221019_s_at	COLEC12	1.13E-03	3309.4	3311.0	3333.1	2456.0	1486.2	2474.6	3873.1	2479.3	2735.7	1771.9	1550.9	640.7	1063.5	1827.1	3309.4	1771.9	0.5
218072_at	COMMD9	2.64E-03	1457.9	1489.5	1379.3	1655.5	1577.9	1513.1	1279.4	1350.3	898.0	689.5	1136.8	1243.4	970.7	805.6	1489.5	970.7	0.7
225747_at	COQ10A	5.19E-03	154.2	180.3	186.9	161.7	156.4	140.6	126.2	158.6	91.6	106.4	112.3	103.0	111.8	66.5	156.4	106.4	0.7
227177_at	CORO2A	1.78E-03	581.4	655.3	625.2	604.2	562.5	581.7	593.2	529.9	393.4	208.1	401.3	274.3	301.1	242.7	593.2	301.1	0.5
1552301_a_at	CORO6	1.75E-03	63.1	84.3	65.7	75.1	78.2	65.6	57.0	43.9	62.9	41.2	54.5	47.6	46.2	51.2	65.7	47.6	0.7
203551_s_at	COX11	1.03E-03	145.0	155.9	178.6	183.3	169.2	143.0	136.0	136.9	96.2	89.6	111.6	100.7	78.6	66.8	155.9	96.2	0.6
221550_at	COX15	3.65E-03	652.9	684.9	1158.6	856.9	917.5	1381.2	941.5	587.7	571.3	581.9	653.9	505.8	651.8	494.3	917.5	581.9	0.6
219547_at	COX15	3.62E-03	515.1	506.9	828.2	747.1	761.3	1091.4	814.8	485.5	401.9	415.5	556.9	397.2	541.2	368.3	761.3	415.5	0.5
203663_s_at	COX5A	7.57E-03	3728.8	3699.9	3569.8	3491.1	3369.9	3480.6	3757.6	3226.7	2955.9	2485.5	2915.8	2966.1	2743.1	2840.7	3569.8	2915.8	0.8
224828_at	CPEB4	3.55E-03	2379.8	2508.4	3491.1	3420.3	3568.7	4116.3	3722.6	1857.5	2182.4	2735.2	2750.0	2031.1	2505.7	2404.3	3491.1	2404.3	0.7
218610_s_at	CPPED1	3.14E-03	214.2	149.2	165.5	196.8	176.0	222.2	149.4	187.9	121.0	105.4	133.7	118.3	122.5	118.8	176.0	121.0	0.7
239135_at	CPPED1	8.72E-03	149.7	250.2	223.9	275.6	211.8	272.2	186.7	158.9	175.5	151.4	216.8	141.3	125.7	118.3	223.9	151.4	0.7
201200_at	CREG1	9.39E-03	2344.4	2879.7	2859.3	3513.2	3274.7	3185.5	2707.1	2061.1	2463.3	2370.6	3026.2	2607.7	2166.7	1999.3	2879.7	2370.6	0.8
225324_at	CRLS1	5.63E-03	208.7	282.3	306.3	517.7	478.9	432.8	347.7	222.5	221.8	180.3	368.0	265.0	222.3	183.8	347.7	222.3	0.6
206914_at	CRTAM	4.78E-03	502.9	469.2	742.2	602.1	653.9	625.5	629.8	458.0	348.0	528.2	486.3	369.3	449.2	315.0	625.5	449.2	0.7
226656_at	CRTAP	1.53E-03	2465.2	2939.4	2791.1	2419.7	3313.0	3479.4	3196.1	2180.5	2064.4	1604.8	1600.0	2441.1	2486.3	1893.3	2939.4	2064.4	0.7
1555889_a_at	CRTAP	3.59E-03	1456.9	1549.8	1935.2	1688.8	1990.6	2054.7	2042.3	1349.3	1320.8	1345.9	1170.9	1341.7	1248.6	1186.9	1935.2	1320.8	0.7
206777_s_at	CRYBB2 /// CRYBB2P1	9.36E-03	303.5	453.7	339.9	265.6	327.7	262.5	232.9	263.0	374.8	263.2	236.5	265.7	212.9	178.3	303.5	263.0	0.9
202950_at	CRYZ	8.97E-03	324.5	387.1	330.0	389.2	260.5	257.9	300.8	299.4	288.9	234.8	364.8	178.1	195.7	230.5	324.5	234.8	0.7
208660_at	CS	8.96E-03	1325.9	1828.8	1647.1	1687.3	1722.8	2086.1	1952.2	1353.8	1435.1	1241.9	1382.9	1209.1	1280.7	1277.0	1722.8	1280.7	0.7
210340_s_at	CSF2RA	8.56E-03	379.1	262.8	449.5	519.1	468.0	444.6	385.6	372.6	215.8	261.5	342.0	367.6	346.4	279.2	444.6	342.0	0.8
212073_at	CSNK2A1 /// CSNK2A1P	5.69E-03	467.6	472.4	676.6	603.4	609.5	658.3	600.1	438.6	386.8	352.4	464.1	440.5	439.5	405.9	603.4	438.6	0.7
204736_s_at	CSPG4	3.37E-03	107.8	98.2	69.2	117.0	128.8	192.2	86.2	101.1	55.2	56.5	75.2	84.6	141.1	55.6	107.8	75.2	0.7
200621_at	CSRP1	2.09E-03	808.4	715.8	770.0	1007.8	839.5	812.5	778.9	714.8	459.3	394.9	677.1	639.2	596.8	478.0	808.4	596.8	0.7
201906_s_at	CTDSPL	7.01E-03	277.8	223.2	316.1	293.3	265.1	252.5	255.0	288.8	175.5	157.4	223.8	175.2	154.0	140.7	265.1	175.2	0.7
222819_at	CTPS2	8.31E-03	96.4	129.7	166.5	139.3	133.9	144.2	114.2	105.9	65.4	66.8	112.2	83.1	96.0	62.6	133.9	83.1	0.6
231234_at	CTSC	6.35E-03	106.9	174.5	219.5	172.7	205.8	223.5	234.9	103.9	108.1	99.2	161.1	73.1	74.4	92.5	205.8	99.2	0.5
1554569_a_at	CUGBP2	8.52E-03	73.3	80.3	83.3	132.5	112.8	121.5	100.4	79.3	63.0	54.5	101.6	74.6	68.7	58.9	100.4	68.7	0.7
202157_s_at	CUGBP2	3.11E-03	785.1	1009.5	780.0	945.5	996.1	1150.7	973.1	680.3	672.9	460.3	782.5	631.9	475.1	485.3	973.1	631.9	0.6
202158_s_at	CUGBP2	2.44E-03	709.9	840.6	841.5	906.4	894.1	1059.9	810.2	523.0	725.6	483.2	715.1	507.6	467.7	467.0	841.5	507.6	0.6
202156_s_at	CUGBP2	1.78E-03	275.5	314.1	294.8	335.9	334.5	382.3	273.4	242.5	177.3	157.3	243.0	249.3	180.7	165.0	314.1	180.7	0.6
227178_at	CUGBP2	1.70E-03	205.5	214.5	229.2	269.5	275.3	307.5	265.3	184.1	108.2	74.5	176.7	170.6	136.7	105.2	265.3	136.7	0.5
221488_s_at	CUTA	1.70E-03	1814.5	1778.7	1522.4	1589.2	1490.2	1637.7	1492.6	1295.9	1217.0	916.7	1046.1	1281.1	1311.9	1066.8	1589.2	1217.0	0.8
218970_s_at	CUTC	5.10E-03	416.8	440.9	593.5	487.9	589.2	654.9	520.4	407.9	323.3	318.0	416.0	339.7	387.2	265.2	520.4	339.7	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203917_at	CXADR	7.30E-03	55.7	190.2	43.8	53.8	355.4	92.5	70.8	49.1	112.4	37.4	48.7	231.7	67.5	44.6	70.8	49.1	0.7
212977_at	CXCR7	3.21E-03	1144.8	1612.0	991.7	1557.2	1215.4	1570.7	1696.7	938.1	1118.5	689.3	1187.0	1031.7	1306.9	1172.8	1557.2	1118.5	0.7
225216_at	CXorf39	3.29E-03	408.2	467.7	533.6	527.6	564.0	583.9	574.0	389.6	362.1	324.2	400.3	303.5	332.2	309.0	533.6	332.2	0.6
202263_at	CYB5R1	7.88E-03	682.0	707.5	918.6	776.7	776.9	774.5	690.1	734.9	509.8	505.1	548.3	559.0	562.6	373.4	774.5	548.3	0.7
223645_s_at	CYorf15B	4.49E-03	113.1	129.7	146.9	130.6	128.4	142.2	121.2	103.8	85.6	99.7	114.6	80.7	68.5	74.7	129.7	85.6	0.7
203979_at	CYP27A1	5.94E-03	7827.2	7151.4	7864.0	7699.0	7509.5	6896.1	7599.3	6146.6	5671.9	5390.6	5391.0	6638.4	6123.4	5682.4	7599.3	5682.4	0.7
226393_at	CYP2U1	6.73E-03	298.8	391.6	478.7	379.4	473.2	592.3	355.5	295.6	292.3	210.3	310.0	311.2	298.6	205.2	391.6	295.6	0.8
226402_at	CYP2U1	2.92E-03	96.2	96.9	128.4	116.3	135.3	170.6	110.7	86.2	76.9	48.7	72.1	75.2	69.0	42.4	116.3	72.1	0.6
228391_at	CYP4V2	5.10E-03	257.1	380.6	334.3	424.2	493.9	392.8	394.6	300.8	211.4	165.3	292.2	300.9	194.9	182.7	392.8	211.4	0.5
231747_at	CYSLTR1	2.38E-03	805.4	1273.7	1580.1	1236.5	1208.0	1794.2	968.7	814.5	694.3	471.5	774.5	586.6	673.3	406.2	1236.5	673.3	0.5
230866_at	CYSLTR1	3.01E-03	178.3	220.5	348.2	298.0	315.1	451.1	251.4	172.2	139.2	93.9	180.4	128.9	123.2	69.7	298.0	128.9	0.4
220813_at	CYSLTR2	8.93E-03	71.5	112.6	122.8	101.4	123.3	110.2	62.6	66.6	70.8	52.5	100.0	77.7	49.0	40.4	110.2	66.6	0.6
212480_at	CYTSA	9.63E-03	446.7	510.1	440.5	454.4	426.2	452.7	423.2	410.9	349.8	332.5	352.2	332.9	375.4	373.8	446.7	352.2	0.8
228738_at	D2HGDH	3.98E-03	769.2	1146.0	874.3	800.8	813.4	926.8	723.3	576.0	757.4	372.4	512.2	680.4	732.3	499.8	813.4	576.0	0.7
240873_x_at	DAB2	3.51E-03	1309.2	1103.1	1138.4	1389.3	1210.0	1108.5	1237.3	1047.0	907.9	788.1	1110.6	760.0	942.9	839.1	1210.0	907.9	0.8
210757_x_at	DAB2	3.78E-03	2227.9	1979.5	2120.4	2308.9	2107.3	2092.2	2520.8	1929.5	1563.6	1337.6	1692.5	1675.1	1576.4	1395.8	2120.4	1576.4	0.7
232898_at	DAB2	9.16E-03	179.9	148.7	206.8	258.0	227.9	227.2	230.2	198.9	98.7	148.7	202.7	126.9	157.0	131.2	227.2	148.7	0.7
201278_at	DAB2	7.88E-04	4332.6	3921.0	4136.4	4611.5	4402.0	4317.4	4680.9	3480.6	2808.3	1969.3	2983.9	2307.6	2787.9	2282.3	4332.6	2787.9	0.6
201280_s_at	DAB2	2.46E-03	960.6	878.0	1131.6	1490.2	1211.9	1237.1	1398.9	976.4	586.2	569.3	885.8	669.3	713.8	574.4	1211.9	669.3	0.6
226640_at	DAGLB	6.76E-03	183.3	156.5	146.5	208.6	172.9	175.9	155.5	155.4	95.3	84.2	151.6	146.7	143.0	130.6	172.9	143.0	0.8
218094_s_at	DBNDD2 /// SYS1 /// SYS1-DBNDD2	8.78E-04	650.9	626.7	838.8	795.7	803.6	845.6	820.3	560.0	436.1	428.2	515.5	488.9	506.3	403.6	803.6	488.9	0.6
224748_at	DCAF7	3.95E-03	777.5	797.4	1038.7	1176.9	793.0	1191.7	838.0	776.4	652.8	607.6	751.6	498.9	669.7	553.4	838.0	652.8	0.8
209592_s_at	DCAF7	2.80E-03	685.2	584.2	518.2	652.0	520.1	700.2	496.2	479.3	465.6	371.9	374.5	442.1	476.6	400.2	584.2	442.1	0.8
224730_at	DCAF7	6.81E-03	1540.1	1545.1	1717.6	1740.0	1393.4	2286.4	1556.2	1623.5	1134.2	1064.3	1335.3	863.4	1168.6	1073.0	1556.2	1134.2	0.7
221745_at	DCAF7	2.70E-03	290.4	232.8	300.9	319.9	214.1	375.1	237.2	259.5	178.6	186.4	235.0	166.9	215.6	148.2	290.4	186.4	0.6
202250_s_at	DCAF8	4.41E-03	348.6	424.3	439.3	384.7	419.5	470.7	402.8	352.9	272.1	212.6	294.0	292.6	289.1	217.3	419.5	289.1	0.7
216885_s_at	DCAF8	1.02E-03	378.0	428.1	416.0	428.1	400.2	427.4	372.4	323.2	306.2	233.7	308.9	268.4	281.7	233.6	416.0	281.7	0.7
219490_s_at	DCLRE1B	2.84E-03	556.6	551.4	593.8	561.0	729.7	607.9	564.5	454.6	404.3	355.3	493.2	431.5	447.9	313.1	564.5	431.5	0.8
203409_at	DDB2	5.58E-03	541.2	524.4	824.1	668.8	452.4	607.4	507.4	572.3	270.0	301.6	463.6	317.8	364.9	249.0	541.2	317.8	0.6
225886_at	DDX5	5.58E-03	836.0	1084.5	1055.1	982.6	905.1	975.8	1036.5	777.1	708.1	597.5	874.0	693.3	644.7	584.9	982.6	693.3	0.7
204909_at	DDX6	5.48E-04	3222.5	3035.6	3435.7	3680.9	3218.2	3863.1	3259.8	2432.8	2195.5	2142.3	2402.5	2388.6	2382.9	2379.4	3259.8	2382.9	0.7
221293_s_at	DEF6	8.87E-03	269.4	229.6	269.0	324.3	237.0	284.7	256.9	189.9	146.6	103.4	185.9	236.3	247.1	115.7	269.0	185.9	0.7
226659_at	DEF6	3.37E-03	308.1	345.3	395.6	450.7	385.0	576.8	349.7	235.0	174.2	100.9	309.5	291.5	300.4	138.8	385.0	235.0	0.6
225637_at	DEF8	9.75E-04	548.1	617.3	603.1	641.2	559.4	536.5	486.8	424.2	329.2	241.6	389.2	413.3	341.7	277.7	559.4	341.7	0.6
226867_at	DENND4C	1.67E-03	1086.5	1499.1	1664.2	2000.8	1734.1	1579.2	1980.9	967.0	1122.2	1045.2	1346.1	925.2	1034.1	1001.5	1664.2	1034.1	0.6
218102_at	DERA	8.21E-03	824.8	749.1	862.9	770.9	941.1	928.2	725.1	814.9	565.3	555.6	644.5	762.6	610.8	501.5	824.8	610.8	0.7
202534_x_at	DHFR	1.82E-03	150.2	138.8	292.1	188.7	148.6	124.8	214.5	115.9	109.1	122.9	137.5	61.9	52.7	84.3	150.2	109.1	0.7
48808_at	DHFR	3.98E-03	86.2	103.4	139.5	116.7	88.7	116.6	121.0	89.5	74.1	74.1	78.8	50.4	48.3	60.8	116.6	74.1	0.6
202481_at	DHRS3	8.32E-03	1019.1	1300.4	1407.3	970.2	840.2	1133.4	898.3	773.2	489.8	261.6	554.3	927.7	495.9	277.3	1019.1	495.9	0.5
229579_s_at	DISP2	8.85E-03	58.5	48.4	68.7	59.5	61.3	91.0	56.1	61.6	25.9	23.0	46.6	41.5	40.1	36.1	59.5	40.1	0.7
236079_at	DKFZp667E0512	6.84E-03	282.2	270.0	354.4	323.2	262.4	232.7	227.5	245.5	207.2	229.9	303.1	186.1	172.1	175.1	270.0	207.2	0.8
208216_at	DLX4	6.71E-03	154.5	221.6	193.4	259.9	176.9	213.6	189.9	162.0	153.7	86.7	168.1	135.5	129.4	84.5	193.4	135.5	0.7
202500_at	DNAJB2	7.37E-03	457.6	441.2	469.8	424.7	432.1	466.0	389.0	390.8	354.3	310.2	321.5	339.2	400.4	331.8	441.2	339.2	0.8
1554258_a_at	DNAJC5B	6.93E-03	591.2	564.0	616.4	356.4	476.7	641.4	391.2	557.0	402.1	296.8	277.9	403.4	395.0	237.3	564.0	395.0	0.7
232798_at	DNAJC5B	8.52E-03	707.8	813.2	913.7	555.8	606.9	939.0	649.0	742.2	553.6	485.5	398.4	468.7	504.9	249.4	707.8	485.5	0.7
213088_s_at	DNAJC9	6.38E-03	508.4	529.1	488.1	478.8	495.7	463.8	523.5	457.7	394.4	317.6	436.3	344.5	346.3	293.5	495.7	346.3	0.7
203912_s_at	DNASE1L1	8.01E-03	2165.7	1906.0	1680.5	1870.3	1650.5	1712.2	1467.8	1558.6	1436.6	962.8	1250.0	1391.2	1588.1	1235.3	1712.2	1391.2	0.8
220380_at	DNASE2B	2.46E-03	325.2	324.4	370.6	199.6	215.2	268.3	190.8	372.8	159.1	170.0	112.0	108.3	116.5	76.6	268.3	116.5	0.4
222640_at	DNMT3A	5.22E-03	984.3	899.9	1171.5	1130.5	809.2	955.7	880.8	831.4	752.0	717.6	887.9	607.1	721.3	728.6	955.7	728.6	0.8
218457_s_at	DNMT3A	1.02E-03	313.0	285.1	373.3	452.0	312.6	352.2	297.0	265.3	169.9	231.0	299.2	211.6	244.1	227.5	313.0	231.0	0.7
226875_at	DOCK11	1.58E-03	4307.7	5197.1	4362.5	4341.7	4340.2	4990.8	4571.2	3620.6	3616.0	1921.7	3228.4	2437.4	3177.8	2700.2	4362.5	3177.8	0.7
238356_at	DOCK11	7.96E-04	1463.8	1531.6	1221.1	1177.6	1292.4	1355.0	1290.1	1048.8	1086.2	569.4	864.8	720.1	957.5	761.3	1292.4	864.8	0.7
213160_at	DOCK2	7.45E-03	835.8	890.5	690.4	805.5	906.0	728.0	700.6	800.8	521.7	390.3	613.7	691.7	610.8	506.6	805.5	610.8	0.8
214054_at	DOK2	3.11E-03	1143.4	1126.2	1117.1	1225.1	1040.5	1345.1	1068.1	859.2	590.8	291.4	712.9	802.8	826.7	410.7	1126.2	712.9	0.6
223553_s_at	DOK3	9.61E-03	1128.5	1097.3	1283.5	1328.3	1100.5	1292.7	1307.9	1116.3	888.7	802.9	1073.5	787.4	1041.0	930.7	1283.5	930.7	0.7
205248_at	DOPEY2	9.97E-03	126.6	136.1	159.7	177.5	156.4	138.9	129.3	133.9	71.6	78.9	141.5	129.4	91.0	64.6	138.9	91.0	0.7
219452_at	DPEP2	1.11E-03	3948.3	3916.4	3750.5	3462.2	3618.0	4290.7	3224.9	2981.0	2465.7	1795.4	1970.4	3017.2	2789.6	2057.6	3750.5	2465.7	0.7
212792_at	DPY19L1	3.73E-03	551.0	500.1	567.5	559.5	623.1	556.5	411.0	488.9	397.5	292.6	437.5	395.3	402.1	268.4	556.5	397.5	0.7
226817_at	DSC2	1.85E-03	836.5	1021.0	1368.2	1308.4	1289.5	1642.1	1184.7	690.8	808.7	718.4	959.3	766.1	740.5	630.5	1289.5	740.5	0.6
229017_s_at	DSTYK	6.63E-03	215.2	283.7	358.5	354.3	325.8	395.4	301.8	240.3	165.9	169.7	273.0	214.8	233.8	172.3	325.8	214.8	0.7
223445_at	DTNBP1	3.06E-03	2040.9	1821.5	1918.2	2196.2	1957.5	1966.4	1902.2	1598.5	1594.1	1346.5	1670.9	1479.5	1552.1	1433.1	1957.5	1552.1	0.8
229984_at	DTWD1	9.81E-03	91.1	101.2	150.4	122.9	114.5	117.4	132.4	93.0	72.9	67.8	102.1	87.5	65.9	74.8	117.4	74.8	0.6
218845_at	DUSP22	8.52E-03	1629.1	1487.9	1439.1	1474.7	1354.4	1528.7	1572.4	1438.6	1280.3	1043.7	1126.3	1196.7	1179.3	1203.5	1487.9	1196.7	0.8
223402_at	DUSP23	5.88E-03	736.4	572.1	752.1	898.4	822.4	839.2	803.4	688.2	451.6	441.0	567.9	673.0	661.5	544.4	803.4	567.9	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
232252_at	DUSP27	7.45E-03	163.4	297.5	26.4	207.8	115.7	351.6	165.8	159.0	196.7	20.4	143.2	72.4	151.5	58.8	165.8	143.2	0.9
201536_at	DUSP3	1.11E-03	1015.9	960.9	1017.7	1087.1	973.5	979.2	946.3	880.5	688.8	564.7	667.0	709.1	640.2	564.6	979.2	667.0	0.7
208955_at	DUT	4.26E-03	180.3	191.0	164.5	170.1	167.5	173.9	140.7	158.1	135.3	131.2	141.4	130.8	106.5	97.7	170.1	131.2	0.8
57532_at	DVL2	5.37E-03	686.5	593.4	695.6	604.4	701.7	640.4	560.4	634.2	508.1	450.5	458.3	498.6	486.1	414.6	640.4	486.1	0.8
202971_s_at	DYRK2	6.41E-03	99.2	77.3	170.6	149.9	114.5	142.9	129.4	110.2	41.0	59.9	95.6	79.9	78.7	46.0	129.4	78.7	0.6
202968_s_at	DYRK2	4.87E-03	93.7	81.2	117.2	122.3	112.4	128.5	117.7	101.4	52.9	68.0	88.2	68.6	79.2	55.4	117.2	68.6	0.6
202969_at	DYRK2	3.05E-03	168.1	106.1	210.6	237.3	190.7	193.1	183.5	161.0	84.8	94.5	156.9	101.2	94.1	99.0	190.7	99.0	0.5
202970_at	DYRK2	3.18E-03	94.5	95.4	189.6	176.0	119.5	173.8	166.0	87.8	66.4	61.9	121.8	55.1	86.0	60.7	166.0	66.4	0.4
241713_s_at	DYX1C1	7.89E-03	270.2	303.3	245.7	297.2	291.9	385.2	284.6	313.2	125.9	65.7	212.9	189.1	181.9	102.7	291.9	181.9	0.6
235273_at	DYX1C1	5.85E-03	301.9	325.6	416.3	486.6	382.8	621.9	432.3	280.5	267.7	102.3	301.2	186.1	233.7	121.7	416.3	233.7	0.6
239785_at	DZIP1L	3.18E-03	232.0	246.9	257.4	230.6	204.1	291.2	233.9	198.9	174.9	161.0	200.2	144.0	179.9	120.2	233.9	174.9	0.7
228361_at	E2F2	2.86E-03	185.3	143.4	148.7	162.3	145.4	103.7	177.7	146.8	117.8	109.0	132.0	109.1	82.8	118.5	148.7	117.8	0.8
202735_at	EBP	1.99E-03	2071.7	1966.8	1324.3	1475.5	1521.7	1575.6	1436.4	1822.2	1172.6	625.4	955.7	1074.4	1177.1	922.3	1521.7	1074.4	0.7
213787_s_at	EBP	5.23E-03	951.1	826.1	611.2	695.4	637.3	687.2	699.9	771.6	429.6	300.9	452.8	547.6	602.0	444.4	695.4	452.8	0.7
200789_at	ECH1	4.57E-03	1737.2	1575.3	1760.7	1945.5	1290.9	1552.4	1563.9	1128.5	955.9	873.2	1202.7	1184.8	1438.9	922.3	1575.3	1128.5	0.7
219974_x_at	ECHDC1	2.12E-03	1038.9	1199.4	1508.4	1419.6	1280.8	1542.6	1271.7	821.0	988.2	972.7	1034.4	982.1	1031.3	1014.0	1280.8	988.2	0.8
223088_x_at	ECHDC1	3.23E-03	1860.7	1966.5	2078.0	2186.6	2175.7	2345.2	1939.5	1602.8	1579.3	1588.9	1663.1	1534.5	1642.8	1575.2	2078.0	1588.9	0.8
233124_s_at	ECHDC1	5.21E-03	1585.5	1810.7	1925.5	1971.9	1974.7	2094.8	1666.9	1434.7	1464.3	1392.2	1493.1	1461.9	1491.1	1412.1	1925.5	1461.9	0.8
223087_at	ECHDC1	5.51E-03	903.5	1245.5	1719.0	1372.0	1586.6	1881.6	1383.2	932.9	941.1	975.6	1063.5	853.8	886.7	770.4	1383.2	932.9	0.7
235305_s_at	ECHDC2	4.99E-03	139.1	137.7	175.7	165.6	147.3	158.7	145.7	128.6	90.0	141.1	115.4	121.6	120.9	93.9	147.3	120.9	0.8
218552_at	ECHDC2	3.71E-03	520.9	609.4	606.5	682.5	596.4	506.8	532.5	489.0	386.6	424.8	491.5	460.1	392.6	388.8	596.4	424.8	0.7
227780_s_at	ECSCR	8.68E-03	338.9	582.4	541.3	611.8	614.5	885.1	513.4	425.0	401.6	248.7	405.0	215.1	429.7	234.5	582.4	401.6	0.7
227779_at	ECSCR	1.74E-03	830.9	864.0	836.5	913.9	783.2	1229.3	711.0	778.5	571.2	336.8	589.2	428.3	702.8	357.3	836.5	571.2	0.7
228339_at	ECSCR	6.13E-03	320.9	454.3	482.5	533.3	537.7	809.0	471.1	385.5	273.3	194.0	364.2	211.5	379.9	150.0	482.5	273.3	0.6
233356_at	EEF1DP3	4.20E-03	61.7	61.7	52.8	51.0	64.2	67.4	46.3	47.5	42.6	38.1	25.9	54.7	49.8	37.1	61.7	42.6	0.7
205249_at	EGR2	1.57E-03	1740.4	1200.0	2688.7	2610.1	2366.5	2627.0	2215.1	1347.3	989.1	1120.3	1310.5	778.8	792.4	797.9	2366.5	989.1	0.4
208670_s_at	EID1	7.95E-03	4382.7	4551.7	4242.4	4776.1	4529.9	4826.1	4323.1	3814.8	3896.8	3266.6	4055.0	3401.0	3937.2	3395.7	4529.9	3814.8	0.8
217736_s_at	EIF2AK1	9.02E-03	559.0	564.2	632.7	663.2	608.3	712.5	633.7	555.2	418.3	461.7	549.7	467.9	564.5	444.3	632.7	467.9	0.7
218287_s_at	EIF2C1	7.55E-03	419.5	449.5	566.1	550.2	554.1	623.7	560.9	423.2	321.0	324.7	458.1	428.0	400.5	318.8	554.1	400.5	0.7
211937_at	EIF4B	4.32E-03	4302.0	4234.3	4406.3	4321.6	4728.4	5407.5	4839.4	3864.7	3402.0	3163.7	3253.0	3804.3	4206.6	3252.2	4406.3	3402.0	0.8
219599_at	EIF4B	1.83E-03	2046.5	2109.2	2912.9	2400.5	2850.3	3236.3	3409.4	1693.7	1705.2	1749.9	1782.4	2164.9	2184.0	2210.2	2850.3	1782.4	0.6
226734_at	EIF4E2	2.58E-03	571.8	656.6	513.4	582.4	552.6	620.0	543.5	498.6	496.0	351.8	487.0	390.0	445.5	362.4	571.8	445.5	0.8
221539_at	EIF4EBP1	7.27E-03	447.7	345.5	421.4	407.5	317.8	318.4	353.6	319.4	193.9	140.1	203.4	319.0	258.1	149.5	353.6	203.4	0.6
208770_s_at	EIF4EBP2	5.80E-03	1821.5	1964.8	2370.9	1870.0	2205.4	2630.7	2198.8	1683.1	1508.9	1386.1	1593.5	1659.1	1436.6	1220.1	2198.8	1508.9	0.7
208769_at	EIF4EBP2	5.19E-03	216.0	277.9	293.7	272.1	346.1	349.2	326.1	222.6	192.0	141.5	214.8	211.2	185.0	148.1	293.7	192.0	0.7
224645_at	EIF4EBP2	3.14E-03	1242.1	1458.0	1504.9	1406.2	1688.0	1519.4	1417.1	1264.8	857.6	582.0	983.7	990.4	772.9	595.4	1458.0	857.6	0.6
224653_at	EIF4EBP2	8.27E-04	732.4	632.9	716.9	768.7	894.8	880.8	701.7	626.4	387.5	306.1	492.1	553.0	429.1	332.3	732.4	429.1	0.6
201935_s_at	EIF4G3	1.76E-03	556.8	655.5	427.4	535.7	433.5	561.9	301.8	461.4	376.9	275.9	386.4	339.0	365.6	236.0	535.7	365.6	0.7
204513_s_at	ELMO1	2.19E-03	593.1	646.5	709.9	703.6	739.3	853.3	655.6	551.9	449.8	304.5	474.5	470.7	481.1	345.6	703.6	470.7	0.7
226502_at	ELMOD2	1.16E-03	337.4	343.9	447.1	446.0	406.7	471.9	440.5	277.1	221.0	233.6	354.5	258.1	243.2	221.3	440.5	243.2	0.6
227075_at	ELP3	3.23E-03	1270.0	1391.4	1446.9	1393.1	1412.1	1363.9	1231.9	1171.5	936.4	703.5	1145.5	900.8	889.5	713.8	1391.4	900.8	0.6
65635_at	ENGASE	1.32E-03	505.8	527.1	429.3	288.3	310.8	477.1	346.6	402.9	334.9	228.4	182.1	244.5	278.0	266.2	429.3	266.2	0.6
220349_s_at	ENGASE	2.92E-03	588.3	622.8	587.9	361.4	386.5	671.2	436.3	526.3	355.9	285.3	224.1	344.9	340.4	243.0	587.9	340.4	0.6
204143_s_at	ENOSF1	5.40E-04	883.0	1451.4	1705.1	1399.7	965.9	867.8	1091.5	688.2	896.5	806.6	878.0	706.2	466.6	634.3	1091.5	706.2	0.6
204142_at	ENOSF1	2.04E-03	541.9	968.2	1209.4	1004.6	706.9	591.8	959.5	541.9	691.7	656.0	630.0	395.3	332.9	521.0	959.5	541.9	0.6
213645_at	ENOSF1	6.54E-04	342.1	435.3	942.4	704.3	657.3	668.6	480.0	293.1	226.1	371.8	421.4	327.3	279.0	167.1	657.3	293.1	0.4
209473_at	ENTPD1	7.17E-03	365.7	424.8	395.7	506.8	446.7	479.4	440.2	353.1	268.1	188.0	472.7	309.3	268.4	263.3	440.2	268.4	0.6
200878_at	EPAS1	2.09E-03	2390.7	2709.5	2865.2	3045.8	3221.2	3018.6	2949.7	2443.4	1582.7	1390.7	2083.1	1745.6	1648.6	1386.6	2949.7	1648.6	0.6
222066_at	EPB41L1	1.91E-03	143.5	158.3	120.7	124.0	144.7	130.8	129.9	100.7	96.7	65.1	97.4	101.8	110.2	94.8	130.8	97.4	0.7
212339_at	EPB41L1	2.67E-04	693.8	695.1	540.6	592.7	625.7	579.7	543.6	481.9	389.2	226.9	386.7	315.2	356.2	226.5	592.7	356.2	0.6
228259_s_at	EPB41L4A	5.61E-03	531.2	563.8	584.7	805.0	547.9	893.0	516.4	495.4	451.2	388.8	691.1	392.2	536.5	336.5	563.8	451.2	0.8
203463_s_at	EPN2	7.85E-03	124.1	125.3	131.0	121.9	138.7	147.5	138.9	104.0	115.0	92.3	85.6	109.5	94.0	119.8	131.0	104.0	0.8
203464_s_at	EPN2	1.94E-03	89.1	76.7	93.0	82.4	77.3	88.1	101.8	66.6	60.5	42.5	56.4	53.5	65.8	58.4	88.1	58.4	0.7
200843_s_at	EPRS	6.13E-03	1111.7	1064.9	977.0	1042.5	907.2	1003.5	1004.7	962.7	624.0	485.2	809.3	752.4	807.7	687.5	1004.7	752.4	0.7
200842_s_at	EPRS	5.68E-03	1275.2	1235.7	1051.7	1206.8	991.6	1155.9	1100.0	1162.1	881.2	592.6	936.8	847.4	861.3	680.3	1155.9	861.3	0.7
91826_at	EPS8L1	4.74E-03	640.5	640.8	511.5	673.2	581.7	573.1	438.5	472.2	577.6	379.2	369.3	435.6	447.8	334.0	581.7	435.6	0.7
218779_x_at	EPS8L1	7.40E-03	390.9	403.0	325.5	415.1	344.2	347.8	280.5	289.8	336.4	250.7	255.2	246.6	293.4	257.0	347.8	257.0	0.7
221665_s_at	EPS8L1	6.86E-03	378.6	391.1	309.2	358.9	325.1	317.7	241.0	263.4	328.5	237.2	228.1	231.4	271.4	220.2	325.1	237.2	0.7
240172_at	ERGIC2	9.51E-03	181.4	240.5	274.4	237.2	315.7	292.5	286.5	221.3	122.5	143.9	191.0	197.6	152.3	135.3	274.4	152.3	0.6
213365_at	ERI2	9.84E-03	198.7	213.4	359.3	248.0	269.1	355.0	285.4	195.0	167.3	207.0	221.4	158.9	156.6	118.6	269.1	167.3	0.6
202444_s_at	ERLIN1	3.93E-03	443.4	530.0	591.3	591.1	550.1	676.0	516.3	420.0	412.9	301.4	439.3	388.6	394.7	304.9	550.1	394.7	0.7
202441_at	ERLIN1	1.27E-03	1321.6	1516.9	1527.1	1820.0	1675.0	1864.7	1639.7	1171.3	1058.1	743.3	1154.6	1073.8	966.3	760.4	1639.7	1058.1	0.6
218342_s_at	ERMP1	8.92E-04	938.5	1131.8	927.1	899.3	960.5	879.1	980.6	734.5	742.6	459.5	715.7	614.2	500.5	590.1	938.5	614.2	0.7
222603_at	ERMP1	7.04E-03	545.5	676.7	698.6	740.5	751.6	691.7	722.2	597.8	518.5	364.8	562.7	394.6	387.2	368.2	698.6	394.6	0.6
201216_at	ERP29	7.29E-03	2774.2	2995.1	3216.6	3053.7	2845.3	3036.4	2694.5	2596.9	2299.8	2394.4	2537.2	2299.1	2301.5	2085.7	2995.1	2301.5	0.8
208858_s_at	ESYT1	3.65E-03	5504.2	5716.6	5019.9	5695.5	4848.0	5299.9	5382.8	4764.6	4273.3	3690.2	4690.2	3555.9	4316.2	4036.7	5382.8	4273.3	0.8

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
204774_at	EVI2A	1.76E-03	912.7	1293.2	1361.7	1402.5	1526.0	1541.1	1404.0	876.6	836.6	532.9	786.0	806.0	564.7	539.1	1402.5	786.0	0.6
211742_s_at	EVI2B	3.84E-03	2220.5	2626.0	3554.3	3005.3	3233.4	4191.3	3202.5	2219.4	1794.6	1191.3	1849.9	1890.5	1588.0	1141.0	3202.5	1794.6	0.6
208297_s_at	EVI5	7.92E-03	582.9	705.8	852.5	885.3	903.7	1037.6	862.5	575.4	551.6	562.1	741.7	627.3	783.4	511.4	862.5	575.4	0.7
209537_at	EXTL2	4.47E-03	88.5	146.4	222.6	143.0	150.1	199.5	108.2	88.0	96.1	53.6	99.9	54.1	70.1	33.1	146.4	70.1	0.5
235978_at	FABP4	4.99E-03	662.6	935.4	1011.9	955.5	623.9	441.5	1089.4	660.7	594.3	598.1	750.9	478.6	306.7	657.5	935.4	598.1	0.6
208962_s_at	FADS1	8.59E-04	821.5	464.6	399.7	273.2	501.7	387.4	563.4	615.4	236.0	197.4	215.6	252.7	274.6	294.7	464.6	252.7	0.5
208964_s_at	FADS1	4.30E-03	683.0	462.5	346.1	243.9	529.7	375.4	529.2	668.6	187.4	180.3	208.4	248.8	229.3	286.5	462.5	229.3	0.5
218080_x_at	FAF1	3.10E-03	1388.1	1460.5	1291.6	1381.6	1343.3	1208.9	1217.8	1162.6	993.4	713.4	874.7	933.7	1111.2	779.3	1343.3	933.7	0.7
224217_s_at	FAF1	1.89E-03	733.4	687.2	746.3	762.3	717.8	729.8	717.7	628.9	479.7	446.7	550.2	480.5	597.2	426.0	729.8	480.5	0.7
244650_at	FAM105A	1.58E-03	726.4	592.1	700.9	637.0	518.6	752.1	501.8	533.0	335.6	202.9	431.2	341.4	392.4	214.3	637.0	341.4	0.5
223058_at	FAM107B	8.57E-03	1800.8	1907.0	1699.8	1558.2	1790.5	1651.2	1943.5	1417.9	1422.8	1217.4	1409.5	1204.0	1571.8	1254.2	1790.5	1409.5	0.8
1553220_at	FAM117B	6.50E-03	65.5	74.6	137.7	99.9	130.7	105.1	74.7	69.6	51.0	48.1	69.6	56.7	24.7	27.8	99.9	51.0	0.5
223386_at	FAM118B	2.98E-03	1402.5	1507.1	1296.1	1525.0	1187.1	1590.9	1097.0	1256.2	1129.5	602.1	1134.2	762.0	1056.1	687.5	1402.5	1056.1	0.8
222129_at	FAM134A	1.71E-03	957.8	904.6	1249.5	1185.4	1255.7	1449.8	1226.6	816.4	649.8	786.6	942.2	674.6	782.0	793.1	1226.6	786.6	0.6
215947_s_at	FAM136A	8.90E-03	450.0	467.2	523.0	600.6	460.8	471.6	470.7	427.8	377.5	456.4	442.5	359.2	342.4	330.6	470.7	377.5	0.8
223203_at	FAM156A /// FAM156B	2.15E-03	944.9	1008.8	1136.0	934.5	877.1	1129.0	828.1	735.1	592.1	333.4	552.8	649.5	584.4	433.6	944.9	584.4	0.6
205308_at	FAM164A	3.67E-03	277.3	246.4	284.8	269.4	345.8	346.5	237.5	286.0	158.6	153.4	195.7	236.7	211.5	149.3	277.3	195.7	0.7
241808_at	FAM164A	5.44E-03	70.7	88.0	127.4	96.7	128.1	145.3	119.2	65.1	74.0	51.4	67.3	50.6	40.3	44.4	119.2	51.4	0.4
228239_at	FAM165B	7.99E-04	496.0	652.9	524.3	411.9	461.8	568.3	443.6	414.8	401.1	249.5	273.7	323.4	301.4	247.2	496.0	301.4	0.6
203482_at	FAM178A	1.06E-03	987.8	943.0	888.4	923.9	836.0	870.3	733.9	794.7	572.4	341.2	619.0	545.7	507.6	385.0	888.4	545.7	0.6
217896_s_at	FAM192A	8.97E-03	313.4	303.2	360.0	350.1	374.3	413.3	309.7	339.2	219.5	252.4	280.3	253.2	261.0	213.5	350.1	253.2	0.7
227194_at	FAM3B	5.49E-03	1561.6	3380.3	1484.5	3615.6	2427.2	2338.8	1501.9	1417.8	2757.3	1035.9	3061.0	1824.9	1721.5	969.4	2338.8	1721.5	0.7
203206_at	FAM53B	1.55E-03	244.1	183.4	239.0	230.7	233.3	261.7	213.2	170.6	143.8	94.9	165.2	149.6	144.4	94.1	233.3	144.4	0.6
228069_at	FAM54A	6.35E-03	122.0	135.4	189.8	200.4	176.3	256.7	162.0	128.4	102.6	81.1	150.0	71.1	105.8	56.7	176.3	102.6	0.6
45749_at	FAM65A	4.68E-03	427.6	348.2	411.5	439.1	381.4	373.1	389.8	321.0	250.4	267.8	288.7	334.0	346.0	251.6	389.8	288.7	0.7
218126_at	FAM82A2	4.37E-03	2641.5	2492.9	2026.4	1867.2	2164.8	1899.3	1914.5	2200.4	1899.3	1561.2	1642.4	1744.7	1391.3	1350.0	2026.4	1642.4	0.8
222665_at	FAM82B	4.01E-03	235.4	244.0	224.0	246.3	260.0	266.0	248.6	199.3	140.5	99.5	184.0	225.2	174.6	128.4	246.3	174.6	0.7
226448_at	FAM89A	1.87E-03	2640.4	2689.3	2926.0	3230.6	2741.8	3420.4	3623.7	2153.8	2287.6	2003.8	2297.2	1502.1	2239.7	2115.5	2926.0	2153.8	0.7
224779_s_at	FAM96A	1.45E-03	2063.0	2242.5	2593.1	2662.5	2350.5	2559.8	2525.4	1643.9	1806.1	1656.0	1960.3	1548.2	1426.8	1322.6	2525.4	1643.9	0.7
220255_at	FANCE	2.34E-03	215.7	127.8	131.4	132.4	132.0	124.4	121.6	142.8	79.2	87.8	83.1	95.4	106.1	106.2	131.4	95.4	0.7
201910_at	FARP1	4.03E-03	911.6	867.1	573.8	756.0	664.8	529.5	499.5	751.9	478.2	345.5	519.2	526.7	450.6	386.3	664.8	478.2	0.7
209696_at	FBP1	7.26E-04	4757.5	4468.2	3759.0	4369.1	3455.9	3873.2	3233.5	3855.9	3193.9	1983.6	3016.4	2224.4	2631.3	2006.6	3873.2	2631.3	0.7
225704_at	FBRSL1	9.10E-03	110.5	75.0	129.6	133.1	139.5	130.5	121.1	109.4	61.1	65.3	108.8	103.6	68.8	66.3	129.6	68.8	0.5
227500_at	FBXL18	7.50E-03	140.7	138.0	123.3	160.3	171.5	132.2	151.6	117.8	71.0	94.6	122.2	103.2	126.8	99.0	140.7	103.2	0.7
235089_at	FBXL20	4.50E-03	158.9	218.0	285.3	255.6	237.6	275.4	182.9	173.2	130.3	163.9	182.6	160.0	156.2	93.2	237.6	160.0	0.7
1558062_at	FBXO10	4.91E-03	186.4	178.2	175.3	209.7	176.1	190.9	207.6	188.2	74.1	73.6	153.0	108.8	131.7	81.2	186.4	108.8	0.6
227222_at	FBXO10	1.89E-03	133.3	129.2	184.2	214.0	192.0	209.0	169.5	123.3	102.6	99.9	126.5	103.9	118.0	79.8	184.2	103.9	0.6
44040_at	FBXO41	1.21E-03	178.3	217.5	230.2	257.4	191.0	201.9	195.8	144.0	167.6	144.4	188.2	125.9	144.4	148.7	201.9	144.4	0.7
208647_at	FDFT1	2.30E-03	6814.7	7694.5	4865.1	5411.7	6394.6	5781.5	6058.0	5930.4	5668.7	2816.6	4375.6	4104.4	4177.7	4099.3	6058.0	4177.7	0.7
210950_s_at	FDFT1	1.49E-03	3000.6	3171.4	1549.7	1629.8	2473.3	1932.5	1965.5	2482.6	1767.9	742.6	1296.2	1522.4	1305.6	1273.3	1965.5	1305.6	0.7
207813_s_at	FDXR	3.38E-03	366.1	360.1	504.5	375.9	347.4	412.9	394.3	293.2	231.3	163.0	267.3	233.3	274.0	188.4	375.9	233.3	0.6
203115_at	FECH	5.62E-03	287.4	300.4	465.1	339.6	376.2	624.5	352.1	262.5	236.0	333.5	274.9	292.7	348.2	213.0	352.1	274.9	0.8
205418_at	FES	9.10E-03	144.2	130.5	243.1	197.2	164.1	167.1	155.1	127.0	69.1	77.6	108.4	158.4	117.8	84.9	164.1	108.4	0.7
226985_at	FGD5	4.16E-03	847.0	911.6	903.5	1039.1	980.8	914.3	978.1	803.9	678.5	507.9	809.0	624.5	693.7	584.9	914.3	678.5	0.7
201540_at	FHL1	4.17E-04	2934.1	3566.6	3746.8	3258.9	3255.7	4302.3	3046.6	2230.7	2296.8	1466.6	1970.2	1535.9	1987.9	1232.2	3258.9	1970.2	0.6
210298_x_at	FHL1	3.41E-04	406.3	428.6	309.2	308.6	273.4	332.8	255.9	287.9	247.7	119.8	171.3	182.3	196.4	121.6	309.2	182.3	0.6
210299_s_at	FHL1	1.29E-03	450.7	564.0	482.1	491.6	506.1	623.2	439.0	418.4	312.2	163.1	288.6	229.6	322.1	159.4	491.6	288.6	0.6
201539_s_at	FHL1	9.83E-04	296.5	281.7	306.9	295.5	288.4	335.1	253.6	255.8	162.1	127.4	171.3	196.9	198.0	123.3	295.5	171.3	0.6
214505_s_at	FHL1	2.55E-04	638.1	590.4	494.0	514.1	441.1	535.6	409.9	395.4	351.1	176.3	273.5	283.3	322.3	210.2	514.1	283.3	0.6
203656_at	FIG4	1.08E-03	1247.6	1496.0	1544.8	1264.3	1489.3	1538.2	1204.2	1011.1	847.0	486.7	770.6	891.6	715.2	459.9	1489.3	770.6	0.5
200894_s_at	FKBP4	1.64E-03	568.3	477.3	778.3	624.3	505.5	573.0	543.4	397.8	383.3	452.7	351.7	400.5	384.1	421.2	568.3	397.8	0.7
200895_s_at	FKBP4	5.70E-04	1199.6	1223.1	1492.4	1064.7	1121.9	1191.1	1077.6	933.3	832.1	874.6	731.6	834.7	721.4	749.2	1191.1	832.1	0.7
212169_at	FKBP9	1.06E-03	1297.9	1620.3	1428.9	1262.6	1379.0	1291.1	1264.1	1006.5	1076.7	675.3	967.5	919.9	859.8	725.0	1297.9	919.9	0.7
204236_at	FLI1	1.34E-03	638.5	726.6	813.4	853.7	772.0	950.3	707.9	535.3	465.4	250.1	521.2	384.1	377.7	350.0	772.0	384.1	0.5
223845_at	FLJ20674	4.13E-03	82.2	56.9	65.8	60.0	57.1	60.1	58.7	53.3	50.8	36.7	34.6	45.1	44.0	48.4	60.0	45.1	0.8
1553991_s_at	FLJ20674	6.89E-04	381.2	329.8	488.0	346.8	329.4	391.4	305.6	286.8	236.0	174.4	199.9	166.9	181.8	166.6	346.8	181.8	0.5
1564208_x_at	FLJ35390	4.22E-03	164.5	223.3	205.1	177.9	151.4	175.8	132.4	142.0	147.7	84.6	141.0	109.7	115.9	83.3	175.8	115.9	0.7
1564207_at	FLJ35390	8.53E-03	217.3	317.1	286.2	235.5	187.4	258.9	153.5	182.7	245.8	91.3	179.8	131.8	114.5	102.3	235.5	131.8	0.6
1558148_x_at	FLJ90757	2.68E-03	156.4	163.7	127.2	151.8	145.6	132.4	115.8	131.2	121.7	95.0	104.9	113.1	84.6	96.4	145.6	104.9	0.7
1566558_x_at	FLJ90757	8.37E-03	173.7	203.4	225.5	206.7	173.4	193.9	156.0	176.8	110.1	78.6	141.6	142.5	92.2	99.7	193.9	110.1	0.6
1566557_at	FLJ90757	2.99E-03	187.0	175.2	238.7	209.0	208.3	216.8	165.9	178.1	106.8	75.0	134.7	128.6	90.3	78.6	208.3	106.8	0.5
219316_s_at	FLVCR2	8.64E-03	1001.8	1073.8	1394.4	1547.1	1408.0	1852.5	1498.4	983.0	983.2	839.6	1206.8	849.2	1102.4	1020.3	1408.0	983.2	0.7
212464_s_at	FN1	6.90E-03	6589.2	5001.7	5557.5	8026.7	2097.5	2408.6	5245.4	4504.1	2714.4	4472.2	6479.6	1070.8	2094.1	4320.1	5245.4	4320.1	0.8
204437_s_at	FOLR1	7.28E-03	383.4	343.0	765.8	477.5	307.7	395.0	320.6	374.4	270.0	464.8	335.4	246.8	310.1	225.1	383.4	310.1	0.8
206371_at	FOLR3	3.04E-03	686.2	2487.3	785.1	917.4	815.3	788.2	723.9	618.9	1740.5	231.9	479.4	477.1	451.4	271.4	788.2	477.1	0.6

