Category	Annotation Cluster 1	Enrichment Score: 13.714996894919818				
	Category	Term	Count	%	PValue	Probes
	SP_PIR_KEYWORDS	disulfide bond	40	58.82	5.57E-16	1448148_AT, 1419298_AT, 1420394_S_AT, 1437726_X_AT, 1455965_AT, 1436996_X_AT, 1419455_AT, 1435903_AT, 1423547_AT, 1451784_X_AT, 1448380_AT, 1449195_S_AT, 1451161_A_AT, 1417963_AT, 1418021_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1417868_A_AT, 1455332_X_AT, 1460248_AT, 1451683_X_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1419483_AT, 1419132_AT, 1419482_AT, 1417870_X_AT, 1452014_A_AT, 1426808_AT, 1456567_X_AT, 1427301_AT, 1419128_AT, 1448591_AT, 1420699_AT, 1448710_AT, 1428018_A_AT, 1421792_S_AT, 1449401_AT, 1435477_S_AT, 1449156_AT, 1419202_AT, 1418910_AT, 1439426_X_AT, 1416340_A_AT, 1419561_AT, 1449164_AT, 1434366_X_AT
	UP_SEQ_FEATURE	disulfide bond	39	57.35	1.85E-15	1451683_X_AT, 1419298_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1437726_X_AT, 1422875_AT, 1436996_X_AT, 1455965_AT, 1419483_AT, 1419132_AT, 1419482_AT, 1419455_AT, 1417870_X_AT, 1452014_A_AT, 1426808_AT, 1435903_AT, 1427301_AT, 1419128_AT, 1423547_AT, 1451784_X_AT, 1448380_AT, 1448591_AT, 1448710_AT, 1420699_AT, 1449401_AT, 1428018_A_AT, 1449195_S_AT, 1421792_S_AT, 1435477_S_AT, 1451161_A_AT, 1418910_AT, 1417963_AT, 1419202_AT, 1449156_AT, 1439426_X_AT, 1425545_X_AT, 1418021_AT, 1421812_AT, 1451941_A_AT, 1416340_A_AT, 1417868_A_AT, 1455332_X_AT, 1434366_X_AT, 1449164_AT, 1419561_AT, 1460248_AT
	SP_PIR_KEYWORDS	signal	42	61.76	3.69E-15	1448148_AT, 1419298_AT, 1420394_S_AT, 1437726_X_AT, 1427076_AT, 1455965_AT, 1436996_X_AT, 1419455_AT, 1435903_AT, 1448891_AT, 1423547_AT, 1451784_X_AT, 1419064_A_AT, 1448380_AT, 1449195_S_AT, 1451161_A_AT, 1417963_AT, 1418021_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1417868_A_AT, 1455332_X_AT, 1418028_AT, 1460248_AT, 1451683_X_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1419132_AT, 1417870_X_AT, 1452014_A_AT, 1456567_X_AT, 1427301_AT, 1419128_AT, 1419100_AT, 1448591_AT, 1428018_A_AT, 1421792_S_AT, 1449401_AT, 1435477_S_AT, 1449156_AT, 1419202_AT, 1418910_AT, 1439426_X_AT, 1416340_A_AT, 1448303_AT, 1434366_X_AT, 1419561_AT, 1449164_AT
	UP_SEQ_FEATURE	signal peptide	42	61.76	7.97E-15	1448148_AT, 1419298_AT, 1420394_S_AT, 1437726_X_AT, 1427076_AT, 1455965_AT, 1436996_X_AT, 1419455_AT, 1435903_AT, 1448891_AT, 1423547_AT, 1451784_X_AT, 1419064_A_AT, 1448380_AT, 1449195_S_AT, 1451161_A_AT, 1417963_AT, 1418021_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1417868_A_AT, 1455332_X_AT, 1418028_AT, 1460248_AT, 1451683_X_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1419132_AT, 1417870_X_AT, 1452014_A_AT, 1456567_X_AT, 1427301_AT, 1419128_AT, 1419100_AT, 1448591_AT, 1428018_A_AT, 1421792_S_AT, 1449401_AT, 1435477_S_AT, 1449156_AT, 1419202_AT, 1418910_AT, 1439426_X_AT, 1416340_A_AT, 1448303_AT, 1434366_X_AT, 1419561_AT, 1449164_AT
	SP_PIR_KEYWORDS	glycoprotein	43	63.24	3.34E-13	1448148_AT, 1419298_AT, 1420394_S_AT, 1437726_X_AT, 1427076_AT, 1455965_AT, 1419455_AT, 1427221_AT, 1435903_AT, 1451784_X_AT, 1419064_A_AT, 1448380_AT, 1449195_S_AT, 1448640_AT, 1451161_A_AT, 1417963_AT, 1418021_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1417868_A_AT, 1455332_X_AT, 1418028_AT, 1460248_AT, 1451683_X_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1420361_AT, 1419483_AT, 1419132_AT, 1419482_AT, 1417870_X_AT, 1456567_X_AT, 1427301_AT, 1448606_AT, 1419128_AT, 1419100_AT, 1448591_AT, 1420699_AT, 1448710_AT, 1428018_A_AT, 1421792_S_AT, 1435477_S_AT, 1449156_AT, 1419202_AT, 1418910_AT, 1428114_AT, 1416340_A_AT, 1448303_AT, 1434366_X_AT, 1449164_AT
	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	41	60.29	5.07E-12	1448148_AT, 1419298_AT, 1420394_S_AT, 1427076_AT, 1455965_AT, 1419455_AT, 1427221_AT, 1435903_AT, 1451784_X_AT, 1419064_A_AT, 1448380_AT, 1448640_AT, 1451161_A_AT, 1417963_AT, 1418021_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1417868_A_AT, 1455332_X_AT, 1418028_AT, 1460248_AT, 1451683_X_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1420361_AT, 1419483_AT, 1419132_AT, 1419482_AT, 1417870_X_AT, 1456567_X_AT, 1427301_AT, 1448606_AT, 1419128_AT, 1419100_AT, 1448591_AT, 1420699_AT, 1448710_AT, 1428018_A_AT, 1421792_S_AT, 1435477_S_AT, 1449156_AT, 1419202_AT, 1418910_AT, 1428114_AT, 1416340_A_AT, 1448303_AT, 1449164_AT
	Annotation Cluster 2	Enrichment Score: 4.658720772381782				
	Category	Term	Count	%	PValue	Genes
immune	INTERPRO	IPR003599:Immunoglobulin subtype	11	16.18	6.62E-08	1424067_AT, 1419315_AT, 1422875_AT, 1428018_A_AT, 1421792_S_AT, 1435477_S_AT, 1449156_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
immune	SP_PIR_KEYWORDS	Immunoglobulin domain	12	17.65	1.36E-07	1420394_S_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1449156_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
immune	SMART	SM00409:IG	11	16.18	1.67E-07	1424067_AT, 1419315_AT, 1422875_AT, 1428018_A_AT, 1421792_S_AT, 1435477_S_AT, 1449156_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
immune	INTERPRO	IPR007110:Immunoglobulin-like	12	17.65	4.91E-07	1451683_X_AT, 1451784_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1428018_A_AT, 1435477_S_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
immune	INTERPRO	IPR013783:Immunoglobulin-like fold	10	14.71	5.71E-05	1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1424067_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
immune	INTERPRO	IPR013106:Immunoglobulin V-set	6	8.82	9.05E-04	1419315_AT, 1421792_S_AT, 1428018_A_AT, 1435903_AT, 1427301_AT, 1449156_AT
immune	UP_SEQ_FEATURE	domain:Ig-like C2-type 1	5	7.35	0.002402145	1424067_AT, 1420394_S_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1427301_AT, 1449156_AT
immune	UP_SEQ_FEATURE	domain:Ig-like C2-type 2	5	7.35	0.002402145	1424067_AT, 1420394_S_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1427301_AT, 1449156_AT
immune	INTERPRO	IPR013151:Immunoglobulin	5	7.35	0.005368799	1424067_AT, 1420394_S_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1427301_AT, 1448891_AT
	Annotation Cluster 3	Enrichment Score: 4.38133131814222				
	Category	Term	Count	%	PValue	Genes

	UP_SEQ_FEATURE	topological domain:Extracellular	26	38.24	2.92E-07	1451683_X_AT, 1420394_S_AT, 1424067_AT, 1419315_AT, 1422875_AT, 1420361_AT, 1427076_AT, 1419483_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1448710_AT, 1420699_AT, 1428018_A_AT, 1449195_S_AT, 1421792_S_AT, 1435477_S_AT, 1451161_A_AT, 1449156_AT, 1425545_X_AT, 1418826_AT, 1451941_A_AT, 1455332_X_AT, 1448303_AT, 1449164_AT
	UP_SEQ_FEATURE	topological domain:Cytoplasmic	29	42.65	1.29E-06	1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1420361_AT, 1427076_AT, 1419483_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1448710_AT, 1420699_AT, 1428018_A_AT, 1449195_S_AT, 1421792_S_AT, 1435477_S_AT, 1451161_A_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1418826_AT, 1451941_A_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	SP_PIR_KEYWORDS	transmembrane	35	51.47	3.82E-06	1426025_S_AT, 1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1425025_AT, 1420361_AT, 1437540_AT, 1427076_AT, 1419483_AT, 1418808_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1419064_A_AT, 1448710_AT, 1420699_AT, 1421792_S_AT, 1428018_A_AT, 1449195_S_AT, 