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
231407_s_at	FOXH1	8.61E-03	159.8	162.5	169.4	123.2	144.7	157.7	129.9	140.3	96.9	94.0	95.4	121.7	139.4	93.4	157.7	96.9	0.6
202724_s_at	FOXO1	1.10E-03	459.9	721.5	524.1	527.0	613.5	559.2	404.5	361.7	312.8	225.7	386.9	421.0	246.0	171.0	527.0	312.8	0.6
219889_at	FRAT1	4.15E-03	145.2	138.1	174.6	172.4	154.6	189.9	137.4	144.1	64.6	47.2	88.1	118.3	91.5	63.1	154.6	88.1	0.6
209864_at	FRAT2	7.82E-03	475.2	332.9	536.3	478.0	431.0	472.9	395.6	387.9	240.3	126.7	308.6	290.6	297.0	195.2	472.9	290.6	0.6
225167_at	FRMD4A	2.93E-03	2233.4	2328.1	1792.4	2000.8	1789.5	2128.6	1773.7	1915.4	1410.8	947.9	1527.5	1448.2	1529.2	963.9	2000.8	1448.2	0.7
225163_at	FRMD4A	2.02E-03	1069.4	1391.8	1015.6	1166.7	1224.8	1226.1	1147.7	886.1	803.1	488.4	970.8	646.8	778.3	463.2	1166.7	778.3	0.7
225168_at	FRMD4A	1.07E-03	1065.3	1086.5	903.5	1052.0	1034.9	1052.1	885.8	892.6	663.3	501.8	833.1	673.7	693.7	502.8	1052.0	673.7	0.6
204072_s_at	FRY	3.78E-03	115.5	151.4	196.3	240.3	269.9	330.1	217.7	126.9	77.8	110.0	169.1	116.7	128.2	85.2	217.7	116.7	0.5
228410_at	GAB3	3.63E-03	367.4	446.7	415.3	409.2	437.8	456.3	349.3	336.4	302.3	278.8	348.1	328.0	321.1	240.0	415.3	321.1	0.8
208868_s_at	GABARAPL1	1.53E-03	863.2	969.0	721.2	960.3	875.1	1094.5	694.9	746.3	740.5	520.0	675.9	574.1	626.4	460.8	875.1	626.4	0.7
208869_s_at	GABARAPL1	2.07E-03	653.7	816.2	629.9	788.9	754.5	925.4	649.3	587.5	570.8	350.2	615.6	462.1	469.6	327.8	754.5	469.6	0.6
211458_s_at	GABARAPL1 /// GABARAPL3	5.16E-03	8273.3	10129.2	7894.7	9349.6	9531.1	10365.5	7677.2	7976.7	7952.0	5151.1	7794.0	6408.4	6553.6	4576.5	9349.6	6553.6	0.7
211810_s_at	GALC	5.77E-03	720.8	975.7	1102.0	856.3	1330.7	1167.1	1181.5	683.0	726.9	540.6	704.5	926.5	796.1	732.3	1102.0	726.9	0.7
204417_at	GALC	1.42E-03	712.9	862.8	1187.3	909.9	1239.7	1089.6	1326.3	638.3	575.0	640.0	637.6	822.2	682.4	659.4	1089.6	640.0	0.6
234974_at	GALM	3.71E-03	209.1	252.7	205.8	172.3	166.9	106.2	128.2	165.0	167.6	123.0	148.6	110.5	72.0	113.3	172.3	123.0	0.7
212256_at	GALNT10	7.93E-03	243.0	343.4	262.0	299.4	280.8	301.5	265.4	240.4	193.1	159.0	273.1	194.5	220.2	156.0	280.8	194.5	0.7
204457_s_at	GAS1	6.09E-03	48.8	72.1	86.5	61.4	64.8	45.5	36.5	39.3	42.0	26.3	46.2	25.3	16.5	32.0	61.4	32.0	0.5
235709_at	GAS2L3	1.53E-03	679.5	574.6	473.7	530.2	536.8	480.8	435.8	523.4	411.2	297.6	304.8	405.9	360.8	207.5	530.2	360.8	0.7
238756_at	GAS2L3	3.66E-03	390.6	321.7	523.1	486.2	521.2	518.0	533.3	275.4	260.6	372.3	359.5	221.6	227.1	179.9	518.0	260.6	0.5
225393_at	GATAD2B	8.83E-03	311.1	433.3	544.5	505.1	478.8	628.2	450.6	320.6	299.3	338.2	459.5	318.0	345.4	289.4	478.8	320.6	0.7
204867_at	GCHFR	8.89E-03	785.4	503.4	644.9	543.2	438.6	465.2	573.0	386.5	231.8	215.9	231.7	485.3	456.4	196.2	543.2	231.8	0.4
226214_at	GDE1	6.66E-03	893.5	1224.2	976.0	864.2	921.9	1047.1	745.7	912.0	762.3	402.7	671.2	672.3	634.4	387.4	921.9	671.2	0.7
202593_s_at	GDE1	3.98E-03	1100.8	1206.2	1127.8	991.9	941.4	1027.5	861.6	1015.3	793.3	497.4	747.3	712.0	642.1	510.1	1027.5	712.0	0.7
219821_s_at	GFOD1	7.59E-03	130.0	125.4	177.0	163.7	164.9	187.8	194.9	129.4	90.2	83.0	121.5	122.1	124.7	85.1	164.9	121.5	0.7
210658_s_at	GGA2	7.55E-03	2017.0	2574.1	2180.3	2058.3	2017.6	2483.4	2046.1	2026.3	1683.8	1023.5	1718.2	1381.5	1785.0	1126.7	2058.3	1683.8	0.8
213772_s_at	GGA2	3.23E-03	3563.3	4963.6	4117.6	3816.8	3430.3	4636.4	3730.4	3059.4	3219.0	1785.0	3110.6	2410.2	2997.2	1948.7	3816.8	2997.2	0.8
208913_at	GGA2	4.65E-03	4050.0	4959.1	4726.3	4609.4	4164.4	5505.4	4882.0	3557.8	3941.1	2265.5	3888.6	2699.0	3585.4	2761.2	4726.3	3557.8	0.8
214190_x_at	GGA2	1.02E-03	1562.2	1710.5	1453.6	1468.4	1289.0	1706.1	1375.6	1226.0	1030.9	583.7	1027.5	840.7	1074.5	726.8	1468.4	1027.5	0.7
208915_s_at	GGA2	9.62E-04	1029.7	1016.7	912.6	939.1	728.0	1054.6	841.8	681.6	542.8	337.7	614.8	551.1	690.1	433.3	939.1	551.1	0.6
208914_at	GGA2	9.01E-04	1627.3	1900.0	1598.3	1816.3	1506.9	1880.4	1650.4	1216.4	958.6	415.7	1097.6	755.8	1013.1	640.1	1650.4	958.6	0.6
228376_at	GGTA1	1.72E-03	820.0	1189.7	1614.8	1460.2	1840.0	1977.0	1324.5	766.4	748.5	691.0	932.1	1164.2	1004.4	569.9	1460.2	766.4	0.5
1552316_a_at	GIMAP1	6.78E-03	890.7	1248.9	1366.9	1379.3	1289.5	1339.7	838.9	851.0	663.3	280.9	964.2	799.7	583.4	395.7	1289.5	663.3	0.5
229367_s_at	GIMAP6	8.56E-03	288.0	241.3	261.9	322.7	289.1	233.1	184.3	303.6	133.3	90.3	273.4	170.4	145.8	95.1	261.9	145.8	0.6
219777_at	GIMAP6	4.34E-03	142.1	137.0	157.7	202.6	148.9	157.2	121.8	128.5	102.8	48.0	143.6	78.8	78.5	59.5	148.9	78.8	0.5
213552_at	GLCE	8.30E-03	285.7	545.3	582.3	449.4	470.6	730.5	456.5	355.1	287.0	139.8	315.2	240.6	265.6	170.8	470.6	265.6	0.6
225918_at	GLG1	9.37E-03	486.0	364.9	448.9	592.1	574.2	528.1	630.8	492.9	237.9	273.1	451.0	501.9	391.8	380.4	528.1	391.8	0.7
225602_at	GLIPR2	6.74E-03	2815.7	2838.4	2258.6	2282.6	2275.4	2519.2	2089.7	2372.4	2038.2	1430.8	1808.7	1765.5	2345.8	1570.0	2282.6	1808.7	0.8
209276_s_at	GLRX	4.99E-03	4559.2	4390.8	4009.7	4667.8	4343.0	4375.7	4369.8	4686.9	3151.4	2621.5	3234.2	3130.7	3252.7	2916.6	4375.7	3151.4	0.7
218473_s_at	GLT25D1	6.22E-03	828.1	771.4	845.4	1016.3	747.3	790.6	908.8	781.6	457.0	554.6	724.1	624.4	658.5	578.2	828.1	624.4	0.8
217202_s_at	GLUL	9.61E-03	3897.8	4441.3	3390.6	4303.1	2844.7	3522.5	2456.0	2695.6	2617.3	1434.7	3053.1	3102.6	2693.1	1456.0	3522.5	2693.1	0.8
200648_s_at	GLUL	4.97E-03	7349.9	7389.1	5622.0	7583.5	5506.1	6380.2	4357.7	5755.8	4674.5	2592.9	5558.1	5171.4	4451.5	2863.4	6380.2	4674.5	0.7
235678_at	GM2A	3.97E-03	822.9	883.4	784.8	752.9	776.4	541.3	778.7	656.1	768.3	563.0	640.0	586.9	377.8	583.7	778.7	586.9	0.8
217990_at	GMPR2	5.99E-03	496.3	556.5	727.0	621.2	666.7	846.6	701.3	477.0	429.2	428.6	509.8	474.9	485.6	350.2	666.7	474.9	0.7
224863_at	GNAQ	2.50E-03	1552.4	1668.7	1807.3	1827.8	1927.4	2057.6	2154.0	1409.5	1340.4	1065.3	1338.6	1116.1	1337.6	1187.0	1827.8	1337.6	0.7
202615_at	GNAQ	1.08E-03	1034.7	1112.5	1533.4	1468.4	1519.9	1640.0	1381.9	874.8	788.2	795.0	1070.2	902.8	879.8	882.1	1468.4	879.8	0.6
224861_at	GNAQ	4.42E-03	169.2	131.8	270.7	275.0	322.7	333.0	242.5	174.2	103.0	125.8	190.9	164.1	158.5	114.7	270.7	158.5	0.6
235139_at	GNGT2	1.57E-03	148.2	139.5	174.8	180.6	129.5	221.1	126.8	103.6	95.0	93.3	136.0	113.5	145.5	75.4	148.2	103.6	0.7
208798_x_at	GOLGA8A	8.16E-03	294.6	673.5	774.2	382.6	604.1	423.1	374.7	322.5	421.8	559.7	307.6	360.3	280.8	214.5	423.1	322.5	0.8
201056_at	GOLGB1	9.54E-03	114.7	146.5	118.9	127.5	132.1	136.6	118.2	112.7	122.0	98.7	81.0	93.4	85.8	91.9	127.5	93.4	0.7
204324_s_at	GOLIM4	7.94E-04	5130.6	4630.7	4723.3	5090.4	4321.5	4074.7	3743.0	3851.7	3436.5	2282.1	3295.8	2830.4	2897.1	2269.8	4630.7	2897.1	0.6
218361_at	GOLPH3L	6.53E-03	495.3	753.8	795.2	657.3	778.9	778.7	736.5	489.5	618.4	378.5	536.0	413.1	411.5	358.6	753.8	413.1	0.5
200708_at	GOT2	3.48E-03	610.9	611.9	708.1	639.6	667.1	609.7	608.8	517.6	512.9	498.8	534.1	424.5	445.1	411.8	611.9	498.8	0.8
205929_at	GPA33	1.02E-03	592.6	796.6	184.4	706.7	409.4	1091.7	378.3	522.0	462.5	62.4	397.2	194.1	449.4	122.6	592.6	397.2	0.7
225420_at	GPAM	3.23E-03	95.8	114.0	167.6	177.1	152.5	173.5	164.9	94.3	74.5	90.8	126.4	74.9	114.5	71.4	164.9	90.8	0.6
1552501_a_at	GPBAR1	1.17E-03	123.0	135.2	143.5	191.9	171.2	158.3	149.9	72.9	96.8	85.8	128.3	152.0	109.6	83.0	149.9	96.8	0.6
204997_at	GPD1	1.22E-03	564.3	499.5	587.3	468.8	383.0	525.9	465.2	408.8	330.5	288.2	280.0	290.8	419.7	246.1	499.5	290.8	0.6
213706_at	GPD1	4.57E-04	814.5	1157.0	1027.1	833.2	768.8	1158.0	882.4	636.1	581.7	384.4	493.2	318.9	662.5	316.9	882.4	493.2	0.6
1563035_x_at	GPD1	2.95E-04	517.3	629.9	572.6	401.6	287.3	589.5	342.1	308.5	210.7	106.0	218.1	114.3	190.4	139.5	517.3	190.4	0.4
1563034_at	GPD1	1.21E-03	617.0	752.5	671.3	446.3	325.5	668.8	395.2	387.4	263.7	80.9	257.5	142.6	165.9	122.5	617.0	165.9	0.3
212510_at	GPD1L	7.55E-03	248.1	344.7	359.6	381.6	350.0	416.3	347.7	250.7	252.7	207.7	304.2	242.0	186.6	157.4	350.0	242.0	0.7
208308_s_at	GPI	4.12E-03	1270.7	1298.7	1256.9	1284.9	1116.9	1711.7	1038.8	992.6	843.0	685.6	900.7	1017.5	1405.6	684.9	1270.7	900.7	0.7
228950_s_at	GPR177	1.24E-03	879.1	946.4	538.3	1044.0	462.9	852.7	468.1	702.0	682.1	374.9	870.4	323.5	570.7	302.6	852.7	570.7	0.7
228949_at	GPR177	4.85E-03	791.8	1049.4	548.7	1237.7	518.1	931.9	444.2	805.7	763.7	374.5	957.2	299.3	520.5	284.2	791.8	520.5	0.7
223620_at	GPR34	6.81E-03	131.7	366.6	382.5	321.7	316.0	451.0	273.1	145.8	160.3	71.1	206.9	189.2	110.8	58.7	321.7	145.8	0.5
228027_at	GPRASP2	2.90E-03	101.3	147.2	208.4	122.5	135.3	161.8	118.3	83.4	107.5	90.2	101.4	79.2	69.5	66.2	135.3	83.4	0.6

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1556698_a_at	GPRIN3	3.12E-03	397.3	468.0	556.7	569.1	590.5	684.0	733.9	377.5	274.3	247.5	459.8	292.9	321.1	262.9	569.1	292.9	0.5
212906_at	GRAMD1B	4.73E-03	113.7	115.2	153.6	166.6	157.7	205.8	124.4	115.7	65.6	90.1	127.0	118.3	102.4	75.9	153.6	102.4	0.7
212856_at	GRAMD4	1.09E-03	104.7	134.8	150.1	150.2	151.3	132.1	135.2	79.8	80.2	50.2	97.9	99.1	65.5	72.5	135.2	79.8	0.6
229397_s_at	GRLF1	5.71E-03	245.0	312.8	342.0	449.8	379.5	407.7	279.0	267.4	222.8	182.2	293.2	227.9	235.5	202.2	342.0	227.9	0.7
229394_s_at	GRLF1	1.50E-03	544.1	531.9	514.7	587.1	590.0	578.4	439.6	455.3	381.6	272.0	446.7	338.0	325.3	313.3	544.1	338.0	0.6
226183_at	GSK3B	5.11E-03	141.8	144.4	167.7	179.9	190.5	210.7	217.0	135.4	115.0	103.5	144.3	118.8	107.8	110.7	179.9	115.0	0.6
234975_at	GSPT1	5.66E-03	246.0	286.2	277.3	300.7	313.3	329.1	329.5	215.5	200.1	233.3	269.4	204.2	228.2	210.0	300.7	215.5	0.7
1554518_at	GSTCD	1.72E-03	70.4	80.8	65.8	89.4	86.3	69.3	64.4	52.1	56.4	39.2	53.7	47.2	54.6	54.4	70.4	53.7	0.8
210912_x_at	GSTM4	1.00E-03	193.0	409.7	369.3	195.4	274.2	255.6	322.3	150.8	235.8	146.6	117.9	201.6	143.0	136.6	274.2	146.6	0.5
218412_s_at	GTF2IRD1	6.33E-03	108.0	104.9	108.4	105.4	91.7	91.1	119.1	90.5	81.8	77.4	79.2	86.0	56.6	67.2	105.4	79.2	0.8
212429_s_at	GTF3C2	9.63E-03	651.6	622.4	766.9	809.6	867.0	916.0	869.3	630.2	504.6	566.8	727.6	517.4	602.4	531.7	809.6	566.8	0.7
213835_x_at	GTPBP3	8.95E-03	399.7	444.3	556.9	502.2	450.6	553.1	458.7	379.6	388.0	349.2	405.3	337.5	361.3	243.2	458.7	361.3	0.8
202487_s_at	H2AFV	7.13E-03	603.9	573.3	568.2	532.3	761.8	586.5	543.2	540.8	410.4	376.4	459.5	571.1	487.7	432.7	573.3	459.5	0.8
227085_at	H2AFV	4.89E-03	220.9	288.7	299.8	272.2	304.9	302.8	291.8	204.1	150.7	181.7	230.5	246.4	168.7	160.7	291.8	181.7	0.6
207168_s_at	H2AFY	2.59E-03	5611.1	5867.9	6222.3	5744.4	6026.7	6641.8	5911.7	4722.3	4874.3	4328.5	4434.2	4639.9	4322.3	3821.2	5911.7	4434.2	0.8
214501_s_at	H2AFY	1.99E-03	4106.9	4096.9	3205.9	3218.9	3871.3	3723.5	3178.0	3206.0	2903.2	1774.5	2504.0	3167.8	2682.0	2091.8	3723.5	2682.0	0.7
214500_at	H2AFY	3.06E-03	650.1	567.4	554.9	532.4	599.0	608.9	526.3	458.0	316.2	279.4	375.5	570.0	453.0	297.6	567.4	375.5	0.7
213911_s_at	H2AFZ	1.80E-03	2206.5	2621.6	3048.0	2581.0	2744.7	3334.0	2790.6	1936.5	1860.5	1761.8	1927.8	1415.4	1586.2	1292.2	2744.7	1761.8	0.6
200853_at	H2AFZ	1.68E-04	1678.3	1582.3	1781.9	1801.1	1451.9	1592.3	1420.9	1201.6	985.1	806.6	956.1	846.3	1002.8	816.4	1592.3	956.1	0.6
201036_s_at	HADH	2.88E-03	384.7	645.8	446.6	452.6	514.7	625.1	376.0	356.2	372.6	224.5	357.4	323.7	302.1	146.7	452.6	323.7	0.7
201035_s_at	HADH	3.40E-03	492.0	781.2	562.1	545.2	603.0	719.0	432.8	501.8	379.2	227.0	342.9	455.2	329.1	193.0	562.1	342.9	0.6
211569_s_at	HADH	4.31E-03	196.5	336.7	277.0	303.2	302.2	372.2	233.6	206.4	167.5	141.3	227.3	202.2	181.5	96.7	302.2	181.5	0.6
217156_at	HADHA	8.67E-03	74.3	61.9	83.4	77.3	60.2	70.7	72.6	58.7	49.9	56.6	55.9	51.1	64.6	60.7	72.6	56.6	0.8
201007_at	HADHB	8.53E-03	2329.5	2721.6	2767.7	2709.9	2461.9	2655.5	2657.7	2162.1	2335.7	2051.6	2299.1	1654.8	1876.3	2079.4	2657.7	2079.4	0.8
213053_at	HAUS5	8.27E-03	186.7	160.0	185.2	202.8	220.8	201.3	179.0	172.7	134.7	137.0	168.1	137.5	157.2	135.4	186.7	137.5	0.7
38037_at	HBEGF	1.80E-03	1257.8	1100.6	1593.8	1442.8	980.0	1241.6	1349.8	1196.9	746.8	623.2	845.0	561.8	563.8	597.4	1257.8	623.2	0.5
203821_at	HBEGF	1.07E-03	1321.2	1126.8	1659.7	1601.0	992.9	1402.0	1387.3	1104.7	809.7	683.5	968.3	519.1	561.8	650.3	1387.3	683.5	0.5
1564548_at	hCG_ 1999814	1.92E-03	82.3	90.0	106.8	114.8	79.7	94.8	61.1	59.7	61.7	39.4	61.6	59.0	59.5	42.3	90.0	59.5	0.7
1556304_s_at	hCG_ 2039027	1.74E-03	115.2	127.3	131.4	133.5	152.7	167.2	126.2	102.0	82.2	79.8	91.2	113.2	90.6	92.9	131.4	91.2	0.7
204225_at	HDAC4	9.83E-03	193.0	111.9	179.9	258.0	238.8	256.1	243.3	179.9	90.9	160.3	197.7	175.8	149.4	148.7	238.8	160.3	0.7
202455_at	HDAC5	3.60E-03	180.5	159.6	199.1	246.9	202.2	173.8	176.9	164.2	112.1	109.2	144.5	159.5	138.1	102.1	180.5	138.1	0.8
203259_s_at	HDDC2	8.48E-03	2000.3	2212.7	3314.3	2765.6	3047.9	3002.7	2670.0	2066.8	1623.2	2106.7	2275.5	2375.0	1829.6	1656.4	2765.6	2066.8	0.7
227008_at	HDDC3	5.82E-03	377.1	379.8	535.2	425.2	479.5	562.8	491.0	383.5	279.0	227.3	267.5	336.1	378.6	242.7	479.5	279.0	0.6
223252_at	HDGF2	8.10E-03	180.7	183.0	194.8	201.1	174.9	178.6	178.0	151.6	149.2	131.0	160.1	142.4	157.9	143.5	180.7	149.2	0.8
209525_at	HDGFRP3	9.78E-03	248.1	466.7	450.3	549.5	440.4	556.1	548.8	278.9	360.6	273.9	392.3	206.4	276.0	199.4	466.7	276.0	0.6
226510_at	HEATR5A	9.33E-03	95.4	138.2	209.1	180.1	240.7	254.7	190.8	105.5	88.5	136.2	148.3	122.6	99.1	99.0	190.8	105.5	0.6
233642_s_at	HEATR5B	1.22E-03	833.3	1118.4	751.8	803.3	825.9	954.8	684.1	696.4	676.4	360.4	648.1	505.8	516.3	388.3	825.9	516.3	0.6
218632_at	HECTD3	8.53E-03	905.0	961.5	802.9	890.3	827.2	842.3	866.9	876.3	716.2	539.6	725.5	674.3	677.7	580.4	866.9	677.7	0.8
218620_s_at	HEMK1	8.95E-03	262.8	272.2	330.7	287.7	258.6	287.9	247.2	252.0	160.3	128.3	194.7	224.7	206.4	145.0	272.2	194.7	0.7
217902_s_at	HERC2	5.74E-03	544.0	585.2	624.4	702.2	816.7	777.4	605.6	529.5	438.4	369.7	526.7	440.5	452.8	490.1	624.4	452.8	0.7
201944_at	HEXB	6.73E-03	11360.2	11136.1	10326.7	10815.4	10211.5	9148.6	9583.4	9966.0	9310.1	7036.1	8122.9	8359.8	7663.1	7414.0	10326.7	8122.9	0.8
227564_at	HGSNAT	4.40E-03	213.2	242.8	199.2	244.2	269.7	236.4	230.2	209.6	168.2	127.3	175.3	216.2	163.6	135.2	236.4	168.2	0.7
215933_s_at	HHEX	2.99E-03	133.8	115.5	164.8	204.5	147.8	151.2	147.3	128.5	74.8	74.1	137.3	108.3	79.3	69.7	147.8	79.3	0.5
224812_at	HIBADH	4.45E-03	1926.5	2150.6	3471.7	2686.2	2667.1	3685.6	2395.4	1770.2	1837.4	1738.8	1969.3	1620.5	1669.9	1223.4	2667.1	1738.8	0.7
224415_s_at	HINT2	2.97E-03	651.2	761.8	710.4	709.5	654.2	810.9	589.1	616.0	447.7	388.2	502.6	523.9	529.6	340.9	709.5	502.6	0.7
204504_s_at	HIRIP3	6.16E-03	102.1	103.0	146.8	128.2	121.7	120.1	97.7	101.5	69.0	81.5	84.1	97.7	94.4	53.4	120.1	84.1	0.7
206951_at	HIST1H4E	1.49E-03	3567.0	3373.6	3623.4	2676.9	3031.4	2845.7	2546.6	2608.0	2482.9	1688.5	2186.1	2067.6	1659.1	1436.7	3031.4	2067.6	0.7
217478_s_at	HLA-DMA /// HLA-DMB	3.49E-03	5419.7	5557.3	5851.3	5290.9	5164.0	5265.2	4523.5	4625.4	3910.9	3425.7	4053.5	4317.0	4088.6	3069.2	5290.9	4053.5	0.8
203932_at	HLA-DMB	2.07E-03	2872.2	3639.3	3799.9	3633.8	3749.9	3653.9	2816.4	2685.3	2196.7	1584.9	2411.0	2581.0	1728.1	1344.4	3639.3	2196.7	0.6
226878_at	HLA-DOA	4.26E-03	1656.7	1335.9	1321.7	1219.2	1457.0	1473.9	1373.9	1537.2	915.2	726.6	1019.6	1068.3	1041.4	859.0	1373.9	1019.6	0.7
211656_x_at	HLA-DQB1 /// LOC100294318	5.68E-03	5383.2	2472.0	1643.6	3203.5	4099.7	7072.6	3639.4	4161.8	1928.6	1173.6	2623.6	3746.4	5597.6	2809.0	3639.4	2809.0	0.8
202983_at	HLTF	1.07E-03	682.9	623.9	805.9	724.6	675.2	865.8	792.4	533.1	345.7	227.2	481.3	325.7	348.8	269.5	724.6	345.7	0.5
208808_s_at	HMGB2	7.07E-03	1585.6	2059.1	2729.1	2063.9	2003.8	2548.2	2336.7	1382.3	1589.1	1403.8	1928.6	1211.3	1010.5	1170.6	2063.9	1382.3	0.7
209377_s_at	HMGN3	9.76E-03	2203.7	2536.4	2915.6	2718.8	2486.2	2744.7	2650.2	1772.3	2426.5	2196.9	2459.7	1503.1	1581.3	1724.7	2650.2	1772.3	0.7
222396_at	HN1	2.77E-03	3116.4	3834.0	2519.4	2757.5	3406.8	3665.3	2658.2	2418.0	2275.3	841.9	1884.7	2643.7	2168.0	1141.1	3116.4	2168.0	0.7
212109_at	HN1L	6.77E-03	253.8	220.7	228.8	217.3	277.4	250.6	261.9	252.1	180.1	119.8	172.5	188.9	141.0	142.4	250.6	172.5	0.7
209068_at	HNRPDL	9.69E-03	798.5	851.0	1270.0	1167.6	943.6	1300.9	1257.7	853.3	569.8	587.9	931.0	730.9	598.5	622.2	1167.6	622.2	0.5
205366_s_at	HOXB6	1.26E-03	558.1	454.7	685.2	721.2	659.2	894.8	351.6	469.6	296.6	279.0	500.9	399.1	536.3	187.5	659.2	399.1	0.6
216973_s_at	HOXB7	5.93E-03	202.9	117.6	230.4	229.4	298.9	334.0	127.3	207.7	96.2	136.2	164.0	177.3	177.3	86.8	229.4	164.0	0.7
224592_x_at	HP1BP3	5.10E-03	1975.1	2216.8	2593.5	2442.9	2372.4	2421.0	2430.7	1668.6	1947.3	1928.0	2044.4	1778.7	1713.6	1831.7	2421.0	1831.7	0.8
224591_at	HP1BP3	8.63E-03	2423.4	2911.3	3214.4	2914.2	2813.3	3275.3	2915.5	2327.0	2316.0	2140.1	2557.2	2054.0	1768.7	1839.0	2914.2	2140.1	0.7
211549_s_at	HPGD	1.96E-03	579.1	287.8	221.6	233.2	232.5	147.7	214.6	428.3	144.7	105.8	153.7	115.6	138.8	123.9	232.5	138.8	0.6

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203914_x_at	HPGD	3.98E-03	433.2	359.2	401.2	450.8	344.4	328.8	350.0	522.5	212.7	139.5	218.6	170.4	153.8	122.6	359.2	170.4	0.5
203913_s_at	HPGD	1.91E-03	125.9	97.2	110.8	145.1	110.7	101.4	111.2	122.0	62.1	43.4	85.5	44.3	50.0	38.0	110.8	50.0	0.5
211548_s_at	HPGD	1.40E-03	423.9	355.7	323.7	368.1	306.7	282.0	306.6	438.0	182.4	96.4	166.4	142.4	114.1	118.9	323.7	142.4	0.4
206726_at	HPGDS	2.15E-04	1494.5	1132.3	979.0	824.9	1200.8	821.9	1123.3	1139.4	792.5	591.8	487.8	715.2	519.9	660.1	1123.3	660.1	0.6
203790_s_at	HRSP12	3.62E-03	129.5	154.3	167.5	175.2	196.8	194.5	131.4	121.7	117.7	122.5	135.7	126.5	140.4	92.9	167.5	122.5	0.7
217989_at	HSD17B11	2.62E-03	1389.0	1706.8	2191.1	2009.0	1889.0	2403.6	1918.6	1330.3	1347.7	1208.2	1324.1	1013.6	1186.7	974.3	1918.6	1208.2	0.6
219113_x_at	HSD17B14	6.61E-03	80.0	74.7	112.1	104.3	95.9	116.4	105.8	61.9	46.8	98.9	72.4	85.6	94.1	77.5	104.3	77.5	0.7
224494_x_at	HSD17B14	5.32E-03	77.5	59.6	114.1	107.9	91.5	117.1	108.8	61.7	49.6	81.4	76.5	85.1	89.5	71.9	107.9	76.5	0.7
228713_s_at	HSD17B14	5.85E-03	88.7	77.3	143.1	150.8	106.3	136.5	141.4	75.9	59.4	106.0	91.6	94.1	106.6	108.1	136.5	94.1	0.7
208814_at	HSPA4	3.41E-03	517.3	632.8	570.3	624.1	691.1	888.8	684.4	499.6	404.8	254.2	442.3	483.5	578.2	361.2	632.8	442.3	0.7
213418_at	HSPA6	9.61E-03	1419.2	1787.1	964.2	1246.4	1427.7	1083.0	1263.3	1146.8	1279.7	832.1	716.9	1123.1	919.7	1083.0	1263.3	1083.0	0.9
219865_at	HSPC157	3.77E-03	224.7	269.3	252.3	256.7	274.6	313.0	202.6	224.7	160.4	127.4	187.5	208.1	169.2	111.6	256.7	169.2	0.7
226188_at	HSPC159	5.75E-03	139.2	152.7	226.3	231.6	164.0	185.2	140.8	132.5	126.7	136.1	122.2	108.1	94.6	48.4	164.0	122.2	0.7
219998_at	HSPC159	3.42E-04	185.6	194.6	254.8	234.3	232.0	214.5	151.7	157.5	119.2	146.8	139.4	136.2	131.0	90.2	214.5	136.2	0.6
208744_x_at	HSPH1	1.76E-03	1973.9	1867.0	1974.5	1663.2	1727.7	1621.1	1617.1	1574.3	1434.5	1343.2	1163.5	1378.3	1254.8	980.3	1727.7	1343.2	0.8
206976_s_at	HSPH1	3.37E-03	1051.8	1119.6	1581.2	1206.5	1232.6	1289.7	1268.2	907.8	972.3	1109.2	879.0	747.7	716.8	671.1	1232.6	879.0	0.7
202390_s_at	HTT	2.55E-03	199.3	165.7	150.0	271.7	246.8	206.0	230.6	128.2	103.2	94.6	189.5	159.1	203.6	166.3	206.0	159.1	0.8
226879_at	HVCN1	1.80E-03	1249.8	1259.1	1215.4	1250.1	1332.7	1494.2	1113.7	1116.8	719.9	357.0	696.5	826.1	715.3	440.4	1250.1	715.3	0.6
217900_at	IARS2	4.83E-03	761.8	831.4	814.7	829.5	765.2	844.4	791.5	695.4	544.3	612.0	703.0	576.4	645.9	564.7	814.7	612.0	0.8
201565_s_at	ID2	3.54E-04	915.5	579.0	1051.2	1016.4	512.4	908.4	754.1	588.9	372.8	383.3	460.3	340.2	436.5	439.9	908.4	436.5	0.5
201566_x_at	ID2	1.42E-03	151.2	103.6	261.3	238.0	137.0	230.8	197.3	113.0	88.4	100.9	124.9	79.9	91.8	90.5	197.3	91.8	0.5
207826_s_at	ID3	1.60E-03	119.3	79.4	100.2	111.1	101.8	110.5	90.5	82.4	62.4	70.4	75.1	78.0	78.6	76.8	101.8	76.8	0.8
242001_at	IDH1	1.54E-03	152.0	167.8	238.4	188.3	152.1	150.4	142.6	129.2	97.2	73.7	119.5	79.1	87.4	69.2	152.1	87.4	0.6
201193_at	IDH1	4.10E-04	3287.0	3618.8	3798.3	3518.3	3076.9	3295.0	3073.9	2221.2	2295.1	1307.7	2314.8	1358.7	1697.8	1348.8	3295.0	1697.8	0.5
1555037_a_at	IDH1	7.95E-04	1823.5	2086.6	2347.0	2133.9	1833.8	2076.9	1990.4	1343.2	1373.9	828.3	1416.0	689.1	832.9	727.6	2076.9	832.9	0.4
202439_s_at	IDS	4.37E-03	2891.4	2957.0	2635.9	3120.4	2971.8	3380.6	2891.3	2651.5	2322.8	1956.5	2559.5	2222.7	2444.4	2045.7	2957.0	2322.8	0.8
209721_s_at	IFFO1	8.01E-03	1300.4	1549.9	1574.7	1479.1	1419.0	1392.4	1300.8	1160.6	1070.8	603.0	1095.1	1168.5	966.3	756.3	1419.0	1070.8	0.8
36030_at	IFFO1	2.01E-03	1162.7	1209.6	1437.7	1331.1	1258.4	1312.6	1177.9	947.5	793.4	537.3	935.1	879.5	738.5	665.0	1258.4	793.4	0.6
210312_s_at	IFT20	2.86E-03	1381.2	1375.4	1184.1	1368.7	1237.6	1469.0	1231.9	1120.1	1060.4	704.9	892.3	1082.6	1076.5	866.8	1368.7	1060.4	0.8
207167_at	IGSF2	3.19E-03	353.9	445.7	390.5	765.9	434.2	566.4	495.8	333.7	309.8	181.7	467.5	324.4	360.9	231.9	445.7	324.4	0.7
204773_at	IL11RA	3.13E-03	345.7	302.8	297.7	278.6	311.6	274.2	251.0	329.7	196.1	147.6	195.6	213.1	170.1	107.5	297.7	195.6	0.7
201888_s_at	IL13RA1	9.40E-03	789.6	956.8	1388.9	1315.0	965.2	1455.9	1187.1	795.6	859.0	783.0	1023.6	659.6	848.7	670.5	1187.1	795.6	0.7
201887_at	IL13RA1	5.96E-03	917.3	1308.3	1535.3	1368.6	1299.8	1671.6	1342.1	927.1	897.3	585.1	1106.5	766.1	858.6	604.4	1342.1	858.6	0.6
224361_s_at	IL17RB	8.13E-03	682.6	708.3	862.7	744.0	519.8	276.6	483.2	666.2	442.6	436.4	433.9	362.7	264.6	297.8	682.6	433.9	0.6
224156_x_at	IL17RB	8.28E-04	1519.1	1459.2	1564.3	1356.3	992.9	506.9	913.5	1185.7	913.3	815.5	707.4	677.0	397.1	506.0	1356.3	707.4	0.5
219255_x_at	IL17RB	9.33E-04	1642.8	1558.9	1656.9	1404.0	1022.1	508.5	1006.9	1263.1	970.5	860.4	725.7	671.3	416.4	530.4	1404.0	725.7	0.5
221688_s_at	IMP3	8.53E-03	918.3	758.6	785.8	842.7	786.9	847.7	739.2	823.1	610.4	497.7	703.4	683.7	650.4	522.3	786.9	650.4	0.8
224743_at	IMPAD1	1.59E-03	1496.4	1485.6	1415.7	1572.5	1430.4	1722.5	1802.0	1217.5	1125.1	1001.8	1283.2	903.9	1012.4	1119.4	1496.4	1119.4	0.7
205981_s_at	ING2	2.31E-03	454.1	484.5	565.2	522.9	506.4	578.5	405.9	417.5	319.8	298.5	343.3	378.2	419.0	232.3	506.4	343.3	0.7
213544_at	ING2	2.63E-03	172.5	176.9	232.6	199.2	205.0	219.7	153.6	162.8	96.0	110.5	162.8	127.0	120.2	89.8	199.2	120.2	0.6
228287_at	ING5	6.78E-03	289.4	273.9	380.6	378.6	491.0	393.2	374.2	305.1	193.8	152.3	305.5	261.7	203.3	201.5	378.6	203.3	0.5
223072_s_at	INO80B /// WBP1	4.54E-03	252.8	248.5	318.6	340.8	297.7	333.5	283.1	232.4	199.4	201.0	188.9	223.7	259.8	159.6	297.7	201.0	0.7
204553_x_at	INPP4A	5.94E-03	308.8	353.0	355.5	377.9	366.3	371.5	284.5	278.2	184.2	163.0	289.9	322.0	251.0	163.9	355.5	251.0	0.7
208364_at	INPP4A	8.32E-04	362.7	417.2	392.9	496.3	344.3	373.1	342.1	224.5	238.5	225.5	385.3	231.1	289.2	252.0	373.1	238.5	0.6
204552_at	INPP4A	3.91E-03	130.7	184.5	191.1	211.4	211.2	237.0	155.1	131.0	104.3	63.8	150.5	127.8	84.1	64.1	191.1	104.3	0.5
227087_at	INPP4A	5.96E-03	207.2	371.8	375.4	340.0	356.4	394.1	312.2	240.7	148.2	117.2	242.3	224.1	146.8	113.3	356.4	148.2	0.4
207851_s_at	INSR	4.90E-03	61.4	70.9	84.3	57.9	72.6	86.6	61.6	61.4	45.0	41.2	39.3	48.6	54.9	48.8	70.9	48.6	0.7
213792_s_at	INSR	1.71E-03	1424.6	2091.2	2289.9	1779.5	1964.9	2611.7	1456.5	1274.9	1507.9	1035.0	1134.3	1283.3	1236.4	781.8	1964.9	1236.4	0.6
226450_at	INSR	1.19E-03	241.9	337.6	385.9	280.5	399.6	492.3	333.1	200.6	223.4	145.6	187.0	191.8	188.8	133.6	337.6	188.8	0.6
205701_at	IPO8	5.66E-03	924.3	1007.5	1138.1	999.7	1133.8	1345.2	961.4	954.6	726.8	692.7	768.4	833.3	867.0	623.6	1007.5	768.4	0.8
225528_at	IPO8	5.30E-03	660.7	893.4	1141.3	1052.6	1015.5	1379.0	1161.7	673.4	710.4	659.8	777.3	531.0	642.9	608.9	1052.6	659.8	0.6
204202_at	IQCE	7.65E-03	80.7	93.3	112.6	110.2	139.2	125.9	104.0	89.9	54.9	62.5	88.7	92.1	82.6	62.0	110.2	82.6	0.7
203906_at	IQSEC1	3.59E-03	912.9	851.6	889.9	1162.8	1199.7	1022.5	1143.1	909.3	481.3	439.5	741.8	840.4	769.5	601.3	1022.5	741.8	0.7
224570_s_at	IRF2BP2	5.91E-03	2140.5	2318.1	3017.7	2794.7	2724.2	3250.3	2695.2	1913.9	1915.4	1411.7	2325.9	1812.5	1581.0	1561.9	2724.2	1812.5	0.7
224571_at	IRF2BP2	1.89E-03	1804.3	1901.8	2399.5	2094.1	2112.0	2818.8	1863.9	1432.9	1076.5	802.7	1589.7	1189.6	966.0	967.0	2094.1	1076.5	0.5
209185_s_at	IRS2	1.40E-03	1302.3	1567.3	1281.1	1750.6	1725.8	2457.8	1795.0	1040.7	843.6	301.1	1148.7	573.2	845.4	483.9	1725.8	843.6	0.5
209184_s_at	IRS2	1.73E-03	648.3	700.0	558.1	821.4	809.4	1097.9	801.2	537.1	453.2	149.7	528.7	331.9	378.8	272.8	801.2	378.8	0.5
209075_s_at	ISCU	5.27E-03	1575.7	1690.1	2017.0	1688.8	1818.8	1993.4	1936.4	1412.7	1372.1	1236.1	1445.9	1360.7	1329.9	1149.7	1818.8	1360.7	0.7
1554240_a_at	ITGAL	5.68E-03	483.3	529.2	639.1	740.6	522.5	619.2	621.1	424.1	389.1	406.8	552.5	440.5	530.9	389.9	619.2	424.1	0.7
201124_at	ITGB5	9.94E-03	100.4	150.4	196.4	180.1	246.8	170.0	171.6	136.0	74.4	78.0	127.7	144.6	74.5	66.9	171.6	78.0	0.5
210740_s_at	ITPK1	1.23E-03	3258.2	3384.9	2942.1	3417.1	2915.4	3061.5	2217.8	2275.1	2397.4	1339.6	1953.8	2103.5	2239.6	1588.1	3061.5	2103.5	0.7
203723_at	ITPKB	2.83E-03	229.7	238.9	388.3	285.9	229.0	259.9	190.1	200.3	124.5	82.9	154.7	143.3	119.6	74.5	238.9	124.5	0.5
209297_at	ITSN1	3.84E-03	372.3	872.3	443.2	437.7	820.0	1233.7	442.2	343.4	500.2	227.4	406.0	391.7	538.8	194.7	443.2	391.7	0.9
203682_s_at	IVD	3.81E-03	107.8	136.0	134.4	145.0	123.2	164.8	130.9	106.0	96.1	77.1	107.2	89.0	105.4	92.5	134.4	96.1	0.7
225311_at	IVD	2.70E-03	210.8	233.9	274.1	260.8	267.7	319.7	256.4	210.9	138.1	115.6	185.9	161.0	179.5	138.8	260.8	161.0	0.6