1435477_S_AT, 1448640_AT, 1451161_A_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1418826_AT, 1451941_A_AT, 1428114_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	UP_SEQ_FEATURE	transmembrane region	34	50.00	7.17E-06	1426025_S_AT, 1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1425025_AT, 1420361_AT, 1437540_AT, 1427076_AT, 1419483_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1419064_A_AT, 1448710_AT, 1420699_AT, 1421792_S_AT, 1428018_A_AT, 1449195_S_AT, 1435477_S_AT, 1448640_AT, 1451161_A_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1418826_AT, 1451941_A_AT, 1428114_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	SP_PIR_KEYWORDS	membrane	38	55.88	1.15E-04	1454268_A_AT, 1426025_S_AT, 1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1418825_AT, 1422875_AT, 1425025_AT, 1420361_AT, 1437540_AT, 1427076_AT, 1419483_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1416612_AT, 1435903_AT, 1427301_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1419064_A_AT, 1448710_AT, 1420699_AT, 1421792_S_AT, 1449195_S_AT, 1428018_A_AT, 1435477_S_AT, 1448640_AT, 1451161_A_AT, 1449156_AT, 1425545_X_AT, 1418826_AT, 1421812_AT, 1451941_A_AT, 1428114_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0016021-integral to membrane	36	52.94	8.97E-04	1426025_S_AT, 1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1425025_AT, 1420361_AT, 1437540_AT, 1427076_AT, 1419483_AT, 1418808_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1419064_A_AT, 1448710_AT, 1420699_AT, 1421792_S_AT, 1428018_A_AT, 1449195_S_AT, 1435477_S_AT, 1448640_AT, 1451161_A_AT, 1424754_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1418826_AT, 1451941_A_AT, 1428114_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0031224-intrinsic to membrane	37	54.41	0.001060222	1426025_S_AT, 1451683_X_AT, 1424067_AT, 1420394_S_AT, 1419315_AT, 1422875_AT, 1425025_AT, 1420361_AT, 1437540_AT, 1427076_AT, 1419483_AT, 1418808_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1419599_S_AT, 1419455_AT, 1419598_AT, 1427221_AT, 1435903_AT, 1427301_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1419064_A_AT, 1448710_AT, 1420699_AT, 1421792_S_AT, 1428018_A_AT, 1449195_S_AT, 1435477_S_AT, 1448640_AT, 1451161_A_AT, 1424754_AT, 1449156_AT, 1425545_X_AT, 1421812_AT, 1418826_AT, 1451941_A_AT, 1428114_AT, 1455332_X_AT, 1418028_AT, 1448303_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0005886-plasma membrane	25	36.76	0.007853312	1426025_S_AT, 1451683_X_AT, 1420394_S_AT, 1424067_AT, 1418825_AT, 1422875_AT, 1437540_AT, 1419483_AT, 1438910_A_AT, 1419132_AT, 1419482_AT, 1427221_AT, 1435903_AT, 1427301_AT, 1448606_AT, 1419128_AT, 1451784_X_AT, 1448710_AT, 1420699_AT, 1421223_A_AT, 1428018_A_AT, 1421792_S_AT, 1435477_S_AT, 1451161_A_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1448303_AT, 1449164_AT
	Annotation Cluster 4	Enrichment Score: 2.8902508251328323				
	Category	Term	Count	%	PValue	Genes
immune	GOTERM_BP_FAT	GO:0006952-defense response	14	20.59	2.78E-08	1451683_X_AT, 1451784_X_AT, 1419100_AT, 1418825_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1435477_S_AT, 1436996_X_AT, 1419132_AT, 1439426_X_AT, 1425545_X_AT, 1418021_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1434366_X_AT, 1419561_AT, 1423547_AT
immune	SP_PIR_KEYWORDS	immune response	10	14.71	7.23E-08	1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1418825_AT, 1437726_X_AT, 1420699_AT, 1449401_AT, 1428018_A_AT, 1419132_AT, 1418021_AT, 1425545_X_AT, 1435903_AT, 1434366_X_AT
	GOTERM_BP_FAT	GO:0006955-immune response	14	20.59	8.55E-08	1451683_X_AT, 1451784_X_AT, 1424067_AT, 1420394_S_AT, 1418825_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1428018_A_AT, 1435477_S_AT, 1419132_AT, 1425545_X_AT, 1418021_AT, 1451941_A_AT, 1455332_X_AT, 1434366_X_AT, 1419561_AT, 1435903_AT
immune	GOTERM_BP_FAT	GO:0045087-innate immune response	7	10.29	7.95E-06	1418021_AT, 1418825_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
immune	SP_PIR_KEYWORDS	innate immunity	6	8.82	1.93E-05	1418021_AT, 1418825_AT, 1437726_X_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0002449-lymphocyte mediated immunity	6	8.82	2.83E-05	1418021_AT, 1424067_AT, 1451941_A_AT, 1437726_X_AT, 1420361_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0002250-adaptive immune response	6	8.82	4.65E-05	1418021_AT, 1424067_AT, 1451941_A_AT, 1437726_X_AT, 1420361_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT

immune	GOTERM_BP_FAT	GO:0002460-adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6	8.82	4.65E-05	1418021_AT, 1424067_AT, 1451941_A_AT, 1437726_X_AT, 1420361_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0002443-leukocyte mediated immunity	6	8.82	6.04E-05	1418021_AT, 1424067_AT, 1451941_A_AT, 1437726_X_AT, 1420361_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0006954-inflammatory response	8	11.76	9.41E-05	1418021_AT, 1419100_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419561_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0019882-antigen processing and presentation	5	7.35	2.54E-04	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1421812_AT, 1424067_AT, 1451941_A_AT, 1420361_AT, 1455332_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0002252-immune effector process	6	8.82	3.19E-04	1418021_AT, 1424067_AT, 1451941_A_AT, 1437726_X_AT, 1420361_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0050778-positive regulation of immune response	6	8.82	3.62E-04	1418021_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
	GOTERM_BP_FAT	GO:0002253-activation of immune response	5	7.35	5.36E-04	1418021_AT, 1437726_X_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0009611-response to wounding	8	11.76	0.001378617	1418021_AT, 1419100_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419561_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0048584-positive regulation of response to stimulus	6	8.82	0.00154885	1418021_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0002684-positive regulation of immune system process	6	8.82	0.002788943	1418021_AT, 1437726_X_AT, 1420361_AT, 1420699_AT, 1449401_AT, 1434366_X_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0016064-immunoglobulin mediated immune response	4	5.88	0.003139579	1418021_AT, 1451941_A_AT, 1437726_X_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0019724-B cell mediated immunity	4	5.88	0.003488663	1418021_AT, 1451941_A_AT, 1437726_X_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	SP_PIR_KEYWORDS	inflammatory response	4	5.88	0.005771685	1418021_AT, 1420699_AT, 1419561_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0002526-acute inflammatory response	4	5.88	0.006865313	1418021_AT, 1419100_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	SP_PIR_KEYWORDS	complement pathway	3	4.41	0.006870333	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0006958-complement activation, classical pathway	3	4.41	0.007768512	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0002455-humoral immune response mediated by circulating immunoglobulin	3	4.41	0.010489602	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0002541-activation of plasma proteins involved in acute inflammatory response	3	4.41	0.010489602	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0006956-complement activation	3	4.41	0.010489602	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	4	5.88	0.011408844	1418021_AT, 1451941_A_AT, 1437726_X_AT, 1455332_X_AT, 1449401_AT, 1434366_X_AT, 1435477_S_AT