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
226267_at	JDP2	7.59E-03	196.9	212.1	187.8	218.5	212.7	202.0	188.7	191.7	164.8	107.1	141.7	164.7	149.0	151.5	202.0	151.5	0.8
224933_s_at	JMJD1C	2.61E-03	1544.7	1511.3	1548.7	1457.8	1519.8	1758.1	1360.3	1098.4	1250.5	996.4	1219.0	1138.0	1164.8	1085.2	1519.8	1138.0	0.7
1568605_at	JRK	8.87E-03	80.0	79.3	92.3	102.5	114.0	121.8	141.2	80.5	57.5	58.9	94.0	77.5	75.5	77.8	102.5	77.5	0.8
201465_s_at	JUN	7.75E-03	1557.3	1419.3	1089.1	1239.2	1034.3	958.1	1072.6	1013.3	838.6	657.7	794.7	782.1	1033.7	847.7	1089.1	838.6	0.8
201466_s_at	JUN	1.46E-03	656.0	701.6	898.9	864.6	655.4	889.9	810.9	522.3	523.0	553.6	715.0	405.2	517.0	431.7	810.9	522.3	0.6
228777_at	KBTBD3	9.36E-03	89.2	90.6	123.1	88.0	102.2	111.9	93.6	94.6	58.3	66.7	83.6	60.2	54.2	50.1	93.6	60.2	0.6
223412_at	KBTBD7	9.06E-04	112.1	140.1	155.6	171.0	150.7	197.2	160.7	99.2	87.7	73.5	116.6	83.2	111.1	78.4	155.6	87.7	0.6
210079_x_at	KCNAB1	1.78E-03	322.6	293.3	696.8	420.2	624.2	596.4	493.5	266.9	198.4	203.2	241.3	345.4	238.5	163.5	493.5	238.5	0.5
208213_s_at	KCNAB1	3.23E-03	391.5	308.3	885.8	489.3	819.7	825.9	651.7	355.4	204.1	239.0	282.0	376.4	272.0	141.3	651.7	272.0	0.4
210471_s_at	KCNAB1	6.00E-03	304.2	343.2	1242.2	612.4	914.7	938.5	748.8	285.2	276.0	295.7	366.9	406.6	217.2	172.5	748.8	285.2	0.4
210078_s_at	KCNAB1	8.92E-03	297.1	495.2	1488.2	874.3	1299.6	1350.6	1086.2	351.1	363.5	462.3	513.6	479.9	330.8	185.0	1086.2	363.5	0.3
203402_at	KCNAB2	1.00E-03	538.9	391.9	603.9	555.3	443.0	455.7	391.2	392.3	251.9	206.0	300.2	293.4	288.9	176.6	455.7	288.9	0.6
211791_s_at	KCNAB2	4.50E-03	195.7	179.7	278.8	280.7	200.4	225.4	233.3	146.1	100.3	107.2	121.8	187.0	177.6	112.3	225.4	121.8	0.5
222923_s_at	KCNE3	6.59E-04	526.2	747.2	683.6	1100.8	848.3	957.0	596.0	429.5	376.6	198.4	476.5	494.3	457.0	273.7	747.2	429.5	0.6
227647_at	KCNE3	1.22E-03	965.0	1137.7	1451.1	1341.4	1526.0	2115.9	1383.4	850.9	621.4	344.8	693.8	620.2	731.4	406.0	1383.4	621.4	0.4
223658_at	KCNK6	4.23E-03	227.9	184.1	306.2	284.5	207.9	261.0	188.4	204.6	130.9	159.2	205.8	168.0	180.5	138.5	227.9	168.0	0.7
221583_s_at	KCNMA1	7.35E-03	422.9	374.9	219.4	477.3	909.8	508.7	572.8	393.0	201.1	127.6	334.1	851.7	351.9	264.2	477.3	334.1	0.7
221584_s_at	KCNMA1	2.62E-04	549.6	490.0	309.1	681.5	1287.1	728.5	697.0	377.4	281.0	155.4	458.8	882.5	378.3	315.2	681.5	377.4	0.6
226518_at	KCTD10	2.89E-03	815.3	776.3	927.6	852.8	853.3	961.8	970.5	673.4	632.5	653.4	696.0	574.7	752.0	615.1	853.3	653.4	0.8
201728_s_at	KIAA0100	7.26E-03	657.3	686.5	586.0	665.2	669.5	690.3	620.4	642.9	414.2	352.1	539.6	539.9	531.3	397.2	665.2	531.3	0.8
201729_s_at	KIAA0100	3.58E-03	791.7	695.9	601.2	726.5	649.2	724.3	609.8	653.1	420.8	378.8	557.8	554.0	584.8	426.5	695.9	554.0	0.8
212523_s_at	KIAA0146	2.98E-03	558.3	898.8	827.4	840.0	794.0	837.9	782.3	533.2	612.9	571.9	654.5	510.8	503.2	424.8	827.4	533.2	0.6
212056_at	KIAA0182	5.91E-03	101.5	161.3	142.1	221.6	164.2	187.2	151.9	125.7	85.3	67.7	129.6	98.3	109.0	86.5	161.3	98.3	0.6
38892_at	KIAA0240	5.92E-03	235.9	271.5	346.6	346.5	346.8	414.4	309.5	247.5	199.7	210.0	276.8	206.1	221.5	180.1	346.5	210.0	0.6
202220_at	KIAA0907	7.22E-03	990.4	1278.4	1459.3	1194.3	1100.1	1264.1	1221.7	964.3	1033.3	899.2	996.8	815.6	745.6	776.5	1221.7	899.2	0.7
235674_at	KIAA0922	6.37E-03	276.4	487.9	460.3	365.4	412.8	500.4	435.0	269.6	301.6	188.0	316.9	286.1	269.2	228.3	435.0	269.6	0.6
226816_s_at	KIAA1143	7.47E-03	320.0	397.2	423.7	433.7	471.7	612.5	552.1	344.1	236.4	263.2	363.7	272.1	281.7	225.2	433.7	272.1	0.6
223110_at	KIAA1429	8.54E-03	395.3	352.4	470.8	435.9	477.4	480.4	486.4	333.0	315.3	360.6	387.9	314.8	373.6	319.9	470.8	333.0	0.7
231850_x_at	KIAA1712	4.85E-03	146.9	207.5	250.2	211.9	209.5	332.8	219.0	148.5	156.4	108.8	156.4	118.4	156.4	96.2	211.9	148.5	0.7
228334_x_at	KIAA1712	7.92E-03	395.2	551.8	713.1	547.8	604.2	886.1	658.7	396.3	381.6	214.9	463.2	301.3	368.2	208.4	604.2	368.2	0.6
229173_at	KIAA1715	5.11E-03	338.8	418.6	554.0	546.4	547.4	561.4	564.7	309.8	312.4	339.2	502.8	330.6	312.8	313.8	547.4	313.8	0.6
225623_at	KIAA1737	6.88E-04	1079.4	1067.7	1176.7	1038.6	853.5	1009.8	958.5	772.0	719.9	548.6	722.0	571.4	709.6	499.6	1038.6	709.6	0.7
243539_at	KIAA1841	4.65E-03	96.4	107.6	109.7	103.5	99.4	105.0	104.0	75.1	87.8	88.3	89.7	59.2	77.7	61.9	104.0	77.7	0.7
202183_s_at	KIF22	7.39E-03	154.5	117.6	171.6	171.6	152.0	148.6	172.5	123.8	94.1	95.7	113.6	143.4	121.6	113.0	154.5	113.6	0.7
220266_s_at	KLF4	9.85E-04	1203.5	1166.8	1426.6	1377.0	1029.5	1267.5	755.3	849.9	785.7	485.8	576.3	697.2	677.7	443.4	1203.5	677.7	0.6
221841_s_at	KLF4	1.62E-03	1114.5	1367.8	2130.8	1924.5	1672.4	2179.1	1315.6	997.2	1004.3	837.4	1005.7	695.5	742.4	456.4	1672.4	837.4	0.5
204334_at	KLF7	2.72E-03	1037.2	933.6	754.7	806.5	1073.5	874.3	849.7	772.1	547.6	246.7	604.6	698.6	601.4	471.5	874.3	601.4	0.7
219930_at	KLF8	4.59E-03	170.6	162.5	177.7	179.5	136.4	152.1	109.1	126.9	122.2	127.0	130.2	111.3	99.9	103.2	162.5	122.2	0.8
230986_at	KLF8	5.91E-03	214.6	335.0	273.5	342.0	302.7	346.3	236.4	252.3	210.9	133.9	217.2	187.2	162.5	143.3	302.7	187.2	0.6
217906_at	KLHDC2	9.63E-04	707.0	820.7	790.9	841.8	889.8	978.9	660.1	599.2	512.2	408.9	587.4	625.0	599.1	441.5	820.7	587.4	0.7
225755_at	KLHDC8B	9.29E-03	1353.0	1179.7	1300.9	1243.7	1081.9	1091.3	1536.5	1186.8	735.7	674.9	825.3	1025.1	930.9	794.3	1243.7	825.3	0.7
1552425_a_at	KLHL10	1.69E-03	139.9	104.1	232.3	144.7	123.8	210.1	165.0	125.7	68.0	118.1	101.5	68.3	87.4	69.3	144.7	87.4	0.6
212882_at	KLHL18	8.06E-03	466.4	622.3	583.9	488.8	570.6	633.1	506.0	463.7	399.5	310.4	464.7	331.3	401.5	335.9	570.6	399.5	0.7
219157_at	KLHL2	5.91E-03	1234.4	1404.1	1811.6	1451.2	1615.5	2149.4	1842.5	1100.2	1104.7	1211.4	1275.3	912.4	1041.1	887.5	1615.5	1100.2	0.7
49329_at	KLHL22	5.64E-03	190.0	170.0	198.3	217.9	188.7	166.3	185.6	150.0	129.6	112.8	171.1	150.4	146.9	137.6	188.7	146.9	0.8
221986_s_at	KLHL24	1.40E-03	393.5	458.3	821.5	658.9	701.0	838.1	583.7	372.7	219.8	315.2	399.7	437.2	361.0	240.0	658.9	361.0	0.5
221985_at	KLHL24	1.60E-03	535.3	635.3	891.6	744.1	741.2	890.5	652.5	475.7	364.6	368.7	446.5	546.2	406.0	285.6	741.2	406.0	0.5
221221_s_at	KLHL3	3.80E-03	76.3	63.4	63.7	82.2	60.4	76.5	73.7	55.2	60.7	35.2	60.7	45.1	53.7	44.2	73.7	53.7	0.7
1560397_s_at	KLHL6	1.94E-03	2142.4	1842.8	1836.4	1819.5	1966.8	1599.4	2163.8	1728.1	1166.9	1311.4	1187.8	1211.3	1428.8	1265.2	1842.8	1265.2	0.7
228167_at	KLHL6	9.75E-03	240.2	261.3	376.6	348.8	383.9	391.1	491.0	264.0	163.0	263.4	256.3	204.6	202.9	160.6	376.6	204.6	0.5
206316_s_at	KNTC1	5.82E-04	217.7	209.0	231.2	248.4	217.0	241.9	199.0	171.1	122.2	121.3	190.8	121.9	114.3	107.8	217.7	121.9	0.6
235252_at	KSR1	3.42E-03	1546.2	1569.4	1924.2	1602.4	1438.0	2196.3	1680.6	1394.1	1023.2	627.2	1194.6	781.0	1256.2	778.8	1602.4	1023.2	0.6
213770_at	KSR1	8.64E-03	226.1	157.4	247.7	206.2	191.5	281.5	226.2	189.0	136.2	106.4	177.1	120.9	204.3	137.1	226.1	137.1	0.6
1552490_at	LACE1	7.55E-03	68.0	63.4	64.8	63.4	66.1	62.8	56.8	60.2	47.9	48.9	53.3	50.7	34.6	45.2	63.4	48.9	0.8
222714_s_at	LACTB2	1.17E-03	466.6	501.8	845.4	682.8	660.7	783.5	673.4	406.2	343.6	350.4	441.1	310.3	406.4	290.5	673.4	350.4	0.5
216264_s_at	LAMB2	5.10E-03	472.8	353.2	220.0	353.4	228.6	119.0	310.9	335.9	202.6	147.0	199.8	183.7	106.4	267.3	310.9	199.8	0.6
200618_at	LASP1	4.97E-03	3128.6	3398.8	3028.8	3147.1	3256.8	3150.7	3355.1	2777.1	2490.6	1565.7	2582.4	2529.7	2274.6	2005.0	3150.7	2490.6	0.8
211005_at	LAT /// SPNS1	2.73E-03	3430.4	4376.8	3575.9	2349.4	2927.2	3609.9	2110.2	2604.8	2675.9	1242.7	1894.8	1913.5	2009.0	1334.1	3430.4	1913.5	0.6
213564_x_at	LDHB	5.71E-03	5621.5	6113.3	6483.9	5465.9	5257.8	6186.7	6280.7	4742.6	5245.6	5218.6	4665.4	3592.9	4633.3	4250.3	6113.3	4665.4	0.8
201030_x_at	LDHB	4.01E-03	5034.1	5597.5	5082.2	4410.2	4228.7	4932.4	4847.4	4463.8	4438.8	4010.7	3563.9	3050.6	3725.1	3529.1	4932.4	3725.1	0.8
229241_at	LDHD	5.57E-03	108.1	93.7	124.4	150.8	134.8	107.2	104.9	82.7	82.4	75.0	107.4	106.3	88.8	84.4	108.1	84.4	0.8
221790_s_at	LDLRAP1	1.84E-03	200.3	126.9	198.6	274.6	184.8	203.7	248.7	167.2	88.3	111.0	150.3	134.4	162.4	131.3	200.3	134.4	0.7
57082_at	LDLRAP1	2.71E-03	438.4	332.9	301.2	333.9	274.3	267.1	327.9	332.8	245.3	162.5	183.1	211.3	234.0	195.2	327.9	211.3	0.6
202595_s_at	LEPROTL1	7.12E-03	669.5	608.7	790.7	732.6	732.9	896.5	778.7	540.1	550.4	658.7	626.0	522.5	578.5	533.6	732.9	550.4	0.8
202594_at	LEPROTL1	2.20E-03	4008.2	4188.2	5256.1	4245.7	4150.3	5487.8	4696.5	3347.4	3138.8	2290.9	3253.5	2561.8	3092.6	2321.3	4245.7	3092.6	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
207170_s_at	LETMD1	7.17E-03	303.3	336.7	368.1	287.7	461.0	430.3	375.8	313.5	257.9	243.9	227.0	303.6	300.8	211.5	368.1	257.9	0.7
208935_s_at	LGALS8	9.68E-03	1563.5	1376.8	1573.8	1919.6	1536.8	1433.8	1499.4	1473.1	1137.2	802.9	1256.4	1228.7	1008.7	1198.7	1536.8	1198.7	0.8
217892_s_at	LIMA1	4.85E-03	1299.9	1598.5	1738.2	1554.9	1828.8	2266.7	1792.1	1017.0	1373.7	1050.0	1451.2	1094.2	1265.5	1176.2	1738.2	1176.2	0.7
206440_at	LIN7A	2.09E-03	348.0	478.6	746.6	651.0	671.6	835.6	727.2	320.7	352.0	301.2	347.7	388.5	451.1	280.0	671.6	347.7	0.5
241957_x_at	LIN7B	5.38E-03	66.1	67.6	107.6	96.2	89.4	94.7	59.8	74.8	43.0	62.7	61.3	49.3	58.0	41.9	89.4	58.0	0.6
201847_at	LIPA	8.11E-03	6213.8	4954.9	4609.8	5164.0	3748.7	5130.0	3712.8	5182.1	3781.7	3110.1	4168.2	3677.7	3606.1	2344.0	4954.9	3677.7	0.7
225793_at	LIX1L	2.99E-03	2487.2	2987.7	2896.7	2984.4	3144.9	3310.2	2869.6	2355.2	2279.6	1664.7	2257.8	2003.4	2078.2	1949.4	2984.4	2078.2	0.7
218191_s_at	LMBRD1	2.64E-03	1493.8	1857.8	1672.2	1812.2	1802.0	1923.0	1527.9	1390.3	1468.6	1022.5	1326.4	1242.6	1210.7	938.7	1802.0	1242.6	0.7
231866_at	LNPEP	4.38E-03	495.5	839.0	969.8	737.6	994.7	1129.5	1049.5	481.8	477.1	333.4	634.5	464.8	415.5	376.0	969.8	464.8	0.5
236874_at	LOC100128071	7.15E-03	198.0	208.0	198.6	188.1	178.9	164.7	166.5	167.5	140.6	130.1	156.8	143.4	123.9	150.7	188.1	143.4	0.8
228791_at	LOC100129502	7.40E-04	486.1	530.2	870.4	794.3	773.7	604.4	466.7	411.2	276.0	241.1	402.1	328.6	194.8	138.6	604.4	276.0	0.5
229699_at	LOC100129550	1.21E-03	478.4	472.0	643.1	626.8	691.6	821.7	591.4	412.0	283.5	291.0	474.3	419.6	431.3	295.3	626.8	412.0	0.7
242364_x_at	LOC100131096	5.71E-03	673.5	674.6	730.7	740.2	627.4	844.2	708.5	511.7	514.2	296.7	524.3	536.5	527.9	507.8	708.5	514.2	0.7
228591_at	LOC100131096	7.59E-03	94.8	109.4	86.6	85.4	99.9	101.9	78.0	77.1	66.5	62.4	65.3	72.1	65.8	79.3	94.8	66.5	0.7
239062_at	LOC100131096	3.94E-03	112.6	86.9	204.5	202.8	152.1	188.1	177.9	106.4	45.4	53.3	98.3	102.9	111.1	55.2	177.9	98.3	0.6
230526_at	LOC100131096	8.55E-04	679.6	761.5	899.8	936.1	801.2	995.9	755.3	542.2	367.1	222.8	410.6	437.0	493.1	239.4	801.2	410.6	0.5
227074_at	LOC100131564	6.52E-03	275.9	435.2	473.1	383.8	306.9	232.2	469.6	299.0	299.1	296.6	305.4	194.7	130.9	259.5	383.8	296.6	0.8
1559514_at	LOC100132077	2.06E-03	76.1	79.6	137.7	106.1	132.9	137.0	146.7	63.0	65.9	82.3	84.4	87.5	82.9	94.8	132.9	82.9	0.6
214189_s_at	LOC100288178	1.62E-03	1283.8	1551.2	1243.6	1196.5	1119.8	1534.9	1215.1	1120.1	875.9	500.9	883.6	700.5	896.1	660.6	1243.6	875.9	0.7
213281_at	LOC100288387	6.87E-03	851.9	1024.7	866.2	889.7	816.9	907.1	1012.3	788.3	730.4	616.9	731.8	593.4	796.5	708.5	889.7	730.4	0.8
231422_x_at	LOC100288438	9.35E-03	420.2	417.9	465.0	497.4	430.0	521.5	371.6	460.6	286.0	205.4	297.9	344.2	349.9	219.5	430.0	297.9	0.7
213789_at	LOC100292959	7.27E-03	765.5	682.7	536.1	553.6	540.0	587.4	582.2	685.9	399.7	277.7	437.1	461.1	477.0	344.9	582.2	437.1	0.8
1563431_x_at	LOC100293219	6.74E-03	2194.8	2164.1	2355.6	2555.6	2084.7	2355.3	2149.1	1934.5	1750.8	1554.7	2112.1	1709.2	1583.7	1752.9	2194.8	1750.8	0.8
231258_at	LOC100293390	5.65E-03	1134.2	974.5	1138.3	990.9	1045.3	1030.1	942.9	949.2	739.8	687.0	696.8	896.3	900.8	663.1	1030.1	739.8	0.7
220219_s_at	LOC100294335 /// LOC644397 /// LRRC37A /// LRRC37A2 /// LRRC37A3 /// LRRC37A4	4.54E-03	1479.1	1036.9	838.7	1192.4	869.6	1210.6	918.2	1122.8	719.1	533.4	882.2	770.5	1058.9	690.0	1036.9	770.5	0.7
240298_at	LOC147791	4.15E-03	88.6	86.0	112.8	128.4	103.2	135.4	103.3	99.7	54.6	51.8	73.2	68.0	64.6	53.2	103.3	64.6	0.6
212098_at	LOC151162 /// MGAT5	1.18E-04	1047.8	1012.4	882.6	1052.2	937.0	846.7	809.4	777.7	610.7	502.7	642.7	559.9	538.5	486.9	937.0	559.9	0.6
213776_at	LOC157562	8.97E-03	93.0	105.7	82.4	74.3	110.9	94.2	95.4	78.2	80.9	79.6	61.6	72.9	65.1	55.6	94.2	72.9	0.8
236832_at	LOC221442	9.30E-03	96.3	134.6	165.5	128.1	141.4	134.2	134.1	92.4	94.8	106.0	115.1	115.1	98.6	86.7	134.2	98.6	0.7
235132_at	LOC254128	8.30E-03	383.5	412.1	551.2	498.9	440.7	557.9	378.9	367.4	329.9	330.4	410.5	343.2	346.0	287.2	440.7	343.2	0.8
236574_at	LOC284373	4.69E-03	50.0	68.1	56.7	57.9	73.2	67.7	56.0	49.5	47.0	41.7	38.6	51.2	50.8	42.8	57.9	47.0	0.8
1563088_a_at	LOC284837	2.23E-04	541.3	785.7	691.0	768.5	450.4	598.2	304.1	394.9	389.4	300.7	358.9	289.5	283.3	187.0	598.2	300.7	0.5
244189_at	LOC284900	2.93E-03	415.9	424.4	492.0	472.0	464.9	458.1	356.6	364.2	321.0	289.2	350.7	347.2	325.6	277.4	458.1	325.6	0.7
235584_at	LOC285033	9.23E-03	198.5	201.8	191.0	178.7	218.3	196.9	175.6	172.6	167.0	113.6	155.0	177.5	157.1	109.6	196.9	157.1	0.8
1561334_at	LOC285181	5.68E-04	368.5	275.9	437.6	436.1	375.9	334.4	352.8	283.0	171.6	239.7	206.4	188.1	255.8	191.4	368.5	206.4	0.6
236321_at	LOC285550	2.96E-03	73.3	76.5	88.9	89.2	105.9	118.3	130.4	67.2	57.7	31.7	56.1	62.2	49.3	56.7	89.2	56.7	0.6
227270_at	LOC285550	6.22E-03	213.8	318.9	330.1	391.7	345.7	435.0	406.5	247.2	212.4	180.1	260.7	213.4	214.0	175.5	345.7	213.4	0.6
238263_at	LOC285965	3.79E-03	78.5	191.7	230.1	165.5	135.1	286.9	203.0	73.5	127.4	149.9	143.1	70.4	177.4	114.0	191.7	127.4	0.7
229015_at	LOC286367	3.11E-03	81.7	114.1	110.0	106.9	84.5	115.0	80.1	79.5	71.9	66.4	62.1	68.3	64.7	38.9	106.9	66.4	0.6
1556266_a_at	LOC400831	4.37E-03	117.5	114.7	94.0	98.8	97.1	150.9	107.7	96.5	74.5	77.0	71.0	82.7	124.5	75.9	107.7	77.0	0.7
1557124_at	LOC440104	9.97E-03	133.3	131.9	109.9	88.7	88.1	112.1	91.5	108.8	93.5	61.2	63.2	82.7	75.1	83.4	109.9	82.7	0.8
227106_at	LOC440104	8.26E-03	147.4	181.3	222.3	223.3	179.9	233.5	169.6	153.6	101.6	77.4	159.8	146.5	124.7	78.7	181.3	124.7	0.7
238511_at	LOC440288	1.53E-03	95.1	102.3	59.7	104.0	97.9	94.6	83.5	54.4	50.0	45.2	48.4	58.5	46.5	75.9	95.1	50.0	0.5
229826_at	LOC440957	5.68E-03	202.4	196.4	194.7	200.7	189.3	182.3	169.8	157.7	126.7	140.9	141.9	148.8	176.1	131.5	194.7	141.9	0.7
230595_at	LOC572558	4.55E-03	87.1	67.2	75.6	70.5	75.3	84.3	68.0	74.1	54.5	55.6	55.0	59.0	58.4	57.8	75.3	57.8	0.8
228908_s_at	LOC642852	1.57E-03	146.2	175.5	204.4	194.7	167.9	182.0	176.9	115.1	118.8	97.2	117.6	95.6	121.4	59.9	176.9	115.1	0.7
226995_at	LOC642852	6.42E-04	104.3	101.9	99.0	110.3	96.0	116.8	95.8	57.9	71.0	82.4	72.0	55.0	65.4	65.4	101.9	65.4	0.6
228909_at	LOC642852	7.57E-03	69.7	121.3	137.9	108.1	98.6	101.4	76.1	78.2	67.9	45.6	75.8	62.5	55.1	43.0	101.4	62.5	0.6
229857_s_at	LOC644246	8.37E-03	323.4	676.9	630.0	210.8	673.4	385.0	238.9	348.5	523.7	445.6	156.7	469.7	243.6	143.0	385.0	348.5	0.9

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1564200_at	LOC646324	9.31E-03	125.1	101.9	89.8	140.4	68.0	82.2	81.2	114.7	61.7	54.3	116.9	55.1	48.7	71.4	89.8	61.7	0.7
218380_at	LOC728392 /// NLRP1	4.35E-04	322.3	422.9	431.6	448.9	335.5	411.8	312.9	247.2	259.8	161.5	250.4	190.0	241.5	152.3	411.8	241.5	0.6
224623_at	LOC728554 /// THOC3	2.65E-03	1214.2	845.3	994.5	1163.3	1132.6	970.4	866.5	1060.4	568.9	549.7	950.2	766.3	726.1	591.1	994.5	726.1	0.7
1568763_s_at	LOC728613 /// PDCD6	4.93E-03	927.4	467.8	1213.7	1497.1	718.4	855.2	854.0	707.4	350.6	1123.7	1263.9	465.7	635.9	569.5	855.2	635.9	0.7
1564474_at	LOC728723	4.26E-03	52.7	21.0	120.6	138.7	131.6	119.1	56.3	53.8	10.7	26.5	91.4	45.9	55.7	26.5	119.1	45.9	0.4
242313_at	LOC728730	2.51E-03	42.9	58.7	90.9	57.8	60.8	78.0	72.5	30.7	35.4	19.5	43.6	29.9	25.8	28.0	60.8	29.9	0.5
237556_at	LOC728804	9.11E-03	121.5	213.3	1296.5	2326.7	228.2	279.6	1545.3	171.4	97.8	321.2	1052.0	138.7	136.9	474.2	279.6	171.4	0.6
235010_at	LOC729013	5.31E-03	391.5	386.2	461.7	415.8	274.6	613.5	473.2	346.7	314.6	293.4	371.8	190.7	368.5	279.0	415.8	314.6	0.8
225332_at	LOC729082	2.59E-03	227.7	230.8	261.0	258.5	311.8	373.2	332.4	223.5	135.9	106.7	191.2	178.9	177.8	155.2	261.0	177.8	0.7
225225_at	LOC729082	5.59E-03	539.2	723.5	914.3	760.1	934.5	1127.0	1244.0	589.0	481.5	367.6	557.7	511.9	486.2	489.2	914.3	489.2	0.5
230952_at	LOC730092	2.69E-03	332.1	531.1	265.0	123.8	362.5	400.8	123.2	231.3	229.6	109.2	98.4	264.8	209.4	94.2	332.1	209.4	0.6
236905_at	LOC731139	8.30E-03	70.9	58.5	52.4	72.4	73.1	69.9	68.5	57.4	51.2	42.7	64.3	55.8	55.6	48.1	69.9	55.6	0.8
220465_at	LOC80054	6.58E-03	111.9	88.0	118.0	103.0	93.7	111.7	86.3	78.7	70.3	56.3	75.7	70.6	72.7	80.8	103.0	72.7	0.7
226842_at	LOC90110	9.71E-04	289.6	372.1	367.3	359.8	397.0	416.5	304.1	263.0	204.9	180.8	213.7	263.8	260.3	151.6	367.3	213.7	0.6
225391_at	LOC93622	5.80E-03	338.6	473.1	425.4	362.5	367.5	483.8	336.5	300.1	240.5	140.7	335.8	251.8	198.7	138.2	367.5	240.5	0.7
206723_s_at	LPAR2	7.63E-03	234.7	371.6	324.4	311.2	343.0	353.4	309.2	221.2	275.5	219.5	247.9	298.9	243.3	238.3	324.4	243.3	0.8
213078_x_at	LPCAT4	2.94E-03	163.9	157.6	165.6	180.3	129.6	144.8	145.3	130.5	123.8	83.1	100.6	99.3	116.5	85.2	157.6	100.6	0.6
40472_at	LPCAT4	4.01E-03	196.3	185.1	184.6	208.6	139.5	164.2	140.9	161.2	128.2	72.1	102.9	123.3	102.3	83.9	184.6	102.9	0.6
235126_at	LQK1	4.86E-03	200.6	193.0	205.0	313.2	511.9	267.7	286.8	208.1	127.9	102.5	241.7	317.9	167.8	138.4	267.7	167.8	0.6
219491_at	LRFN4	2.09E-03	192.7	188.5	205.8	219.1	214.5	233.2	175.4	164.1	122.9	165.7	140.6	152.3	164.9	137.9	205.8	152.3	0.7
1555353_at	LRP1	8.95E-03	93.6	107.8	80.6	95.9	87.3	89.7	82.4	60.2	70.2	56.5	79.4	67.4	94.0	56.6	89.7	67.4	0.8
1569042_at	LRP1	5.17E-03	59.1	57.7	68.2	78.3	75.5	79.5	74.7	53.7	38.7	42.5	64.0	51.4	69.1	52.0	74.7	52.0	0.7
200785_s_at	LRP1	7.23E-03	251.0	202.5	236.3	298.0	293.0	298.7	312.8	214.4	141.5	120.9	202.6	266.8	249.2	198.6	293.0	202.6	0.7
200784_s_at	LRP1	9.39E-03	695.6	549.2	560.0	810.3	708.0	703.5	669.6	464.3	300.2	343.9	436.4	656.4	712.1	484.9	695.6	464.3	0.7
201186_at	LRPAP1	7.57E-03	4613.1	4708.4	4285.2	4201.0	3811.0	4091.7	3564.9	3694.8	3657.8	3044.4	3284.5	3450.2	3585.2	2727.2	4201.0	3450.2	0.8
230793_at	LRRC16A	1.98E-03	318.5	536.6	337.5	351.2	177.1	173.0	332.5	223.6	321.6	102.2	230.7	120.0	114.6	170.3	332.5	170.3	0.5
220220_at	LRRC37A4	7.85E-03	209.1	124.3	122.6	434.9	120.9	332.4	236.9	212.3	64.0	95.1	310.0	90.1	244.5	133.5	209.1	133.5	0.6
218684_at	LRRC8D	2.56E-03	2143.1	2724.2	2336.2	2240.4	2032.0	2240.3	1761.8	1660.9	1809.6	921.4	1790.4	1360.2	1431.9	1103.1	2240.3	1431.9	0.6
212924_s_at	LSM4	3.46E-03	2002.0	1775.6	1862.2	1952.1	1724.6	1923.2	1646.2	1561.9	1257.7	951.9	1360.7	1479.8	1489.4	1171.1	1862.2	1360.7	0.7
202737_s_at	LSM4	1.78E-03	2044.7	1881.4	1999.7	2127.1	1832.8	2004.0	1758.2	1567.9	1415.3	1050.2	1358.2	1332.8	1635.9	1195.6	1999.7	1358.2	0.7
208771_s_at	LTA4H	5.74E-03	12444.7	12213.9	12669.6	12614.2	12366.7	12756.6	11516.2	10619.2	10083.1	6863.1	9883.1	9746.5	9952.7	7222.4	12444.7	9883.1	0.8
221831_at	LUZP1	7.25E-03	389.5	421.0	520.6	491.2	426.3	389.4	452.8	334.1	294.6	420.2	405.3	249.3	284.0	396.6	426.3	334.1	0.8
223414_s_at	LYAR	6.36E-03	1617.3	939.1	1023.5	1004.8	1003.0	1026.3	896.6	1049.4	808.0	658.1	714.7	734.5	862.7	819.9	1004.8	808.0	0.8
218437_s_at	LZTFL1	1.92E-03	652.7	617.5	787.9	713.7	867.8	761.0	716.0	513.5	472.1	251.4	403.9	502.7	440.5	326.2	716.0	440.5	0.6
206363_at	MAF	3.28E-03	607.7	400.0	633.1	471.0	534.7	379.1	425.2	346.3	268.2	188.5	304.8	357.2	314.3	215.0	471.0	304.8	0.6
209348_s_at	MAF	1.75E-03	349.7	356.9	582.8	493.3	535.8	465.7	483.0	298.5	237.5	202.8	346.4	279.5	236.4	215.2	483.0	237.5	0.5
218176_at	MAGEF1	5.91E-03	133.9	91.8	126.9	125.7	76.3	93.8	80.7	99.1	80.4	67.8	103.6	53.0	77.5	58.5	93.8	77.5	0.8
202032_s_at	MAN2A2	8.98E-04	2223.4	2072.5	2143.2	2238.9	2072.6	2180.3	1957.5	1727.0	1518.5	1113.2	1506.8	1386.0	1619.0	1224.8	2143.2	1506.8	0.7
219999_at	MAN2A2	3.99E-03	237.0	213.2	302.6	317.7	280.5	321.7	275.0	230.6	134.1	142.2	203.0	227.0	194.9	130.3	280.5	194.9	0.7
203778_at	MANBA	7.18E-04	2862.2	3397.0	3055.0	3208.7	3387.4	2959.9	2849.5	2115.7	2483.0	1438.9	2271.9	2157.6	1940.5	1653.3	3055.0	2115.7	0.7
214786_at	MAP3K1	3.95E-03	413.0	451.2	532.0	593.8	511.4	572.7	456.6	409.9	277.0	242.4	429.0	354.9	322.0	307.3	511.4	322.0	0.6
225927_at	MAP3K1	4.46E-03	1195.3	1664.9	1872.0	1863.6	1706.9	2063.7	1745.1	1091.7	1133.6	747.8	1582.2	1012.2	1029.4	1029.5	1745.1	1029.5	0.6
205447_s_at	MAP3K12	1.91E-03	78.4	86.6	84.7	76.0	89.2	86.5	80.8	70.6	51.1	49.2	60.3	60.0	47.6	40.1	84.7	51.1	0.6
226441_at	MAP3K2	3.14E-03	1022.0	1129.3	1347.2	1448.5	1641.8	1583.4	1668.6	894.0	839.9	793.8	1223.0	972.9	1173.0	1067.0	1448.5	972.9	0.7
227131_at	MAP3K3	4.63E-03	202.0	169.3	251.5	249.0	278.6	252.9	161.7	170.0	119.9	131.0	149.5	238.2	175.5	132.0	249.0	149.5	0.6
216199_s_at	MAP3K4	7.09E-03	360.1	347.3	386.4	394.9	398.5	348.3	338.7	355.0	263.9	253.3	307.2	288.8	284.6	238.7	360.1	284.6	0.8
203901_at	MAP3K7IP1	5.85E-03	74.2	66.8	99.0	91.7	86.6	91.6	92.0	68.1	53.6	54.0	68.9	66.4	70.9	59.0	91.6	66.4	0.7
212566_at	MAP4	9.05E-03	2471.4	2446.4	1999.4	2180.8	2142.5	2203.1	2270.5	2426.7	1760.4	1226.5	1845.5	1430.0	1873.5	1474.8	2203.1	1760.4	0.8
202530_at	MAPK14	5.08E-03	1698.4	1624.7	1639.5	2132.5	1815.5	2270.1	1991.6	1367.9	1333.3	999.0	1909.1	1157.7	1828.2	1357.8	1815.5	1357.8	0.7
202788_at	MAPKAPK3	5.53E-03	2465.2	2190.1	2333.1	2572.9	2158.6	2413.1	2246.0	2152.1	1620.4	1426.2	2028.4	1779.0	2008.0	1635.1	2333.1	1779.0	0.8
223095_at	MARVELD1	2.38E-03	639.8	724.0	509.2	584.3	608.3	557.1	515.3	500.9	345.7	130.7	393.0	415.4	282.3	216.0	584.3	345.7	0.6
40016_g_at	MAST4	2.00E-03	376.5	511.8	523.3	559.4	374.3	435.0	262.9	275.2	322.8	135.4	286.2	252.8	246.3	129.9	435.0	252.8	0.6
225613_at	MAST4	7.41E-04	345.5	523.0	643.0	644.1	485.2	562.3	294.3	234.7	267.2	111.4	280.4	232.7	167.3	80.5	523.0	232.7	0.4
225611_at	MAST4	1.15E-03	334.1	770.2	751.6	798.4	572.9	672.1	370.4	296.2	296.8	159.3	346.2	275.6	173.0	75.9	672.1	275.6	0.4
228798_x_at	MAZ	5.89E-03	551.9	468.4	469.2	510.9	474.2	480.7	441.5	429.6	329.5	274.9	379.4	394.4	421.3	365.3	474.2	379.4	0.8
212064_x_at	MAZ	8.12E-04	1400.6	1139.8	1261.2	1415.3	1329.9	1314.5	1235.2	1063.5	894.8	845.4	983.4	934.1	1004.0	823.8	1314.5	934.1	0.7
227833_s_at	MBD6	7.17E-03	2965.3	3220.8	3103.8	3347.9	2640.5	2525.3	2374.6	2558.5	2455.4	2204.7	2580.5	2152.3	2223.8	1952.4	2965.3	2223.8	0.7
203640_at	MBNL2	3.04E-03	208.9	294.6	319.5	303.3	314.6	315.5	277.1	208.5	140.1	73.1	186.4	164.4	97.1	103.5	303.3	140.1	0.5
227379_at	MBOAT1	9.02E-03	1271.4	1417.3	1944.1	1293.1	1192.7	1473.4	1514.2	1235.0	1112.3	949.5	1120.9	839.9	758.2	706.7	1417.3	949.5	0.7
225408_at	MBP	3.06E-03	326.5	308.0	311.1	393.1	306.7	331.4	292.1	309.9	200.0	139.6	224.7	235.7	220.1	160.9	311.1	220.1	0.7
1554544_a_at	MBP	2.19E-03	513.2	434.2	441.4	518.0	435.2	480.7	353.5	394.0	294.4	189.8	264.8	371.4	316.1	214.6	441.4	294.4	0.7
228938_at	MBP	1.78E-03	797.4	683.4	670.7	763.4	682.5	761.3	646.5	666.6	408.3	254.5	472.9	517.1	424.1	288.5	683.4	424.1	0.6
225407_at	MBP	9.06E-04	2351.9	2260.7	2137.6	2677.8	2355.8	2528.8	2029.6	1990.5	1487.8	811.2	1431.9	1434.0	1275.0	1102.2	2351.9	1431.9	0.6

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
210136_at	MBP	2.41E-03	2205.4	2077.0	2131.3	2358.0	2008.3	2307.5	1676.4	1968.4	1437.0	803.9	1282.0	1472.2	1237.9	867.0	2131.3	1282.0	0.6
226797_at	MBTD1	6.71E-03	345.0	561.4	684.2	579.0	668.0	738.0	592.0	369.9	368.1	319.9	479.0	406.0	366.7	267.0	592.0	368.1	0.6
243552_at	MBTD1	9.69E-03	94.0	130.1	170.0	169.0	187.4	202.9	126.8	112.8	95.6	101.3	120.0	107.4	101.3	72.0	169.0	101.3	0.6
202107_s_at	MCM2	2.22E-03	249.4	224.5	198.7	224.5	188.7	182.5	205.5	217.0	143.4	104.3	184.7	125.7	108.7	145.1	205.5	143.4	0.7
201555_at	MCM3	8.65E-03	646.1	577.2	556.3	623.9	516.0	502.8	449.4	548.5	415.9	303.6	551.8	414.7	403.1	340.4	556.3	414.7	0.7
222037_at	MCM4	7.74E-04	368.0	392.6	346.8	402.2	317.8	303.4	346.3	312.4	234.0	188.9	303.2	190.2	185.1	215.8	346.8	215.8	0.6
222036_s_at	MCM4	9.84E-03	149.4	204.2	252.0	307.2	224.0	268.5	291.6	176.0	156.5	138.7	229.3	112.7	137.0	138.3	252.0	138.7	0.6
201930_at	MCM6	7.45E-03	238.9	278.6	297.2	311.5	284.9	282.5	254.3	278.0	161.4	134.1	245.6	171.7	140.9	139.0	282.5	161.4	0.6
224320_s_at	MCM8	6.24E-03	83.8	93.6	93.1	100.8	99.8	102.7	93.3	82.2	64.1	55.2	86.8	59.2	76.9	50.7	93.6	64.1	0.7
219952_s_at	MCOLN1	4.49E-03	799.5	638.9	908.2	700.0	596.7	647.5	663.3	513.6	448.9	310.3	353.4	518.7	513.9	351.9	663.3	448.9	0.7
200978_at	MDH1	4.80E-03	2203.4	2474.1	2238.6	2101.7	2126.3	2553.2	2106.8	1989.8	1788.7	1522.3	1879.7	1620.6	1635.7	1432.7	2203.4	1635.7	0.7
212693_at	MDN1	8.05E-03	256.1	284.7	296.1	322.7	342.4	363.0	331.7	232.7	220.2	217.6	289.2	182.6	237.4	244.3	322.7	232.7	0.7
204058_at	ME1	3.73E-03	69.0	85.2	125.3	129.7	139.8	120.1	127.0	68.0	58.1	92.7	94.3	83.8	69.7	64.5	125.3	69.7	0.6
226958_s_at	MED11	6.75E-03	1874.1	1356.7	1589.3	1763.5	1823.8	1856.4	1535.5	1584.1	1055.9	988.2	1310.5	1549.7	1614.6	1167.6	1763.5	1310.5	0.7
212872_s_at	MED20	9.85E-03	356.4	405.1	384.5	389.5	404.6	505.8	336.2	365.1	263.3	258.7	346.3	289.6	330.2	253.2	389.5	289.6	0.7
222447_at	METTL9	6.14E-03	117.5	126.2	288.2	236.0	183.9	307.6	247.0	93.2	94.5	201.3	185.3	171.8	209.3	205.7	236.0	185.3	0.8
204153_s_at	MFNG	2.09E-03	1063.2	1332.5	1090.2	1201.4	1019.8	1212.6	1012.3	937.5	866.0	508.0	776.7	737.6	880.4	611.9	1090.2	776.7	0.7
225325_at	MFSD6	5.82E-04	2541.6	2808.9	2844.0	2329.5	2145.5	2705.3	2964.8	1946.7	2045.7	1535.0	1537.7	1357.1	1863.8	2081.9	2705.3	1863.8	0.7
213403_at	MFSD9	6.06E-03	223.9	242.4	274.9	244.2	232.2	232.3	199.2	220.2	157.5	120.7	210.9	135.0	154.7	111.3	232.3	154.7	0.7
230848_s_at	MGA	9.59E-03	803.1	955.1	1172.7	1311.0	1409.3	1438.2	1319.9	780.0	801.4	748.7	1090.9	792.5	981.8	1009.1	1311.0	801.4	0.6
209764_at	MGAT3	9.51E-03	677.2	691.7	754.6	912.7	657.7	801.7	799.0	646.7	573.3	480.1	615.5	398.9	742.0	512.5	754.6	573.3	0.8
231283_at	MGAT4A	3.10E-04	786.2	1071.0	916.8	909.5	878.7	1126.0	737.4	583.2	639.2	432.4	600.6	593.4	610.7	372.8	909.5	593.4	0.7
219797_at	MGAT4A	4.01E-03	584.8	911.2	879.2	709.7	780.2	1020.4	735.3	498.8	569.8	459.5	693.1	395.7	500.2	312.4	780.2	498.8	0.6
226039_at	MGAT4A	3.59E-03	1108.8	1646.0	1650.0	1327.6	1486.2	1853.6	1277.0	970.7	1010.9	594.7	1140.8	870.5	850.8	534.4	1486.2	870.5	0.6
1556154_a_at	MGC23284	7.39E-03	119.0	175.2	110.3	122.0	69.7	197.4	143.8	114.7	105.8	36.8	79.0	58.2	82.6	42.6	122.0	79.0	0.6
204168_at	MGST2	6.60E-04	1080.1	2376.0	2406.4	2441.2	1720.3	2382.9	2067.1	853.5	1569.3	1167.7	1611.0	1187.5	1155.4	1138.9	2376.0	1167.7	0.5
218376_s_at	MICAL1	4.16E-03	4296.2	3832.2	4233.1	3771.7	3616.1	3258.6	3019.0	2917.7	2534.0	2524.1	2217.7	3351.3	2839.9	2188.8	3771.7	2534.0	0.7
223411_at	MIF4GD	5.65E-03	770.2	843.9	929.2	868.8	821.4	1033.0	772.7	711.4	602.7	413.8	608.0	683.7	613.4	507.2	843.9	608.0	0.7
231727_s_at	MIF4GD	4.38E-03	246.0	428.0	552.8	449.9	349.5	532.8	356.0	244.5	210.8	162.7	280.4	249.8	283.7	148.8	428.0	244.5	0.6
1554874_at	MITF	4.01E-03	71.9	96.9	63.7	64.4	51.8	59.9	64.1	56.9	78.8	35.9	60.3	32.9	37.8	40.7	64.1	40.7	0.6
207233_s_at	MITF	1.11E-03	890.0	666.5	831.2	874.6	945.3	806.0	959.1	781.4	421.4	512.4	622.4	595.3	535.9	485.0	874.6	535.9	0.6
226066_at	MITF	1.35E-03	2360.7	1813.6	2670.0	2953.8	3078.9	2748.3	3171.7	1828.0	1447.7	1325.4	1881.4	1222.0	1519.1	1352.7	2748.3	1447.7	0.5
1570202_a_at	MKL2	7.48E-03	210.0	199.7	192.1	223.8	201.5	225.0	201.6	187.0	182.2	127.0	187.2	152.7	150.5	130.4	201.6	152.7	0.8
209467_s_at	MKNK1	2.64E-03	1040.8	1180.4	1138.8	1529.0	1192.9	1347.8	1097.2	918.9	858.9	621.0	1270.4	747.5	908.4	710.8	1180.4	858.9	0.7
243256_at	MKNK1	1.42E-03	448.5	593.4	573.2	1078.0	564.5	741.1	501.8	396.0	354.8	328.4	799.4	387.1	514.0	341.6	573.2	387.1	0.7
218071_s_at	MKRN2	4.92E-03	456.4	419.4	566.4	523.4	538.0	582.9	458.7	428.9	346.8	356.7	420.9	328.3	400.2	321.0	523.4	356.7	0.7
200617_at	MLEC	3.13E-03	636.9	525.3	502.2	533.7	448.7	486.8	552.0	475.5	367.8	282.5	429.2	377.1	393.2	353.1	525.3	377.1	0.7
229304_s_at	MLF1IP	1.49E-03	384.5	415.9	476.1	382.3	392.3	451.5	388.8	322.9	284.8	267.5	305.0	267.6	266.2	204.7	392.3	267.6	0.7
218883_s_at	MLF1IP	5.40E-03	157.6	177.9	214.1	209.1	216.4	164.2	187.2	161.0	137.0	94.5	144.4	88.1	98.4	101.6	187.2	101.6	0.5
218211_s_at	MLPH	6.52E-04	1785.2	2390.0	2019.0	2189.6	1827.7	2543.0	2245.8	1370.6	1332.3	667.6	1318.2	880.6	1351.3	773.1	2189.6	1318.2	0.6
242082_at	MMAB	9.67E-03	211.9	158.5	97.2	109.9	114.0	95.5	132.9	145.1	108.5	77.0	82.3	98.1	90.8	110.7	114.0	98.1	0.9
203414_at	MMD	5.10E-03	5664.7	7742.2	7448.6	5931.8	6158.8	8189.1	7158.9	5224.2	6119.0	4161.6	5140.2	3838.5	5326.4	3943.6	7158.9	5140.2	0.7
203435_s_at	MME	4.47E-03	2392.8	4024.9	3559.3	2693.4	2973.3	2132.9	2430.2	2501.3	2720.5	1941.7	2039.6	1934.4	1239.9	1555.3	2693.4	1941.7	0.7
203434_s_at	MME	4.03E-03	1692.9	2945.1	3298.4	2317.7	2275.5	1635.5	2248.8	1548.7	2475.2	2284.6	1772.1	1314.0	910.8	1307.4	2275.5	1548.7	0.7
204574_s_at	MMP19	1.37E-03	182.1	219.5	261.6	252.5	203.3	260.3	206.1	161.0	123.4	96.9	148.3	135.5	136.3	85.7	219.5	135.5	0.6
219265_at	MOBKL2B	9.74E-03	1371.2	1242.5	1310.7	1423.1	1190.6	1412.3	1311.7	1283.0	1130.8	575.0	938.5	724.2	927.3	1009.6	1311.7	938.5	0.7
226844_at	MOBKL2B	1.35E-03	498.0	612.2	638.0	742.9	576.3	760.7	604.3	462.6	353.9	175.7	386.0	209.7	323.4	267.3	612.2	323.4	0.5
229568_at	MOBKL2B	3.83E-03	131.4	145.4	225.9	228.0	173.7	245.3	198.7	122.9	106.6	64.0	141.5	79.0	67.7	69.6	198.7	79.0	0.4
1553062_at	MOGAT1	5.26E-03	161.4	217.0	182.0	186.6	143.4	238.6	217.0	141.0	115.6	67.9	155.4	104.0	148.5	85.0	186.6	115.6	0.6
218853_s_at	MOSPD1	4.26E-03	133.5	156.8	368.3	281.6	302.4	302.6	317.6	133.1	104.2	134.8	180.4	166.4	122.5	88.7	302.4	133.1	0.4
221895_at	MOSPD2	3.84E-03	697.7	907.3	1000.2	1045.7	866.5	873.6	1203.6	648.1	714.0	576.2	803.3	487.4	534.7	555.0	907.3	576.2	0.6
64883_at	MOSPD2	3.88E-03	231.5	301.9	424.5	476.5	377.9	405.3	471.1	227.3	208.8	253.4	353.3	213.5	243.6	198.3	405.3	227.3	0.6
219070_s_at	MOSPD3	9.62E-03	214.2	180.1	201.0	211.4	188.5	192.7	203.0	192.8	139.6	156.4	144.5	158.3	174.7	140.9	201.0	156.4	0.8
203466_at	MPV17	7.51E-03	1050.5	1043.0	935.4	1106.2	937.3	858.7	825.9	910.6	670.4	617.2	734.9	815.6	792.6	593.0	937.3	734.9	0.8
230518_at	MPZL2	1.11E-03	199.4	349.0	251.7	272.7	232.6	231.0	171.4	164.8	179.7	102.0	163.4	169.3	116.7	66.7	232.6	163.4	0.7
203779_s_at	MPZL2	5.65E-03	194.2	374.1	397.1	509.8	382.4	451.3	307.2	219.1	206.1	119.4	325.6	201.0	169.1	74.2	382.4	201.0	0.5
203780_at	MPZL2	2.45E-03	218.0	320.6	400.3	471.1	416.0	495.0	317.5	180.3	207.3	117.4	305.4	172.0	159.3	71.4	400.3	172.0	0.4
204438_at	MRC1 /// MRC1L1	5.29E-03	6826.6	8320.9	9730.9	8602.1	9114.7	10289.7	8527.3	5766.3	6624.1	6645.1	7504.4	4347.3	6822.7	5486.5	8602.1	6624.1	0.8
212199_at	MRFAP1L1	1.26E-03	1565.0	1645.4	1977.1	1816.5	1456.4	1812.5	1723.3	1351.0	1262.8	1184.2	1308.7	880.0	1143.9	1153.1	1723.3	1184.2	0.7
228077_at	MRI1	4.45E-03	378.5	463.4	227.0	444.0	388.5	548.6	432.5	410.8	236.4	131.3	295.2	267.3	230.5	197.2	432.5	236.4	0.5
204386_s_at	MRP63	9.35E-03	1326.6	1316.7	1486.9	1422.8	1491.6	1655.1	1472.5	1340.0	1088.1	1079.5	1111.0	1136.8	1213.9	1022.8	1472.5	1111.0	0.8
221692_s_at	MRPL34	8.57E-03	339.7	327.0	376.7	384.9	353.4	323.7	311.4	319.6	190.0	198.6	309.5	297.8	259.1	186.3	339.7	259.1	0.8
218281_at	MRPL48	3.00E-03	565.0	571.9	635.7	638.8	631.8	1141.9	539.4	461.2	498.7	390.2	494.4	484.2	754.0	345.1	631.8	484.2	0.8
201717_at	MRPL49	8.89E-03	565.9	537.6	602.7	529.6	544.1	583.0	515.9	497.9	400.1	401.0	435.8	433.8	495.8	440.0	544.1	435.8	0.8
223291_at	MRPS15	6.61E-03	499.7	445.5	442.4	513.5	453.8	565.2	398.8	419.9	391.9	351.8	390.7	368.2	454.6	310.5	453.8	390.7	0.9