immune	KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	4	5.88	0.011878829	1418021_AT, 1419482_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT, 1419483_AT
immune	GOTERM_BP_FAT	GO:0010033-response to organic substance	7	10.29	0.016092162	1419100_AT, 1420361_AT, 1420699_AT, 1422660_AT, 1416612_AT, 1427301_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0006959-humoral immune response	3	4.41	0.023764772	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0001819-positive regulation of cytokine production	3	4.41	0.028051453	1420361_AT, 1420699_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0051605-protein maturation by peptide bond cleavage	3	4.41	0.035012467	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0016485-protein processing	3	4.41	0.062264083	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0051604-protein maturation	3	4.41	0.068366612	1418021_AT, 1437726_X_AT, 1449401_AT, 1434366_X_AT
immune	GOTERM_BP_FAT	GO:0001817-regulation of cytokine production	3	4.41	0.136242797	1420361_AT, 1420699_AT, 1419132_AT
immune	GOTERM_BP_FAT	GO:0051240-positive regulation of multicellular organismal process	3	4.41	0.171199099	1420361_AT, 1420699_AT, 1419132_AT
	GOTERM_BP_FAT	GO:0006508-proteolysis	7	10.29	0.263621423	1418021_AT, 1417870_X_AT, 1437726_X_AT, 1417868_A_AT, 1448591_AT, 1449401_AT, 1434366_X_AT, 1455965_AT, 1460248_AT
	UP_SEQ_FEATURE	mutagenesis site	5	7.35	0.483181551	1418825_AT, 1420699_AT, 1428018_A_AT, 1435903_AT, 1419132_AT
	Annotation Cluster 5	Enrichment Score: 2.7407592738577513				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0009897-external side of plasma membrane	8	11.76	1.87E-04	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1424067_AT, 1451941_A_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT, 1427301_AT, 1451161_A_AT, 1419128_AT, 1419132_AT
	GOTERM_CC_FAT	GO:0009986-cell surface	9	13.24	3.35E-04	1451683_X_AT, 1451784_X_AT, 1424067_AT, 1420361_AT, 1420699_AT, 1435477_S_AT, 1451161_A_AT, 1419132_AT, 1425545_X_AT, 1451941_A_AT, 1455332_X_AT, 1427301_AT, 1419128_AT
	GOTERM_CC_FAT	GO:0044459-plasma membrane part	14	20.59	0.095714156	1426025_S_AT, 1451683_X_AT, 1451784_X_AT, 1424067_AT, 1420699_AT, 1421223_A_AT, 1435477_S_AT, 1451161_A_AT, 1438910_A_AT, 1419132_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1427221_AT, 1448303_AT, 1427301_AT, 1419128_AT
	Annotation Cluster 6	Enrichment Score: 2.5795838206287387				

	Category	Term	Count	%	PValue	Genes
	KEGG_PATHWAY	mmu04142:Lysosome	6	8.82	7.46E-04	1426025_S_AT, 1417870_X_AT, 1416340_A_AT, 1417868_A_AT, 1420361_AT, 1448591_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0005773-vacuole	7	10.29	0.001574594	1426025_S_AT, 1417870_X_AT, 1416340_A_AT, 1418825_AT, 1417868_A_AT, 1420361_AT, 1448591_AT, 1449164_AT
	SP_PIR_KEYWORDS	lysosome	5	7.35	0.004755445	1426025_S_AT, 1417870_X_AT, 1416340_A_AT, 1417868_A_AT, 1448591_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0005764-lysosome	6	8.82	0.004759808	1426025_S_AT, 1417870_X_AT, 1416340_A_AT, 1417868_A_AT, 1420361_AT, 1448591_AT, 1449164_AT
	GOTERM_CC_FAT	GO:0000323-lytic vacuole	6	8.82	0.004759808	1426025_S_AT, 1417870_X_AT, 1416340_A_AT, 1417868_A_AT, 1420361_AT, 1448591_AT, 1449164_AT
	Annotation Cluster 7	Enrichment Score: 2.3216805623472023				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0050829-defense response to Gram-negative bacterium	3	4.41	8.34E-04	1420361_AT, 1436996_X_AT, 1423547_AT, 1439426_X_AT
	GOTERM_BP_FAT	GO:0050830-defense response to Gram-positive bacterium	3	4.41	0.004899368	1436996_X_AT, 1423547_AT, 1419132_AT, 1439426_X_AT
	GOTERM_BP_FAT	GO:0042742-defense response to bacterium	4	5.88	0.005586037	1420361_AT, 1436996_X_AT, 1423547_AT, 1419132_AT, 1439426_X_AT
	GOTERM_BP_FAT	GO:0009617-response to bacterium	4	5.88	0.022631172	1420361_AT, 1436996_X_AT, 1423547_AT, 1419132_AT, 1439426_X_AT
	Annotation Cluster 8	Enrichment Score: 2.2370588137102074				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	Secreted	16	23.53	6.04E-04	1448148_AT, 1419298_AT, 1419100_AT, 1437726_X_AT, 1448380_AT, 1421792_S_AT, 1449401_AT, 1435477_S_AT, 1455965_AT, 1418910_AT, 1417963_AT, 1419202_AT, 1418021_AT, 1451941_A_AT, 1452014_A_AT, 1455332_X_AT, 1434366_X_AT, 1419561_AT, 1456567_X_AT, 1460248_AT
	GOTERM_CC_FAT	GO:0005576-extracellular region	18	26.47	0.005096219	1448148_AT, 1419298_AT, 1419100_AT, 1437726_X_AT, 1448380_AT, 1421792_S_AT, 1449195_S_AT, 1449401_AT, 1435477_S_AT, 1455965_AT, 1418910_AT, 1417963_AT, 1419202_AT, 1418021_AT, 1451941_A_AT, 1452014_A_AT, 1455332_X_AT, 1426808_AT, 1434366_X_AT, 1419561_AT, 1456567_X_AT, 1460248_AT
	GOTERM_CC_FAT	GO:0044421-extracellular region part	11	16.18	0.012600953	1418021_AT, 1448148_AT, 1419298_AT, 1452014_A_AT, 1448380_AT, 1449195_S_AT, 1426808_AT, 1419561_AT, 1456567_X_AT, 1455965_AT, 1460248_AT, 1418910_AT
immune	GOTERM_CC_FAT	GO:0005615-extracellular space	8	11.76	0.029046853	1418021_AT, 1448148_AT, 1419298_AT, 1452014_A_AT, 1449195_S_AT, 1419561_AT, 1456567_X_AT, 1460248_AT, 1418910_AT
	Annotation Cluster 9	Enrichment Score: 1.9176920910086395				
	Category	Term	Count	%	PValue	Genes
immune	INTERPRO	IPR013783:Immunoglobulin-like fold	10	14.71	5.71E-05	1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1424067_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1435903_AT, 1427301_AT, 1448891_AT
	SP_PIR_KEYWORDS	cell membrane	17	25.00	7.40E-04	1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1418825_AT, 1422875_AT, 1448710_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1419483_AT, 1451161_A_AT, 1438910_A_AT, 1419132_AT, 1425545_X_AT, 1419482_AT, 1451941_A_AT, 1455332_X_AT, 1427221_AT, 1435903_AT, 1449164_AT, 1427301_AT, 1448606_AT
	SP_PIR_KEYWORDS	alternative splicing	17	25.00	0.698753839	1454268_A_AT, 1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1424067_AT, 1418825_AT, 1422875_AT, 1448710_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1425545_X_AT, 1426509_S_AT, 1426508_AT, 1421812_AT, 1451941_A_AT, 1436890_AT, 1452014_A_AT, 1455332_X_AT, 1435903_AT, 1449164_AT, 1448606_AT
	UP_SEQ_FEATURE	splice variant	17	25.00	0.722999178	1454268_A_AT, 1451683_X_AT, 1451784_X_AT, 1420394_S_AT, 1424067_AT, 1418825_AT, 1422875_AT, 1448710_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1425545_X_AT, 1426509_S_AT, 1426508_AT, 1421812_AT, 1451941_A_AT, 1436890_AT, 1452014_A_AT, 1455332_X_AT, 1435903_AT, 1449164_AT, 1448606_AT
	Annotation Cluster 10	Enrichment Score: 1.6649392451162597				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0007155-cell adhesion	8	11.76	0.011406839	1424067_AT, 1422875_AT, 1448380_AT, 1420699_AT, 1448303_AT, 1460248_AT, 1419128_AT, 1449156_AT
	GOTERM_BP_FAT	GO:0022610-biological adhesion	8	11.76	0.011538761	1424067_AT, 1422875_AT, 1448380_AT, 1420699_AT, 1448303_AT, 1460248_AT, 1419128_AT, 1449156_AT
	SP_PIR_KEYWORDS	cell adhesion	5	7.35	0.076887856	1424067_AT, 1422875_AT, 1448380_AT, 1419128_AT, 1449156_AT
	Annotation Cluster 11	Enrichment Score: 1.5393972778930243				
	Category	Term	Count	%	PValue	Genes