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
226296_s_at	MRPS15	8.36E-03	2802.0	2866.5	2276.2	2570.1	2549.9	2664.5	1914.7	2531.1	2337.4	1599.5	1960.1	2089.0	2100.5	1640.6	2570.1	2089.0	0.8
224357_s_at	MS4A4A	2.57E-03	1954.3	2342.1	2008.0	2299.4	2172.2	2041.4	1941.5	1610.0	1825.6	1397.9	1897.0	1494.9	1636.8	1316.2	2041.4	1610.0	0.8
224356_x_at	MS4A6A	5.98E-04	3306.0	4240.9	3470.3	4973.2	4713.3	3189.4	1483.6	2275.0	2596.7	1635.0	3408.3	3395.6	1687.1	1060.7	3470.3	2275.0	0.7
230550_at	MS4A6A	9.12E-04	362.4	603.8	375.2	674.2	561.9	362.5	205.8	242.6	277.1	99.8	406.8	382.9	121.4	89.8	375.2	242.6	0.6
223280_x_at	MS4A6A	8.10E-04	3247.2	4129.5	3561.8	4884.7	4537.6	3119.0	1453.0	2161.8	2662.4	1640.5	3381.0	3286.1	1675.5	1080.8	3561.8	2161.8	0.6
223922_x_at	MS4A6A	3.50E-04	1049.1	1348.6	1204.9	1629.1	1626.9	1092.8	570.8	624.4	887.4	641.9	1198.8	1100.5	494.1	345.1	1204.9	641.9	0.5
219666_at	MS4A6A	5.40E-04	754.4	1338.0	978.2	1325.0	1309.1	874.1	345.6	463.4	710.2	286.8	760.5	900.1	311.8	141.1	978.2	463.4	0.5
209421_at	MSH2	6.51E-03	164.3	334.5	317.6	263.4	229.1	244.6	199.8	201.7	202.3	153.2	150.7	150.4	133.8	88.9	244.6	150.7	0.6
225238_at	MSI2	8.95E-03	67.1	99.8	78.5	75.1	111.3	109.2	79.0	65.3	53.8	50.4	73.6	53.5	72.7	49.0	79.0	53.8	0.7
225240_s_at	MSI2	6.70E-03	299.1	541.7	577.3	630.5	551.2	729.1	545.2	338.8	393.0	217.6	385.2	340.3	307.0	274.5	551.2	338.8	0.6
216685_s_at	MTAP	4.34E-03	130.7	106.9	116.2	131.3	124.9	137.3	106.1	115.2	85.7	69.7	97.4	98.0	109.8	68.7	124.9	97.4	0.8
203346_s_at	MTF2	6.97E-03	189.1	198.1	205.8	222.3	176.1	167.8	201.8	160.6	146.8	139.0	197.0	138.8	127.1	105.2	198.1	139.0	0.7
235689_at	MTFMT	6.98E-03	224.7	262.2	250.4	235.0	274.9	287.6	224.5	248.5	172.6	156.7	187.4	164.9	174.9	117.9	250.4	172.6	0.7
202309_at	MTHFD1	8.51E-03	646.5	824.6	1055.6	867.5	841.3	1037.4	798.0	735.3	612.8	559.8	659.8	488.0	611.1	477.8	841.3	611.1	0.7
226969_at	MTR	4.44E-03	257.5	239.8	327.1	285.5	329.0	345.8	254.0	236.4	160.7	116.2	220.8	179.9	183.5	164.2	285.5	179.9	0.6
219822_at	MTRF1	5.79E-03	515.2	505.0	478.1	526.1	458.6	457.8	439.3	439.7	360.1	346.2	439.7	398.2	366.2	333.9	478.1	366.2	0.8
212095_s_at	MTUS1	1.78E-03	48.7	82.8	285.5	83.6	47.4	58.3	58.1	40.8	59.4	185.4	58.2	37.6	46.0	38.6	58.3	46.0	0.8
212096_s_at	MTUS1	4.41E-03	44.9	139.8	362.8	66.7	52.7	89.8	48.9	47.6	56.5	186.6	45.9	34.3	45.3	17.0	66.7	45.9	0.7
223348_x_at	MUM1	3.62E-03	251.9	196.2	231.6	204.1	193.6	193.2	182.3	207.2	153.7	111.5	144.8	133.6	152.8	127.1	196.2	144.8	0.7
241749_at	MURC	2.04E-03	93.7	126.4	161.0	159.5	138.7	187.8	162.7	95.1	71.6	51.7	69.4	45.7	60.9	32.2	159.5	60.9	0.4
202364_at	MXI1	1.74E-03	181.7	224.4	507.6	325.6	386.8	358.3	251.2	183.1	133.0	161.1	163.6	175.7	120.2	108.3	325.6	161.1	0.5
204798_at	MYB	4.34E-03	579.5	1341.5	1125.1	1396.7	1331.7	2044.0	881.9	545.6	860.4	169.1	793.6	471.5	559.2	181.2	1331.7	545.6	0.4
227761_at	MYO5A	4.54E-03	306.0	333.7	568.8	566.6	601.6	682.5	724.3	288.9	217.6	322.0	489.2	289.6	297.0	289.2	568.8	289.6	0.5
203215_s_at	MYO6	4.54E-03	1000.2	1053.6	1010.5	1183.3	1094.8	1066.8	982.8	950.3	786.6	712.6	847.6	734.9	885.2	706.7	1053.6	786.6	0.7
205610_at	MYOM1	4.50E-03	140.8	146.2	136.2	97.4	126.4	138.2	130.2	117.9	94.8	93.6	75.7	82.3	106.8	118.8	136.2	94.8	0.7
221820_s_at	MYST1	5.07E-03	952.3	1095.0	901.3	1263.4	1008.8	1207.7	961.8	951.9	589.6	311.1	687.1	741.5	840.0	400.9	1008.8	687.1	0.7
40569_at	MZF1	6.10E-03	276.9	317.5	295.1	300.8	324.1	280.6	248.4	225.1	205.1	181.0	218.1	253.2	253.4	210.8	295.1	218.1	0.7
202944_at	NAGA	2.89E-03	616.3	553.7	603.6	669.6	596.8	532.1	580.6	576.1	426.6	356.2	501.4	414.6	360.6	360.9	596.8	414.6	0.7
204860_s_at	NAIP	1.60E-03	719.1	824.3	721.5	689.6	737.3	481.6	473.2	637.1	403.9	264.7	435.3	519.4	249.0	232.6	719.1	403.9	0.6
228608_at	NALCN	4.39E-03	155.7	131.1	413.3	258.7	230.4	555.5	177.4	169.1	96.7	155.3	134.4	77.5	186.3	91.5	230.4	134.4	0.6
208754_s_at	NAP1L1	7.96E-03	678.6	738.1	1069.1	1014.5	1199.7	1358.9	1513.9	659.8	635.3	747.0	806.0	782.1	744.3	821.1	1069.1	747.0	0.7
200027_at	NARS	3.79E-03	1521.9	1815.7	2017.4	2118.0	2099.4	2385.2	1981.5	1491.4	1241.7	1143.8	1720.0	1181.1	1124.0	1067.6	2017.4	1181.1	0.6
219217_at	NARS2	2.39E-03	310.3	351.3	399.6	366.5	303.8	370.6	343.0	301.2	203.4	235.5	257.9	222.0	219.0	179.6	351.3	222.0	0.6
222369_at	NAT11	6.30E-03	215.0	420.1	373.3	326.6	315.0	391.9	307.1	222.1	275.8	124.6	276.3	139.3	157.3	117.1	326.6	157.3	0.5
223040_at	NAT5	6.95E-03	1567.7	1488.2	1561.3	1615.9	1439.5	1586.9	1350.4	1482.9	1191.1	1024.2	1301.7	1085.4	1142.6	1085.5	1561.3	1142.6	0.7
212854_x_at	NBPF10	5.93E-03	2553.2	2671.8	4207.4	2979.5	3100.2	4165.4	2982.1	2553.5	1893.2	1930.8	2511.2	1936.5	2385.4	1633.3	2982.1	1936.5	0.6
207677_s_at	NCF4	5.73E-03	2261.2	2118.6	1715.6	2072.0	1733.6	1980.8	1566.1	1811.5	1377.7	914.8	1433.4	1462.9	1787.1	1139.5	1980.8	1433.4	0.7
205147_x_at	NCF4	9.74E-03	1210.9	1190.8	963.1	1186.7	928.4	1082.7	898.6	1078.1	769.1	521.7	805.3	771.8	1033.5	626.0	1082.7	771.8	0.7
215857_at	NCLN	8.13E-04	196.9	236.2	243.6	324.3	176.3	199.2	187.8	168.4	121.6	81.5	169.6	104.4	108.6	91.7	199.2	108.6	0.5
243807_at	NCOA7	3.55E-03	66.9	57.5	50.6	59.0	62.2	55.9	50.2	50.7	30.4	32.6	44.0	43.7	39.0	46.9	57.5	43.7	0.8
200854_at	NCOR1	7.46E-03	321.1	402.6	460.3	553.4	560.5	635.0	569.4	331.2	309.2	307.4	454.7	314.6	344.4	357.8	553.4	331.2	0.6
228993_s_at	NCRNA00081	1.09E-03	3314.6	4145.5	3875.1	3926.3	4002.7	5510.9	3384.4	2686.5	2833.5	1573.6	2618.1	2554.3	2994.6	1660.2	3926.3	2618.1	0.7
213788_s_at	NCRNA00094	9.38E-03	523.8	669.5	791.8	776.1	684.3	787.9	608.5	567.1	429.9	364.9	617.6	501.9	478.8	386.1	684.3	478.8	0.7
200632_s_at	NDRG1	4.19E-03	1464.6	1049.1	3030.6	1744.2	2588.9	3146.6	1837.0	1229.5	920.0	1156.6	900.2	1220.3	1082.7	1273.8	1837.0	1156.6	0.6
217286_s_at	NDRG3	1.94E-03	612.5	854.0	702.2	771.0	835.8	916.3	721.4	568.5	640.8	428.0	562.3	545.1	587.3	455.2	771.0	562.3	0.7
201740_at	NDUFS3	3.77E-03	780.1	747.0	721.3	783.2	667.8	730.9	658.4	668.7	500.0	479.9	545.8	584.8	589.8	473.2	730.9	545.8	0.7
219396_s_at	NEIL1	7.94E-03	45.8	83.7	74.4	73.8	63.9	89.9	54.1	50.5	46.7	30.9	57.5	43.3	53.4	32.2	73.8	46.7	0.6
226585_at	NEIL2	1.75E-03	2796.3	3436.4	2301.2	2301.9	2299.5	1997.3	2265.2	2344.0	2240.6	931.0	1623.0	1416.7	1181.9	935.0	2301.2	1416.7	0.6
223159_s_at	NEK6	8.24E-03	2402.6	1962.7	2323.7	2541.9	2161.7	2168.5	2557.0	2156.9	1669.3	1180.2	1891.2	1654.7	1728.8	1608.4	2323.7	1669.3	0.7
212299_at	NEK9	5.92E-03	2191.7	2259.2	2724.5	2370.6	2328.4	2921.3	2489.7	1902.4	1968.2	1751.2	2087.7	1656.8	2015.6	1703.6	2370.6	1902.4	0.8
201830_s_at	NET1	9.71E-03	374.3	734.0	408.3	624.7	684.9	537.8	784.3	307.0	488.3	248.9	675.4	467.5	291.3	329.0	624.7	329.0	0.5
201829_at	NET1	2.32E-03	698.6	1129.8	770.2	1210.3	1266.9	1159.2	1251.5	464.4	852.3	456.9	1040.9	839.9	535.7	531.6	1159.2	535.7	0.5
210555_s_at	NFATC3	7.81E-03	349.0	353.2	470.4	540.0	470.4	483.3	398.3	387.6	262.3	274.5	365.8	343.8	300.2	258.1	470.4	300.2	0.6
209930_s_at	NFE2	1.07E-03	118.4	82.6	181.8	325.7	182.4	190.7	160.3	95.6	65.5	85.8	145.2	81.8	113.1	69.1	181.8	85.8	0.5
224975_at	NFIA	1.39E-04	362.8	527.7	485.2	513.9	590.3	681.9	372.0	220.5	269.5	155.5	309.5	292.8	262.8	138.6	513.9	262.8	0.5
224970_at	NFIA	4.11E-04	646.4	927.8	853.4	824.1	943.7	1087.9	605.2	392.5	496.1	244.7	443.6	580.0	419.9	181.1	853.4	419.9	0.5
229994_at	NFIA	6.14E-03	80.9	151.5	251.6	184.0	263.2	289.0	159.5	75.0	106.4	49.2	127.2	112.2	79.5	33.4	184.0	79.5	0.4
226806_s_at	NFIA	1.75E-03	227.4	508.6	576.1	496.8	671.8	711.2	380.2	193.1	262.5	99.2	264.8	260.2	191.4	92.7	508.6	193.1	0.4
218946_at	NFU1	3.95E-03	954.4	940.6	1110.3	960.8	1076.5	1036.0	981.3	908.2	770.5	738.6	729.9	709.7	709.2	659.3	981.3	729.9	0.7
217722_s_at	NGRN	9.60E-03	2890.7	3438.0	3342.3	3352.9	3331.0	3643.1	3066.6	2602.8	3173.1	2726.6	2705.0	2366.2	2481.7	2232.4	3342.3	2602.8	0.8
201076_at	NHP2L1	1.57E-03	779.1	748.3	733.0	857.7	852.4	916.0	827.6	693.6	493.5	445.8	639.7	636.0	564.2	489.6	827.6	564.2	0.7
218133_s_at	NIF3L1	8.84E-03	610.3	636.1	654.1	698.0	615.6	638.8	532.8	641.2	421.7	351.6	504.4	471.9	479.0	382.5	636.1	471.9	0.7
225921_at	NIN	1.60E-03	1379.1	1543.5	1617.4	1815.3	1944.6	2058.9	2000.2	1227.3	1030.8	785.1	1388.6	1185.8	1141.3	1130.2	1815.3	1141.3	0.6
225876_at	NIPAL3	2.68E-03	650.5	857.8	734.2	803.5	669.4	741.5	652.8	601.4	595.2	409.7	597.0	490.9	531.1	411.0	734.2	531.1	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
201709_s_at	NIPSNAP1	2.98E-03	176.6	161.8	203.0	199.2	175.3	200.5	155.6	156.2	122.5	87.7	135.4	111.2	140.1	91.6	176.6	122.5	0.7
201708_s_at	NIPSNAP1	4.16E-03	147.1	134.3	180.9	163.7	154.5	184.9	144.5	133.9	90.3	64.3	127.1	93.0	105.8	62.6	154.5	93.0	0.6
221104_s_at	NIPSNAP3B	9.60E-03	69.4	102.3	147.5	87.1	102.8	154.1	116.8	55.0	63.5	94.3	94.3	55.7	50.6	63.2	102.8	63.2	0.6
225930_at	NKIRAS1	5.96E-03	388.7	486.1	455.6	490.0	508.1	491.6	476.9	365.5	376.5	365.1	372.1	363.3	338.9	387.1	486.1	365.5	0.8
222589_at	NLK	8.01E-03	876.0	964.6	896.8	968.8	947.8	1134.2	767.3	771.8	814.5	665.4	873.1	631.3	709.5	586.4	947.8	709.5	0.7
1552553_a_at	NLRC4	2.46E-03	1303.2	1591.1	1526.5	1513.2	1410.6	1794.1	1576.9	1013.7	1092.1	517.8	1145.8	880.6	1020.4	808.3	1526.5	1013.7	0.7
211822_s_at	NLRP1	3.10E-03	254.3	198.7	308.9	381.4	248.7	256.9	274.4	179.8	170.0	155.6	210.9	182.3	216.3	162.9	256.9	179.8	0.7
211824_x_at	NLRP1	2.01E-04	211.3	144.7	235.7	261.3	186.1	214.2	194.7	127.1	99.4	133.9	149.9	135.4	146.6	109.0	211.3	133.9	0.6
210113_s_at	NLRP1	1.78E-04	375.4	280.2	376.4	382.0	337.8	359.2	333.0	273.8	153.1	198.0	235.5	215.5	242.8	195.7	359.2	215.5	0.6
218036_x_at	NMD3	6.66E-03	596.3	572.5	633.0	660.9	635.0	620.9	738.0	532.0	430.2	537.0	562.1	388.9	457.2	454.1	633.0	457.2	0.7
221210_s_at	NPL	9.27E-03	568.0	586.3	600.4	698.5	737.5	714.6	599.7	493.2	414.2	388.8	542.2	745.7	417.2	327.6	600.4	417.2	0.7
205259_at	NR3C2	2.93E-04	70.0	69.5	75.6	63.2	92.6	91.3	63.1	42.7	42.8	42.7	42.8	46.1	34.6	39.1	70.0	42.7	0.6
212298_at	NRP1	7.81E-03	598.2	512.0	599.3	650.7	635.2	448.0	964.3	542.7	327.5	256.0	622.2	379.2	293.5	387.5	599.3	379.2	0.6
226880_at	NUCKS1	9.29E-03	1734.5	2014.2	2500.9	2278.2	2307.8	2764.6	2774.6	1676.7	1715.9	1726.1	1959.5	1504.8	1574.2	1517.0	2307.8	1676.7	0.7
224582_s_at	NUCKS1	7.68E-03	1013.5	1034.9	1153.0	1027.4	1026.5	1113.0	1070.6	1014.6	783.2	555.6	832.7	704.7	748.1	662.0	1034.9	748.1	0.7
217802_s_at	NUCKS1	5.72E-03	3534.1	4018.1	4355.5	3929.0	4046.4	5001.9	4264.7	3063.0	3208.2	2873.8	3637.0	2833.4	2887.4	2858.4	4046.4	2887.4	0.7
223661_at	NUCKS1	1.94E-03	1118.2	1162.9	1198.0	1157.6	1080.2	1246.8	1219.8	922.0	870.1	577.2	874.8	774.0	751.8	726.5	1162.9	774.0	0.7
224581_s_at	NUCKS1	2.27E-03	851.1	941.0	1129.0	1014.1	1037.0	1280.1	1180.5	695.9	688.9	679.7	857.6	597.2	596.1	649.6	1037.0	679.7	0.7
201270_x_at	NUDCD3	3.19E-03	786.1	715.7	702.5	697.8	700.8	792.1	634.9	673.2	549.7	448.2	554.9	568.8	594.6	430.1	702.5	554.9	0.8
224830_at	NUDT21	8.83E-03	292.7	382.1	537.3	531.5	461.6	553.9	557.0	316.9	248.9	391.5	436.6	254.3	322.6	371.0	531.5	322.6	0.6
206303_s_at	NUDT4	2.46E-03	206.9	167.1	200.7	211.6	198.3	203.9	162.0	169.2	120.1	121.5	191.8	125.7	139.5	107.4	200.7	125.7	0.6
206302_s_at	NUDT4 /// NUDT4P1	8.02E-03	450.0	521.1	701.8	634.9	555.6	698.2	528.8	447.4	394.8	318.9	518.9	394.4	369.3	322.7	555.6	394.4	0.7
212181_s_at	NUDT4 /// NUDT4P1	1.66E-03	1333.1	1238.3	1677.0	1621.9	1458.9	1537.8	1356.6	1127.5	964.4	818.1	1182.1	833.0	793.6	796.2	1458.9	833.0	0.6
230329_s_at	NUDT6	1.32E-03	196.3	249.4	276.4	276.0	219.9	259.5	197.8	186.5	154.6	102.0	142.4	122.0	131.7	86.3	249.4	131.7	0.5
200747_s_at	NUMA1	9.10E-03	394.0	369.6	456.9	492.0	399.8	446.5	431.8	322.5	222.9	237.5	381.6	387.7	367.4	269.0	431.8	322.5	0.7
214251_s_at	NUMA1	6.78E-03	210.2	198.0	235.2	285.0	200.9	225.5	192.1	157.0	125.8	144.2	199.1	179.3	215.4	139.5	210.2	157.0	0.7
202155_s_at	NUP214	9.86E-03	2078.1	2098.9	2123.1	2152.7	2373.5	2572.8	2149.2	2003.6	1601.4	1043.5	1638.2	1963.1	1866.7	1442.0	2149.2	1638.2	0.8
219978_s_at	NUSAP1	3.52E-03	241.7	234.9	271.2	266.6	251.0	191.0	200.2	231.8	126.7	168.5	209.7	123.2	129.9	133.5	241.7	133.5	0.6
205441_at	OCEL1	1.09E-03	257.6	219.0	200.8	281.5	184.1	226.2	178.2	197.2	113.5	99.3	180.4	137.7	172.9	105.4	219.0	137.7	0.6
213273_at	ODZ4	6.71E-04	85.8	107.2	122.2	86.1	170.1	184.3	83.4	75.9	70.5	62.7	49.4	101.1	106.8	52.1	107.2	70.5	0.7
209240_at	OGT	3.85E-03	2103.3	2234.2	2431.8	2335.0	2086.4	2369.1	2008.2	1730.4	1684.4	1234.4	1943.1	1645.4	1409.6	1342.0	2234.2	1645.4	0.7
229787_s_at	OGT	5.33E-03	580.9	910.0	1148.2	1046.5	847.4	1036.3	883.1	594.4	653.8	596.7	822.4	541.5	524.4	549.0	910.0	594.4	0.7
221864_at	ORAI3	2.46E-03	960.7	1052.9	1200.4	1231.7	1022.0	1208.0	883.9	862.0	582.9	440.5	760.3	765.8	683.0	497.0	1052.9	683.0	0.6
229527_s_at	OSBPL11	5.91E-04	689.4	648.8	591.7	683.6	597.9	745.0	604.5	526.6	331.5	230.5	421.7	395.8	458.1	324.7	648.8	395.8	0.6
222586_s_at	OSBPL11	1.25E-03	1288.5	1579.0	1452.5	1781.2	1542.1	1999.2	1445.2	1186.7	1026.7	590.4	1010.5	866.2	902.6	593.3	1542.1	902.6	0.6
218304_s_at	OSBPL11	1.19E-03	2184.5	3014.5	2951.2	3050.3	2807.1	3814.5	2670.1	1822.2	1971.4	1169.4	2089.4	1238.0	1529.2	1030.9	2951.2	1529.2	0.5
209485_s_at	OSBPL1A	7.87E-03	3206.3	3736.8	3419.2	3096.6	2812.1	2740.5	2722.5	2674.1	3301.9	2248.3	2235.7	2381.1	2206.9	2208.4	3096.6	2248.3	0.7
209627_s_at	OSBPL3	1.44E-03	58.7	57.9	60.8	94.0	62.5	123.3	64.2	50.7	34.6	27.3	48.2	34.7	36.1	20.0	62.5	34.7	0.6
230032_at	OSGEPL1	9.34E-03	80.7	104.6	152.2	144.3	117.5	140.8	121.9	85.4	56.9	49.1	112.0	88.5	50.2	38.5	121.9	56.9	0.5
1559201_a_at	OSTF1	9.36E-03	96.0	95.6	102.0	107.0	91.1	112.6	105.3	94.1	75.0	75.7	88.2	74.1	76.4	78.2	102.0	76.4	0.7
208717_at	OXA1L	4.37E-03	1115.4	1257.6	1441.4	1325.5	1281.3	1403.2	1303.5	1089.8	857.6	753.2	895.4	1002.3	1007.9	811.3	1303.5	895.4	0.7
218957_s_at	PAAF1	7.85E-03	211.8	181.5	309.9	225.6	300.3	307.7	250.2	218.4	108.1	123.6	192.3	209.4	171.9	127.1	250.2	171.9	0.7
1555824_a_at	PACS2	4.22E-03	238.7	205.1	218.1	259.3	222.8	217.0	172.6	176.2	164.6	133.6	154.3	119.9	150.5	166.4	218.1	154.3	0.7
205233_s_at	PAFAH2	4.37E-03	191.2	165.3	187.4	208.3	213.5	206.7	169.3	191.2	107.1	97.1	165.4	133.7	140.3	110.6	191.2	133.7	0.7
205232_s_at	PAFAH2	9.71E-03	80.0	64.6	84.4	95.9	96.0	94.6	92.0	74.4	66.7	50.2	69.7	56.3	59.5	57.2	92.0	59.5	0.6
230100_x_at	PAK1	6.00E-03	52.6	62.0	80.3	78.8	89.0	78.4	72.4	52.5	42.6	26.2	63.4	37.9	35.6	38.5	78.4	38.5	0.5
212858_at	PAQR4	9.35E-03	179.0	133.5	138.2	139.3	161.2	135.1	126.1	165.3	80.9	69.2	111.2	115.4	116.3	96.2	138.2	111.2	0.8
220333_at	PAQR5	8.11E-03	86.6	92.6	126.5	92.2	129.7	64.6	79.9	90.6	74.4	85.9	72.4	67.8	36.0	45.4	92.2	72.4	0.8
242871_at	PAQR5	4.34E-03	160.3	194.8	248.7	150.7	214.8	108.6	172.8	158.8	135.9	117.7	115.4	95.6	40.5	67.8	172.8	115.4	0.7
213534_s_at	PASK	3.19E-03	165.4	170.2	220.3	197.5	178.1	151.0	138.7	133.9	121.9	107.4	148.7	100.3	116.5	106.9	170.2	116.5	0.7
216945_x_at	PASK	8.86E-04	173.1	183.4	166.4	198.2	152.3	137.2	105.3	118.3	141.6	94.9	147.9	99.6	99.5	78.5	166.4	99.6	0.6
214177_s_at	PBXIP1	1.37E-03	1369.7	1595.8	1661.9	1814.0	1585.2	1776.7	1290.1	1102.7	1259.5	986.1	1340.6	1138.4	1164.6	939.7	1595.8	1138.4	0.7
223712_at	PCBD2	6.40E-03	87.8	103.1	94.7	101.6	91.9	114.8	110.0	74.1	95.8	60.4	83.0	67.9	86.6	73.8	101.6	74.1	0.7
203860_at	PCCA	2.98E-04	893.6	931.0	746.6	897.6	713.1	827.1	553.1	593.1	622.2	328.3	532.3	490.8	520.4	316.1	827.1	520.4	0.6
212694_s_at	PCCB	6.45E-03	516.5	579.8	590.9	558.1	530.3	535.2	492.1	489.8	328.8	424.0	442.0	426.8	392.8	357.6	535.2	424.0	0.8
209996_x_at	PCM1	7.27E-03	448.3	384.1	452.2	442.4	395.8	459.2	438.9	354.2	297.3	311.8	330.0	388.5	353.4	337.0	442.4	337.0	0.8
209997_x_at	PCM1	1.64E-03	610.5	573.9	632.7	619.8	582.3	698.3	624.0	510.0	395.6	404.2	440.0	487.5	495.3	413.6	619.8	440.0	0.7
214118_x_at	PCM1	1.53E-03	246.8	235.4	307.6	272.1	251.3	357.8	320.4	195.3	183.2	195.3	217.8	158.7	187.6	187.9	272.1	187.9	0.7
214937_x_at	PCM1	1.53E-03	552.6	554.6	694.7	609.9	604.5	668.0	720.4	472.1	436.4	392.0	454.2	343.2	400.0	418.1	609.9	418.1	0.7
202174_s_at	PCM1	6.86E-04	1091.2	1057.0	1352.9	1198.9	1197.7	1294.9	1348.9	858.9	778.7	747.2	891.9	752.4	781.4	850.9	1198.9	781.4	0.7
212406_s_at	PCMTD2	9.37E-03	164.8	220.7	463.9	313.8	324.9	364.3	293.0	198.1	150.6	232.0	230.3	188.4	144.7	127.4	313.8	188.4	0.6
233387_s_at	PCNT	3.60E-03	334.5	338.6	300.1	344.3	283.7	297.1	296.4	269.8	226.6	194.2	238.0	198.2	273.5	236.6	300.1	236.6	0.8
203660_s_at	PCNT	6.92E-03	489.8	679.3	603.0	595.4	528.6	571.7	507.5	500.0	397.1	280.0	464.9	372.7	406.6	329.8	571.7	397.1	0.7
219295_s_at	PCOLCE2	8.35E-03	4799.7	5745.9	4199.8	4853.0	4515.4	5004.1	4825.0	4446.3	4751.9	3186.4	4295.4	3352.0	3520.7	3514.7	4825.0	3520.7	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
225274_at	PCYOX1	4.10E-03	220.0	301.1	331.8	301.8	341.1	324.4	310.2	239.4	212.4	147.8	186.0	197.6	170.3	137.4	310.2	186.0	0.6
218953_s_at	PCYOX1L	1.47E-03	455.8	828.9	572.9	733.4	456.6	835.4	540.9	367.7	423.7	157.5	474.0	271.2	292.8	198.5	572.9	292.8	0.5
212593_s_at	PDCD4	2.46E-03	3031.7	3767.6	4215.2	3960.7	3736.3	5217.7	3531.7	2562.7	2944.2	1727.6	2772.3	2367.1	2871.4	1696.4	3767.6	2562.7	0.7
202730_s_at	PDCD4	1.63E-03	468.2	601.0	728.4	638.2	589.3	884.2	498.4	425.0	408.5	310.1	406.9	370.6	435.4	230.3	601.0	406.9	0.7
202731_at	PDCD4	2.38E-03	307.0	436.0	537.4	423.0	416.5	673.4	363.8	284.0	271.6	191.2	299.5	229.2	272.8	149.9	423.0	271.6	0.6
238153_at	PDE6B	4.22E-04	197.8	155.6	193.4	170.0	150.6	171.5	131.2	145.9	93.4	131.4	125.5	107.5	108.2	91.9	170.0	108.2	0.6
204091_at	PDE6D	4.15E-03	719.1	890.4	944.3	936.6	726.1	938.3	809.6	709.3	508.1	647.4	771.9	477.8	552.3	524.7	890.4	552.3	0.6
222860_s_at	PDGFD	6.84E-03	257.1	400.7	635.6	487.5	547.5	422.6	151.6	286.0	277.0	374.5	358.6	350.7	288.4	91.3	422.6	288.4	0.7
208911_s_at	PDHB	9.87E-03	418.6	430.6	549.8	448.2	434.7	467.6	447.1	406.4	338.0	294.3	355.9	357.9	341.7	279.9	447.1	341.7	0.8
202590_s_at	PDK2	8.38E-03	86.2	85.5	103.1	98.3	91.8	108.7	79.0	66.2	60.2	55.8	72.3	80.9	77.7	74.0	91.8	72.3	0.8
206348_s_at	PDK3	5.26E-03	227.7	229.4	272.6	241.8	299.4	266.5	246.3	228.4	183.5	172.4	185.1	202.7	176.6	153.7	246.3	183.5	0.7
205960_at	PDK4	8.85E-03	411.4	727.2	296.6	271.7	348.9	502.1	283.7	350.8	300.9	52.3	215.9	282.2	171.1	68.9	348.9	215.9	0.6
208690_s_at	PDLIM1	8.89E-03	3268.0	3239.0	2094.9	2973.2	2567.7	2820.7	2084.9	2663.1	2343.9	1514.2	2497.7	1897.9	2540.3	1840.9	2820.7	2343.9	0.8
219165_at	PDLIM2	6.61E-03	291.1	232.7	330.5	318.2	291.4	376.2	295.2	246.6	127.1	150.7	220.3	237.4	331.5	193.8	295.2	220.3	0.7
221244_s_at	PDPK1	4.74E-03	710.6	764.3	754.1	842.0	781.4	787.8	703.8	660.9	589.5	544.4	592.8	607.8	630.4	534.2	764.3	592.8	0.8
223290_at	PDXP	1.10E-03	95.5	91.5	108.7	112.6	114.7	88.3	94.5	60.8	56.7	58.3	75.9	72.2	80.8	61.4	95.5	61.4	0.6
205353_s_at	PEBP1	3.83E-03	5548.6	6089.2	6168.5	5738.6	5854.8	6393.2	5789.6	4735.7	5003.8	4668.9	4842.6	3962.0	4751.4	4057.7	5854.8	4735.7	0.8
210825_s_at	PEBP1	7.22E-03	4970.3	5475.3	5872.4	5507.2	5179.1	5815.2	5717.4	4606.1	4827.2	4300.9	4419.3	3724.5	4411.5	3856.9	5507.2	4411.5	0.8
1559921_at	PECAM1	9.38E-03	361.7	371.8	336.8	378.2	353.2	368.6	335.9	313.3	284.3	226.0	278.3	328.6	318.1	244.6	361.7	284.3	0.8
208981_at	PECAM1	9.75E-04	3240.9	3741.8	3553.1	4090.7	4355.2	4403.5	3337.4	2663.2	2720.5	2250.3	3094.4	2882.5	2499.1	2238.4	3741.8	2663.2	0.7
208983_s_at	PECAM1	1.48E-03	8133.7	8764.6	7201.9	8474.2	8982.7	8670.2	7398.6	6922.7	5807.3	4135.8	5935.9	7060.2	6213.5	4681.7	8474.2	5935.9	0.7
221142_s_at	PECR	8.91E-04	258.7	341.4	483.4	497.0	513.5	587.7	366.5	210.4	277.5	272.1	320.3	315.1	350.1	225.9	483.4	277.5	0.6
230068_s_at	PEG3	7.46E-03	76.7	75.9	88.3	105.7	111.2	113.0	102.0	62.6	71.6	63.9	92.3	71.1	80.3	62.6	102.0	71.1	0.7
235431_s_at	PELI3	7.00E-04	1648.1	1865.5	1585.6	2068.0	1749.3	2355.1	1401.7	1138.8	994.9	337.8	853.9	894.0	1189.7	523.1	1749.3	894.0	0.5
205251_at	PER2	4.35E-03	732.4	909.2	905.9	816.2	698.0	1029.0	800.7	667.0	670.4	358.7	677.1	375.8	555.2	419.9	816.2	555.2	0.7
208518_s_at	PER2	3.77E-03	129.7	94.3	126.6	125.3	101.8	122.5	101.3	89.8	73.0	59.1	113.5	73.5	81.2	52.1	122.5	73.5	0.6
1555131_a_at	PER3	8.40E-03	86.4	77.0	162.8	137.6	98.3	84.1	151.3	73.0	70.0	88.4	58.1	67.0	68.6	63.0	98.3	68.6	0.7
221045_s_at	PER3	7.99E-03	115.5	164.1	211.2	189.0	129.9	140.1	208.9	107.8	132.1	100.1	144.3	75.0	112.3	97.8	164.1	107.8	0.7
205160_at	PEX11A	4.13E-03	160.6	258.4	224.1	200.5	186.6	404.2	201.3	142.2	155.6	108.5	153.1	126.7	140.6	69.3	201.3	140.6	0.7
201707_at	PEX19	6.99E-03	735.4	849.2	937.1	918.7	788.4	986.2	851.4	759.0	635.1	504.2	732.7	515.8	670.3	563.0	851.4	635.1	0.7
213302_at	PFAS	1.93E-03	395.9	388.4	461.1	479.6	403.1	428.0	468.4	317.7	325.3	265.8	372.5	281.6	279.2	284.9	428.0	284.9	0.7
238450_at	PFKFB2	2.06E-03	96.8	86.8	104.9	100.8	108.0	121.9	82.1	75.8	53.5	74.8	85.8	61.5	85.7	62.4	100.8	74.8	0.7
209992_at	PFKFB2	4.22E-03	59.1	71.3	104.6	92.8	101.7	118.4	76.6	62.8	45.1	40.7	66.3	55.8	51.7	39.9	92.8	51.7	0.6
226733_at	PFKFB2	9.01E-04	141.4	183.7	210.7	231.8	209.7	229.1	166.0	104.8	123.4	54.4	118.0	82.0	70.9	49.4	209.7	82.0	0.4
55616_at	PGAP3	6.35E-03	506.3	434.0	380.4	519.8	485.0	468.2	412.6	422.3	278.8	236.9	349.4	384.2	461.4	286.2	468.2	349.4	0.7
238004_at	PGBD2	8.35E-03	148.4	167.9	146.8	143.5	135.3	125.7	132.8	118.5	148.9	98.1	123.7	116.8	96.9	96.7	143.5	116.8	0.8
201118_at	PGD	9.12E-03	1395.4	1246.0	1434.6	1497.5	1364.5	1403.6	1424.9	1250.2	884.9	717.3	1114.3	1126.4	1207.5	981.0	1403.6	1114.3	0.8
201968_s_at	PGM1	2.68E-03	1704.6	2235.7	2065.9	1973.3	1875.4	1852.5	2062.9	1607.3	1692.4	1204.6	1483.0	1220.3	1176.9	1375.0	1973.3	1375.0	0.7
229553_at	PGM2L1	1.97E-03	315.6	239.5	224.5	221.9	198.7	199.1	216.7	241.1	166.1	163.8	191.9	158.2	135.5	151.4	221.9	163.8	0.7
226303_at	PGM5	2.47E-03	353.1	245.6	330.5	468.1	445.5	293.6	202.0	360.3	140.8	114.1	267.8	247.7	166.3	87.1	330.5	166.3	0.5
218410_s_at	PGP	8.76E-03	124.1	131.2	119.4	119.3	113.3	118.5	138.2	101.0	73.7	73.3	92.1	102.5	107.8	92.5	119.4	92.5	0.8
237202_at	PGPEP1	3.33E-03	162.8	156.2	155.2	147.4	146.7	155.3	161.2	126.9	109.2	98.7	126.7	108.3	133.8	110.3	155.3	110.3	0.7
201121_s_at	PGRMC1	5.18E-03	1375.6	1391.7	1688.4	1761.5	1569.6	1712.1	1493.7	1286.2	1201.2	1090.7	1345.2	1103.6	1208.2	1075.7	1569.6	1201.2	0.8
213638_at	PHACTR1	1.43E-03	2579.8	1946.7	2149.4	2581.3	2214.1	1987.7	3079.6	1770.5	1470.1	1723.2	1395.7	1332.2	1581.0	1816.4	2214.1	1581.0	0.7
200659_s_at	PHB	9.02E-03	691.5	568.8	504.7	542.3	469.5	469.7	530.1	483.4	375.8	279.4	434.4	424.7	451.4	311.7	530.1	424.7	0.8
217952_x_at	PHF3	2.93E-03	880.3	1013.3	1298.1	1053.4	1208.1	1376.9	900.8	796.6	778.1	847.8	805.9	777.8	779.8	667.7	1053.4	779.8	0.7
215718_s_at	PHF3	9.33E-04	931.4	1078.0	1362.5	1379.3	1138.6	1546.0	1258.8	706.7	895.1	785.8	972.0	705.9	841.2	782.5	1258.8	785.8	0.6
209439_s_at	PHKA2	7.11E-03	374.9	475.2	490.3	487.8	473.7	547.9	488.1	369.1	316.3	346.3	403.3	385.8	387.2	324.6	487.8	369.1	0.8
209438_at	PHKA2	5.32E-03	67.5	85.8	115.8	97.9	112.9	96.5	88.3	57.9	62.8	64.7	81.9	69.3	83.0	61.6	96.5	64.7	0.7
230434_at	PHOSPHO2	7.34E-03	64.1	87.8	67.0	77.8	58.9	88.5	72.7	55.5	59.2	59.7	58.3	36.0	60.3	63.7	72.7	59.2	0.8
209780_at	PHTF2	8.70E-03	2195.6	2549.5	3183.6	2696.3	2885.0	3458.1	2440.8	1986.5	2155.4	2204.3	2383.6	1383.2	1752.7	1471.0	2696.3	1986.5	0.7
203335_at	PHYH	1.57E-03	1191.7	1669.4	2089.7	1791.0	1698.3	1819.5	1817.4	1038.0	1251.7	1039.9	1289.5	901.6	943.0	903.9	1791.0	1038.0	0.6
214442_s_at	PIAS2	8.45E-03	456.6	405.2	615.4	458.7	555.4	593.0	501.0	479.1	298.4	376.0	393.7	365.4	353.2	333.9	501.0	365.4	0.7
212688_at	PIK3CB	2.22E-03	2628.0	3193.1	3172.3	3302.8	3093.1	3581.0	3137.0	2309.6	2429.0	1673.8	2555.2	1951.7	2371.8	1816.5	3172.3	2309.6	0.7
212239_at	PIK3R1	5.10E-03	527.8	559.0	743.3	754.2	710.0	670.4	756.3	571.3	358.8	382.5	556.2	443.4	357.2	329.6	710.0	382.5	0.5
1568629_s_at	PIK3R2	8.00E-03	206.3	200.8	232.8	222.1	230.8	247.4	207.3	203.8	161.8	163.0	187.1	161.3	168.8	151.9	222.1	163.0	0.7
212740_at	PIK3R4	7.90E-03	181.6	194.7	249.3	234.0	227.6	275.1	228.3	197.6	130.5	146.0	176.9	173.5	159.5	150.8	228.3	159.5	0.7
214224_s_at	PIN4	2.65E-03	1779.0	2178.3	2405.6	2083.0	2084.2	2221.2	2000.4	1606.5	1733.2	1601.1	1541.5	1468.7	1662.5	1345.7	2084.2	1601.1	0.8
204571_x_at	PIN4	3.04E-03	1591.2	1866.3	1950.9	1750.8	1814.5	1794.0	1646.5	1337.7	1488.3	1323.3	1353.0	1363.1	1461.3	1237.8	1794.0	1353.0	0.8
209019_s_at	PINK1	8.57E-04	2221.6	2194.2	2355.2	2126.6	1993.0	1990.7	1694.7	1728.9	1498.6	1021.7	1136.5	1358.5	1282.6	1067.7	2126.6	1282.6	0.6
212829_at	PIP4K2A	5.85E-03	2752.0	3072.0	2883.3	2957.9	3073.6	3197.0	2763.2	2545.0	2345.8	1773.4	2501.1	2336.8	2421.0	1951.1	2957.9	2345.8	0.8
201080_at	PIP4K2B	4.85E-03	157.9	137.2	183.6	215.4	209.3	207.0	229.1	151.7	102.1	88.7	151.6	125.7	143.7	95.3	207.0	125.7	0.6
218942_at	PIP4K2C	7.09E-03	1311.1	1507.0	1336.3	1398.2	1300.8	1336.9	1228.1	1170.3	1193.4	1084.5	1209.8	936.1	1004.9	969.2	1336.3	1084.5	0.8
219155_at	PITPNC1	3.46E-03	827.0	1279.0	986.2	943.0	1004.3	1040.2	852.0	648.8	798.7	426.4	601.5	832.9	831.3	524.7	986.2	648.8	0.7
221061_at	PKD2L1	5.58E-03	411.0	196.2	343.5	308.4	308.9	458.2	350.1	321.1	150.5	270.6	202.0	300.2	327.8	237.2	343.5	270.6	0.8
204267_x_at	PKMYT1	7.88E-03	104.9	79.9	103.4	105.8	89.3	89.9	109.7	86.4	65.6	72.1	83.3	80.0	67.6	93.2	103.4	80.0	0.8

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
212629_s_at	PKN2	7.69E-04	1832.2	2631.2	2302.2	1997.2	1954.3	2892.6	1963.5	1313.3	1705.4	935.7	1397.7	1323.1	1332.4	969.3	1997.2	1323.1	0.7
212628_at	PKN2	4.28E-03	770.8	1425.3	1247.8	1091.1	1200.1	1851.5	1363.4	719.6	789.1	464.9	833.1	815.5	685.6	464.3	1247.8	719.6	0.6
201928_at	PKP4	2.18E-03	387.3	371.2	390.1	304.0	378.1	358.3	354.7	310.2	270.4	242.9	272.2	244.3	204.4	237.1	371.2	244.3	0.7
204458_at	PLA2G15	3.21E-03	359.5	337.5	324.8	396.3	308.9	415.4	342.9	321.0	149.2	118.0	235.7	258.7	214.3	121.8	342.9	214.3	0.6
235110_at	PLA2G16	1.82E-03	253.2	286.9	296.9	265.3	246.4	254.4	266.7	212.3	219.2	158.3	210.8	141.3	165.4	151.2	265.3	165.4	0.6
210647_x_at	PLA2G6	8.86E-03	117.3	74.6	135.4	141.4	111.1	146.3	116.1	84.5	79.6	85.1	87.0	92.2	97.1	83.1	117.3	85.1	0.7
204691_x_at	PLA2G6	1.43E-03	93.5	83.5	109.7	103.3	78.9	113.0	92.5	72.6	65.6	65.2	63.9	59.2	75.2	72.7	93.5	65.6	0.7
215938_s_at	PLA2G6	4.41E-03	68.5	56.2	105.2	103.0	79.1	102.7	90.6	54.0	44.8	52.6	67.8	61.7	88.2	55.5	90.6	55.5	0.6
211668_s_at	PLAU	1.15E-03	155.6	131.1	210.0	186.3	161.8	186.2	167.6	138.2	72.1	84.2	84.1	100.9	109.5	104.9	167.6	100.9	0.6
205479_s_at	PLAU	4.60E-04	568.5	556.6	740.9	641.7	618.8	727.0	715.5	491.4	343.5	308.0	291.4	309.2	351.6	332.4	641.7	332.4	0.5
218454_at	PLBD1	2.64E-03	4526.1	4435.5	3754.3	3748.2	3937.9	4041.1	3151.2	4298.1	3298.5	2345.4	2538.6	2903.9	2677.6	2207.1	3937.9	2677.6	0.7
227276_at	PLXDC2	8.45E-04	2580.6	2803.8	2572.9	2870.9	2953.2	3195.8	2857.4	2182.0	1778.8	1183.5	1894.2	1924.6	1967.4	1529.6	2857.4	1894.2	0.7
210139_s_at	PMP22	8.55E-05	938.7	492.5	426.9	269.2	720.0	553.9	634.3	691.5	211.3	197.8	113.7	367.0	230.0	270.1	553.9	230.0	0.4
225298_at	PNKD	4.86E-03	229.5	271.7	301.5	276.6	289.8	302.2	228.0	199.2	145.9	115.3	214.6	210.5	224.1	112.1	276.6	199.2	0.7
1567213_at	PNN	5.71E-03	622.9	803.0	1019.4	911.4	632.8	737.1	774.3	610.9	635.2	788.1	688.0	435.2	444.1	499.1	774.3	610.9	0.8
220675_s_at	PNPLA3	9.91E-03	167.5	163.2	211.0	139.4	128.9	154.8	223.4	143.1	94.7	49.4	78.9	107.1	91.5	47.9	163.2	91.5	0.6
233030_at	PNPLA3	1.32E-03	1582.7	2352.9	2042.8	1346.8	1302.8	1729.1	1980.2	1204.0	973.7	310.9	565.7	684.9	518.0	403.3	1729.1	565.7	0.3
203718_at	PNPLA6	1.80E-03	919.3	1040.0	901.8	1285.8	728.3	943.8	847.2	677.9	470.2	227.4	574.4	471.1	674.6	347.7	919.3	471.1	0.5
218511_s_at	PNPO	2.77E-03	1048.1	1551.9	1352.2	1318.2	1041.8	1253.2	1150.1	934.5	955.7	639.4	1103.8	711.6	742.8	629.0	1253.2	742.8	0.6
218229_s_at	POGK	8.72E-03	1544.6	1548.7	1928.9	1640.0	1666.0	1679.9	1525.3	1374.5	1321.1	1370.9	1431.6	1039.6	1128.4	1251.5	1640.0	1321.1	0.8
204835_at	POLA1	3.99E-03	146.8	155.1	175.9	176.9	191.8	155.5	190.8	149.1	94.5	121.1	139.6	123.1	97.8	114.8	175.9	121.1	0.7
205811_at	POLG2	1.08E-03	208.8	278.0	235.8	244.0	196.9	267.5	216.5	177.3	161.0	112.3	173.0	140.8	148.0	115.9	235.8	148.0	0.6
223269_at	POLR3GL	1.83E-03	717.9	877.1	987.9	965.0	864.5	1091.1	930.3	629.5	682.6	554.2	678.6	542.9	530.6	517.5	930.3	554.2	0.6
201876_at	PON2	7.10E-03	513.9	1199.0	988.6	582.7	437.1	837.6	504.6	481.7	873.1	689.1	461.9	348.0	636.2	423.7	582.7	481.7	0.8
210830_s_at	PON2	3.84E-03	278.6	510.0	528.2	333.5	235.0	458.8	274.5	239.4	429.1	383.9	248.2	195.2	312.8	194.7	333.5	248.2	0.7
204839_at	POP5	7.00E-03	623.1	680.0	527.4	557.0	553.5	612.3	643.0	651.7	360.3	229.4	436.0	436.4	314.1	321.3	612.3	360.3	0.6
209147_s_at	PPAP2A	7.83E-03	318.2	419.2	420.3	462.1	571.0	539.8	335.1	330.1	293.6	267.5	360.4	389.1	394.8	261.0	420.3	330.1	0.8
208510_s_at	PPARG	1.54E-03	4180.1	4064.2	3839.7	4020.0	3686.5	4739.6	3357.6	3524.9	2218.3	973.9	2116.7	1916.0	2363.3	1008.5	4020.0	2116.7	0.5
208994_s_at	PPIG	7.98E-03	1516.1	1602.8	1762.9	1711.2	1647.0	1706.8	1567.1	1242.3	1414.1	1351.7	1433.3	1187.8	1405.1	1297.4	1647.0	1351.7	0.8
224364_s_at	PPIL3	1.02E-03	1062.6	1199.0	1034.1	1201.2	1084.3	1518.4	1220.6	938.0	772.4	437.5	784.5	540.9	707.0	540.4	1199.0	707.0	0.6
235344_at	PPM1A	8.52E-03	184.9	218.3	272.7	216.4	288.0	300.9	250.5	209.6	154.3	136.9	173.6	172.9	159.3	132.0	250.5	159.3	0.6
227728_at	PPM1A	7.14E-03	142.2	170.1	242.1	198.4	215.2	239.6	233.3	149.7	98.9	98.4	173.6	135.3	108.1	105.0	215.2	108.1	0.5
200726_at	PPP1CC	3.68E-04	1192.0	1358.4	1713.4	1674.4	1653.2	1668.4	1421.7	873.4	967.0	741.7	1057.9	851.7	858.5	743.4	1653.2	858.5	0.5
229001_at	PPP1R3E	7.16E-03	190.8	196.7	208.3	222.3	174.5	175.5	158.6	155.4	118.2	104.0	149.8	158.5	157.7	94.7	190.8	149.8	0.8
227412_at	PPP1R3E	4.69E-03	140.4	189.9	172.9	157.9	154.1	193.8	134.6	137.9	100.4	66.0	111.3	119.5	100.0	55.1	157.9	100.4	0.6
202187_s_at	PPP2R5A	2.15E-03	1042.3	1150.0	1268.7	1466.8	1519.9	1892.0	1335.6	1073.1	648.1	539.2	916.2	929.3	890.1	621.3	1335.6	890.1	0.7
200975_at	PPT1	8.54E-03	3907.5	4900.6	5581.9	5612.5	5275.8	5260.7	5633.5	3757.3	4195.2	4074.1	4612.1	3911.7	3264.0	3880.5	5275.8	3911.7	0.7
213483_at	PPWD1	6.73E-03	643.3	732.3	896.8	795.7	813.2	789.8	704.0	594.1	637.9	633.4	657.2	562.1	581.0	506.4	789.8	594.1	0.8
235085_at	PRAGMIN	4.14E-03	233.1	253.0	314.1	296.9	296.7	297.0	301.5	219.5	134.6	88.7	214.5	171.7	169.1	117.1	296.9	169.1	0.6
241742_at	PRAM1	1.34E-03	2502.0	2511.3	2381.3	2295.4	1955.3	2044.5	2142.0	1224.2	1088.2	283.7	866.3	1032.4	1112.3	493.0	2295.4	1032.4	0.4
230015_at	PRCD	9.42E-03	103.0	108.8	134.4	120.4	117.7	82.9	85.6	88.5	88.1	69.9	84.8	97.3	61.8	72.9	108.8	84.8	0.8
205277_at	PRDM2	5.22E-03	610.5	750.9	607.5	587.4	508.2	522.6	447.4	508.8	512.7	240.6	400.2	393.6	402.1	286.3	587.4	400.2	0.7
212217_at	PREPL	2.97E-03	233.2	281.6	268.1	265.9	281.7	331.3	253.4	221.3	162.0	100.0	194.8	182.6	169.0	114.4	268.1	169.0	0.6
212215_at	PREPL	4.30E-03	350.4	384.1	457.6	493.0	519.3	551.7	497.5	314.5	313.1	157.8	357.3	250.9	259.4	197.9	493.0	259.4	0.5
205053_at	PRIM1	8.39E-03	132.6	167.5	204.7	170.7	183.2	207.2	175.9	163.5	78.9	68.3	139.4	95.6	90.9	67.8	175.9	90.9	0.5
235780_at	PRKACB	4.47E-03	60.4	63.6	96.3	101.6	101.0	84.1	92.8	68.0	38.2	47.1	71.8	58.4	44.4	42.8	92.8	47.1	0.5
202741_at	PRKACB	3.71E-04	1741.2	1928.1	1824.6	1702.7	1733.1	1756.9	1206.2	1260.0	1047.6	579.6	1036.6	810.5	648.3	464.1	1741.2	810.5	0.5
202742_s_at	PRKACB	1.71E-03	1169.9	1438.8	1386.4	1186.7	1340.7	1502.2	1000.2	955.5	839.2	471.1	903.7	598.5	488.1	363.6	1340.7	598.5	0.4
206099_at	PRKCH	6.11E-03	1294.7	1643.0	1180.6	1194.4	1323.3	1332.5	1245.9	1264.2	954.5	798.7	996.7	931.6	1035.5	775.6	1294.7	954.5	0.7
207808_s_at	PROS1	3.77E-03	2170.1	2903.3	2688.4	2960.9	2738.2	2437.7	2261.0	1950.6	2383.0	1561.7	2325.3	1738.5	1797.8	1452.3	2688.4	1797.8	0.7
223230_at	PRPF38A	3.22E-03	967.2	851.6	972.7	926.3	961.1	881.9	959.0	781.9	695.0	577.0	745.6	705.7	684.9	699.2	959.0	699.2	0.7
203401_at	PRPS2	4.10E-03	1011.3	973.9	1243.7	1136.1	1053.8	1042.3	1012.9	885.7	737.5	837.0	1007.6	633.3	722.3	732.1	1042.3	737.5	0.7
221734_at	PRRC1	7.30E-03	2215.0	1866.1	1855.5	1839.3	1897.1	2309.9	1722.4	2020.1	1552.8	1220.4	1625.1	1382.7	1684.9	1261.5	1866.1	1552.8	0.8
224643_at	PRRC1	7.42E-03	537.4	557.0	775.3	844.3	726.8	919.1	822.9	532.5	475.0	464.0	665.0	374.9	531.4	546.6	775.3	531.4	0.7
211373_s_at	PSEN2	8.95E-03	756.4	733.7	739.7	636.4	585.5	636.5	518.7	656.8	597.8	495.3	526.4	516.5	521.1	379.6	636.5	521.1	0.8
205961_s_at	PSIP1	9.71E-03	165.1	183.9	275.2	236.5	187.7	240.2	191.9	171.2	127.3	89.4	178.7	132.6	126.6	85.4	191.9	127.3	0.7
209337_at	PSIP1	2.68E-03	220.6	238.7	390.7	387.5	346.3	384.4	292.1	226.7	129.9	121.3	248.0	164.8	181.0	142.4	346.3	164.8	0.5
228020_at	PTCD3	1.49E-03	176.7	193.6	210.4	298.3	251.1	267.2	201.5	157.6	131.3	128.0	220.2	173.7	170.5	108.8	210.4	157.6	0.7
224950_at	PTGFRN	1.73E-04	1012.6	1044.3	1230.9	1151.3	791.8	757.3	761.3	598.4	693.9	558.2	767.2	490.8	445.0	363.6	1012.6	558.2	0.6
231897_at	PTGR1	4.01E-03	924.4	1398.2	1347.0	1317.0	1702.4	1344.1	957.5	831.9	1080.1	824.6	1083.6	1234.2	1008.6	676.5	1344.1	1008.6	0.8
208617_s_at	PTP4A2	7.72E-03	2258.3	2317.3	2494.5	2409.5	2543.3	2602.7	2532.6	2035.7	1954.6	1486.3	2058.3	1929.8	1680.0	1923.3	2494.5	1929.8	0.8
208615_s_at	PTP4A2	2.60E-03	1247.5	1408.4	1348.2	1325.1	1666.1	1563.4	1398.1	1136.3	952.6	770.4	1121.6	942.6	855.1	862.9	1398.1	942.6	0.7
222404_x_at	PTPLAD1	4.74E-03	1317.4	1749.8	1402.6	1223.1	1201.4	1227.5	1158.5	1229.6	1315.1	887.7	977.4	974.0	858.9	757.8	1227.5	974.0	0.8
244050_at	PTPLAD2	2.93E-03	803.7	1128.6	1604.7	1472.5	1234.6	1463.8	874.9	674.0	880.8	991.7	1181.2	744.6	656.8	470.2	1234.6	744.6	0.6
225901_at	PTPMT1	6.46E-03	1464.7	1425.4	1456.0	1394.0	1425.5	1665.8	1317.5	1374.7	1081.4	847.3	1053.0	1191.5	1270.0	885.1	1425.5	1081.4	0.8
223808_s_at	PTPMT1	5.83E-03	3349.8	3115.1	3879.3	3547.2	3254.8	3660.7	3022.0	3189.1	2629.2	2370.2	2505.3	2421.0	2708.6	2207.1	3349.8	2505.3	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
229535_at	PTPMT1	2.27E-03	279.4	242.6	311.7	276.4	273.2	311.2	279.7	253.8	144.3	156.5	215.7	183.8	212.3	162.3	279.4	183.8	0.7
203555_at	PTPN18	5.62E-03	1716.4	2070.1	1593.2	1750.1	1601.9	1840.7	1217.3	1606.3	1181.2	770.3	1240.8	1333.2	1310.3	849.8	1716.4	1240.8	0.7
213521_at	PTPN18	6.73E-03	663.1	785.7	772.9	782.3	656.7	743.7	644.3	565.5	493.5	290.0	506.4	598.8	516.7	366.4	743.7	506.4	0.7
206060_s_at	PTPN22	1.97E-03	282.1	421.4	387.0	359.5	378.6	445.2	336.5	245.4	210.4	92.9	215.5	209.1	148.5	96.1	378.6	209.1	0.6
208010_s_at	PTPN22	9.22E-03	184.2	392.7	487.2	415.5	383.9	483.3	398.3	253.5	189.8	145.1	272.2	215.9	176.8	141.2	398.3	189.8	0.5
1555579_s_at	PTPRM	2.60E-03	927.6	907.6	928.5	1042.8	1167.3	958.2	872.9	774.5	748.5	680.5	823.4	865.3	722.9	628.3	928.5	748.5	0.8
203329_at	PTPRM	2.53E-03	816.0	798.7	774.4	826.8	931.1	728.7	714.1	694.4	636.1	536.5	624.6	699.0	568.9	534.9	798.7	624.6	0.8
1555578_at	PTPRM	7.95E-03	55.3	47.5	75.2	69.2	81.5	83.8	74.9	52.8	41.4	49.7	56.5	43.7	46.8	36.7	74.9	46.8	0.6
208121_s_at	PTPRO	8.34E-03	3361.1	4262.1	4307.8	3851.9	3722.2	4382.5	3773.3	3075.8	3707.0	2746.5	3487.1	2474.2	2877.8	2583.0	3851.9	2877.8	0.7
211846_s_at	PVRL1	8.26E-03	170.9	127.3	125.4	151.7	159.7	140.7	145.7	137.6	115.5	108.0	127.5	121.7	103.2	105.2	145.7	115.5	0.8
1558290_a_at	PVT1	5.84E-03	208.7	322.9	230.2	284.6	154.6	305.7	265.2	203.8	203.7	153.4	189.3	138.3	178.0	182.4	265.2	182.4	0.7
221666_s_at	PYCARD	4.89E-03	1911.0	1907.9	2020.3	2247.0	1777.1	2343.2	1942.4	1545.8	1189.1	592.1	1262.1	1329.9	1750.5	868.2	1942.4	1262.1	0.6
202990_at	PYGL	5.68E-04	1833.0	1262.1	1530.2	1070.6	1574.3	1741.6	1130.0	1382.6	834.5	623.2	681.7	897.0	896.1	466.2	1530.2	834.5	0.5
239857_at	QDPR	7.19E-03	155.7	173.9	229.5	228.9	189.3	218.6	186.4	143.7	133.4	121.6	193.6	111.5	156.7	143.7	189.3	143.7	0.8
1556205_at	QDPR	4.26E-04	242.1	212.3	204.5	267.9	180.0	191.6	190.5	153.3	116.7	96.9	144.4	119.9	151.1	122.7	204.5	122.7	0.6
242414_at	QPRT	8.30E-03	133.2	159.7	139.2	152.1	159.4	192.3	122.5	134.3	127.0	78.8	121.7	122.8	118.6	73.7	152.1	121.7	0.8
203831_at	R3HDM2	4.91E-03	1409.0	1559.2	2288.1	1951.9	1975.0	2117.4	2090.4	1195.0	1445.2	1586.6	1580.5	1252.9	1294.5	1343.1	1975.0	1343.1	0.7
219681_s_at	RAB11FIP1	4.49E-03	749.4	896.4	1084.2	1042.9	951.8	1154.7	1090.7	688.4	684.8	403.1	828.9	483.8	583.1	525.7	1042.9	583.1	0.6
225177_at	RAB11FIP1	1.40E-03	1578.4	1698.1	1197.9	1332.1	1128.9	1216.3	900.0	1181.3	796.0	221.5	657.7	586.6	597.2	341.9	1216.3	597.2	0.5
224482_s_at	RAB11FIP4	8.10E-03	61.4	55.6	83.4	108.1	61.9	85.3	58.1	49.5	47.6	40.7	49.7	49.0	46.0	50.4	61.9	49.0	0.8
213440_at	RAB1A	9.31E-03	1725.1	1536.9	2108.8	2069.0	1815.5	1980.7	2029.8	1455.3	1482.6	1625.7	1694.9	1388.1	1439.9	1479.9	1980.7	1479.9	0.7
209515_s_at	RAB27A	1.32E-03	707.2	688.2	686.9	971.1	695.0	737.7	993.4	596.7	526.3	421.3	691.0	481.3	547.2	630.8	707.2	547.2	0.8
203581_at	RAB4A	4.05E-03	479.7	542.2	598.9	579.8	555.5	777.7	521.6	430.4	448.9	380.9	447.4	270.2	410.8	326.1	555.5	410.8	0.7
203582_s_at	RAB4A	4.22E-03	674.6	666.1	725.0	671.0	599.7	712.1	548.1	657.8	482.2	437.8	495.2	410.3	505.5	419.1	671.0	482.2	0.7
209849_s_at	RAD51C	8.00E-03	223.6	302.0	280.6	266.0	406.8	356.8	314.5	193.9	243.8	166.5	253.7	253.3	232.5	149.2	302.0	232.5	0.8
224880_at	RALA	3.95E-03	1581.6	1378.9	1405.1	1588.7	1656.7	1338.5	1802.6	1371.1	1189.7	953.8	1263.8	1119.5	914.3	1383.5	1581.6	1189.7	0.8
202844_s_at	RALBP1	3.64E-03	882.5	938.7	1042.4	993.8	1003.5	1043.2	839.8	748.0	801.3	710.4	798.8	635.9	733.9	643.5	993.8	733.9	0.7
213019_at	RANBP6	3.26E-03	428.6	449.2	562.5	625.5	552.7	620.1	679.8	370.5	394.4	417.0	465.7	351.2	404.1	441.6	562.5	404.1	0.7
229905_at	RAP1GDS1	3.54E-03	476.4	520.7	505.8	591.1	501.8	696.9	536.3	442.0	420.1	325.0	456.6	326.2	465.8	302.8	520.7	420.1	0.8
210051_at	RAPGEF3	2.80E-03	270.4	202.9	240.8	223.0	239.8	240.0	208.2	189.4	180.1	143.9	117.6	188.1	183.0	117.2	239.8	180.1	0.8
216300_x_at	RARA	4.00E-03	205.6	170.4	261.6	268.0	204.6	282.1	204.0	168.8	128.2	117.2	194.2	163.9	190.4	135.6	205.6	163.9	0.8
203749_s_at	RARA	4.53E-03	395.2	390.7	492.9	495.0	396.3	502.9	353.4	364.4	233.1	197.0	348.8	277.2	363.7	227.4	396.3	277.2	0.7
234343_s_at	RASAL2	4.79E-03	724.5	866.7	874.8	798.2	796.5	979.4	686.3	678.2	548.0	350.7	635.3	581.7	544.9	362.7	798.2	548.0	0.7
222810_s_at	RASAL2	3.05E-03	267.0	322.9	280.6	288.5	355.7	317.7	228.4	263.1	184.3	118.1	233.0	171.7	150.4	121.4	288.5	171.7	0.6
234910_at	RASAL2	3.11E-03	528.1	815.3	753.2	839.1	789.8	934.7	655.3	588.3	438.9	305.5	553.4	390.6	467.9	326.2	789.8	438.9	0.6
219026_s_at	RASAL2	9.76E-04	332.2	375.6	415.0	472.1	388.1	502.3	357.4	284.4	209.7	163.9	335.1	207.3	255.6	159.7	388.1	209.7	0.5
227036_at	RASAL2	3.29E-03	1056.6	1600.7	1736.3	1821.2	1818.2	2179.5	1764.0	1040.6	965.0	503.0	1298.1	681.5	797.2	560.2	1764.0	797.2	0.5
214369_s_at	RASGRP2	3.14E-03	204.4	213.7	176.9	317.8	194.3	267.7	172.3	167.9	111.8	94.9	200.4	163.2	209.6	121.9	204.4	163.2	0.8
208206_s_at	RASGRP2	1.72E-03	190.6	203.7	198.7	344.8	197.7	270.7	234.3	139.7	124.2	85.4	197.7	155.2	207.5	107.5	203.7	139.7	0.7
204346_s_at	RASSF1	1.45E-03	267.1	315.1	290.2	259.7	244.8	290.4	238.9	219.0	188.0	125.5	183.8	172.8	191.0	144.9	267.1	183.8	0.7
225396_at	RBBP4	8.31E-03	218.6	187.2	206.4	236.1	274.7	256.9	248.7	228.8	149.1	117.4	184.1	182.5	178.4	164.9	236.1	178.4	0.8
210371_s_at	RBBP4	8.37E-03	824.2	919.8	1388.4	1269.5	1102.3	1362.8	1339.4	790.9	727.0	951.5	1122.2	815.4	857.0	772.9	1269.5	815.4	0.6
237333_at	RBBP4	6.80E-03	217.4	227.7	358.0	379.4	393.3	385.0	426.1	231.6	153.5	222.8	306.8	241.8	212.1	196.8	379.4	222.8	0.6
212331_at	RBL2	9.40E-03	306.8	323.3	558.7	487.6	492.1	563.2	494.1	303.4	295.7	370.0	373.7	264.3	276.2	287.2	492.1	295.7	0.6
213852_at	RBM8A	1.53E-03	352.0	339.0	423.7	485.3	397.9	391.2	430.0	315.5	252.8	194.7	322.1	208.6	204.4	220.8	397.9	220.8	0.6
225778_at	RBMS2	8.17E-03	701.7	963.4	694.6	796.5	788.5	770.2	785.4	739.6	547.3	409.5	637.8	597.5	467.6	570.3	785.4	570.3	0.7
211974_x_at	RBPJ	5.22E-03	5215.4	4793.5	4577.4	5089.6	4659.8	4701.2	3859.0	4443.7	3606.8	2398.4	3798.7	3684.8	3754.1	2865.3	4701.2	3684.8	0.8
207785_s_at	RBPJ	3.77E-03	1732.7	1677.1	2162.1	2475.8	2086.5	2433.5	1923.8	1482.2	1418.8	1355.0	2033.8	1253.5	1261.6	1213.6	2086.5	1355.0	0.6
226272_at	RCAN3	5.51E-03	253.6	334.0	298.6	308.4	286.8	310.5	269.4	254.8	218.3	185.7	264.8	187.4	181.6	185.4	298.6	187.4	0.6
224578_at	RCC2	9.76E-03	3484.5	3235.7	3340.5	4028.5	3422.4	3133.4	3189.4	2969.1	2307.9	1647.4	2915.9	2755.7	2800.9	2449.1	3340.5	2755.7	0.8
226488_at	RCCD1	4.14E-03	242.7	225.4	302.8	257.3	220.1	227.2	218.9	215.7	178.5	164.2	194.4	173.2	156.1	127.2	227.2	173.2	0.8
222666_s_at	RCL1	9.62E-03	452.2	556.1	517.9	509.4	489.2	485.5	398.2	415.6	371.9	294.4	459.5	338.8	405.2	300.1	489.2	371.9	0.8
218544_s_at	RCL1	2.43E-03	201.3	291.6	253.6	304.3	245.5	298.3	229.7	186.1	170.7	144.0	248.3	150.8	197.0	118.0	253.6	170.7	0.7
201485_s_at	RCN2	8.12E-03	386.0	354.2	382.5	386.7	316.9	349.0	362.7	307.3	251.4	229.0	311.7	302.1	281.8	270.7	362.7	281.8	0.8
227467_at	RDH10	4.39E-04	687.6	815.6	888.6	987.7	965.0	1035.8	517.6	421.6	461.0	196.6	485.8	469.7	348.0	149.5	888.6	421.6	0.5
1552378_s_at	RDH10	1.49E-03	184.5	236.1	286.7	332.8	280.5	308.7	175.4	166.7	113.7	81.4	170.4	163.7	109.7	49.0	280.5	113.7	0.4
226021_at	RDH10	1.69E-03	287.5	492.6	712.9	781.4	640.2	725.3	426.5	291.4	209.7	147.7	341.9	256.2	199.6	86.1	640.2	209.7	0.3
1559190_s_at	RDH13	3.06E-03	78.1	97.6	90.1	69.6	76.4	92.5	59.5	62.4	70.0	50.3	59.7	47.7	46.5	45.8	78.1	50.3	0.6
208873_s_at	REEP5	1.09E-03	3307.2	3392.3	3412.3	3323.9	3010.6	3600.0	2940.9	2891.4	2335.5	1559.5	2123.6	1905.0	2009.0	1740.7	3323.9	2009.0	0.6
233613_x_at	REXO2	2.06E-03	110.3	148.0	107.7	125.8	105.4	126.7	100.4	92.4	94.0	67.6	90.2	84.3	93.3	52.6	110.3	90.2	0.8
218194_at	REXO2	6.60E-04	2168.6	2243.2	1739.4	1919.6	1676.6	1928.1	1674.0	1594.4	1584.8	1046.8	1415.7	1256.3	1418.2	1064.3	1919.6	1415.7	0.7
204127_at	RFC3	5.17E-03	267.8	254.5	487.5	481.9	364.9	367.2	426.5	288.2	198.5	239.7	304.3	231.6	197.7	226.7	367.2	231.6	0.6
204023_at	RFC4	4.33E-03	323.3	282.3	293.9	324.3	305.0	282.0	273.6	285.4	190.4	185.1	280.4	170.5	196.1	215.9	293.9	196.1	0.7
208492_at	RFXAP	7.20E-03	122.7	96.3	141.6	148.3	136.2	121.4	123.5	95.8	59.4	93.9	110.6	124.9	110.1	89.4	123.5	95.8	0.8
229431_at	RFXAP	4.35E-03	29.1	46.1	71.8	49.3	58.7	65.0	58.1	26.3	33.3	31.9	39.2	41.0	28.9	29.1	58.1	31.9	0.5
228877_at	RGL3	5.48E-03	254.1	268.3	353.6	294.7	287.5	278.3	174.4	256.6	143.5	163.7	190.1	243.2	174.9	105.1	278.3	174.9	0.6

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1560348_at	RGNEF	1.49E-03	396.2	560.2	609.0	766.3	377.5	469.0	440.0	286.9	321.2	97.7	381.6	137.0	194.9	114.0	469.0	194.9	0.4
1554003_at	RGNEF	1.57E-03	911.9	1184.9	1258.1	1957.6	1162.4	1522.8	1409.9	685.1	729.6	187.0	911.2	353.1	502.4	347.9	1258.1	502.4	0.4
232994_s_at	RGNEF	2.27E-03	347.3	565.3	532.8	642.9	423.5	449.0	424.5	287.5	324.2	84.7	362.0	133.8	154.0	103.5	449.0	154.0	0.3
219610_at	RGNEF	3.37E-03	158.6	202.8	298.7	409.2	174.5	207.3	176.9	154.8	119.6	47.1	188.6	64.4	62.9	32.1	202.8	64.4	0.3
1554004_a_at	RGNEF	1.21E-03	358.1	579.2	466.2	728.0	434.7	507.9	494.5	294.1	268.2	66.0	328.9	122.7	146.5	99.9	494.5	146.5	0.3
205823_at	RGS12	6.45E-03	288.6	252.8	334.3	280.4	221.2	254.7	255.0	224.0	197.4	205.2	202.0	209.8	212.5	169.3	255.0	205.2	0.8
223809_at	RGS18	7.99E-03	78.1	234.4	216.7	263.8	315.4	626.7	173.4	69.1	176.5	107.1	156.6	263.7	177.8	78.4	234.4	156.6	0.7
232053_x_at	RHBDD2	9.29E-03	292.1	322.8	452.1	483.0	274.6	407.4	337.0	300.8	141.4	141.3	282.2	221.6	301.8	149.1	337.0	221.6	0.7
222995_s_at	RHBDD2	3.24E-03	857.2	793.6	867.5	1105.2	589.5	864.0	851.5	610.4	381.3	230.6	549.3	466.3	627.6	423.3	857.2	466.3	0.5
212099_at	RHOB	2.86E-04	2336.7	2867.1	2173.5	2185.7	1666.6	2303.2	1843.5	1594.5	1772.8	889.4	1287.0	1147.7	1186.3	1002.3	2185.7	1186.3	0.5
212651_at	RHOBTB1	2.61E-03	93.0	101.2	228.6	185.8	177.0	225.6	200.9	94.0	46.8	53.3	114.6	49.9	47.1	43.6	185.8	49.9	0.3
209441_at	RHOBTB2	3.19E-03	109.8	77.4	138.5	141.0	95.2	125.1	97.7	89.3	50.0	43.5	70.7	80.7	63.0	48.0	109.8	63.0	0.6
1554586_a_at	RHOBTB2	1.10E-03	318.1	273.2	333.1	311.7	244.2	361.4	276.7	262.4	125.7	109.0	168.1	159.5	196.8	96.4	311.7	159.5	0.5
230062_at	RIMBP3 /// RIMBP3B /// RIMBP3C	7.10E-03	174.3	169.1	192.5	198.9	199.3	270.4	216.2	174.2	104.4	76.3	96.2	180.2	155.2	129.3	198.9	129.3	0.7
219457_s_at	RIN3	8.90E-03	302.4	337.2	361.9	448.1	331.6	375.4	372.9	262.3	182.1	119.4	238.4	308.4	299.8	175.8	361.9	238.4	0.7
1555201_a_at	RMND1	1.61E-03	330.8	287.7	296.0	326.4	315.7	369.9	283.5	287.2	196.6	214.8	215.4	240.1	272.8	206.0	315.7	215.4	0.7
220329_s_at	RMND1	7.65E-03	333.7	388.2	499.5	442.6	451.5	595.9	433.4	392.8	255.6	276.2	327.8	276.9	340.8	236.3	442.6	276.9	0.6
212479_s_at	RMND5A	2.64E-03	701.4	1005.7	902.7	841.8	860.3	984.7	846.4	643.6	708.5	576.8	682.1	610.8	583.1	532.1	860.3	610.8	0.7
212482_at	RMND5A	3.16E-03	146.4	196.7	208.5	199.7	207.2	210.0	188.1	152.8	119.8	117.1	147.6	126.9	113.4	99.3	199.7	119.8	0.6
229285_at	RNASEL	4.15E-03	1212.8	1353.3	1426.6	1374.2	1488.4	1732.7	1508.7	1086.0	1047.8	972.6	1143.7	747.6	1016.2	813.2	1426.6	1016.2	0.7
221287_at	RNASEL	4.11E-03	449.3	451.7	428.3	440.7	469.7	487.7	419.2	422.1	316.1	275.5	374.5	304.4	344.3	303.7	449.3	316.1	0.7
217983_s_at	RNASET2	1.71E-03	1244.4	1518.6	1610.8	1431.4	1217.0	1259.2	1039.3	1098.2	1093.1	909.1	1003.8	921.6	815.1	613.6	1259.2	921.6	0.7
217984_at	RNASET2	1.72E-03	3011.8	3304.4	3121.5	3009.1	2747.8	2682.8	2036.4	2550.5	2316.9	1601.8	2006.1	2192.0	1702.4	1304.8	3009.1	2006.1	0.7
209565_at	RNF113A	4.50E-03	518.8	559.0	565.3	543.4	521.5	542.7	467.6	473.3	372.9	347.5	431.2	418.2	397.2	359.2	542.7	397.2	0.7
217865_at	RNF130	9.70E-03	3331.0	3530.4	3612.9	3124.1	3541.6	3083.3	2701.4	3126.1	2569.3	2198.8	2384.1	3109.2	2522.1	2011.5	3331.0	2522.1	0.8
1553127_a_at	RNF168	3.11E-03	294.7	342.1	299.8	344.6	362.9	432.1	353.6	295.7	227.2	169.3	245.0	260.4	267.1	203.1	344.6	245.0	0.7
203286_at	RNF44	7.29E-03	262.9	218.9	325.7	318.1	285.5	331.7	282.7	238.1	192.4	201.1	258.3	219.2	191.3	157.8	285.5	201.1	0.7
202683_s_at	RNMT	3.95E-03	1344.4	1233.7	1343.1	1405.4	1344.7	1406.2	1481.9	1168.2	981.9	993.6	1197.6	1003.3	1030.2	1084.4	1344.7	1030.2	0.8
218291_at	ROBLD3	8.92E-03	847.8	780.9	825.6	920.4	730.5	781.5	689.8	668.8	577.9	477.3	656.2	669.3	697.0	533.0	781.5	656.2	0.8
219550_at	ROBO3	4.85E-03	126.3	174.5	247.5	165.2	170.9	135.7	212.5	92.9	107.0	189.0	155.4	107.4	113.5	147.0	170.9	113.5	0.7
218394_at	ROGDI	4.85E-03	330.2	624.6	483.1	540.1	363.1	576.1	350.2	346.3	312.3	160.1	380.9	247.3	274.0	149.9	483.1	274.0	0.6
217122_s_at	RP11-345P4.4	8.12E-03	1039.7	1268.0	1150.5	1135.3	1064.4	1195.8	836.4	1027.8	676.7	476.2	900.6	782.0	837.9	543.6	1135.3	782.0	0.7
213478_at	RP1-21O18.1	3.99E-03	337.6	347.6	421.5	365.1	396.2	474.0	445.2	319.9	178.5	175.8	250.5	263.1	297.4	145.3	396.2	250.5	0.6
229144_at	RP1-21O18.1	2.93E-03	77.6	73.5	104.6	70.1	96.5	127.6	89.1	61.9	45.5	25.6	49.5	56.2	53.3	38.2	89.1	49.5	0.6
224826_at	RP5-1022P6.2	1.95E-03	2378.5	2148.3	2365.8	2657.8	2895.8	3140.6	2855.5	1995.3	1566.9	1356.6	2240.0	1846.2	2135.6	1695.3	2657.8	1846.2	0.7
230492_s_at	RP5-1022P6.2	4.51E-03	844.1	725.3	930.7	1222.9	1035.3	1097.7	1185.6	670.1	679.6	716.3	774.4	677.6	869.3	764.1	1035.3	716.3	0.7
224835_at	RP5-1022P6.2	4.92E-04	2815.3	2671.8	2436.4	2978.5	3255.4	3427.6	3000.3	2000.9	1756.7	979.3	1945.6	1828.0	2224.6	1579.8	2978.5	1828.0	0.6
201529_s_at	RPA1	4.14E-03	349.3	272.1	332.8	309.5	307.7	260.5	303.2	306.5	159.3	144.5	211.5	249.7	196.1	166.1	307.7	196.1	0.6
225040_s_at	RPE	5.40E-03	668.8	858.2	1001.1	781.9	760.1	895.7	670.1	611.7	689.5	527.3	677.9	481.4	525.2	433.9	781.9	527.3	0.7
225039_at	RPE	1.78E-03	300.0	420.5	439.1	397.4	375.6	470.7	358.5	269.0	275.1	245.8	312.6	236.3	237.5	189.1	397.4	245.8	0.6
221476_s_at	RPL15	9.59E-03	3883.2	4071.9	4946.7	4498.3	5109.9	5482.5	5604.8	3868.1	3327.0	3544.0	3868.2	3618.0	3534.3	3428.0	4946.7	3544.0	0.7
223415_at	RPP25	7.30E-03	96.4	76.5	97.1	125.9	105.7	98.8	82.1	72.4	68.3	40.2	64.1	72.9	71.9	66.9	97.1	68.3	0.7
219143_s_at	RPP25	5.95E-03	167.9	135.3	211.0	186.8	185.1	186.8	171.5	150.4	93.4	71.7	108.0	147.3	126.7	75.8	185.1	108.0	0.6
212553_at	RPRD2	8.22E-03	290.6	386.4	593.8	497.0	492.3	613.7	545.6	362.9	237.0	273.2	358.7	279.4	277.2	255.5	497.0	277.2	0.6
226527_at	RPRD2	5.02E-03	207.5	261.1	288.5	318.7	323.2	373.8	330.1	210.9	172.3	123.6	240.1	181.6	173.9	112.1	318.7	173.9	0.5
235415_at	RPRD2	5.68E-03	221.8	258.2	336.7	298.2	338.3	439.7	337.2	221.2	163.2	155.1	259.5	179.9	164.9	173.2	336.7	173.2	0.5
235309_at	RPS15A	2.09E-03	403.0	512.3	349.9	419.1	371.7	457.7	388.8	379.7	267.5	168.1	243.7	270.3	223.7	142.0	403.0	243.7	0.6
218007_s_at	RPS27L	5.01E-03	4518.3	4759.3	5110.3	4647.2	4628.6	5545.0	5286.6	4150.3	3846.9	3183.7	3926.5	3174.8	3829.2	3069.3	4759.3	3829.2	0.8
222487_s_at	RPS27L	1.52E-03	4423.2	4780.5	5037.7	4808.4	4675.9	5311.3	4789.3	3743.7	3783.1	3207.6	3653.5	3123.2	3506.0	2888.1	4789.3	3506.0	0.7
203379_at	RPS6KA1	4.73E-03	1092.9	1041.4	1041.9	1219.3	1057.7	1069.6	1078.9	1049.8	687.5	554.5	760.7	868.1	818.6	634.6	1069.6	760.7	0.7
212912_at	RPS6KA2	3.20E-03	204.3	145.5	253.7	132.6	170.3	184.4	176.5	180.3	70.3	113.7	98.1	136.4	101.2	73.6	176.5	101.2	0.6
221524_s_at	RRAGD	1.02E-03	3267.7	2655.0	3453.1	2819.2	2814.1	2450.1	2491.3	2555.0	2089.6	2300.3	1782.8	1884.1	1907.9	1726.2	2814.1	1907.9	0.7
221523_s_at	RRAGD	1.06E-03	922.9	962.3	1171.0	977.4	998.3	981.9	915.9	832.2	625.8	583.9	663.5	527.6	542.2	434.8	977.4	583.9	0.6
203704_s_at	RREB1	2.00E-03	2113.9	2280.1	2281.9	2560.8	2480.1	2824.5	2443.5	1854.7	1549.8	1259.4	2121.4	1578.5	1730.6	1634.9	2443.5	1634.9	0.7
214764_at	RRP15	4.14E-03	61.2	67.1	67.0	77.9	88.2	79.8	97.3	39.7	45.1	59.0	65.7	56.1	59.0	46.3	77.9	56.1	0.7
209567_at	RRS1	4.85E-03	802.1	805.5	1089.8	989.3	940.4	1427.8	1009.5	785.0	606.4	549.3	769.9	607.2	759.2	665.2	989.3	665.2	0.7
225780_at	RSC1A1	3.10E-03	416.2	431.6	598.5	463.2	520.7	580.9	555.7	360.7	258.4	277.4	410.2	326.6	318.7	241.7	520.7	318.7	0.6
223713_at	RSPH3	8.22E-03	677.1	767.5	579.4	610.0	577.9	612.6	518.5	589.3	564.2	378.9	444.5	431.2	550.7	454.3	610.0	454.3	0.7
203485_at	RTN1	5.32E-03	608.5	732.7	792.5	764.1	700.2	731.9	705.6	592.5	473.0	496.5	672.0	496.5	492.4	429.7	731.9	496.5	0.7
209360_s_at	RUNX1	3.87E-03	2165.7	2090.1	2184.7	2187.1	2494.4	2329.7	2453.9	1898.8	1681.9	1483.7	1752.9	1674.2	1868.2	1812.0	2187.1	1752.9	0.8
202449_s_at	RXRA	8.06E-03	2387.5	2626.2	2138.9	2497.1	2516.8	2467.6	2323.7	2031.5	2063.9	1680.0	2039.7	1738.0	2242.5	1832.2	2467.6	2031.5	0.8