immune	GOTERM_BP_FAT	GO:0042098-T cell proliferation	3	4.41	0.009083018	1420361_AT, 1448710_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0046651-lymphocyte proliferation	3	4.41	0.017902453	1420361_AT, 1448710_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0032943-mononuclear cell proliferation	3	4.41	0.018830422	1420361_AT, 1448710_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0070661-leukocyte proliferation	3	4.41	0.018830422	1420361_AT, 1448710_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0045321-leukocyte activation	5	7.35	0.019305064	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1448710_AT, 1435477_S_AT, 1427301_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0042110-T cell activation	4	5.88	0.0200143	1420361_AT, 1448710_AT, 1427301_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0001775-cell activation	5	7.35	0.029086386	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1448710_AT, 1435477_S_AT, 1427301_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0046649-lymphocyte activation	4	5.88	0.060262652	1420361_AT, 1448710_AT, 1427301_AT, 1419128_AT
immune	GOTERM_BP_FAT	GO:0008283-cell proliferation	3	4.41	0.357941461	1420361_AT, 1448710_AT, 1419128_AT
	Annotation Cluster 12	Enrichment Score: 1.52574686796283				

	Category	Term	Count	%	PValue	Genes
	GOTERM_MF_FAT	GO:0004866-endopeptidase inhibitor activity	4	5.88	0.019097955	1418021_AT, 1419100_AT, 1452352_AT, 1419202_AT
	GOTERM_MF_FAT	GO:0030414-peptidase inhibitor activity	4	5.88	0.022548735	1418021_AT, 1419100_AT, 1452352_AT, 1419202_AT
	GOTERM_MF_FAT	GO:0004857-enzyme inhibitor activity	4	5.88	0.061468178	1418021_AT, 1419100_AT, 1452352_AT, 1419202_AT
	Annotation Cluster 13	Enrichment Score: 1.3607610489878275				
	Category	Term	Count	%	PValue	Genes
immune	GOTERM_CC_FAT	GO:0005615-extracellular space	8	11.76	0.029046853	1418021_AT, 1448148_AT, 1419298_AT, 1452014_A_AT, 1449195_S_AT, 1419561_AT, 1456567_X_AT, 1460248_AT, 1418910_AT
immune	GOTERM_MF_FAT	GO:0005125-cytokine activity	4	5.88	0.042370762	1448148_AT, 1449195_S_AT, 1419561_AT, 1456567_X_AT, 1418910_AT
immune	SP_PIR_KEYWORDS	cytokine	4	5.88	0.043738306	1448148_AT, 1449195_S_AT, 1419561_AT, 1456567_X_AT, 1418910_AT
	KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	5	7.35	0.06697743	1419455_AT, 1448710_AT, 1449195_S_AT, 1419561_AT, 1418910_AT
	Annotation Cluster 14	Enrichment Score: 1.2560398176710135				
	Category	Term	Count	%	PValue	Genes
immune	GOTERM_BP_FAT	GO:0050766-positive regulation of phagocytosis	3	4.41	0.004399266	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0050764-regulation of phagocytosis	3	4.41	0.005424421	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0045807-positive regulation of endocytosis	3	4.41	0.009774934	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0006909-phagocytosis	3	4.41	0.019778346	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0030100-regulation of endocytosis	3	4.41	0.020745983	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0060627-regulation of vesicle-mediated transport	3	4.41	0.046555602	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0051130-positive regulation of cellular component organization	3	4.41	0.119462989	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0051050-positive regulation of transport	3	4.41	0.134352312	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0006897-endocytosis	3	4.41	0.221817505	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0010324-membrane invagination	3	4.41	0.221817505	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0016044-membrane organization	3	4.41	0.374087963	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