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
202598_at	S100A13	6.23E-03	3258.1	3144.3	2587.9	2546.6	1652.1	2258.4	2766.1	2887.7	2177.1	1358.2	1689.5	1406.4	1915.3	1832.4	2587.9	1832.4	0.7
206437_at	S1PR4	6.74E-03	154.6	131.4	184.2	196.8	126.5	144.0	132.6	123.4	115.5	92.1	116.7	92.1	122.8	97.2	144.0	115.5	0.8
205449_at	SAC3D1	2.09E-03	1178.3	1488.1	1059.5	1247.3	1054.2	1170.1	936.0	1010.1	964.8	434.7	931.8	641.1	776.9	508.7	1170.1	776.9	0.7
201569_s_at	SAMM50	5.38E-03	1060.9	1298.2	908.3	957.2	838.2	1040.1	874.8	955.6	629.2	308.3	698.7	658.3	665.8	449.1	957.2	658.3	0.7
201570_at	SAMM50	3.37E-03	536.8	592.9	554.0	585.5	470.6	606.2	501.7	445.4	278.7	192.6	405.5	374.6	385.4	245.8	554.0	374.6	0.7
204900_x_at	SAP30	7.22E-03	156.6	218.5	181.2	214.0	164.7	146.1	177.0	150.3	176.7	150.6	158.3	115.3	87.8	126.7	177.0	150.3	0.8
225509_at	SAP30L	1.79E-03	244.8	300.4	314.0	333.5	396.4	362.5	246.1	217.0	207.7	161.5	247.2	225.5	157.1	124.4	314.0	207.7	0.7
213257_at	SARM1 /// TMEM199	1.06E-03	161.2	138.0	197.3	181.8	180.4	177.8	138.7	129.7	88.4	105.0	123.2	128.5	131.6	98.5	177.8	123.2	0.7
213435_at	SATB2	6.73E-03	136.7	148.8	186.5	135.6	189.6	167.7	145.7	145.3	97.4	64.5	110.3	67.4	78.1	48.2	148.8	78.1	0.5
212417_at	SCAMP1	2.84E-03	1017.7	1366.3	1994.0	1697.0	1630.2	2120.3	1694.9	895.2	1181.5	1184.4	1217.5	873.5	1233.9	1081.1	1694.9	1181.5	0.7
212416_at	SCAMP1	3.75E-03	1315.6	1678.9	2058.6	1426.0	1668.4	2148.2	1680.5	1124.1	1429.3	1137.7	1169.0	1085.6	1355.4	1138.2	1678.9	1138.2	0.7
1552256_a_at	SCARB1	1.90E-03	111.5	120.1	128.6	139.6	98.1	179.9	256.2	69.7	77.3	68.2	72.0	100.2	98.2	122.7	128.6	77.3	0.6
201825_s_at	SCCPDH	4.93E-03	2838.6	2842.6	2369.0	2308.4	2072.9	2396.6	2425.4	2099.4	2024.3	1889.9	2077.4	1601.4	2030.3	1676.8	2396.6	2024.3	0.8
201826_s_at	SCCPDH	4.50E-03	711.5	957.1	740.2	735.9	649.9	721.7	677.6	603.2	707.9	588.8	638.7	479.7	571.5	452.9	721.7	588.8	0.8
211162_x_at	SCD	7.92E-03	4872.6	4197.2	3539.0	3469.6	3221.7	3765.1	4953.2	4279.1	2738.4	2554.5	2699.3	3008.0	3029.1	3164.9	3765.1	3008.0	0.8
201339_s_at	SCP2	2.38E-03	3033.8	3002.5	3285.0	3343.5	3005.9	3420.2	3107.4	2326.6	2646.6	2259.6	2570.0	2047.0	2495.5	1826.4	3107.4	2326.6	0.7
226693_at	SDHALP2	4.28E-03	757.0	893.7	910.7	640.7	562.9	821.3	710.2	666.4	664.2	551.0	447.3	472.1	623.2	551.7	757.0	551.7	0.7
1552790_a_at	SEC62	4.09E-03	113.0	150.3	163.1	166.7	181.3	196.3	184.5	117.1	77.7	74.8	140.2	99.3	97.5	86.2	166.7	97.5	0.6
1552789_at	SEC62	8.21E-03	73.1	73.4	127.9	140.4	133.2	136.6	137.2	80.4	53.6	62.5	109.8	76.8	70.6	55.6	133.2	70.6	0.5
209879_at	SELPLG	4.16E-03	1317.7	1546.6	1284.6	1393.9	1407.7	1884.7	1352.3	1134.7	936.8	346.1	972.8	801.8	1193.2	628.2	1393.9	936.8	0.7
215113_s_at	SENP3	3.84E-03	283.5	340.2	448.8	362.0	283.9	374.7	293.9	298.0	165.0	146.4	214.1	178.7	222.3	148.4	340.2	178.7	0.5
215114_at	SENP3	2.84E-04	180.8	203.3	299.1	206.6	166.1	206.0	175.2	140.1	101.5	131.8	129.8	65.7	106.3	90.6	203.3	106.3	0.5
203871_at	SENP3	6.86E-04	1084.7	1228.1	1322.2	971.5	853.4	1147.6	774.3	832.5	673.4	397.1	515.0	519.1	570.1	368.3	1084.7	519.1	0.5
217977_at	SEPX1	7.91E-03	379.3	378.6	427.0	467.2	394.0	436.7	378.9	354.1	272.2	194.7	333.9	338.8	306.8	241.5	394.0	306.8	0.8
227369_at	SERBP1	4.98E-03	404.3	519.0	563.4	503.9	543.6	642.5	608.6	395.3	367.0	319.4	437.0	344.5	347.6	357.8	543.6	357.8	0.7
232983_s_at	SERGEF	8.71E-03	473.9	445.2	381.8	397.0	470.7	392.3	329.0	429.3	312.0	260.9	305.5	369.6	366.1	248.2	397.0	312.0	0.8
224928_at	SETD7	4.24E-04	883.3	1147.0	948.8	1030.9	1018.5	1056.4	911.2	708.1	696.1	433.6	688.2	612.2	554.3	479.1	1018.5	612.2	0.6
235338_s_at	SETDB2	7.55E-03	444.5	396.0	808.5	562.3	567.4	537.0	363.7	460.5	338.6	551.3	393.6	390.3	315.4	225.3	537.0	390.3	0.7
238684_at	SETDB2	1.31E-03	300.0	215.8	482.6	328.3	351.4	319.7	132.2	224.9	172.3	215.3	194.3	175.7	140.1	92.0	319.7	175.7	0.5
203818_s_at	SF3A3	3.07E-03	543.7	606.1	495.9	450.4	513.1	538.0	452.1	450.3	407.1	256.5	345.5	398.6	391.4	340.5	513.1	391.4	0.8
227210_at	SFMBT2	7.88E-03	193.5	101.5	213.3	214.5	147.4	131.0	209.7	197.9	92.0	87.3	121.7	98.2	72.1	105.8	193.5	98.2	0.5
212176_at	SFRS18	9.33E-03	428.2	557.1	674.8	520.8	511.7	537.6	417.9	360.0	455.9	437.4	488.2	349.3	336.2	355.6	520.8	360.0	0.7
212179_at	SFRS18	3.37E-03	386.7	532.8	785.1	715.7	592.2	771.0	703.2	369.4	371.2	381.8	523.9	405.8	355.0	374.3	703.2	374.3	0.5
225336_at	SFRS2IP	2.31E-03	1689.1	2096.2	1607.1	2597.8	2367.5	2675.6	2282.9	1579.5	1604.6	1062.7	1889.7	1618.7	1726.7	1497.9	2282.9	1604.6	0.7
217226_s_at	SFXN3	7.20E-03	693.1	749.7	567.0	726.9	587.0	710.9	573.5	595.2	423.7	387.8	531.4	510.3	582.4	460.7	693.1	510.3	0.7
226373_at	SFXN5	7.32E-03	176.4	133.5	165.1	170.0	144.1	210.4	151.6	136.1	91.6	111.8	144.6	142.3	151.5	109.9	165.1	136.1	0.8
243141_at	SGMS2	8.35E-03	530.0	649.2	448.9	512.8	580.1	744.6	568.6	501.8	409.6	327.8	506.4	360.4	437.7	343.6	568.6	409.6	0.7
222258_s_at	SH3BP4	1.06E-03	347.9	430.5	264.4	525.0	278.3	368.2	247.0	350.8	183.6	98.8	263.0	145.5	169.5	113.9	347.9	169.5	0.5
201810_s_at	SH3BP5	9.56E-03	845.7	914.6	979.4	1064.7	1024.3	1009.9	1294.2	678.4	736.8	897.0	776.6	674.8	902.1	999.8	1009.9	776.6	0.8
213252_at	SH3PXD2A	6.31E-03	150.3	112.6	134.2	110.2	105.7	112.4	107.8	116.3	88.9	79.9	89.2	81.6	90.3	94.8	112.4	89.2	0.8
224817_at	SH3PXD2A	3.82E-03	157.8	123.2	243.2	268.0	208.5	230.9	192.8	159.9	95.7	113.8	175.1	111.9	109.7	82.5	208.5	111.9	0.5
230459_s_at	SHB	1.69E-03	132.7	96.8	135.2	95.9	91.3	104.0	89.5	90.1	82.2	44.2	50.2	56.2	58.6	44.2	96.8	56.2	0.6
204656_at	SHB	1.35E-03	257.1	222.5	234.6	171.9	182.0	206.7	160.3	183.1	154.8	86.4	118.5	124.2	118.7	93.5	206.7	118.7	0.6
204657_s_at	SHB	4.37E-04	206.6	126.4	220.4	157.8	145.9	176.9	129.1	142.8	82.0	89.1	89.5	99.3	112.1	68.5	157.8	89.5	0.6
1557458_s_at	SHB	3.29E-03	265.7	272.8	478.2	307.9	312.6	310.4	319.4	271.1	139.2	101.4	127.0	129.2	154.8	60.8	310.4	129.2	0.4
224954_at	SHMT1	2.18E-03	386.9	440.8	390.1	385.4	301.1	403.5	284.2	267.4	255.8	112.4	231.0	234.1	235.9	151.2	386.9	234.1	0.6
225056_at	SIPA1L2	5.24E-03	1099.5	1831.4	1452.5	1901.0	1575.8	1063.1	1269.5	966.1	1482.1	997.6	1339.8	1167.0	902.4	1026.4	1452.5	1026.4	0.7
37831_at	SIPA1L3	8.76E-03	100.3	97.2	111.7	108.5	116.3	106.9	97.5	92.3	69.1	77.2	93.0	82.7	94.2	74.8	106.9	82.7	0.8
206934_at	SIRPB1	1.28E-03	2144.2	2201.6	1403.0	2334.5	2088.9	1615.2	651.8	1738.0	1419.9	656.8	1532.2	1415.1	965.6	496.3	2088.9	1415.1	0.7
1559034_at	SIRPB2	4.54E-03	238.9	370.6	403.9	306.7	423.8	396.1	378.1	242.0	137.2	138.5	193.1	307.7	225.4	184.9	378.1	193.1	0.5
221562_s_at	SIRT3	5.10E-03	94.0	102.6	108.2	117.7	115.3	115.2	91.9	78.9	84.5	75.3	91.6	101.2	88.5	62.3	108.2	84.5	0.8
219185_at	SIRT5	3.37E-03	221.9	188.0	252.6	211.7	243.7	262.0	183.4	213.4	147.7	129.5	134.4	174.2	160.7	102.7	221.9	147.7	0.7
229112_at	SIRT5	6.25E-04	165.3	150.6	143.4	134.9	147.4	168.4	124.3	132.8	109.7	97.8	93.3	91.4	109.6	89.3	147.4	97.8	0.7
204270_at	SKI	7.87E-05	369.1	400.4	314.8	539.0	451.3	537.9	385.5	263.4	221.5	165.5	337.5	243.0	282.5	204.0	400.4	243.0	0.6
203625_x_at	SKP2	4.58E-03	708.0	926.1	902.1	795.7	743.1	848.1	736.2	599.0	666.7	480.9	667.4	628.1	527.0	481.2	795.7	599.0	0.8
203761_at	SLA	9.99E-03	2063.8	2523.6	2640.9	2820.2	2453.3	3113.8	2847.1	2062.7	2047.0	1226.8	2352.5	1698.4	1857.1	1403.3	2640.9	1857.1	0.7
203760_s_at	SLA	5.71E-03	1784.7	1963.8	1597.0	2039.0	1360.1	1867.2	1815.3	1488.2	1188.4	651.0	1486.7	1203.2	1330.0	923.9	1815.3	1203.2	0.7
210422_x_at	SLC11A1	9.38E-03	4680.1	5853.4	5103.5	5419.6	4890.4	5069.3	5679.2	3902.6	4409.1	2630.5	3663.2	4233.0	4691.7	3316.3	5103.5	3902.6	0.8
210423_s_at	SLC11A1	2.97E-03	2379.1	3234.8	2273.5	2762.9	3211.7	3473.9	2318.1	1893.9	1896.6	1196.3	1860.0	2743.9	2853.7	1360.7	2762.9	1893.9	0.7
230382_at	SLC11A1	8.13E-03	125.3	113.7	145.4	172.5	109.7	113.6	172.1	97.0	63.5	80.9	76.4	105.3	103.6	78.4	125.3	80.9	0.6
217507_at	SLC11A1	1.63E-03	723.4	588.9	568.6	589.9	438.5	386.3	628.2	500.6	345.4	231.9	254.4	326.0	315.8	305.2	588.9	315.8	0.5
226741_at	SLC12A6	7.86E-03	654.2	909.0	1021.1	975.0	997.0	1335.1	1369.2	718.4	688.1	499.8	772.8	557.7	688.9	697.8	997.0	688.9	0.7
220740_s_at	SLC12A6	6.35E-04	2204.9	2083.2	2050.9	2396.2	2250.0	2654.2	2307.1	1679.7	1431.6	1065.0	1746.1	1532.1	1787.5	1482.0	2250.0	1532.1	0.7
220371_s_at	SLC12A9	5.58E-03	192.3	170.5	242.1	256.2	191.6	225.5	203.9	163.0	102.5	88.7	172.9	149.7	178.5	102.1	203.9	149.7	0.7
221041_s_at	SLC17A5	1.07E-03	1572.7	1662.8	1506.1	1446.5	1320.3	1474.1	1331.8	1185.7	1357.3	874.2	966.9	864.9	1100.4	937.3	1474.1	966.9	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
229639_s_at	SLC19A1	2.93E-03	151.9	127.3	126.9	145.0	131.5	156.9	114.2	131.6	86.1	99.6	92.3	109.0	114.4	82.5	131.5	99.6	0.8
1555952_at	SLC19A1	2.99E-03	57.7	66.7	76.7	88.9	88.6	106.2	82.8	55.3	41.4	41.0	69.0	62.6	53.5	47.0	82.8	53.5	0.6
1555953_at	SLC19A1	3.58E-03	124.4	161.1	122.7	136.3	137.0	133.7	91.8	92.8	72.4	45.2	84.4	92.4	59.2	85.4	133.7	84.4	0.6
209777_s_at	SLC19A1	3.76E-03	162.5	179.4	165.0	153.9	119.4	137.6	137.8	138.5	115.6	76.0	129.3	89.6	90.9	73.5	153.9	90.9	0.6
220736_at	SLC19A3	1.43E-03	1203.4	1105.9	1876.0	1458.2	1483.4	2017.4	1021.1	987.0	763.4	430.1	677.2	490.9	594.0	396.7	1458.2	594.0	0.4
239345_at	SLC19A3	5.01E-03	313.4	365.3	754.3	650.1	651.7	940.8	439.4	395.3	247.5	191.0	271.1	214.9	289.9	167.7	650.1	247.5	0.4
208916_at	SLC1A5	8.84E-03	139.6	100.9	147.4	207.1	104.6	139.2	151.2	121.5	50.2	83.7	117.7	90.3	133.3	94.1	139.6	94.1	0.7
243969_at	SLC24A4	8.39E-03	167.1	242.8	537.8	387.9	548.1	968.1	383.9	207.4	140.3	98.5	254.4	220.0	272.4	81.5	387.9	207.4	0.5
203658_at	SLC25A20	7.07E-03	431.9	700.7	515.1	570.2	456.8	557.0	411.7	420.0	396.4	196.1	442.7	356.6	351.9	203.7	515.1	356.6	0.7
228836_at	SLC25A35	4.69E-03	76.4	64.9	83.8	85.9	94.5	76.5	63.9	71.7	56.3	37.9	56.5	58.3	48.4	37.9	76.5	56.3	0.7
201919_at	SLC25A36	2.46E-03	291.7	360.2	425.7	402.7	421.1	459.0	412.9	241.4	268.3	318.3	308.8	272.7	227.4	224.3	412.9	268.3	0.6
1563498_s_at	SLC25A45	9.03E-03	53.7	74.3	82.0	74.5	93.0	96.0	63.3	58.4	41.9	34.1	70.7	43.6	41.3	36.1	74.5	41.9	0.6
226679_at	SLC26A11	6.58E-04	917.7	540.1	801.6	576.5	715.3	423.9	649.8	567.5	318.1	497.5	262.3	554.6	315.2	338.9	649.8	338.9	0.5
226728_at	SLC27A1	7.75E-03	121.1	104.8	135.0	143.1	117.7	116.1	127.4	103.6	84.5	63.3	82.3	102.5	91.6	79.6	121.1	84.5	0.7
201802_at	SLC29A1	3.43E-03	748.7	864.4	1304.0	979.0	762.9	1311.7	897.5	529.9	506.7	396.9	640.1	651.6	794.1	389.0	897.5	529.9	0.6
219344_at	SLC29A3	8.28E-03	513.1	410.0	568.9	533.2	419.6	408.0	495.7	439.8	234.0	145.6	311.1	356.6	260.2	148.1	495.7	260.2	0.5
239426_at	SLC2A8	7.82E-03	44.4	35.7	50.5	99.5	78.9	59.3	69.7	38.4	26.3	43.1	82.4	56.7	51.2	44.4	59.3	44.4	0.7
232678_at	SLC2A9	6.14E-03	66.8	58.5	53.8	72.5	72.2	65.7	65.4	51.8	55.3	36.0	54.8	45.7	53.8	51.1	65.7	51.8	0.8
226894_at	SLC35A3	7.25E-03	130.0	172.1	284.9	230.6	242.3	260.2	288.8	137.4	116.9	154.9	187.7	156.1	118.3	127.2	242.3	137.4	0.6
222647_at	SLC35C1	5.99E-03	306.5	285.3	387.5	384.9	363.5	375.3	307.6	291.8	194.5	225.5	265.6	307.1	294.5	217.4	363.5	265.6	0.7
202830_s_at	SLC37A4	9.78E-03	132.7	115.6	159.2	154.4	142.5	134.9	127.1	124.6	92.4	90.9	128.2	118.3	94.1	94.1	134.9	94.1	0.7
227046_at	SLC39A11	4.39E-03	1141.8	1478.5	1486.0	1445.9	1505.7	1369.6	1577.1	1205.0	852.8	658.1	1083.8	929.5	700.3	640.0	1478.5	852.8	0.6
224609_at	SLC44A2	8.56E-03	250.0	263.3	255.1	303.2	217.4	257.9	166.2	215.9	150.5	123.4	196.2	226.5	188.4	97.3	255.1	188.4	0.7
225175_s_at	SLC44A2	6.42E-04	592.9	556.7	570.6	726.4	498.7	571.7	321.5	459.9	343.0	250.5	415.5	366.1	339.9	161.7	570.6	343.0	0.6
225598_at	SLC45A4	2.36E-03	528.6	665.3	496.9	376.0	496.0	561.0	468.8	471.2	299.0	155.4	252.1	329.7	287.2	178.7	496.9	287.2	0.6
1552278_a_at	SLC46A1	8.59E-04	65.5	79.5	80.6	62.2	71.5	72.7	50.6	49.0	48.9	44.5	37.1	61.5	46.8	28.5	71.5	46.8	0.7
1558703_at	SLC46A1	8.22E-04	310.6	384.2	267.7	271.4	251.0	257.4	150.4	165.1	151.5	75.6	116.5	229.1	101.5	70.7	267.7	116.5	0.4
214719_at	SLC46A3	1.79E-03	545.7	661.6	801.4	702.9	751.6	715.0	484.5	468.4	351.3	192.9	383.5	450.2	267.0	166.2	702.9	351.3	0.5
219525_at	SLC47A1	4.65E-03	1320.8	1308.2	1518.5	1838.8	1608.3	1747.1	1907.3	1357.7	913.4	563.3	1159.1	998.5	760.5	679.5	1608.3	913.4	0.6
223748_at	SLC4A11	7.40E-03	302.6	396.7	442.9	351.2	365.1	263.2	284.5	294.6	323.3	158.3	240.0	254.3	116.3	133.1	351.2	240.0	0.7
1554113_a_at	SLC4A8	2.90E-03	170.0	235.6	190.5	159.0	171.4	269.6	181.7	147.1	132.2	60.6	116.2	99.2	150.4	110.1	181.7	116.2	0.6
232057_at	SLC7A6OS	5.54E-03	759.8	858.1	958.6	910.4	748.2	929.9	735.4	707.9	700.0	688.8	730.6	564.6	688.2	554.8	858.1	688.8	0.8
229153_at	SLC7A6OS	7.59E-03	175.2	156.1	230.2	208.1	220.3	194.8	163.3	180.1	107.1	146.9	177.3	154.4	140.4	108.8	194.8	146.9	0.8
216092_s_at	SLC7A8	1.57E-03	716.0	1646.0	1042.4	682.9	839.3	999.9	1064.0	625.7	885.9	387.5	400.2	555.1	474.3	351.3	999.9	474.3	0.5
216603_at	SLC7A8	1.09E-03	511.3	1151.0	911.2	467.8	543.5	709.9	874.4	335.9	520.2	199.0	259.4	348.1	331.0	267.3	709.9	331.0	0.5
217248_s_at	SLC7A8	3.66E-03	374.7	671.2	665.2	403.1	375.5	547.5	655.6	306.7	241.1	152.9	205.7	324.3	266.2	199.4	547.5	241.1	0.4
202752_x_at	SLC7A8	2.44E-03	380.2	933.0	625.1	380.5	478.6	577.8	627.7	369.7	427.7	199.0	243.5	303.8	252.4	239.5	577.8	252.4	0.4
216604_s_at	SLC7A8	5.76E-04	1293.3	2893.4	2024.0	1080.9	1202.4	1843.2	2149.5	780.6	1605.5	515.6	589.7	698.6	691.5	601.1	1843.2	691.5	0.4
209453_at	SLC9A1	3.37E-03	320.9	354.0	407.5	388.3	336.2	406.0	369.2	315.5	198.5	176.1	272.1	233.1	255.9	173.2	369.2	233.1	0.6
203909_at	SLC9A6	4.01E-03	1264.7	1523.2	1560.1	1590.2	1602.1	1825.4	1377.2	1170.7	1155.6	941.6	1298.9	1131.5	1187.4	1015.4	1560.1	1155.6	0.7
211557_x_at	SLCO2B1	5.81E-03	421.5	396.2	464.8	451.8	326.0	354.2	420.3	316.9	236.6	157.8	284.2	278.4	270.2	154.0	420.3	270.2	0.6
203472_s_at	SLCO2B1	3.66E-03	512.8	497.6	558.8	598.4	393.6	447.0	454.5	394.1	266.8	177.2	310.5	318.5	338.8	181.8	497.6	310.5	0.6
203473_at	SLCO2B1	2.29E-03	2730.3	3126.8	2821.1	2933.8	2615.6	2786.7	2534.7	2263.9	1996.6	901.4	1959.5	1565.6	1490.8	906.7	2786.7	1565.6	0.6
226743_at	SLFN11	1.48E-03	2840.4	3041.7	2946.3	2567.5	2674.4	2463.2	2315.2	2176.4	2236.6	1798.9	1993.2	1430.0	1671.8	1776.4	2674.4	1798.9	0.7
206565_x_at	SMA4	6.74E-03	1067.3	886.7	1144.8	992.7	1124.2	891.4	757.4	926.4	562.3	673.7	760.4	1036.3	692.3	552.3	992.7	692.3	0.7
215043_s_at	SMA4 /// SMA5	3.93E-03	603.6	480.3	816.2	665.3	712.3	549.9	435.5	560.4	255.3	353.2	393.9	540.2	385.5	308.3	603.6	385.5	0.6
235598_at	SMAD2	4.81E-03	705.8	741.0	857.4	789.7	824.7	947.1	877.2	616.7	596.3	625.4	659.6	535.0	619.1	710.4	824.7	619.1	0.8
235725_at	SMAD4	2.73E-03	519.4	608.6	571.3	545.9	566.0	610.7	577.5	424.3	435.8	386.6	466.9	387.8	490.0	432.8	571.3	432.8	0.8
207069_s_at	SMAD6	3.90E-03	145.4	197.3	150.1	189.6	159.8	165.2	195.9	152.3	103.8	68.7	127.6	106.9	99.2	127.2	165.2	106.9	0.6
212257_s_at	SMARCA2	3.16E-03	518.5	487.2	516.2	539.4	566.5	561.6	439.7	455.1	308.2	267.4	405.2	434.5	421.3	233.1	518.5	405.2	0.8
206544_x_at	SMARCA2	4.55E-03	496.0	572.9	801.1	768.1	609.6	804.0	601.9	509.3	421.4	364.4	540.4	391.1	439.0	300.9	609.6	421.4	0.7
206542_s_at	SMARCA2	2.88E-03	808.1	859.8	1100.4	1007.3	1013.3	1176.5	834.2	622.1	732.6	483.2	806.1	508.1	595.1	489.7	1007.3	595.1	0.6
223197_s_at	SMARCAD1	9.29E-03	398.9	389.6	401.9	412.0	423.0	429.4	398.0	375.2	315.9	319.8	365.9	302.5	302.1	282.5	401.9	315.9	0.8
211988_at	SMARCE1	8.31E-03	721.6	782.2	1086.2	1024.8	1086.1	870.4	819.0	652.2	674.3	858.1	884.3	757.5	592.7	614.8	870.4	674.3	0.8
204240_s_at	SMC2	2.52E-03	99.7	130.2	176.1	141.6	172.1	141.2	131.6	97.0	70.9	80.7	113.5	82.3	65.1	69.7	141.2	80.7	0.6
231701_s_at	SMCR8	2.51E-03	78.6	89.2	160.8	117.7	98.2	143.4	120.2	69.8	56.1	58.9	86.4	57.7	63.0	45.2	117.7	58.9	0.5
210465_s_at	SNAPC3	7.93E-03	190.3	220.7	296.4	297.9	219.5	282.3	236.9	197.5	188.6	157.7	205.2	153.2	174.0	121.5	236.9	174.0	0.7
204001_at	SNAPC3	2.02E-03	254.3	369.2	321.5	364.6	302.6	319.4	296.0	245.5	254.3	180.3	239.9	211.6	201.9	171.2	319.4	211.6	0.7
223773_s_at	SNHG12	8.52E-03	2543.8	2601.9	3675.6	3087.7	3067.6	3181.3	3758.3	2484.6	2148.1	2249.4	2643.5	2255.9	2045.6	2275.6	3087.7	2255.9	0.7
223774_at	SNHG12	8.01E-03	420.5	400.5	632.2	513.0	638.8	598.5	573.8	453.3	245.4	326.6	410.1	436.2	422.0	366.2	573.8	410.1	0.7
218493_at	SNRNP25	2.06E-03	882.5	831.8	604.5	636.2	590.0	530.4	563.6	639.5	564.2	364.8	449.7	487.2	458.9	364.1	604.5	458.9	0.8
206042_x_at	SNRPN /// SNURF	7.47E-03	407.4	524.9	554.5	427.4	490.0	513.7	393.8	344.4	378.5	336.8	340.1	421.7	446.4	296.0	490.0	344.4	0.7
213364_s_at	SNX1	5.15E-03	348.0	416.4	601.8	565.2	681.6	732.6	664.3	397.2	260.2	206.1	369.7	326.3	357.7	236.6	601.8	326.3	0.5
226683_at	SNX18	2.77E-03	862.1	1111.9	1723.1	1680.3	1441.5	1857.9	1511.5	823.3	725.3	660.3	1117.7	897.2	782.9	636.1	1511.5	782.9	0.5

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
1553961_s_at	SNX21	9.47E-03	133.4	161.9	169.7	153.4	182.7	157.9	136.0	110.3	116.2	43.4	112.6	130.7	93.5	74.3	157.9	110.3	0.7
222716_s_at	SNX24	3.46E-03	352.0	307.6	326.3	330.2	264.5	284.0	273.4	259.6	187.1	194.0	275.9	224.0	232.0	165.2	307.6	224.0	0.7
225624_at	SNX29	6.78E-03	138.2	119.9	128.5	192.0	174.1	153.0	144.6	130.1	82.9	83.2	135.3	145.0	100.2	62.6	144.6	100.2	0.7
226249_at	SNX30	5.14E-03	312.3	390.7	436.0	498.0	523.1	483.7	447.1	302.5	262.0	232.8	447.4	327.8	262.0	233.2	447.1	262.0	0.6
222417_s_at	SNX5	2.77E-03	2297.7	2458.6	2887.6	2554.2	2470.9	2925.0	2471.1	2172.1	1433.4	1111.7	1746.6	1716.1	1625.6	1229.6	2471.1	1625.6	0.7
217792_at	SNX5	9.35E-03	581.3	742.6	928.7	781.9	847.0	910.2	807.2	694.4	493.9	346.1	512.9	564.8	492.5	374.3	807.2	493.9	0.6
229980_s_at	SNX5	1.06E-03	2285.1	2552.2	3723.6	3207.8	2981.0	3927.6	3463.3	1819.2	1958.8	1754.9	2113.1	1726.9	1955.0	1538.0	3207.8	1819.2	0.6
203372_s_at	SOCS2	5.88E-03	100.6	133.9	140.0	165.9	120.1	188.1	109.3	126.3	67.2	74.3	104.7	63.1	83.3	61.8	133.9	74.3	0.6
222513_s_at	SORBS1	9.63E-03	91.3	108.6	71.6	65.0	71.3	62.8	67.3	81.8	85.7	56.7	46.9	54.7	45.3	63.0	71.3	56.7	0.8
201562_s_at	SORD	1.45E-03	266.5	300.8	345.0	322.8	298.9	289.0	300.5	196.9	238.1	175.1	239.9	181.8	168.4	129.8	300.5	181.8	0.6
201563_at	SORD	1.69E-03	322.0	365.2	542.2	523.0	478.6	453.0	396.6	298.0	254.5	244.1	315.8	272.0	180.1	199.3	453.0	254.5	0.6
212797_at	SORT1	1.86E-03	409.6	366.9	514.2	449.4	431.2	558.1	572.8	354.2	287.4	348.9	334.5	250.1	335.6	312.0	449.4	334.5	0.7
224818_at	SORT1	1.10E-03	2877.0	2732.4	2797.1	2609.7	2730.5	3142.1	2688.7	2523.2	1708.5	1500.2	1807.6	1653.8	2025.1	1932.4	2732.4	1807.6	0.7
204432_at	SOX12	6.86E-03	117.3	142.7	98.6	85.8	75.6	93.2	71.4	104.4	86.0	48.9	41.0	62.1	65.8	61.0	93.2	62.1	0.7
209736_at	SOX13	8.83E-03	75.6	66.5	93.0	84.8	91.7	86.3	77.6	78.3	50.8	54.4	58.0	46.8	64.8	59.4	84.8	58.0	0.7
201417_at	SOX4	1.53E-03	982.3	982.0	1273.3	1204.0	1119.6	832.4	907.9	788.2	549.7	621.8	781.2	655.7	585.0	314.6	982.3	621.8	0.6
201416_at	SOX4	7.80E-03	470.4	590.5	599.9	528.7	512.7	420.6	441.3	521.2	281.4	243.7	369.6	318.6	287.8	146.3	512.7	287.8	0.6
224754_at	SP1	8.91E-03	852.5	876.4	942.8	1037.5	1050.7	1083.6	1009.2	797.0	740.4	754.5	883.1	752.0	752.5	744.4	1009.2	752.5	0.7
200665_s_at	SPARC	6.89E-03	2063.6	2163.8	5589.0	4542.2	3279.0	4379.6	4130.1	2004.3	1377.5	2492.0	3339.0	2813.6	2085.9	1808.2	4130.1	2085.9	0.5
237807_at	SPATA12	8.34E-03	149.1	130.8	109.1	119.6	106.1	105.2	109.7	140.7	77.3	45.5	80.6	104.9	59.5	53.9	109.7	77.3	0.7
211704_s_at	SPIN2A /// SPIN2B	5.68E-03	341.9	492.3	420.7	445.3	376.7	419.9	297.7	354.7	274.7	264.8	334.0	252.6	301.6	214.2	419.9	274.7	0.7
228654_at	SPIN4	9.31E-03	78.3	76.2	119.5	141.9	117.5	106.0	149.2	82.8	70.8	61.7	93.3	48.6	44.0	53.2	117.5	61.7	0.5
202826_at	SPINT1	7.87E-03	220.0	159.4	179.2	198.3	179.6	146.8	150.1	161.9	107.6	63.3	99.0	176.3	112.4	86.1	179.2	107.6	0.6
1569723_a_at	SPIRE2	4.16E-04	264.1	118.5	144.8	182.4	134.9	232.3	139.8	222.4	73.1	73.5	91.9	83.1	118.0	65.8	144.8	83.1	0.6
1568916_at	SPIRE2	4.03E-03	164.7	191.0	262.9	181.7	209.5	275.5	204.7	163.0	108.5	101.4	149.8	116.4	139.7	86.0	204.7	116.4	0.6
243594_x_at	SPIRE2	1.39E-03	269.3	294.5	422.3	367.2	277.6	542.4	370.5	217.3	167.3	142.3	252.5	165.0	322.0	175.7	367.2	175.7	0.5
1568964_x_at	SPN	2.65E-03	643.4	713.4	522.3	625.7	434.3	497.4	459.9	517.4	415.5	229.7	440.1	317.0	403.6	260.1	522.3	403.6	0.8
216981_x_at	SPN	1.96E-03	2659.6	2189.2	2143.3	2361.1	1878.5	2064.0	1910.5	1885.1	1576.5	1388.0	1784.8	1483.3	1795.3	1331.7	2143.3	1576.5	0.7
206057_x_at	SPN	1.34E-03	2814.3	2320.4	2319.3	2568.8	1956.6	2085.3	2034.6	1897.1	1649.2	1412.4	1839.5	1383.8	1857.6	1334.7	2319.3	1649.2	0.7
223173_at	SPNS1	1.97E-03	293.0	225.5	256.2	253.5	222.7	274.0	195.5	199.0	172.7	136.2	164.5	168.4	237.7	120.9	253.5	168.4	0.7
46256_at	SPSB3	7.50E-03	790.8	960.6	1087.7	1016.4	928.6	967.3	789.7	700.2	657.3	585.6	714.5	824.9	775.8	595.2	960.6	700.2	0.7
226080_at	SSH2	5.48E-04	1912.3	1690.6	1680.0	1927.1	1854.4	1819.1	1337.7	1291.3	1121.0	665.7	1224.0	1122.7	1206.8	815.7	1819.1	1122.7	0.6
200957_s_at	SSRP1	5.46E-03	756.8	830.7	891.7	876.7	897.0	875.2	788.0	678.7	594.1	603.2	678.7	763.9	653.6	639.5	875.2	653.6	0.7
203016_s_at	SSX2IP	3.37E-03	125.2	166.7	244.2	213.8	196.7	222.8	183.5	132.4	109.1	106.5	146.1	100.0	94.6	81.8	196.7	106.5	0.5
207040_s_at	ST13	4.99E-03	5519.8	5612.5	5881.8	5328.7	5805.4	5988.7	5336.3	4819.8	4634.9	4371.4	4264.9	4603.6	4767.1	4034.6	5612.5	4603.6	0.8
213355_at	ST3GAL6	2.34E-03	1120.7	1155.8	1417.6	1434.9	1235.1	1396.0	1549.7	1015.1	876.3	1078.6	1014.9	740.9	877.9	905.8	1396.0	905.8	0.6
210942_s_at	ST3GAL6	2.88E-03	805.5	767.5	893.1	944.3	933.5	966.3	878.8	779.7	537.4	669.3	668.9	540.8	576.5	548.4	893.1	576.5	0.6
202440_s_at	ST5	3.97E-03	268.2	228.6	419.3	384.6	205.5	372.2	265.1	213.5	122.2	100.4	214.6	176.9	142.1	86.9	268.2	142.1	0.5
236123_at	ST7L	4.23E-03	195.7	182.3	116.5	111.8	108.9	184.8	122.4	166.9	131.2	71.3	90.2	93.7	99.2	76.2	122.4	93.7	0.8
205743_at	STAC	2.36E-03	1517.5	1660.8	2106.9	2021.0	1788.6	2540.1	1701.7	1307.5	1238.0	807.3	1233.7	509.1	856.9	627.1	1788.6	856.9	0.5
227108_at	STARD9	9.77E-03	90.8	105.0	119.2	130.3	91.3	98.3	88.4	72.6	84.7	86.0	72.8	78.6	69.6	81.9	98.3	78.6	0.8
231017_at	STK11	3.78E-03	499.1	650.5	605.1	593.9	554.3	671.7	568.0	419.7	460.0	353.8	376.0	453.9	561.3	426.9	593.9	426.9	0.7
1553117_a_at	STK38	9.29E-03	109.6	146.5	202.8	180.6	174.1	193.5	127.1	123.5	91.3	107.2	127.7	132.7	101.1	89.0	174.1	107.2	0.6
202786_at	STK39	1.07E-03	280.7	321.5	382.2	485.5	539.7	635.6	433.5	250.2	182.8	211.6	302.7	261.8	251.0	163.8	433.5	250.2	0.6
200783_s_at	STMN1	6.42E-04	922.2	1175.8	1100.9	925.2	758.0	1078.6	932.0	802.7	608.3	357.9	476.3	362.2	391.5	324.2	932.0	391.5	0.4
231795_at	STON1	5.80E-03	363.9	282.3	347.4	375.9	461.6	371.2	451.3	270.0	256.8	190.6	224.7	110.5	206.6	153.6	371.2	206.6	0.6
1552618_at	STX6	9.84E-03	630.1	582.2	430.1	482.1	484.0	447.9	461.6	449.3	384.1	306.4	430.4	401.7	432.9	322.7	482.1	401.7	0.8
244041_at	STX6	4.62E-03	74.6	87.0	117.6	103.7	118.3	99.4	96.4	71.8	57.5	36.9	57.5	80.3	53.6	57.9	99.4	57.5	0.6
212632_at	STX7	5.69E-03	1814.9	1776.8	2132.1	1931.2	2048.8	2112.9	1686.3	1569.4	1482.1	1276.7	1419.9	1654.2	1629.1	1323.9	1931.2	1482.1	0.8
203615_x_at	SULT1A1	9.91E-03	1676.2	1284.3	2082.7	2661.7	1119.9	1090.0	1258.3	1365.8	781.2	871.5	1843.3	1084.7	871.4	810.0	1284.3	871.5	0.7
226850_at	SUMF1	4.37E-03	1409.6	1445.2	1254.9	1372.3	1482.1	1772.2	1933.5	1286.0	1185.9	813.6	1114.6	1052.0	1161.5	1116.9	1445.2	1116.9	0.8
204067_at	SUOX	7.14E-04	704.6	815.4	892.3	638.7	675.2	1028.3	683.3	530.2	540.6	351.3	403.6	431.2	451.1	319.7	704.6	431.2	0.6
222566_at	SUV420H1	8.29E-04	606.2	569.8	629.9	614.0	614.2	651.0	430.8	453.2	410.9	322.0	440.5	398.5	402.1	318.6	614.0	402.1	0.7
202566_s_at	SVIL	2.38E-03	817.0	795.5	915.2	976.7	919.7	1247.0	921.0	809.5	543.8	478.5	652.9	586.6	794.8	569.6	919.7	586.6	0.6
202565_s_at	SVIL	1.68E-03	3352.2	3498.1	3653.4	4163.2	4139.8	5464.9	4368.8	2646.1	2542.7	2618.8	3303.1	2022.3	3201.4	2524.7	4139.8	2618.8	0.6
226068_at	SYK	3.53E-03	2325.2	2217.4	2373.5	2318.6	2284.5	2327.7	2181.6	2027.6	1423.9	1176.2	1753.2	1627.1	1887.8	1399.6	2318.6	1627.1	0.7
209269_s_at	SYK	7.65E-03	446.8	405.7	490.5	491.3	454.1	501.0	476.6	479.5	292.5	285.6	358.2	320.7	374.5	292.4	476.6	320.7	0.7
224669_at	SYS1	5.17E-03	757.0	840.1	886.3	763.5	879.3	929.8	749.3	762.2	650.3	572.6	592.2	560.0	604.6	419.9	840.1	592.2	0.7
1554690_a_at	TACC1	6.66E-03	337.6	346.1	392.8	370.4	404.0	409.3	368.4	364.1	197.6	244.1	273.0	300.2	284.0	207.4	370.4	273.0	0.7
200911_s_at	TACC1	6.31E-03	795.1	916.6	784.4	835.5	941.0	951.3	768.3	742.5	592.0	424.3	717.3	716.8	603.6	582.3	835.5	603.6	0.7
218308_at	TACC3	3.60E-04	622.0	624.6	629.8	681.0	565.3	541.4	535.0	436.7	397.2	294.6	458.3	367.5	372.4	295.7	622.0	372.4	0.6
235154_at	TAF3	9.54E-03	758.7	776.5	784.9	730.8	680.0	753.4	685.6	596.5	680.7	606.9	614.0	579.7	638.4	538.0	753.4	606.9	0.8
208425_s_at	TANC2	3.65E-03	158.6	176.9	152.4	190.1	217.9	214.7	173.8	179.3	78.8	90.5	120.9	111.8	123.3	83.9	176.9	111.8	0.6
224952_at	TANC2	5.40E-03	208.9	238.6	221.2	268.2	307.1	313.7	329.8	196.6	139.6	138.6	205.8	120.9	165.0	94.7	268.2	139.6	0.5
202813_at	TARBP1	6.20E-03	244.9	321.6	340.9	355.2	295.0	305.1	264.2	266.7	167.4	168.5	253.8	215.3	202.6	144.4	305.1	202.6	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
203677_s_at	TARBP2	4.92E-03	116.6	107.3	142.0	134.6	142.2	130.6	116.6	111.9	73.0	79.7	103.6	107.5	95.0	85.1	130.6	95.0	0.7
209154_at	TAX1BP3	3.18E-03	2700.7	3225.2	3783.6	3586.1	3745.6	3584.5	3397.0	2349.6	2597.9	2507.0	2979.7	2486.4	2121.5	1965.5	3584.5	2486.4	0.7
228258_at	TBC1D10C	1.99E-03	339.8	327.9	378.6	324.5	307.2	422.4	274.8	283.1	168.2	128.0	233.8	183.5	241.1	97.5	327.9	183.5	0.6
224622_at	TBC1D14	6.66E-03	188.2	157.5	246.0	264.0	271.9	203.2	224.1	188.1	116.0	152.1	181.0	201.9	168.3	133.2	224.1	168.3	0.8
230072_at	TBC1D15	8.63E-03	88.1	103.8	207.8	182.7	190.4	216.3	182.3	102.7	75.3	97.0	133.1	77.2	69.8	74.2	182.7	77.2	0.4
222173_s_at	TBC1D2	1.58E-03	501.0	265.0	400.1	385.7	399.6	331.0	359.2	332.5	144.6	184.4	218.5	343.9	261.9	187.5	385.7	218.5	0.6
227908_at	TBC1D24	1.01E-03	371.4	395.2	327.3	357.9	367.1	309.4	252.4	321.2	212.5	152.5	247.4	203.4	213.3	140.4	357.9	212.5	0.6
203387_s_at	TBC1D4	5.92E-03	1544.2	2439.7	2231.9	1811.7	2114.7	2391.0	1525.4	1440.7	1906.2	1214.7	1585.2	1407.5	1237.4	853.7	2114.7	1407.5	0.7
201814_at	TBC1D5	3.22E-03	959.8	959.6	994.5	963.8	1145.2	1146.7	976.4	869.7	707.2	567.2	755.9	845.7	832.6	623.3	976.4	755.9	0.8
222633_at	TBL1XR1	7.78E-03	1383.9	1214.9	1455.6	1489.6	1541.0	1586.4	2000.7	1265.0	987.1	978.7	1318.1	1016.4	1090.2	1020.6	1489.6	1020.6	0.7
223013_at	TBL1XR1	6.84E-03	1939.3	2275.0	2825.6	2530.9	2719.5	2838.0	3133.2	1813.0	1709.8	1593.5	2382.9	1686.7	1689.4	1634.7	2719.5	1689.4	0.6
230320_at	TBRG1	5.92E-03	262.5	341.5	352.3	355.0	346.1	382.6	325.0	278.9	232.5	188.5	288.8	209.9	214.0	202.4	346.1	214.0	0.6
226388_at	TCEA3	8.51E-04	792.1	630.6	964.5	756.7	743.6	833.0	512.9	585.0	332.5	370.8	349.7	559.6	536.2	226.1	756.7	370.8	0.5
204045_at	TCEAL1	8.13E-03	267.0	258.1	412.7	327.0	342.2	371.2	307.4	238.8	230.2	287.4	288.3	214.6	206.2	184.6	327.0	230.2	0.7
213877_x_at	TCEB2	2.49E-03	519.5	425.6	355.3	469.1	423.8	431.4	356.3	357.6	329.8	211.7	242.7	328.2	351.8	266.8	425.6	328.2	0.8
210776_x_at	TCF3	8.28E-03	943.7	741.6	840.3	890.9	830.3	743.8	842.8	801.0	656.6	607.8	681.8	650.1	615.7	711.1	840.3	656.6	0.8
213730_x_at	TCF3	6.24E-03	417.7	395.6	411.3	386.6	374.5	341.3	347.4	373.2	304.9	263.0	305.3	268.5	273.6	296.1	386.6	296.1	0.8
213811_x_at	TCF3	9.47E-03	923.2	744.2	901.5	889.9	807.3	723.6	854.3	850.4	635.2	636.4	670.3	667.2	612.8	602.6	854.3	636.4	0.7
209153_s_at	TCF3	3.50E-03	269.6	264.8	391.0	310.5	330.4	320.9	304.1	284.0	112.3	154.3	210.4	195.9	190.7	125.7	310.5	190.7	0.6
213780_at	TCHH	5.22E-03	142.3	83.3	211.7	221.1	246.2	188.5	150.0	131.0	77.5	107.6	130.4	104.6	65.6	52.3	188.5	104.6	0.6
203054_s_at	TCTA	7.74E-03	250.0	293.7	226.8	263.7	243.0	238.5	224.1	240.6	172.6	171.7	179.4	190.2	205.5	151.4	243.0	179.4	0.7
219715_s_at	TDP1	5.99E-03	127.4	149.9	186.5	165.1	115.2	174.4	126.4	130.9	85.4	96.1	137.2	85.2	96.7	73.3	149.9	96.1	0.6
225840_at	TEF	5.44E-03	164.5	148.6	214.1	178.8	127.0	174.9	143.3	148.9	90.8	87.8	130.5	100.2	88.7	103.6	164.5	100.2	0.6
221035_s_at	TEX14	3.92E-04	710.2	922.1	952.0	892.3	645.0	1078.9	905.4	506.9	455.2	311.5	427.7	392.0	482.5	276.0	905.4	427.7	0.5
218099_at	TEX2	5.87E-04	1108.2	1324.2	1113.5	1232.6	1132.5	1372.3	1080.1	883.3	729.8	393.5	739.9	639.8	591.3	418.2	1132.5	639.8	0.6
227642_at	TFCP2L1	9.22E-03	85.1	122.2	101.0	95.4	129.7	107.1	75.2	83.1	76.3	65.0	86.1	69.7	82.8	35.2	101.0	76.3	0.8
219735_s_at	TFCP2L1	5.38E-04	189.5	318.6	267.3	267.0	249.6	214.1	155.7	147.8	165.0	152.4	188.5	130.4	88.5	92.0	249.6	147.8	0.6
226157_at	TFDP2	8.22E-03	61.2	100.7	122.2	159.7	129.0	136.7	153.8	71.1	56.5	57.8	125.6	86.3	75.7	73.2	129.0	73.2	0.6
206943_at	TGFBR1	9.36E-03	215.8	182.3	249.5	235.4	236.1	268.2	272.4	228.7	128.5	172.6	189.5	156.9	188.3	137.9	236.1	172.6	0.7
224793_s_at	TGFBR1	4.69E-03	626.9	563.6	987.8	891.3	876.1	1032.5	1177.0	568.6	479.7	594.3	692.6	521.7	550.6	549.5	891.3	550.6	0.6
208944_at	TGFBR2	1.47E-03	2760.4	2874.8	3054.5	2894.5	2897.5	2987.2	2522.7	2314.6	2218.9	1881.0	2229.5	1897.0	1943.7	1812.8	2894.5	1943.7	0.7
203888_at	THBD	1.76E-03	2730.3	3035.5	1502.2	1910.8	1518.9	1977.0	3609.3	1820.8	2588.3	1063.9	1352.5	1122.9	1602.0	2562.4	1977.0	1602.0	0.8
203887_s_at	THBD	4.06E-03	929.7	1151.0	570.3	651.0	605.0	804.9	1494.6	784.6	880.1	388.6	585.6	427.6	606.1	924.0	804.9	606.1	0.8
239336_at	THBS1	6.70E-03	40.9	276.3	68.0	37.1	41.9	62.5	204.3	32.0	156.3	33.3	30.4	35.8	37.2	65.3	62.5	35.8	0.6
204064_at	THOC1	8.91E-03	1436.2	1369.5	1478.2	1418.8	1354.1	1261.6	1264.7	1183.4	1192.5	1021.9	1152.8	995.6	1132.7	1014.1	1369.5	1132.7	0.8
223711_s_at	THYN1	4.62E-03	723.5	683.5	649.3	717.1	656.2	778.9	710.4	618.7	437.6	256.2	501.0	545.2	488.8	302.3	710.4	488.8	0.7
206409_at	TIAM1	7.93E-03	203.6	186.8	243.4	245.1	271.6	227.8	249.9	194.4	132.2	191.0	178.5	231.7	182.3	176.6	243.4	182.3	0.7
213135_at	TIAM1	8.25E-04	1536.8	1506.7	1711.1	1921.2	1927.0	1836.3	1726.7	1340.3	1034.0	1139.6	1215.3	1286.0	1026.3	1087.3	1726.7	1139.6	0.7
224365_s_at	TIGD7	3.09E-03	412.0	434.3	536.5	445.7	346.5	353.7	381.4	325.2	327.2	296.1	402.7	216.5	211.3	279.8	412.0	296.1	0.7
224560_at	TIMP2	3.42E-03	8277.7	8841.7	8528.6	8045.4	8416.0	8651.7	8380.6	7240.2	7545.7	5163.8	6137.6	6164.9	6038.5	5631.9	8416.0	6137.6	0.7
231579_s_at	TIMP2	3.51E-03	9198.3	9378.3	9767.4	9349.9	9680.0	10222.5	9958.0	7783.6	8383.1	6516.0	7322.3	6869.2	7052.8	6451.3	9680.0	7052.8	0.7
204227_s_at	TK2	7.54E-03	227.2	259.5	258.0	262.3	234.8	341.9	226.8	215.2	136.0	120.9	207.1	212.9	206.6	122.3	258.0	206.6	0.8
204276_at	TK2	7.95E-04	836.3	1105.6	1032.6	1134.2	983.7	1423.2	986.5	681.5	625.0	348.2	690.8	546.4	712.1	394.9	1032.6	625.0	0.6
204277_s_at	TK2	9.24E-04	1384.2	1486.6	1390.9	1647.6	1230.6	1566.4	1072.3	843.6	828.3	416.8	834.1	871.2	1048.3	529.1	1390.9	834.1	0.6
208700_s_at	TKT	2.86E-03	4310.1	4944.8	5616.4	5202.9	5007.8	6230.7	4926.4	3648.3	3087.6	2240.2	3246.4	3929.8	4345.5	2714.2	5007.8	3246.4	0.6
208699_x_at	TKT	5.95E-03	1973.0	2190.2	2933.8	2925.4	2297.6	3307.7	2627.0	1572.7	1293.3	1088.6	1491.6	2277.0	2360.3	1357.6	2627.0	1491.6	0.6
221060_s_at	TLR4	4.37E-03	671.9	844.3	831.2	791.7	827.8	764.4	702.8	460.0	680.5	658.3	678.1	614.7	500.0	597.0	791.7	614.7	0.8
210166_at	TLR5	9.51E-03	228.2	300.1	441.8	344.4	397.4	345.2	256.6	244.7	178.2	85.6	205.7	263.4	159.0	93.0	344.4	178.2	0.5
219892_at	TM6SF1	8.25E-03	265.4	571.7	531.6	568.3	428.3	617.5	506.5	325.1	375.4	251.5	358.4	283.3	268.9	214.6	531.6	283.3	0.5
222477_s_at	TM7SF3	8.11E-03	875.9	1126.1	822.7	894.4	811.9	870.2	733.4	863.3	721.7	438.0	724.6	645.2	664.1	464.3	870.2	664.1	0.8
217974_at	TM7SF3	7.31E-03	209.2	238.5	257.4	190.0	259.9	269.5	250.6	231.8	142.8	137.2	157.2	167.7	153.9	152.2	250.6	153.9	0.6
221266_s_at	TM7SF4	1.26E-03	1294.3	1180.2	1644.0	1683.5	1496.2	478.5	1652.9	1111.8	648.2	468.5	860.1	857.8	189.3	509.0	1496.2	648.2	0.4
224755_at	TM9SF3	7.17E-03	828.3	827.6	889.5	1207.3	977.5	990.0	1316.5	823.3	712.1	517.2	933.5	675.3	617.2	772.2	977.5	712.1	0.7
204328_at	TMC6	4.34E-03	3521.6	3768.2	4062.8	3990.2	3441.5	3131.9	3569.4	3119.3	3067.4	2084.6	2760.5	2512.6	2419.3	2228.0	3569.4	2512.6	0.7
242644_at	TMC8	7.53E-03	111.6	114.3	170.7	149.1	126.4	149.8	148.9	108.3	76.3	91.2	124.6	90.0	101.4	117.9	148.9	101.4	0.7
227353_at	TMC8	6.40E-04	722.1	747.5	719.0	808.9	698.0	801.5	803.6	428.1	374.7	165.7	425.2	407.9	444.3	333.7	747.5	407.9	0.5
212352_s_at	TMED10	7.33E-03	2752.7	3296.5	3266.0	2680.3	2887.7	3301.9	3079.3	2512.5	2559.9	1947.3	2543.3	2011.2	2150.1	2001.6	3079.3	2150.1	0.7
225004_at	TMEM101	5.29E-03	1197.3	1231.6	1190.5	1310.3	1158.5	1302.3	1092.9	1059.2	906.8	701.9	1039.5	982.6	984.7	783.7	1197.3	982.6	0.8
220097_s_at	TMEM104	1.61E-03	466.2	508.3	494.5	486.9	512.6	553.6	485.9	409.1	294.4	210.5	364.2	300.9	250.9	199.7	494.5	294.4	0.6
226529_at	TMEM106B	5.69E-03	438.5	525.1	770.7	693.3	685.3	833.7	743.5	356.0	453.8	591.2	594.5	391.7	437.6	430.4	693.3	437.6	0.6
217882_at	TMEM111	2.56E-03	1489.0	1545.5	1495.0	1489.7	1381.0	1385.3	1296.0	1312.9	1069.9	981.2	1081.1	1128.1	1042.1	930.9	1489.0	1069.9	0.7
219154_at	TMEM120B	5.89E-03	97.3	85.9	99.3	95.8	97.0	129.0	94.4	77.5	67.6	62.8	70.6	80.4	52.6	60.8	97.0	67.6	0.7
225588_s_at	TMEM129	3.01E-03	1294.7	1262.0	1127.7	1167.8	1073.9	1120.7	976.7	1031.2	888.6	724.4	842.5	846.7	942.2	797.2	1127.7	846.7	0.8
228624_at	TMEM144	2.62E-03	251.9	313.5	423.0	339.9	404.4	467.9	354.3	237.7	198.8	161.5	240.9	229.2	196.7	139.8	354.3	198.8	0.6
223105_s_at	TMEM14B /// TMEM14C	8.01E-03	2410.7	2507.9	2986.6	3048.2	2752.0	3392.7	3054.8	2267.6	2321.9	2090.0	2333.2	2020.3	2156.5	2045.7	2986.6	2156.5	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
228981_at	TMEM169	6.67E-03	55.9	117.0	102.2	85.4	102.0	157.6	76.8	51.7	74.5	37.4	76.9	63.9	56.9	31.3	102.0	56.9	0.6
224929_at	TMEM173	8.92E-04	984.2	917.1	1090.8	1279.4	841.3	1218.8	959.4	668.5	561.4	271.2	668.6	445.8	668.2	423.1	984.2	561.4	0.6
224916_at	TMEM173	1.07E-03	669.1	473.0	616.5	764.1	531.1	684.8	547.9	447.4	296.3	166.9	371.7	334.4	409.1	249.8	616.5	334.4	0.5
1555790_a_at	TMEM192 /// ZNF320	7.18E-03	150.1	181.6	208.2	220.2	202.3	202.2	218.1	152.1	131.2	143.6	186.0	140.2	120.1	120.8	202.3	140.2	0.7
228671_at	TMEM201	3.89E-03	187.6	175.7	193.9	218.5	176.2	209.0	181.5	150.9	158.2	147.7	142.6	134.7	142.5	141.3	187.6	142.6	0.8
238831_at	TMEM33	8.00E-03	3120.6	3478.7	4409.6	4428.1	3516.6	4403.8	4401.3	2981.1	2992.7	3239.0	3599.6	2334.0	3090.7	3313.7	4401.3	3090.7	0.7
226361_at	TMEM42	9.35E-03	392.8	417.1	498.1	393.4	455.7	466.4	359.0	415.9	275.0	285.5	282.4	364.0	359.2	244.5	417.1	285.5	0.7
234672_s_at	TMEM48	2.29E-03	374.7	432.3	488.5	495.4	451.2	511.2	497.1	349.9	266.5	240.5	392.1	253.0	259.9	221.7	488.5	259.9	0.5
219462_at	TMEM53	5.27E-03	461.4	497.4	450.0	416.1	411.1	469.0	403.7	480.2	300.2	213.9	260.5	290.3	357.0	242.0	450.0	290.3	0.6
1554077_a_at	TMEM53	8.22E-03	333.2	287.8	360.7	376.4	297.2	356.7	353.6	315.6	170.3	160.0	212.4	227.3	328.8	213.8	353.6	213.8	0.6
234980_at	TMEM56	5.10E-03	100.4	217.2	199.9	136.6	146.1	219.1	177.3	114.1	126.0	96.5	102.9	72.1	91.5	90.3	177.3	96.5	0.5
237515_at	TMEM56	9.23E-03	27.4	81.1	93.0	76.4	99.9	106.1	88.0	38.5	42.4	25.5	42.5	43.6	19.6	15.8	88.0	38.5	0.4
221951_at	TMEM80	1.15E-03	113.7	130.0	139.3	192.8	216.3	190.4	193.7	93.2	90.7	91.1	134.7	160.7	101.4	104.6	190.4	101.4	0.5
227570_at	TMEM86A	9.28E-03	190.1	270.6	236.4	229.1	194.8	228.7	159.9	171.7	131.9	81.3	161.4	198.6	122.3	67.9	228.7	131.9	0.6
238710_at	TMEM86A	2.92E-03	386.1	386.5	412.5	423.7	454.1	437.9	334.2	378.0	170.2	175.6	251.1	351.5	222.4	131.9	412.5	222.4	0.5
229957_at	TMEM91	2.43E-03	362.4	345.9	539.2	557.7	349.9	474.8	435.3	298.2	281.9	220.7	366.0	216.7	303.4	241.0	435.3	281.9	0.6
214283_at	TMEM97	1.40E-03	774.4	766.3	634.4	699.4	671.4	739.8	594.1	617.3	536.7	425.8	498.7	524.0	501.7	482.2	699.4	501.7	0.7
226186_at	TMOD2	8.75E-03	212.3	181.0	344.0	240.7	301.5	309.2	287.1	203.1	133.0	135.8	203.9	211.8	184.4	160.6	287.1	184.4	0.6
226322_at	TMTC1	6.23E-03	66.0	51.2	64.3	144.4	101.1	117.2	34.2	61.9	32.6	26.2	109.0	54.7	54.0	28.6	66.0	54.0	0.8
225666_at	TMTC4	6.21E-03	263.3	360.3	533.9	408.4	349.0	526.6	263.8	269.1	281.4	277.9	319.2	212.0	254.2	154.4	360.3	269.1	0.7
223583_at	TNFAIP8L2	4.24E-03	850.6	982.9	967.3	1082.4	908.0	1104.3	865.0	760.3	628.9	396.2	794.4	693.0	694.9	559.3	967.3	693.0	0.7
205611_at	TNFSF12	6.72E-04	486.7	581.1	521.1	639.2	562.4	656.5	579.6	441.8	346.9	266.4	364.2	354.6	350.1	318.5	579.6	350.1	0.6
211495_x_at	TNFSF12-TNFSF13 /// TNFSF13	8.92E-03	1581.0	1492.7	1560.3	1693.7	1168.9	1457.3	1445.9	1358.7	1024.2	676.3	1138.7	1106.9	1116.9	818.9	1492.7	1106.9	0.7
209499_x_at	TNFSF12-TNFSF13 /// TNFSF13	5.03E-03	2037.6	2038.6	2014.3	2127.6	1495.2	1881.0	1889.5	1609.8	1298.4	946.2	1408.3	1392.1	1494.8	1091.4	2014.3	1392.1	0.7
209500_x_at	TNFSF12-TNFSF13 /// TNFSF13	2.08E-03	2660.7	2683.7	2668.9	2626.4	2133.3	2742.1	2397.1	2040.9	1819.0	1138.5	1652.5	1526.3	2195.0	1404.9	2660.7	1652.5	0.6
229326_at	TNFSF13	1.13E-03	5110.9	5425.3	4910.2	5117.2	4106.6	5346.3	4294.8	3804.8	3925.3	2189.4	3318.7	2773.4	3880.2	2620.2	5110.9	3318.7	0.6
210314_x_at	TNFSF13	9.79E-04	1976.0	1926.0	1869.1	2058.7	1552.2	2028.2	1796.1	1411.8	1287.1	830.5	1174.7	1169.5	1482.1	996.0	1926.0	1174.7	0.6
206393_at	TNNI2	2.16E-03	474.1	380.0	461.1	375.4	360.5	429.8	290.2	336.2	261.2	209.3	227.9	287.5	352.9	167.5	380.0	261.2	0.7
221747_at	TNS1	2.76E-03	637.3	185.2	279.7	123.8	159.7	116.9	135.3	261.2	100.5	91.5	72.4	126.1	74.7	109.3	159.7	100.5	0.6
221748_s_at	TNS1	2.26E-03	393.6	134.0	212.1	86.5	117.1	76.0	124.7	197.3	40.8	59.4	59.7	91.5	51.1	43.7	124.7	59.4	0.5
228834_at	TOB1	8.90E-03	1929.5	1631.5	1644.8	1709.6	1032.3	2237.6	1602.0	1541.8	1391.3	765.2	1312.8	886.3	1272.5	1203.2	1644.8	1272.5	0.8
200662_s_at	TOMM20	2.20E-03	2302.3	2313.6	3044.6	2553.6	2545.5	2967.7	2634.0	2059.0	1751.6	1856.7	1980.2	1808.9	2004.3	1653.9	2553.6	1856.7	0.7
225802_at	TOP1MT	4.26E-03	572.8	666.0	569.1	502.8	625.4	730.9	550.8	513.8	441.6	330.4	369.2	540.2	553.1	337.9	572.8	441.6	0.8
203786_s_at	TPD52L1	9.72E-03	126.4	220.1	539.5	292.0	430.2	490.1	361.7	117.1	163.3	221.1	187.7	407.0	211.8	139.5	361.7	187.7	0.5
210987_x_at	TPM1	4.68E-03	230.0	178.2	307.6	308.2	309.9	268.3	249.6	236.5	95.6	136.7	227.5	178.2	196.2	143.1	268.3	178.2	0.7
204083_s_at	TPM2	6.46E-03	594.5	709.0	771.6	432.1	647.2	451.7	651.5	388.8	471.9	404.1	316.0	600.0	418.0	403.4	647.2	404.1	0.6
224871_at	TPRG1L	6.11E-03	904.7	923.6	1036.7	1046.7	903.4	946.9	1017.9	777.8	729.3	681.6	679.1	751.5	839.7	731.4	946.9	731.4	0.8
204079_at	TPST2	2.99E-03	724.5	822.0	831.6	958.9	703.0	728.6	1062.6	724.9	537.7	501.7	641.1	503.2	514.2	632.3	822.0	537.7	0.7
202080_s_at	TRAK1	1.32E-03	563.2	537.5	499.2	494.5	480.8	421.0	416.8	436.8	345.3	300.3	382.9	366.2	324.4	293.8	494.5	345.3	0.7
219937_at	TRHDE	7.82E-03	279.0	506.3	726.1	529.7	561.6	734.9	367.5	323.7	371.3	327.6	349.0	266.6	252.8	115.8	529.7	323.7	0.6
218403_at	TRIAP1	5.04E-03	2446.9	2332.1	2693.3	2538.3	2521.9	2796.2	2586.6	2046.8	1963.9	1722.6	2217.5	1811.8	2095.6	1938.6	2538.3	1963.9	0.8
242056_at	TRIM45	2.98E-03	46.5	54.5	80.0	57.4	73.7	77.4	54.8	48.7	31.6	35.6	41.4	38.9	43.6	27.0	57.4	38.9	0.7
221897_at	TRIM52	8.81E-03	348.0	564.5	514.1	416.1	482.0	483.7	403.3	357.0	303.0	296.4	392.3	329.8	304.4	227.1	482.0	304.4	0.6
223132_s_at	TRIM8	4.67E-03	3515.3	3560.2	3769.1	3707.5	3726.3	4112.7	3542.2	3258.5	2787.7	1956.7	2796.2	2767.3	2896.8	2182.2	3707.5	2787.7	0.8
221012_s_at	TRIM8	1.98E-03	2282.8	2175.7	2605.5	2858.1	2528.7	2690.2	2153.9	2132.3	1505.3	1270.9	1902.4	1720.0	1680.8	1319.4	2528.7	1680.8	0.7
208178_x_at	TRIO	4.82E-03	377.9	413.7	416.6	413.4	410.7	420.3	377.1	352.4	228.1	214.7	300.7	341.1	304.1	194.2	413.4	300.7	0.7
209013_x_at	TRIO	3.32E-03	342.0	381.4	425.1	389.7	374.3	416.3	341.4	331.6	206.8	203.0	271.7	280.8	257.8	220.0	381.4	257.8	0.7
209012_at	TRIO	1.14E-03	578.2	610.9	778.2	727.5	637.8	711.3	688.6	499.8	402.3	385.4	489.3	447.4	449.7	373.1	688.6	447.4	0.6
221952_x_at	TRMT5	6.21E-03	7142.0	7250.8	9366.4	8223.0	7892.7	8883.8	8623.3	6243.1	6488.8	6687.1	7020.1	5656.6	6066.9	6012.9	8223.0	6243.1	0.8
228997_at	TRNAU1AP	8.60E-03	1160.5	1105.2	1424.5	1505.0	1191.9	1211.7	1440.1	1111.5	875.4	903.5	1134.8	1059.7	855.8	895.0	1211.7	903.5	0.7
218502_s_at	TRPS1	3.17E-03	261.0	222.6	234.6	316.7	301.7	215.7	244.7	186.5	167.6	152.1	243.6	233.9	149.9	224.4	244.7	186.5	0.8
219632_s_at	TRPV1	6.88E-03	91.4	100.1	149.6	111.3	127.4	134.4	112.2	91.0	56.7	68.3	97.1	84.2	67.6	40.0	112.2	68.3	0.6
207001_x_at	TSC22D3	5.87E-03	335.3	349.0	269.8	322.7	253.1	337.8	268.3	266.6	261.1	182.1	251.3	247.4	242.9	194.5	322.7	247.4	0.8
208763_s_at	TSC22D3	8.11E-03	2420.9	3182.7	2044.7	1957.5	1996.6	2254.7	1472.2	2280.4	2261.5	806.1	1497.4	1515.2	1323.1	999.4	2044.7	1497.4	0.7
244391_at	TSEN2	3.96E-03	130.4	153.8	222.9	185.6	165.6	255.2	156.6	110.9	93.2	105.4	128.2	107.1	88.4	40.3	165.6	105.4	0.6
219581_at	TSEN2	7.79E-03	137.9	158.6	210.0	212.4	154.1	255.5	191.5	165.4	112.7	76.9	136.2	62.5	98.1	50.6	191.5	98.1	0.5
223283_s_at	TSHZ1	7.59E-03	163.3	187.8	287.0	214.0	220.4	252.8	176.3	176.1	96.3	104.9	164.4	156.3	139.1	95.8	214.0	139.1	0.6
218245_at	TSKU	5.38E-03	153.0	122.5	101.5	200.0	82.7	128.3	98.2	131.2	84.0	57.7	112.1	82.1	73.2	67.7	122.5	82.1	0.7
203983_at	TSNAX	6.25E-03	2118.3	2290.5	2629.2	2684.6	2572.4	2884.0	2551.6	2016.5	1869.2	1681.8	2303.6	1628.3	1673.8	1700.0	2572.4	1700.0	0.7
209263_x_at	TSPAN4	6.97E-03	194.5	153.3	228.5	205.0	207.5	188.2	187.1	160.7	112.5	138.4	120.0	202.0	152.8	112.3	194.5	138.4	0.7
213122_at	TSPYL5	4.18E-03	274.8	165.4	387.5	244.7	372.3	311.6	296.8	244.4	144.9	229.6	185.3	189.2	153.2	152.2	296.8	185.3	0.6
209605_at	TST	3.22E-03	476.1	517.1	572.4	522.0	492.8	521.1	378.3	439.7	300.7	266.9	321.4	363.9	398.0	244.8	517.1	321.4	0.6

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
234004_at	TTC28	9.28E-03	57.0	65.7	87.6	87.2	69.0	84.0	67.4	46.5	44.4	46.8	69.4	59.4	72.2	53.3	69.0	53.3	0.8
213058_at	TTC28	6.44E-03	40.8	59.0	76.1	70.2	81.0	91.3	56.1	42.1	48.2	31.2	50.4	34.2	36.6	28.6	70.2	36.6	0.5
208662_s_at	TTC3	3.97E-03	412.9	433.5	455.9	478.5	488.7	543.5	485.4	380.2	275.3	248.2	392.6	381.6	363.4	311.5	478.5	363.4	0.8
208073_x_at	TTC3	6.85E-03	1295.2	1673.7	1714.1	1683.7	1871.1	1875.0	1651.6	1389.9	1172.6	916.2	1335.9	1198.9	1238.5	945.1	1683.7	1198.9	0.7
224912_at	TTC7A	1.89E-03	3025.6	3168.9	2487.0	2921.0	2477.0	2531.5	2213.3	2325.0	1983.0	888.5	1857.1	1703.7	1780.1	1242.1	2531.5	1780.1	0.7
224923_at	TTC7A	6.07E-03	532.1	486.3	479.3	512.8	414.9	415.3	379.2	444.9	296.6	203.8	355.8	357.8	325.3	247.5	479.3	325.3	0.7
205652_s_at	TTLL1	4.26E-03	126.3	145.1	163.4	148.8	164.8	162.5	145.9	132.4	88.6	60.9	94.3	106.6	97.5	70.5	148.8	94.3	0.6
213266_at	TUBGCP4	3.55E-03	116.9	104.2	120.3	134.4	129.2	141.6	159.9	104.5	84.1	64.4	104.2	80.5	92.9	80.3	129.2	84.1	0.7
224170_s_at	TULP4	2.64E-03	78.6	82.8	79.5	66.7	78.3	101.1	66.4	59.5	48.5	58.4	50.2	65.3	65.1	54.6	78.6	58.4	0.7
218184_at	TULP4	6.45E-04	522.5	603.1	566.8	540.5	673.3	692.1	534.7	443.2	321.8	319.4	390.8	330.2	373.4	306.5	566.8	330.2	0.6
203246_s_at	TUSC4	5.70E-03	431.2	413.6	465.7	441.7	403.3	401.6	353.6	393.7	259.6	193.4	327.0	296.8	299.6	229.7	413.6	296.8	0.7
217684_at	TYMS	9.55E-03	87.0	88.4	199.8	121.4	98.0	99.3	105.8	74.2	69.4	99.7	96.3	75.3	87.5	71.2	99.3	75.3	0.8
238462_at	UBASH3B	6.46E-03	339.7	394.8	382.5	464.6	347.3	298.8	488.7	375.4	240.7	132.3	308.7	232.9	159.2	215.4	382.5	232.9	0.6
228359_at	UBASH3B	1.81E-03	1252.1	1285.4	830.7	1009.7	768.2	790.9	1081.1	964.8	572.6	248.4	616.9	485.6	554.8	450.3	1009.7	554.8	0.5
238587_at	UBASH3B	2.68E-03	747.2	882.7	586.5	661.6	522.7	508.3	833.8	595.4	353.9	120.5	410.4	281.3	307.2	340.5	661.6	340.5	0.5
1557053_s_at	UBE2G2	8.24E-03	1878.2	2237.5	2522.6	2582.6	2246.5	2722.7	2636.2	1826.1	1920.2	1782.4	2100.5	1496.3	2005.4	1869.9	2522.6	1869.9	0.7
223014_at	UBE2R2	1.37E-03	2373.0	2181.3	2519.7	2213.1	2542.0	2687.9	2151.9	1849.8	1808.0	1625.1	1603.5	1826.0	1760.4	1617.4	2373.0	1760.4	0.7
218521_s_at	UBE2W	8.91E-03	390.9	431.4	829.9	795.5	632.5	844.4	672.7	403.8	393.9	484.8	549.2	386.5	456.5	453.4	672.7	453.4	0.7
202038_at	UBE4A	3.53E-03	2002.6	2272.8	2413.2	2653.9	2531.7	2764.6	2455.9	1697.2	1906.0	1741.0	2230.5	1764.3	1741.0	1635.8	2455.9	1741.0	0.7
210685_s_at	UBE4B	7.79E-03	246.0	258.6	296.3	282.6	271.5	287.7	247.9	261.4	176.8	154.1	209.6	205.9	187.3	168.3	271.5	187.3	0.7
202317_s_at	UBE4B	2.75E-03	1490.7	1627.8	1680.6	1590.1	1672.3	1664.7	1556.5	1351.7	1042.7	712.2	1227.3	985.2	1064.2	954.6	1627.8	1042.7	0.6
226746_s_at	UBE4B	1.55E-03	564.0	575.9	571.3	567.8	511.9	570.0	450.6	474.1	403.7	279.8	413.9	359.7	304.0	286.7	567.8	359.7	0.6
1555888_at	UBR5	9.18E-03	64.1	78.6	141.6	123.0	104.9	177.4	105.7	71.0	52.2	78.9	89.1	79.2	76.9	62.4	105.7	76.9	0.7
208884_s_at	UBR5	9.60E-03	703.3	830.4	1101.9	1094.7	1065.2	1394.4	814.8	640.8	719.6	770.9	888.0	690.6	751.7	664.1	1065.2	719.6	0.7
225982_at	UBTF	7.14E-03	193.6	195.6	182.1	213.8	207.4	210.8	189.3	161.3	179.8	146.1	168.7	162.3	145.7	146.4	195.6	161.3	0.8
213100_at	UNC5B	6.16E-03	162.6	159.3	215.1	286.8	232.7	290.7	244.3	169.6	95.6	84.6	204.1	166.0	179.4	109.5	232.7	166.0	0.7
41856_at	UNC5B	1.76E-03	277.5	250.8	265.7	405.9	343.0	379.1	335.6	235.9	156.4	134.9	271.4	262.3	277.2	180.2	335.6	235.9	0.7
226899_at	UNC5B	4.02E-03	284.0	317.1	276.8	462.9	462.8	493.8	456.5	296.2	149.2	122.2	343.3	300.9	283.0	202.7	456.5	283.0	0.6
208970_s_at	UROD	7.46E-03	4312.9	4446.7	3645.6	4374.1	3620.1	4222.6	3458.7	3764.0	3575.8	2617.9	3716.0	2763.4	3569.4	2773.8	4222.6	3569.4	0.8
226567_at	USP14	7.33E-03	1189.5	1222.1	1203.2	1180.7	1322.8	1469.0	1229.1	1162.8	960.1	833.6	911.1	909.4	1105.6	1002.2	1222.1	960.1	0.8
226652_at	USP3	5.86E-03	808.1	698.3	661.8	773.3	744.2	849.3	772.1	763.7	474.5	361.6	596.2	595.6	644.1	540.1	772.1	595.6	0.8
220079_s_at	USP48	2.50E-03	720.6	1100.7	1000.0	995.8	1068.7	1003.2	839.4	679.9	688.9	504.4	814.7	580.1	542.9	488.7	1000.0	580.1	0.6
213480_at	VAMP4	4.67E-03	318.2	399.0	385.7	441.5	467.1	421.9	412.9	291.9	269.7	301.5	368.9	248.9	224.7	258.7	412.9	269.7	0.7
202546_at	VAMP8	2.66E-03	8623.0	8548.4	8918.2	9784.4	8136.0	7953.0	7389.7	6718.4	6777.7	5548.6	7187.7	6704.7	6430.3	5122.2	8548.4	6704.7	0.8
230546_at	VASH1	2.12E-03	1143.6	1358.8	1068.8	1313.8	1239.8	1095.2	958.2	946.0	751.7	491.7	1078.7	751.2	708.9	673.5	1143.6	751.2	0.7
208626_s_at	VAT1	2.52E-03	4779.4	4369.0	4688.7	4420.0	4645.1	3892.6	3802.8	3893.4	3271.9	2769.2	3187.0	3540.8	3273.2	2549.3	4420.0	3271.9	0.7
226063_at	VAV2	8.10E-03	265.2	281.2	332.3	307.6	332.8	308.7	275.7	226.4	246.2	213.7	243.7	182.5	261.2	199.6	307.6	226.4	0.7
200931_s_at	VCL	4.32E-03	360.5	429.8	714.0	278.3	391.6	563.3	568.8	330.4	289.0	305.0	224.9	275.0	282.6	260.4	429.8	282.6	0.7
225483_at	VPS26B	7.12E-03	226.4	252.5	278.2	275.3	286.6	278.7	245.4	229.2	169.2	158.4	213.0	203.9	218.6	129.6	275.3	203.9	0.7
233864_s_at	VPS35	9.63E-03	1049.2	1052.7	1125.9	1318.6	1174.5	1215.3	1297.4	1024.9	878.6	897.8	989.0	941.4	901.3	923.7	1174.5	923.7	0.8
222478_at	VPS36	6.30E-03	230.9	307.4	353.7	399.7	297.7	426.9	348.1	239.7	244.0	206.5	312.6	166.7	225.5	194.3	348.1	225.5	0.6
209268_at	VPS45	8.53E-03	488.8	621.6	622.4	640.6	708.9	652.2	579.1	547.5	395.6	368.7	496.0	486.6	460.4	337.4	622.4	460.4	0.7
209553_at	VPS8	6.95E-03	297.7	381.6	632.4	517.5	556.0	652.6	447.1	354.1	228.2	309.6	377.4	341.1	351.4	214.5	517.5	341.1	0.7
203856_at	VRK1	3.63E-03	546.8	497.9	550.0	646.1	579.7	606.5	557.4	468.4	443.6	398.8	487.0	382.9	440.3	395.9	557.4	440.3	0.8
204787_at	VSIG4	6.97E-03	7608.0	8346.5	7469.3	8394.7	8296.9	8517.5	7416.2	7098.6	6125.9	4775.8	6408.8	7285.0	6649.2	4880.8	8296.9	6408.8	0.8
209452_s_at	VTI1B	9.17E-03	3880.8	3704.0	3610.0	3676.3	3712.9	3524.0	3304.1	3079.7	3147.3	2985.9	2828.2	3018.8	2997.4	2848.5	3676.3	2997.4	0.8
205011_at	VWA5A	6.53E-04	674.2	556.2	622.1	718.8	563.3	527.7	791.9	553.7	314.8	329.0	492.1	344.1	380.3	480.3	622.1	380.3	0.6
227490_at	WDFY2	3.09E-03	218.8	220.7	229.2	270.9	244.0	260.8	241.8	185.1	153.8	105.0	198.8	181.7	190.4	132.4	241.8	181.7	0.8
229597_s_at	WDFY4	1.54E-03	784.3	686.7	680.4	801.8	735.5	688.1	653.6	589.9	458.9	398.9	528.4	580.2	546.9	503.9	688.1	528.4	0.8
218512_at	WDR12	8.34E-03	251.1	313.2	355.2	373.2	297.0	341.2	376.4	265.7	191.8	241.2	332.2	189.8	186.6	207.1	341.2	207.1	0.6
211383_s_at	WDR37	4.61E-03	1495.7	1449.5	1667.3	1696.4	1470.0	1841.3	1478.8	1352.4	1140.9	883.4	1419.5	919.5	1025.0	1038.3	1495.7	1038.3	0.7
217734_s_at	WDR6	3.37E-03	6736.2	5121.1	4191.1	6155.2	3873.5	6907.0	7192.8	5193.0	3646.8	2238.8	4506.6	3031.7	5744.1	5486.2	6155.2	4506.6	0.7
214061_at	WDR67	9.73E-03	362.0	569.9	624.7	549.3	466.6	555.4	472.4	363.5	451.0	370.7	421.8	360.5	344.5	375.1	549.3	370.7	0.7
212880_at	WDR7	7.93E-03	320.0	547.8	467.3	488.9	480.7	509.1	439.1	363.5	323.9	273.7	381.6	325.8	298.3	282.1	480.7	323.9	0.7
201421_s_at	WDR77	3.93E-03	1273.4	1254.1	1382.0	1313.9	1150.0	1240.6	1196.9	1009.4	974.1	759.6	1068.8	945.7	930.8	801.3	1254.1	945.7	0.8
226738_at	WDR81	8.90E-03	534.9	484.3	533.9	570.5	492.3	485.2	418.1	453.9	302.1	283.9	421.0	450.7	426.0	278.0	492.3	421.0	0.9
218971_s_at	WDR91	1.73E-03	323.3	255.0	395.8	271.8	300.9	360.8	267.1	265.6	188.4	175.7	184.1	209.1	193.0	123.1	300.9	188.4	0.6
226668_at	WDSUB1	6.01E-03	793.8	782.0	954.6	884.6	847.6	801.0	788.6	674.2	670.0	710.4	607.7	635.5	672.8	648.1	801.0	670.0	0.8
202664_at	WIPF1	9.53E-03	1067.5	1243.6	1645.1	1525.8	1481.2	1606.2	1502.3	1038.7	1084.3	966.7	1292.6	979.6	834.8	947.9	1502.3	979.6	0.7
214699_x_at	WIPI2	2.97E-03	182.2	202.2	186.8	224.0	176.4	210.9	193.6	143.6	182.6	130.5	164.7	122.3	166.3	132.2	193.6	143.6	0.7
202132_at	WWTR1	7.07E-03	141.9	137.7	190.2	174.5	111.7	128.2	188.3	134.0	92.8	116.3	105.3	106.2	81.3	89.3	141.9	105.3	0.7
205672_at	XPA	8.73E-03	505.6	571.2	683.6	576.6	615.6	693.3	580.0	523.3	377.1	410.3	512.8	424.8	481.4	386.1	580.0	424.8	0.7
208775_at	XPO1	3.81E-03	676.9	741.9	866.8	774.2	770.8	838.4	732.2	570.5	592.3	487.4	685.1	507.6	463.5	461.9	770.8	507.6	0.7
212166_at	XPO7	9.54E-03	682.2	646.6	699.2	768.2	762.1	825.5	708.9	640.9	561.3	537.6	578.9	618.2	656.4	512.1	708.9	578.9	0.8
203655_at	XRCC1	1.75E-03	828.3	705.6	850.8	823.2	813.6	855.7	744.0	651.0	485.5	564.4	629.3	551.1	736.5	536.9	823.2	564.4	0.7
227678_at	XRCC6BP1	6.39E-03	123.9	125.3	127.9	195.7	180.7	249.8	111.2	134.1	84.8	59.0	148.9	114.5	107.6	55.3	127.9	107.6	0.8

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
229060_at	YPEL2	5.95E-03	193.7	184.5	187.6	194.8	224.1	230.0	156.5	172.7	138.3	70.4	138.7	173.1	129.1	67.7	193.7	138.3	0.7
201020_at	YWHAH	2.09E-03	2446.0	2840.5	2112.6	2527.4	2186.9	2628.1	2408.4	2106.7	2089.1	1275.4	2022.7	1644.1	1785.4	1606.3	2446.0	1785.4	0.7
224711_at	YY1	6.54E-04	609.4	657.2	616.1	653.1	722.0	655.6	627.8	511.9	392.7	375.5	464.2	450.4	463.1	391.0	653.1	450.4	0.7
224718_at	YY1	7.23E-03	625.7	733.8	723.3	684.1	807.3	782.5	652.5	638.4	464.7	364.3	475.0	634.4	563.2	466.4	723.3	475.0	0.7
227977_at	ZADH2	3.30E-03	130.7	177.7	144.6	178.3	129.6	171.0	140.7	131.6	88.9	75.8	131.9	90.3	103.5	75.5	144.6	90.3	0.6
1554239_s_at	ZADH2	3.48E-03	521.6	571.8	504.5	654.4	474.6	607.4	565.5	510.7	390.6	268.8	498.8	323.0	309.7	340.5	565.5	340.5	0.6
227049_at	ZADH2	9.74E-03	125.6	188.2	162.5	212.0	155.7	212.6	195.5	146.6	122.1	54.8	151.5	103.0	92.5	75.0	188.2	103.0	0.5
226255_at	ZBTB33	1.61E-03	971.4	1185.3	1786.2	1498.3	1544.6	1667.1	1320.9	819.4	887.6	1104.3	1216.4	892.9	1011.3	788.1	1498.3	892.9	0.6
227047_x_at	ZBTB4	3.94E-03	256.6	269.4	357.4	289.0	338.0	367.5	294.4	257.3	168.6	181.8	209.6	253.0	211.7	185.8	294.4	209.6	0.7
225629_s_at	ZBTB4	8.51E-04	6430.7	6766.5	7174.8	7104.7	7443.1	7630.6	7250.7	5065.3	5285.4	3617.4	4368.2	5058.1	4558.3	4566.2	7174.8	4566.2	0.6
203959_s_at	ZBTB40	8.53E-03	494.1	518.8	512.9	553.3	531.3	552.0	503.5	435.3	364.0	353.2	460.4	382.7	471.9	441.9	518.8	435.3	0.8
1554470_s_at	ZBTB44	7.98E-03	243.0	339.1	395.8	411.8	437.3	479.7	392.2	301.6	237.6	186.7	265.8	234.5	258.8	195.8	395.8	237.6	0.6
226148_at	ZBTB44	9.35E-03	692.8	923.2	1183.4	965.3	1246.0	1487.3	1182.8	722.9	718.4	630.5	840.8	575.2	653.1	622.6	1182.8	653.1	0.6
226500_at	ZBTB47	3.53E-03	254.5	235.1	183.3	222.7	191.3	193.6	168.2	193.4	145.6	95.8	166.2	154.8	147.4	138.3	193.6	147.4	0.8
227782_at	ZBTB7C	3.37E-03	161.0	148.6	178.6	179.4	148.8	97.6	118.6	179.2	96.4	82.2	104.9	82.2	49.2	67.1	148.8	82.2	0.6
235142_at	ZBTB8A	6.58E-03	94.0	80.5	150.6	136.0	135.8	110.9	121.2	99.7	52.3	88.8	101.6	64.1	79.1	54.0	121.2	79.1	0.7
223107_s_at	ZCCHC17	2.65E-03	656.7	668.7	569.8	589.5	625.5	601.7	532.1	564.0	468.2	375.2	426.5	498.2	484.0	399.2	601.7	468.2	0.8
212423_at	ZCCHC24	6.26E-03	151.2	175.4	189.8	241.1	135.1	156.4	127.4	160.6	109.7	74.2	137.0	103.7	99.7	68.5	156.4	103.7	0.7
212419_at	ZCCHC24	3.93E-03	355.1	422.2	459.1	631.7	321.6	398.2	262.2	353.4	204.3	127.2	330.6	218.3	225.5	132.2	398.2	218.3	0.5
225394_s_at	ZCRB1	7.32E-03	2690.0	2415.1	2448.1	2761.3	2466.9	2910.4	2511.9	2144.0	1984.4	2081.0	2184.3	1966.9	2469.7	2064.8	2511.9	2081.0	0.8
221646_s_at	ZDHHC11	4.54E-03	2052.5	1131.2	333.1	278.6	491.9	475.8	115.5	1443.7	344.2	135.2	105.5	435.6	359.1	68.9	475.8	344.2	0.7
243786_at	ZDHHC20	3.98E-03	1884.5	1886.6	1612.1	1986.1	1731.0	1976.5	1413.3	1687.5	1404.0	1199.5	1558.6	1216.6	1435.4	1178.2	1884.5	1404.0	0.7
202456_s_at	ZER1	9.44E-03	327.6	282.7	368.8	322.0	359.2	378.4	287.7	267.0	173.7	204.4	229.5	324.4	306.6	252.5	327.6	252.5	0.8
226137_at	ZFHX3	8.24E-04	775.2	693.1	761.3	937.5	992.4	1009.9	862.9	588.9	491.1	461.9	614.7	606.3	677.1	711.3	862.9	606.3	0.7
222407_s_at	ZFP106	8.28E-04	420.6	344.8	403.0	427.7	473.6	426.7	476.1	334.0	218.0	282.6	332.2	330.2	301.1	289.3	426.7	301.1	0.7
217781_s_at	ZFP106	1.78E-03	1080.9	1088.5	1378.6	1309.7	1433.1	1664.5	1440.9	921.2	736.1	850.4	1100.3	761.3	978.7	924.1	1378.6	921.2	0.7
201368_at	ZFP36L2	6.95E-03	3549.1	3725.3	4182.9	3861.7	3757.6	4124.8	3233.4	3085.2	3092.7	2026.6	3171.8	2761.5	2840.5	2244.3	3757.6	2840.5	0.8
227796_at	ZFP62	2.73E-03	710.1	726.5	1130.7	947.6	830.6	1149.3	917.5	649.5	571.5	724.8	733.6	469.6	695.1	568.8	917.5	649.5	0.7
225843_at	ZFYVE19	6.33E-03	249.5	232.7	285.3	249.8	249.6	246.4	212.1	209.8	192.1	190.7	180.7	198.7	221.8	131.5	249.5	192.1	0.8
224445_s_at	ZFYVE21	1.75E-03	793.4	834.5	922.0	881.4	835.6	1163.0	814.8	686.1	605.2	460.7	631.3	548.4	627.6	379.7	835.6	605.2	0.7
37943_at	ZFYVE26	3.36E-03	852.5	1059.4	1311.1	1289.5	1121.3	1544.1	1080.1	834.1	708.3	817.8	840.7	727.4	638.5	657.8	1121.3	727.4	0.6
213073_at	ZFYVE26	7.81E-04	2461.6	2795.6	2959.8	2844.1	2694.3	3372.7	2329.4	2051.6	1811.1	1629.8	1777.4	1641.6	1496.3	1517.4	2795.6	1641.6	0.6
212545_s_at	ZHX3	4.25E-03	80.9	72.7	71.7	66.3	71.1	64.5	64.4	52.1	53.6	60.4	46.1	59.3	54.6	49.7	71.1	53.6	0.8
1562305_x_at	ZKSCAN3	2.27E-03	135.9	164.7	183.4	152.3	147.0	192.1	138.6	132.4	115.9	110.9	107.5	75.9	107.5	76.6	152.3	107.5	0.7
219628_at	ZMAT3	8.63E-03	333.7	522.6	614.8	489.5	497.4	592.3	457.4	347.3	330.6	299.2	449.2	330.4	323.0	219.8	497.4	330.4	0.7
212124_at	ZMIZ1	8.84E-03	1938.7	1839.4	1800.4	2285.9	2355.1	1919.7	2173.5	2002.4	1117.6	1018.8	1808.7	1604.3	1567.8	1526.6	1938.7	1567.8	0.8
1554172_a_at	ZMYM3	5.89E-03	82.5	74.0	91.1	84.4	91.9	91.8	77.8	72.4	42.5	47.9	64.6	75.6	55.8	65.6	84.4	64.6	0.8
1554171_at	ZMYM3	1.60E-03	211.2	295.5	280.4	248.4	285.8	239.7	269.2	181.6	150.4	104.4	176.6	190.8	110.6	138.9	269.2	150.4	0.6
219925_at	ZMYM6	1.41E-03	781.2	935.2	914.7	811.7	831.8	985.5	724.7	660.3	609.1	498.3	653.6	523.7	523.1	473.9	831.8	523.7	0.6
202136_at	ZMYND11	9.56E-03	1310.3	1262.5	1457.6	1375.1	1381.2	1442.8	1154.5	1173.4	1068.7	1058.1	1156.2	1070.9	1118.8	980.3	1375.1	1070.9	0.8
235408_x_at	ZNF117	3.51E-03	155.0	154.8	154.3	250.9	231.3	412.9	320.9	132.5	110.2	103.5	167.8	156.1	160.8	131.7	231.3	132.5	0.6
235166_at	ZNF148	1.75E-03	72.4	86.9	86.7	109.8	103.3	113.3	97.6	63.4	67.7	61.3	67.5	71.6	80.8	69.3	97.6	67.7	0.7
230821_at	ZNF148	5.71E-03	91.8	108.7	146.0	133.3	156.4	171.7	151.6	76.8	85.5	81.2	116.3	119.7	86.5	74.5	146.0	85.5	0.6
219314_s_at	ZNF219	5.66E-03	165.8	127.0	197.2	207.6	176.1	172.5	159.1	132.1	102.8	117.7	128.5	119.9	130.1	151.3	172.5	128.5	0.7
219123_at	ZNF232	3.10E-03	211.4	206.0	273.7	194.8	224.2	225.4	199.1	179.3	147.1	128.1	122.0	192.8	134.7	128.2	211.4	134.7	0.6
236328_at	ZNF285A	1.88E-03	178.3	192.3	187.5	198.0	208.7	220.5	175.3	145.6	155.8	121.7	157.2	120.2	152.1	108.2	192.3	145.6	0.8
219228_at	ZNF331	8.20E-04	473.1	640.8	492.9	480.4	505.9	472.4	399.1	381.9	380.9	289.5	314.5	388.2	341.9	241.2	480.4	341.9	0.7
231864_at	ZNF33A	6.36E-03	306.1	419.8	449.9	431.8	476.2	562.3	407.5	310.2	287.5	241.1	355.2	343.7	289.9	206.2	431.8	289.9	0.7
226820_at	ZNF362	4.56E-03	406.9	510.1	648.6	547.4	546.0	588.6	488.3	411.6	336.5	223.4	368.5	350.5	299.4	221.6	546.0	336.5	0.6
1570121_at	ZNF365	2.68E-03	166.6	238.8	355.0	331.8	228.6	385.3	181.6	143.6	159.4	52.2	148.6	74.0	129.0	45.6	238.8	129.0	0.5
229551_x_at	ZNF367	9.02E-03	79.8	74.6	74.5	120.8	68.2	56.1	80.9	80.9	50.8	47.6	88.4	24.0	40.6	41.2	74.6	47.6	0.6
1559988_at	ZNF483	2.44E-03	121.5	137.1	246.9	152.4	206.8	387.7	177.0	80.7	68.4	61.1	118.0	132.1	103.0	71.8	177.0	80.7	0.5
225050_at	ZNF512	6.12E-03	298.5	273.6	403.2	362.3	358.1	397.9	354.2	268.8	245.4	270.1	279.6	180.1	196.7	210.8	358.1	245.4	0.7
203604_at	ZNF516	5.40E-03	185.9	161.3	176.9	145.3	200.8	203.6	176.0	156.3	121.8	156.3	109.7	139.2	158.4	145.1	176.9	145.1	0.8
242697_at	ZNF540	6.21E-03	64.7	53.5	66.2	55.4	62.4	93.4	56.6	46.5	46.2	39.3	43.0	44.1	56.2	53.5	62.4	46.2	0.7
219968_at	ZNF589	9.76E-04	721.7	1170.6	973.9	689.9	679.9	930.2	673.3	479.0	472.8	150.6	322.2	343.0	356.8	150.6	721.7	343.0	0.5
210062_s_at	ZNF589	8.51E-04	1149.7	1907.9	1329.9	923.7	966.9	1358.8	924.8	627.8	811.8	238.2	569.5	540.2	470.4	237.5	1149.7	540.2	0.5
210061_at	ZNF589	8.70E-04	600.0	880.0	682.4	447.6	457.8	649.0	465.6	408.3	312.2	140.1	240.3	270.1	253.4	119.0	600.0	253.4	0.4
227507_at	ZNF592	2.99E-03	207.0	213.0	263.0	295.2	314.9	334.4	263.4	201.9	155.5	159.3	191.0	198.0	237.5	191.4	263.4	191.4	0.7
212617_at	ZNF609	3.68E-03	138.6	137.4	234.4	200.5	183.6	236.8	178.5	137.0	89.2	87.3	115.5	132.1	130.3	97.2	183.6	115.5	0.6
212620_at	ZNF609	9.47E-04	511.0	590.7	681.7	647.9	550.8	746.2	501.0	434.8	318.0	268.6	381.7	374.4	364.1	288.4	590.7	364.1	0.6
225266_at	ZNF652	5.10E-03	218.7	345.1	447.3	567.9	454.9	511.8	333.7	244.4	208.9	163.1	372.9	256.0	241.4	194.7	447.3	241.4	0.5
242915_at	ZNF682	3.81E-03	107.5	94.5	65.4	80.0	64.2	98.0	68.3	59.3	79.7	54.8	53.4	43.0	44.6	51.0	80.0	53.4	0.7
227331_at	ZNF740	3.93E-03	309.0	362.6	421.0	423.9	387.2	432.4	322.9	286.0	220.7	183.6	275.9	278.3	330.2	207.8	387.2	275.9	0.7
1558277_at	ZNF740	2.49E-03	317.7	381.4	389.5	495.6	441.0	559.5	406.9	324.5	239.9	193.7	342.0	229.1	306.9	249.9	406.9	249.9	0.6
239083_at	ZNF786	3.69E-03	482.2	441.7	497.1	478.5	381.8	449.7	373.7	421.8	294.7	207.7	293.7	284.1	338.9	239.6	449.7	293.7	0.7

Continued

Supplementary Table S2. ***Continued.***

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
244552_at	ZNF788	7.59E-03	183.2	164.2	240.3	206.5	200.4	290.3	232.2	188.1	88.2	37.2	131.0	108.0	118.5	59.6	206.5	108.0	0.5
238148_s_at	ZNF818P	9.30E-03	75.6	102.4	119.4	84.1	99.5	125.4	102.9	68.4	74.0	80.2	72.6	81.5	86.0	89.2	102.4	80.2	0.8
205494_at	ZNF821	9.02E-03	76.9	72.3	97.9	97.8	86.6	93.3	77.2	64.2	65.0	72.5	80.7	56.4	71.1	66.4	86.6	66.4	0.8
1569077_x_at	ZNF836	2.58E-03	396.0	441.9	637.4	387.0	457.2	492.1	456.0	363.7	327.5	297.5	278.2	289.5	285.1	285.8	456.0	289.5	0.6
228719_at	ZSWIM7	7.31E-03	1413.6	720.6	1369.4	1332.0	1059.6	1331.4	884.4	1293.2	464.3	917.5	1045.7	795.5	1099.2	756.3	1331.4	917.5	0.7
204026_s_at	ZWINT	3.62E-03	416.7	460.2	610.3	610.7	479.4	463.9	611.5	403.8	342.3	307.4	428.3	179.5	201.8	272.6	479.4	307.4	0.6
225350_s_at	ZYG11B	2.49E-03	471.4	803.5	664.7	599.7	640.5	832.0	626.7	452.1	420.5	281.7	462.2	360.7	336.9	258.1	640.5	360.7	0.6
239347_at	—	9.68E-03	84.3	86.0	91.2	76.5	78.8	78.5	73.6	77.8	67.2	70.2	70.2	58.3	49.1	55.2	78.8	67.2	0.9
226374_at	—	3.93E-03	86.3	404.0	56.4	81.8	530.4	158.2	96.8	81.2	193.8	43.6	60.2	323.6	109.1	59.4	96.8	81.2	0.8
1562059_at	—	8.32E-03	106.7	102.1	109.5	126.6	103.5	154.8	122.2	79.4	90.3	97.1	110.2	67.3	93.2	89.7	109.5	90.3	0.8
1569478_s_at	—	4.93E-03	717.3	668.6	636.6	589.6	792.3	688.6	671.8	559.2	582.4	426.2	428.6	547.9	597.2	545.7	671.8	547.9	0.8
229606_at	—	9.00E-03	4828.9	4366.4	4572.3	5492.4	4589.8	4670.1	4464.1	3940.6	3653.0	3284.7	3939.3	3488.9	4372.3	3737.2	4589.8	3737.2	0.8
217300_at	—	2.68E-03	1188.7	999.5	982.9	1001.6	1155.1	1009.6	937.1	916.9	814.9	671.4	862.2	865.6	758.8	668.9	1001.6	814.9	0.8
213979_s_at	—	9.46E-03	4886.8	5027.6	4695.7	5059.7	4814.5	5137.4	4503.9	4537.5	4114.6	3474.7	4290.5	3536.3	3957.5	3756.6	4886.8	3957.5	0.8
227095_at	—	4.05E-03	1409.7	1545.0	1328.5	1895.4	1528.4	1869.0	1727.5	1251.1	1267.2	1033.8	1526.5	1035.5	1253.5	1085.7	1545.0	1251.1	0.8
230096_at	—	3.81E-03	177.9	204.7	162.0	244.4	192.2	277.9	191.7	170.0	146.7	99.6	170.6	136.5	175.9	155.6	192.2	155.6	0.8
229713_at	—	7.81E-03	2795.2	3267.1	3132.1	3189.0	3123.2	3691.8	3110.0	2446.0	2680.2	2297.2	2830.8	2463.3	2751.8	2496.1	3132.1	2496.1	0.8
1556553_at	—	6.36E-03	84.6	58.4	72.1	78.5	94.4	74.3	72.7	56.0	50.8	63.0	65.5	69.3	59.1	52.0	74.3	59.1	0.8
241114_s_at	—	2.69E-03	305.8	225.2	263.8	419.8	523.9	391.8	313.9	315.7	138.1	176.1	264.2	346.4	247.3	193.4	313.9	247.3	0.8
238944_at	—	6.50E-03	213.8	253.5	268.0	246.5	304.6	425.3	443.3	197.2	207.1	150.8	208.8	218.4	294.0	251.2	268.0	208.8	0.8
230967_s_at	—	9.76E-03	373.0	327.9	475.1	426.1	496.1	519.4	509.9	306.1	219.9	297.8	369.9	449.7	440.4	381.1	475.1	369.9	0.8
227683_x_at	—	4.33E-03	141.9	147.1	148.5	145.1	139.2	141.7	129.6	127.7	111.6	98.4	122.2	95.3	110.3	96.3	141.9	110.3	0.8
230407_at	—	9.51E-03	294.3	299.8	320.8	336.3	349.1	366.1	399.3	316.0	187.0	185.7	272.3	264.7	260.9	217.4	336.3	260.9	0.8
229189_s_at	—	7.55E-03	130.4	124.0	157.6	120.4	120.4	260.8	133.2	126.3	84.9	87.7	101.6	100.7	155.8	76.0	130.4	100.7	0.8
238517_at	—	6.56E-03	103.8	107.3	99.3	115.9	132.8	141.5	108.1	109.8	64.6	46.2	93.2	88.2	83.2	70.0	108.1	83.2	0.8
237627_at	—	4.68E-03	153.9	296.8	191.2	177.7	166.2	272.2	292.9	140.5	220.1	135.7	145.8	120.0	194.4	158.9	191.2	145.8	0.8
216112_at	—	7.56E-03	83.2	112.5	110.6	122.7	110.1	149.9	116.7	63.7	93.1	81.1	117.0	57.0	86.1	85.5	112.5	85.5	0.8
227121_at	—	8.34E-03	78.5	56.7	61.8	72.1	88.8	113.7	96.5	66.1	41.6	46.2	69.8	62.9	59.6	49.5	78.5	59.6	0.8
227221_at	—	7.85E-03	357.6	468.5	638.1	448.5	563.5	565.3	428.9	354.2	349.8	366.7	409.0	318.4	363.3	273.6	468.5	354.2	0.8
235379_at	—	9.86E-04	122.3	135.8	99.3	132.0	86.9	100.9	72.0	84.3	92.7	63.8	86.9	67.4	76.2	58.2	100.9	76.2	0.8
239734_at	—	6.91E-03	94.4	72.9	63.9	72.6	88.6	107.3	74.5	52.9	77.4	47.0	56.1	61.0	56.4	45.7	74.5	56.1	0.8
214148_at	—	5.10E-03	82.0	87.7	99.2	98.6	91.6	97.0	93.3	72.7	55.7	71.9	90.4	51.4	70.2	63.3	93.3	70.2	0.8
231101_at	—	8.15E-03	227.7	278.9	348.8	293.9	328.4	376.6	293.8	253.8	175.0	248.0	221.0	228.3	215.1	156.5	293.9	221.0	0.8
239632_at	—	9.96E-03	66.9	85.5	63.6	72.1	83.8	91.7	78.4	58.3	52.1	43.7	67.2	58.2	63.7	70.6	78.4	58.3	0.7
227959_at	—	3.78E-03	79.9	83.9	49.8	62.4	48.0	57.4	57.1	67.4	51.0	24.3	54.6	33.5	33.5	42.5	57.4	42.5	0.7
217549_at	—	2.76E-03	304.5	244.1	265.8	303.9	296.2	279.5	291.6	242.5	184.9	161.9	221.4	252.8	215.7	213.3	291.6	215.7	0.7
1558011_at	—	4.83E-03	73.4	37.1	104.4	93.5	101.1	110.2	68.9	57.6	34.0	69.2	71.5	85.7	71.9	45.1	93.5	69.2	0.7
226250_at	—	9.87E-03	115.8	104.6	91.0	94.6	114.3	129.6	106.9	85.6	108.4	53.0	79.0	88.2	73.2	70.6	106.9	79.0	0.7
222297_x_at	—	5.86E-03	72.2	71.7	86.0	90.5	81.4	100.8	96.3	45.6	62.2	78.9	64.8	61.8	63.4	75.5	86.0	63.4	0.7
228457_at	—	6.00E-03	69.2	62.9	59.0	62.8	71.5	62.7	50.5	49.6	53.4	31.2	38.6	55.0	45.8	46.2	62.8	46.2	0.7
1555904_at	—	5.45E-03	122.0	109.9	120.6	110.7	128.1	119.2	102.6	104.1	102.3	70.0	87.5	89.3	81.5	69.7	119.2	87.5	0.7
236476_at	—	7.21E-03	73.6	69.2	72.8	78.4	85.3	85.5	79.4	57.5	60.5	47.8	72.5	46.4	64.4	44.4	78.4	57.5	0.7
235293_at	—	9.48E-03	267.5	353.9	259.5	266.8	258.5	270.7	244.8	283.0	239.7	187.2	197.3	195.8	190.9	193.0	266.8	195.8	0.7
229874_x_at	—	8.13E-03	1124.2	978.3	1376.8	1283.2	1418.6	1422.3	1474.0	1076.9	806.8	975.2	1010.0	1097.9	1018.8	829.3	1376.8	1010.0	0.7
227897_at	—	2.65E-03	4596.9	4109.6	6073.8	5245.4	4809.0	3802.8	4691.3	3576.6	3353.1	3439.3	4051.4	3912.8	2635.6	3078.6	4691.3	3439.3	0.7
233729_at	—	2.43E-03	187.1	229.9	178.0	219.4	189.4	224.5	170.0	171.8	138.4	116.8	173.9	111.5	165.3	100.9	189.4	138.4	0.7
229541_at	—	7.21E-03	411.8	421.8	411.0	465.9	492.0	510.7	512.1	316.3	294.5	317.0	433.2	419.2	339.5	414.7	465.9	339.5	0.7
228240_at	—	3.52E-03	66.5	73.9	68.4	74.7	60.6	62.3	61.0	52.4	54.4	48.4	63.5	44.8	42.7	30.2	66.5	48.4	0.7
235072_s_at	—	2.54E-03	998.4	1414.3	1232.1	1105.8	1341.6	1458.8	1035.8	895.9	1000.3	731.1	922.6	907.0	834.3	626.5	1232.1	895.9	0.7
226116_at	—	4.67E-03	306.6	337.8	458.8	328.4	400.2	471.3	376.6	279.8	204.6	239.5	304.7	273.8	274.7	189.0	376.6	273.8	0.7
234439_at	—	3.98E-03	69.0	71.4	83.4	102.2	72.9	82.9	97.5	53.4	51.0	60.3	62.5	64.4	71.0	59.7	82.9	60.3	0.7
229204_at	—	3.06E-03	3012.0	3417.9	3611.3	3619.5	3457.0	3850.9	3314.5	2750.2	2642.9	2404.4	2857.2	2511.5	2397.5	2031.5	3457.0	2511.5	0.7
227805_at	—	4.31E-03	112.6	117.6	134.1	117.6	133.0	106.6	103.4	92.6	100.1	85.4	88.6	62.2	75.9	71.6	117.6	85.4	0.7
211976_at	—	2.22E-03	988.6	1135.7	1158.0	1287.4	1300.9	1325.9	1193.1	864.7	846.9	645.9	946.4	936.6	946.5	842.8	1193.1	864.7	0.7
1569127_at	—	5.00E-03	290.7	235.5	327.5	266.7	217.0	264.8	193.4	238.9	148.1	191.9	204.4	156.6	207.8	176.1	264.8	191.9	0.7
229704_at	—	5.94E-03	846.5	828.2	884.4	1051.0	838.3	862.0	803.8	750.7	730.6	551.4	872.2	612.4	540.5	571.0	846.5	612.4	0.7
244661_at	—	9.36E-03	1740.7	2374.9	1987.0	2042.7	2208.4	2317.8	2184.1	1931.3	1659.3	1361.2	1602.6	1577.4	1418.3	1348.9	2184.1	1577.4	0.7
230350_at	—	6.74E-03	184.2	233.3	243.4	321.2	293.4	295.4	256.8	189.4	185.2	111.5	221.9	170.3	203.1	162.5	256.8	185.2	0.7
239069_s_at	—	7.46E-03	160.1	244.1	162.5	179.2	203.0	239.5	154.3	151.4	131.8	118.4	157.5	128.9	92.7	81.5	179.2	128.9	0.7
244343_at	—	1.67E-03	57.2	56.2	49.9	63.4	83.3	50.2	65.2	32.0	41.5	41.1	41.2	64.6	27.3	47.1	57.2	41.2	0.7
229949_at	—	8.00E-03	461.5	604.1	653.1	546.7	477.5	610.5	551.6	454.2	387.7	435.0	457.5	395.4	368.1	396.4	551.6	396.4	0.7
229571_at	—	5.50E-03	181.2	174.6	205.2	164.4	133.0	142.9	143.4	130.6	143.6	109.4	142.2	101.5	87.2	117.7	164.4	117.7	0.7
239324_at	—	7.08E-03	546.9	657.4	623.8	575.4	742.3	674.1	650.9	509.4	474.9	403.9	534.9	380.2	465.4	391.2	650.9	465.4	0.7
242966_x_at	—	5.53E-03	122.1	159.0	144.6	136.2	145.6	142.9	141.6	123.3	117.2	91.5	107.7	100.6	88.5	102.1	142.9	102.1	0.7
237444_at	—	1.78E-03	1391.8	1852.1	1608.4	1687.6	2027.5	2151.6	1446.6	1252.8	1204.7	897.6	1291.2	1359.8	1206.0	996.0	1687.6	1206.0	0.7
1558890_at	—	3.11E-04	201.9	173.7	178.2	209.8	160.9	204.8	159.1	128.8	129.0	98.0	127.2	105.0	146.5	109.0	178.2	127.2	0.7

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
231972_at	—	1.15E-03	3912.9	3333.5	4057.9	5048.4	4846.8	3420.5	5798.4	2929.0	2604.6	2981.2	2869.4	2887.1	2655.8	3590.9	4057.9	2887.1	0.7
214176_s_at	—	2.68E-03	1313.9	1700.0	1552.2	1773.2	1613.5	1741.4	1347.4	1208.8	1228.2	982.5	1400.0	1147.5	1072.1	951.7	1613.5	1147.5	0.7
230293_at	—	3.39E-03	70.1	57.2	66.0	60.2	75.0	62.9	74.0	60.2	36.1	46.9	52.9	37.8	34.4	49.7	66.0	46.9	0.7
226252_at	—	6.63E-03	96.7	79.5	99.3	106.8	142.1	155.4	133.0	87.3	61.7	62.2	99.5	80.8	75.8	69.5	106.8	75.8	0.7
214857_at	—	4.84E-03	362.1	744.5	510.4	388.8	477.7	387.0	292.2	326.8	399.8	208.6	254.1	380.8	275.9	196.8	388.8	275.9	0.7
228389_at	—	9.36E-03	101.8	88.0	142.8	137.5	141.4	133.8	142.5	97.4	76.1	101.0	119.6	98.1	93.9	95.9	137.5	97.4	0.7
213755_s_at	—	2.56E-03	692.3	783.3	557.1	814.5	572.0	640.6	513.9	520.0	445.9	241.8	453.3	488.8	491.0	328.1	640.6	453.3	0.7
240121_x_at	—	1.06E-03	294.7	602.7	568.5	387.4	403.2	548.5	401.7	212.3	480.3	285.1	301.1	218.5	286.5	232.2	403.2	285.1	0.7
235573_at	—	1.80E-03	177.2	161.9	235.6	174.3	182.4	193.6	165.3	137.6	125.2	139.3	137.6	122.6	91.5	91.7	177.2	125.2	0.7
229735_s_at	—	1.78E-03	516.7	558.5	487.0	522.6	509.6	532.2	455.5	449.6	364.4	235.7	390.3	340.2	370.0	260.3	516.7	364.4	0.7
235213_at	—	4.02E-03	68.0	48.5	85.1	82.5	73.4	76.5	54.8	66.8	36.2	51.6	60.0	39.1	51.6	38.4	73.4	51.6	0.7
239300_at	—	5.37E-03	72.6	76.8	88.4	97.2	100.4	96.4	95.8	71.6	38.1	39.5	74.5	72.7	67.3	52.7	95.8	67.3	0.7
225923_at	—	4.48E-03	162.9	169.7	219.6	251.6	232.4	197.3	268.5	147.4	106.4	127.8	212.4	154.2	162.9	168.8	219.6	154.2	0.7
226377_at	—	1.75E-03	252.1	212.8	304.2	301.7	313.1	283.7	283.9	234.9	129.8	155.9	206.5	206.7	199.1	173.2	283.9	199.1	0.7
235902_at	—	6.30E-03	613.8	326.5	584.3	601.5	508.7	482.0	373.8	457.6	274.6	355.3	514.0	444.3	284.0	278.9	508.7	355.3	0.7
227191_at	—	6.81E-03	69.9	70.2	94.9	91.5	101.5	109.9	108.9	65.7	52.9	80.4	72.3	54.4	66.2	68.1	94.9	66.2	0.7
243972_at	—	8.67E-03	89.1	78.6	134.4	131.9	146.7	147.6	135.4	83.6	56.7	99.3	127.4	93.7	98.4	83.5	134.4	93.7	0.7
226742_at	—	2.91E-03	536.0	604.3	733.3	727.5	726.4	843.0	764.1	479.8	477.7	517.3	585.0	505.4	537.9	500.9	727.5	505.4	0.7
237845_at	—	4.90E-03	44.5	57.7	68.4	66.0	70.1	75.3	66.3	36.1	40.2	52.3	61.0	46.0	60.5	40.6	66.3	46.0	0.7
228309_at	—	2.46E-03	4144.4	4175.7	4199.2	4185.9	3874.9	4505.2	4099.5	3340.9	2820.4	1812.8	2897.4	3018.2	3140.5	2441.3	4175.7	2897.4	0.7
238882_at	—	1.78E-03	225.6	213.8	282.4	357.7	262.4	428.6	325.8	195.8	128.1	207.8	271.3	183.8	264.3	173.7	282.4	195.8	0.7
243086_at	—	2.55E-03	657.2	810.3	810.9	834.3	684.8	719.0	652.8	539.3	497.8	534.9	773.7	447.6	491.2	430.0	719.0	497.8	0.7
225139_at	—	3.49E-03	1050.5	998.4	1277.4	1273.6	951.2	1103.7	879.2	956.7	779.5	693.6	889.0	721.6	647.7	626.5	1050.5	721.6	0.7
236772_s_at	—	5.92E-03	227.7	173.0	237.4	346.0	438.3	343.5	316.2	231.7	137.2	132.8	257.0	260.1	215.8	147.4	316.2	215.8	0.7
235227_at	—	8.45E-03	41.0	46.4	81.1	54.9	74.9	86.2	67.5	37.6	31.6	50.0	57.0	46.0	46.8	41.0	67.5	46.0	0.7
243687_at	—	6.78E-03	172.5	192.0	197.3	146.8	115.8	192.4	150.5	135.7	156.1	64.8	89.9	70.2	125.6	117.6	172.5	117.6	0.7
235406_x_at	—	5.87E-03	1289.1	1438.1	2034.1	1287.6	1476.7	1599.4	1721.4	1263.2	1097.0	995.5	928.5	1005.9	1154.0	865.5	1476.7	1005.9	0.7
238728_at	—	5.80E-03	61.9	59.5	78.8	65.1	74.0	111.2	80.5	58.6	41.2	44.8	50.3	59.9	51.2	47.0	74.0	50.3	0.7
238431_at	—	4.66E-03	400.4	421.6	467.7	536.3	516.6	572.3	562.0	342.7	335.7	362.7	453.8	369.5	325.3	351.3	516.6	351.3	0.7
228487_s_at	—	2.09E-03	1818.1	2015.1	2105.8	2216.5	2175.3	2613.1	1991.7	1476.3	1302.2	1158.2	1948.2	1405.5	1500.5	1430.8	2105.8	1430.8	0.7
235630_at	—	5.68E-03	172.5	207.6	219.8	261.4	210.9	233.7	177.1	179.1	160.7	114.0	179.4	85.0	142.0	91.8	210.9	142.0	0.7
229150_at	—	6.71E-04	159.8	128.4	149.0	179.0	122.9	164.2	131.1	107.9	87.1	78.8	124.1	90.0	100.3	101.8	149.0	100.3	0.7
227533_at	—	6.89E-03	46.2	59.6	58.8	91.7	69.9	96.4	66.9	46.1	40.7	31.6	78.1	49.8	45.0	38.3	66.9	45.0	0.7
238115_at	—	1.73E-03	82.9	69.2	96.9	77.0	83.9	97.8	96.7	57.7	56.3	49.5	63.8	44.3	65.5	54.1	83.9	56.3	0.7
212812_at	—	3.30E-03	1018.2	767.4	1354.6	1018.1	1474.1	1120.1	1461.1	898.6	604.2	927.0	788.5	752.2	671.0	737.4	1120.1	752.2	0.7
242130_at	—	1.76E-03	102.7	83.7	105.5	101.0	109.6	106.0	101.6	68.9	66.3	74.8	86.9	80.7	62.3	66.6	102.7	68.9	0.7
227117_at	—	6.78E-03	201.9	305.3	246.8	255.5	254.9	246.0	254.3	209.6	176.9	109.8	207.6	167.0	170.0	138.4	254.3	170.0	0.7
227052_at	—	7.20E-03	2360.0	3338.2	3491.1	3104.5	3406.8	4008.7	3472.8	2329.5	2684.2	1903.5	2610.5	2274.8	2183.4	2079.1	3406.8	2274.8	0.7
228479_at	—	7.28E-03	605.1	797.5	645.4	784.9	726.6	892.1	827.4	697.6	537.8	381.8	519.5	522.3	509.6	447.3	784.9	519.5	0.7
1559776_at	—	5.09E-03	773.9	776.8	580.6	606.2	629.8	397.5	723.4	796.9	547.0	390.6	415.7	425.4	282.1	371.2	629.8	415.7	0.7
225345_s_at	—	3.82E-03	75.7	64.3	77.0	75.9	72.4	97.3	62.5	66.7	47.2	49.9	47.1	63.5	67.9	46.8	75.7	49.9	0.7
225902_at	—	4.39E-03	770.6	961.8	1153.6	987.7	918.0	1190.8	913.3	790.6	659.9	561.3	719.6	575.7	633.7	612.4	961.8	633.7	0.7
242465_at	—	1.63E-03	511.0	487.2	1023.1	610.5	563.1	1118.0	730.8	435.2	349.4	550.8	401.8	329.9	628.2	281.9	610.5	401.8	0.7
228548_at	—	2.55E-03	283.9	323.8	300.8	329.7	383.1	354.0	219.6	277.5	186.3	139.7	233.3	213.0	213.8	150.0	323.8	213.0	0.7
214977_at	—	5.70E-03	751.1	738.6	877.1	851.3	516.0	648.1	665.2	472.1	650.7	449.8	596.2	392.8	568.0	485.1	738.6	485.1	0.7
226397_s_at	—	4.70E-03	1015.8	1021.8	1440.4	1306.2	1356.6	1287.7	1670.6	924.6	848.1	1177.5	796.5	717.7	856.2	950.3	1306.2	856.2	0.7
238113_at	—	5.73E-04	147.0	86.3	130.3	227.8	125.2	215.6	200.2	125.7	51.8	72.3	111.7	82.4	123.7	96.1	147.0	96.1	0.7
240736_at	—	6.23E-03	63.9	60.7	74.8	67.4	60.2	82.7	60.2	62.9	35.8	41.2	57.2	41.7	60.0	41.4	63.9	41.7	0.7
236350_at	—	9.76E-03	149.7	143.1	210.6	219.0	180.0	208.7	200.5	165.8	92.3	131.0	171.1	142.1	124.6	123.3	200.5	131.0	0.7
235352_at	—	7.15E-03	412.5	505.3	645.4	515.8	642.9	824.1	627.7	428.4	365.8	370.5	420.1	409.0	440.0	281.2	627.7	409.0	0.7
242134_at	—	2.02E-04	364.3	356.7	269.2	363.8	426.3	541.9	447.4	236.5	265.3	149.3	235.4	225.6	278.7	276.5	364.3	236.5	0.6
228070_at	—	3.54E-03	127.2	177.1	200.2	151.5	184.7	189.7	181.5	121.1	113.3	125.8	128.6	113.8	117.7	94.4	181.5	117.7	0.6
227815_at	—	1.93E-03	512.6	497.8	583.9	539.6	587.7	683.3	670.1	463.1	338.0	354.1	435.2	318.5	409.1	378.4	583.9	378.4	0.6
235805_at	—	6.78E-03	93.2	107.4	125.1	112.5	150.6	132.2	131.2	75.0	80.9	80.2	102.8	101.4	58.2	95.9	125.1	80.9	0.6
1554597_at	—	2.19E-03	691.3	743.2	805.6	899.2	812.0	910.4	807.7	653.5	501.5	513.4	701.7	501.0	548.0	522.4	807.7	522.4	0.6
238709_at	—	6.46E-04	276.5	253.9	335.0	360.2	329.2	335.3	330.5	213.1	196.3	228.6	246.7	240.1	211.8	213.0	330.5	213.1	0.6
236101_at	—	2.93E-03	153.0	208.2	150.1	255.8	215.5	281.1	180.6	165.3	133.5	78.3	156.1	115.8	143.7	76.8	208.2	133.5	0.6
213964_x_at	—	1.83E-03	329.2	547.4	527.8	361.3	469.1	425.7	333.1	273.0	343.0	229.5	293.3	302.6	209.5	160.6	425.7	273.0	0.6
1558397_at	—	8.90E-04	1362.0	1648.1	423.4	1602.8	1193.1	1438.0	1103.1	1091.6	844.2	193.5	922.6	873.0	963.1	512.1	1362.0	873.0	0.6
244354_at	—	5.29E-03	59.6	60.0	81.6	83.3	99.3	85.0	84.4	53.4	52.3	57.5	68.4	67.9	51.7	51.7	83.3	53.4	0.6
226343_at	—	1.65E-03	1272.8	1327.7	1156.8	1601.7	1463.2	1526.1	1421.6	1056.4	901.8	465.7	1157.3	938.2	870.9	725.8	1421.6	901.8	0.6
228932_at	—	8.05E-03	91.7	105.8	139.9	159.1	157.3	148.9	160.5	104.0	67.8	97.4	120.8	84.3	94.4	92.5	148.9	94.4	0.6
217922_at	—	3.87E-03	285.1	331.9	291.7	349.1	410.7	382.6	334.1	286.7	182.6	176.7	288.3	244.1	207.4	211.7	334.1	211.7	0.6
244018_at	—	9.10E-03	42.0	55.2	121.9	69.5	79.2	93.1	50.5	44.0	33.2	33.8	45.2	51.7	57.0	28.6	69.5	44.0	0.6
235534_at	—	3.30E-03	489.3	456.8	475.9	650.5	550.0	504.2	642.6	467.3	318.4	236.6	450.8	291.5	355.4	281.6	504.2	318.4	0.6
228159_at	—	3.86E-03	189.1	163.0	212.1	286.4	245.4	285.9	246.3	181.3	93.4	70.8	196.7	154.9	154.8	85.7	245.4	154.8	0.6

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
232198_at	—	5.86E-03	81.8	56.1	84.5	98.0	88.4	73.2	83.0	68.2	52.3	47.2	69.9	70.7	38.5	46.2	83.0	52.3	0.6
229004_at	—	4.96E-03	99.0	192.4	88.2	136.7	113.4	185.4	163.1	70.5	117.2	56.1	105.3	114.4	86.2	82.9	136.7	86.2	0.6
227116_at	—	1.97E-03	1125.7	1562.6	1475.3	1089.9	1504.5	1640.8	1569.5	982.1	1232.1	828.0	835.1	850.9	947.7	951.0	1504.5	947.7	0.6
227082_at	—	7.65E-03	43.4	43.3	52.7	66.2	68.5	79.1	65.0	40.8	38.8	28.6	30.1	42.8	60.5	41.7	65.0	40.8	0.6
215306_at	—	6.54E-03	90.7	99.0	115.6	130.8	170.9	185.3	88.3	87.5	83.8	49.1	72.5	36.3	81.4	34.6	115.6	72.5	0.6
227630_at	—	8.52E-03	711.5	903.2	1000.0	875.1	971.4	1023.9	883.4	815.8	653.1	508.2	680.6	564.6	555.8	485.2	903.2	564.6	0.6
227665_at	—	7.65E-03	168.8	205.8	191.4	178.5	200.8	239.7	200.4	160.1	120.6	105.4	180.0	124.5	155.5	104.9	200.4	124.5	0.6
229214_at	—	1.08E-03	344.3	370.7	387.9	352.2	327.8	316.6	340.5	252.4	203.7	213.5	301.5	213.7	205.8	235.1	344.3	213.7	0.6
240397_x_at	—	4.20E-03	103.7	111.4	100.3	141.2	78.4	95.0	135.0	107.5	81.4	57.4	84.0	31.0	58.6	64.4	103.7	64.4	0.6
237186_at	—	7.30E-03	101.2	56.0	80.0	43.5	64.5	54.7	92.0	79.2	41.5	39.7	30.6	64.1	33.8	39.9	64.5	39.9	0.6
220033_at	—	3.17E-03	65.2	68.6	103.6	85.7	100.2	83.6	77.5	69.3	42.9	46.6	52.7	54.1	51.3	48.1	83.6	51.3	0.6
236488_s_at	—	3.46E-03	818.0	783.0	837.6	1159.7	982.6	1378.4	1225.6	733.4	514.5	449.7	1005.0	599.5	672.3	539.1	982.6	599.5	0.6
214807_at	—	6.12E-04	4250.3	4266.0	3657.9	4350.7	4648.5	4939.9	4693.7	3502.5	2588.0	1537.7	2825.2	2653.8	2640.7	2148.6	4350.7	2640.7	0.6
243417_at	—	3.37E-03	89.2	94.8	116.3	99.2	89.1	94.7	94.0	78.5	56.8	47.7	80.5	57.2	58.5	39.3	94.7	57.2	0.6
238379_x_at	—	2.87E-03	81.9	85.4	105.4	125.9	152.2	148.8	141.8	88.4	40.9	44.7	86.3	76.0	79.8	56.8	125.9	76.0	0.6
230085_at	—	3.83E-03	116.2	109.3	136.1	118.8	136.8	141.6	170.1	97.7	73.7	46.7	82.0	94.7	84.8	64.1	136.1	82.0	0.6
244375_at	—	1.45E-03	174.3	106.1	216.7	240.5	120.1	171.3	148.5	145.7	86.5	156.1	158.4	69.1	103.1	95.6	171.3	103.1	0.6
228275_at	—	8.12E-03	158.9	190.2	187.1	157.7	143.6	211.4	147.5	146.8	140.9	85.9	152.2	88.3	95.6	74.6	158.9	95.6	0.6
239355_at	—	9.47E-03	277.0	287.1	405.3	336.9	354.7	453.6	293.6	314.6	201.3	173.9	260.9	222.9	202.2	163.1	336.9	202.2	0.6
228006_at	—	1.48E-03	539.3	633.5	715.8	629.4	675.8	758.9	655.0	459.4	390.4	353.0	511.0	375.6	391.5	413.6	655.0	391.5	0.6
227432_s_at	—	4.24E-04	1672.3	2084.0	2170.5	1963.5	1983.0	2494.6	1369.0	1264.3	1433.3	889.0	1062.2	1184.0	1321.3	782.4	1983.0	1184.0	0.6
238700_at	—	1.60E-03	486.8	584.6	809.5	651.5	614.2	871.3	661.7	394.9	345.7	318.7	499.2	388.7	418.4	272.3	651.5	388.7	0.6
1562848_at	—	6.90E-03	103.6	150.5	139.8	137.9	167.8	125.7	99.4	119.1	82.1	59.4	98.9	94.5	75.9	64.4	137.9	82.1	0.6
243781_at	—	6.60E-03	95.4	134.4	198.6	161.5	164.7	169.7	178.9	99.1	96.6	87.9	99.3	113.8	97.8	62.7	164.7	97.8	0.6
242951_at	—	8.95E-04	420.9	589.9	446.5	426.5	555.6	469.8	285.5	312.7	264.7	124.0	277.6	329.6	171.4	122.7	446.5	264.7	0.6
1560625_s_at	—	2.93E-03	638.9	782.6	607.1	652.0	603.4	900.4	702.3	604.1	386.5	205.9	355.0	439.8	551.4	288.8	652.0	386.5	0.6
238378_at	—	5.44E-03	120.3	134.9	170.2	157.2	170.8	186.9	172.2	114.0	66.0	51.8	131.6	105.9	100.6	65.9	170.2	100.6	0.6
230313_at	—	1.41E-03	1313.8	1491.0	1421.5	1583.1	1234.9	1626.7	1125.9	928.3	808.1	437.5	840.0	906.0	1074.2	509.2	1421.5	840.0	0.6
226910_at	—	4.60E-03	588.1	672.5	785.7	799.7	821.2	770.2	850.1	573.3	464.3	343.7	646.0	520.0	405.3	413.7	785.7	464.3	0.6
225328_at	—	9.07E-03	66.0	87.2	74.7	57.6	64.2	93.9	48.4	52.2	54.2	38.9	62.1	38.4	35.2	33.1	66.0	38.9	0.6
232331_at	—	5.93E-04	410.9	391.7	444.2	487.7	434.0	565.7	413.5	347.4	252.7	209.1	282.9	255.7	328.9	188.8	434.0	255.7	0.6
236660_at	—	1.36E-03	61.9	75.0	93.7	61.1	73.6	76.0	77.2	60.2	44.2	48.9	29.1	44.4	31.9	31.7	75.0	44.2	0.6
226832_at	—	4.02E-03	503.5	680.0	659.1	616.0	674.5	820.6	725.5	502.6	402.4	306.3	532.7	340.4	396.2	350.3	674.5	396.2	0.6
1570375_at	—	7.02E-03	96.1	127.0	186.6	216.8	180.8	180.6	129.2	105.8	67.5	57.2	121.9	119.3	109.3	77.3	180.6	105.8	0.6
229383_at	—	4.87E-03	621.6	753.9	988.6	985.1	1034.7	1118.2	937.1	579.5	578.6	368.7	751.7	572.0	430.9	407.9	985.1	572.0	0.6
1560169_at	—	5.94E-03	225.0	240.7	218.2	260.8	181.4	214.7	171.1	227.1	115.4	95.4	190.7	125.0	161.6	91.2	218.2	125.0	0.6
235761_at	—	5.00E-04	167.9	132.1	285.4	212.3	305.7	281.4	462.9	126.7	77.2	187.8	140.7	212.0	161.0	214.4	281.4	161.0	0.6
1561705_at	—	9.95E-04	295.8	419.7	526.1	485.3	460.4	608.1	477.0	254.0	257.9	324.4	382.0	272.2	361.7	270.3	477.0	272.2	0.6
244368_x_at	—	4.11E-03	186.4	242.8	310.3	291.9	288.9	366.3	331.5	175.9	166.5	150.0	252.5	146.8	173.8	149.5	291.9	166.5	0.6
225716_at	—	3.04E-03	242.7	278.1	280.9	287.7	326.4	322.5	250.6	223.3	159.4	74.7	203.0	170.9	140.4	97.2	280.9	159.4	0.6
240856_at	—	4.00E-03	688.7	1468.0	715.0	673.7	585.8	1101.4	710.4	581.3	680.7	77.8	399.9	204.0	445.7	156.6	710.4	399.9	0.6
1554007_at	—	8.80E-03	41.0	48.8	88.0	59.7	112.4	143.6	69.9	39.3	42.3	29.2	48.8	39.1	43.4	25.9	69.9	39.3	0.6
236297_at	—	2.09E-03	819.3	791.8	895.9	985.1	1399.8	1304.9	1212.9	821.6	492.2	388.6	649.7	577.9	554.1	514.2	985.1	554.1	0.6
230894_s_at	—	1.94E-03	211.6	330.0	352.5	321.2	322.4	344.6	246.4	186.6	244.2	135.6	186.0	180.7	139.0	140.9	322.4	180.7	0.6
233176_at	—	5.73E-03	119.7	108.2	192.2	201.0	131.0	137.5	155.1	99.7	63.7	38.9	81.6	103.1	76.8	70.4	137.5	76.8	0.6
244652_at	—	2.13E-03	246.2	408.6	334.7	441.5	287.7	537.6	318.4	243.5	213.3	110.0	280.1	153.3	187.0	137.5	334.7	187.0	0.6
1569346_a_at	—	6.92E-04	260.0	240.2	280.0	260.8	221.9	289.9	312.4	211.7	123.3	145.5	183.4	141.6	159.4	135.3	260.8	145.5	0.6
239236_at	—	6.07E-03	99.6	142.7	182.4	131.9	183.9	207.9	171.8	95.0	95.7	99.2	124.9	84.2	95.8	83.6	171.8	95.7	0.6
229934_at	—	6.72E-03	438.1	927.7	831.9	1073.2	743.7	1065.6	885.3	478.2	575.5	407.8	862.9	490.9	530.5	414.0	885.3	490.9	0.6
229327_s_at	—	3.11E-03	1823.5	1622.1	1870.9	1476.1	1613.5	1343.4	1169.1	1298.0	867.6	509.1	892.7	1125.5	966.0	644.0	1613.5	892.7	0.6
238455_at	—	2.11E-04	729.1	645.7	879.6	1110.3	990.2	1173.2	1209.5	545.5	384.4	421.7	610.1	556.1	553.1	483.1	990.2	545.5	0.6
238668_at	—	4.53E-03	391.1	502.5	591.2	613.9	624.4	656.3	655.3	337.2	405.8	289.3	539.2	352.9	327.3	324.7	613.9	337.2	0.5
240432_x_at	—	5.15E-03	318.8	353.0	392.9	470.6	568.3	528.7	477.5	327.7	270.9	182.7	346.0	257.9	221.3	242.9	470.6	257.9	0.5
239050_s_at	—	2.57E-03	170.4	172.4	219.7	282.7	268.2	275.9	319.8	151.8	113.8	154.4	210.5	142.4	145.8	136.0	268.2	145.8	0.5
240690_at	—	2.60E-03	78.1	110.7	118.6	123.5	118.5	135.3	139.9	63.1	61.4	64.4	120.7	63.0	64.5	71.4	118.6	64.4	0.5
215287_at	—	7.53E-03	53.7	55.3	92.1	87.9	95.7	81.8	104.3	47.3	37.7	45.1	79.2	56.0	65.8	47.1	87.9	47.3	0.5
225176_at	—	3.95E-03	1162.6	1574.3	1577.6	1364.3	1623.8	1741.4	1530.3	1155.1	942.3	610.3	1133.0	770.6	837.8	662.8	1574.3	837.8	0.5
235385_at	—	6.35E-03	407.2	540.8	837.0	708.7	768.4	760.8	690.4	394.0	375.7	277.9	584.8	429.2	368.0	270.7	708.7	375.7	0.5
226280_at	—	6.12E-04	1177.4	1431.8	1523.4	1531.6	1623.6	1681.7	1577.2	986.4	809.2	676.0	1053.0	914.2	804.5	757.9	1531.6	809.2	0.5
241417_at	—	3.45E-04	163.7	215.5	146.7	201.1	209.1	192.5	132.1	128.4	101.6	94.1	108.2	91.0	117.3	70.9	192.5	101.6	0.5
230268_at	—	6.45E-03	142.2	126.1	192.4	250.7	189.5	222.9	195.3	149.3	93.4	90.1	178.8	100.4	119.3	67.1	192.4	100.4	0.5
230391_at	—	5.78E-03	492.1	528.4	569.3	838.5	772.7	710.9	559.4	490.8	296.2	207.9	477.5	693.0	292.9	232.2	569.3	296.2	0.5
222824_at	—	2.90E-03	134.6	147.1	169.8	142.9	151.3	151.2	133.0	136.2	76.2	74.9	101.6	88.0	69.8	47.4	147.1	76.2	0.5
230913_at	—	4.66E-03	2389.1	3152.5	2515.0	2279.8	2691.2	2943.7	2796.5	1997.4	1392.2	333.3	1407.6	1412.2	1206.2	565.7	2691.2	1392.2	0.5
235286_at	—	4.62E-03	85.1	84.8	69.9	94.4	76.6	80.7	89.3	84.5	55.2	38.0	72.1	43.9	28.7	41.4	84.8	43.9	0.5
230958_s_at	—	2.91E-03	218.8	429.9	417.6	405.8	532.1	575.0	314.3	200.4	254.4	89.0	225.4	270.8	215.7	89.2	417.6	215.7	0.5

Continued

Supplementary Table S2. *Continued.*

ID	Gene Symbol	p-value	VW3_ Saline	VW6_ Saline	VW7_ Saline	VW13_ Saline	VW22_ Saline	VW23_ Saline	VW25_ Saline	VW3_ LPS	VW6_ LPS	VW7_ LPS	VW13_ LPS	VW22_ LPS	VW23_ LPS	VW25_ LPS	Median_ saline	Median_ LPS	Fold change
227929_at	—	8.22E-03	73.5	114.2	211.7	167.1	166.0	254.7	203.6	85.7	87.8	53.8	90.6	85.0	86.1	56.7	167.1	85.7	0.5
226865_at	—	6.10E-04	1126.0	1143.8	1372.5	1510.8	1521.6	1479.3	1679.2	889.2	625.8	509.1	958.2	762.1	734.7	588.4	1479.3	734.7	0.5
1554609_at	—	8.85E-03	143.5	211.6	295.9	223.8	227.3	350.7	214.3	149.9	139.0	61.7	169.1	110.7	107.2	49.8	223.8	110.7	0.5
244551_at	—	4.81E-03	28.4	44.5	64.4	49.3	67.5	83.0	59.4	29.2	24.7	29.7	38.7	39.0	29.3	21.7	59.4	29.3	0.5
241359_at	—	2.04E-03	455.6	615.5	189.5	162.3	354.6	541.1	386.6	450.1	362.6	71.2	105.5	190.1	284.9	174.1	386.6	190.1	0.5
242714_at	—	1.44E-03	609.6	805.9	1050.9	985.2	929.0	1440.3	787.1	497.9	459.0	320.2	582.5	455.0	441.8	201.1	929.0	455.0	0.5
228175_at	—	3.50E-04	341.5	408.4	266.5	241.3	281.4	377.4	256.2	216.8	256.0	74.7	126.9	136.8	193.5	110.0	281.4	136.8	0.5
242868_at	—	1.22E-03	75.4	73.1	131.6	123.8	114.8	125.7	87.3	67.8	52.2	57.7	71.1	55.0	55.6	48.9	114.8	55.6	0.5
230178_s_at	—	1.02E-03	210.5	236.6	393.2	305.0	339.6	297.8	299.5	172.2	139.4	144.9	207.6	152.8	143.2	103.8	299.5	144.9	0.5
226134_s_at	—	5.19E-03	42.6	48.1	99.7	107.4	125.8	114.8	98.9	47.5	36.4	40.6	64.2	57.8	47.7	34.5	99.7	47.5	0.5
227995_at	—	8.88E-04	396.0	465.6	480.2	553.6	539.0	558.6	635.8	329.6	220.6	164.3	330.1	250.7	261.6	175.9	539.0	250.7	0.5
235109_at	—	3.95E-03	129.6	128.0	220.9	199.2	179.0	171.5	153.8	132.6	79.5	65.8	122.0	106.8	67.2	56.3	171.5	79.5	0.5
232828_at	—	3.01E-03	176.8	383.2	547.1	356.3	315.0	468.7	166.7	162.5	189.3	84.2	179.4	121.5	165.8	77.9	356.3	162.5	0.5
1558742_at	—	4.34E-03	107.4	149.2	244.7	180.5	152.0	170.6	183.8	113.7	75.5	92.1	126.3	77.5	45.5	54.4	170.6	77.5	0.5
228959_at	—	8.86E-04	405.9	551.9	426.9	348.6	481.0	520.8	484.2	333.0	277.9	127.1	215.2	261.2	201.9	196.2	481.0	215.2	0.4
243495_s_at	—	1.95E-03	384.8	839.1	977.7	934.3	1010.4	911.5	732.3	330.0	563.0	379.9	709.9	484.8	406.8	401.8	911.5	406.8	0.4
240173_at	—	1.78E-03	291.0	365.2	457.9	462.4	451.1	456.0	660.4	266.6	186.3	183.3	265.9	198.2	256.6	174.5	456.0	198.2	0.4
228560_at	—	2.49E-04	680.8	432.5	618.2	535.6	642.9	375.3	307.8	464.2	232.0	180.2	253.6	257.0	201.9	106.9	535.6	232.0	0.4
1557275_a_at	—	1.53E-03	2806.9	3444.3	1036.7	677.9	1809.1	2376.4	1726.2	2315.5	1951.0	388.2	442.4	758.5	1715.7	750.1	1809.1	758.5	0.4
232081_at	—	2.89E-03	892.0	1041.0	815.0	678.4	936.1	882.4	904.8	877.4	356.9	157.2	411.3	454.1	329.7	208.9	892.0	356.9	0.4
241652_x_at	—	4.42E-03	64.9	79.5	196.9	194.5	170.6	270.0	218.7	65.3	64.9	66.6	97.3	58.4	64.9	59.5	194.5	64.9	0.3