immune	GOTERM_BP_FAT	GO:0016192-vesicle-mediated transport	3	4.41	0.642887442	1451941_A_AT, 1420361_AT, 1455332_X_AT, 1420699_AT, 1435477_S_AT
	Annotation Cluster 15	Enrichment Score: 1.221327586084469				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0005887-integral to plasma membrane	7	10.29	0.044611228	1426025_S_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1427221_AT, 1448303_AT, 1435477_S_AT, 1419128_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0031226-intrinsic to plasma membrane	7	10.29	0.050768799	1426025_S_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1427221_AT, 1448303_AT, 1435477_S_AT, 1419128_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0044459-plasma membrane part	14	20.59	0.095714156	1426025_S_AT, 1451683_X_AT, 1451784_X_AT, 1424067_AT, 1420699_AT, 1421223_A_AT, 1435477_S_AT, 1451161_A_AT, 1438910_A_AT, 1419132_AT, 1425545_X_AT, 1421812_AT, 1451941_A_AT, 1455332_X_AT, 1427221_AT, 1448303_AT, 1427301_AT, 1419128_AT
	Annotation Cluster 16	Enrichment Score: 1.085074596499677				
	Category	Term	Count	%	PValue	Genes
extracellular matrix/adhesion	GOTERM_MF_FAT	GO:0030246-carbohydrate binding	5	7.35	0.04388825	1416340_A_AT, 1420699_AT, 1448303_AT, 1426808_AT, 1418910_AT
extracellular matrix/adhesion	GOTERM_MF_FAT	GO:0001871-pattern binding	3	4.41	0.112515919	1420699_AT, 1448303_AT, 1418910_AT
extracellular matrix/adhesion	GOTERM_MF_FAT	GO:0030247-polysaccharide binding	3	4.41	0.112515919	1420699_AT, 1448303_AT, 1418910_AT
	Annotation Cluster 17	Enrichment Score: 1.0831038273109155				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	chemotaxis	3	4.41	0.033710359	1419482_AT, 1449195_S_AT, 1419561_AT, 1419483_AT
	GOTERM_BP_FAT	GO:0042330-taxis	3	4.41	0.101512971	1419482_AT, 1449195_S_AT, 1419561_AT, 1419483_AT
	GOTERM_BP_FAT	GO:0006935-chemotaxis	3	4.41	0.101512971	1419482_AT, 1449195_S_AT, 1419561_AT, 1419483_AT
	GOTERM_BP_FAT	GO:0007610-behavior	5	7.35	0.10463346	1419482_AT, 1416340_A_AT, 1437540_AT, 1449195_S_AT, 1419561_AT, 1419483_AT
	GOTERM_BP_FAT	GO:0007626-locomotory behavior	4	5.88	0.10568268	1419482_AT, 1437540_AT, 1449195_S_AT, 1419561_AT, 1419483_AT
	Annotation Cluster 18	Enrichment Score: 0.9116367543075803				
	Category	Term	Count	%	PValue	Genes

	GOTERM_BP_FAT	GO:0001503-ossification	3	4.41	0.096290258	1452014_A_AT, 1448303_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0060348-bone development	3	4.41	0.113995571	1452014_A_AT, 1448303_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0001501-skeletal system development	4	5.88	0.167733345	1452014_A_AT, 1448303_AT, 1426808_AT, 1418910_AT
	Annotation Cluster 19	Enrichment Score: 0.7598296521261833				
	Category	Term	Count	%	PValue	Genes
	INTERPRO	IPR013128:Peptidase C1A, papain	3	4.41	0.008105518	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1452352_AT
	GOTERM_MF_FAT	GO:0008234-cysteine-type peptidase activity	3	4.41	0.115979532	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1452352_AT
	GOTERM_MF_FAT	GO:0070011-peptidase activity, acting on L-amino acid peptides	5	7.35	0.203253743	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1452352_AT, 1455965_AT, 1460248_AT
	GOTERM_MF_FAT	GO:0008233-peptidase activity	5	7.35	0.225789104	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1452352_AT, 1455965_AT, 1460248_AT
	SP_PIR_KEYWORDS	zymogen	3	4.41	0.234813039	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1455965_AT
	GOTERM_BP_FAT	GO:0006508-proteolysis	7	10.29	0.263621423	1418021_AT, 1417870_X_AT, 1437726_X_AT, 1417868_A_AT, 1448591_AT, 1449401_AT, 1434366_X_AT, 1455965_AT, 1460248_AT
	GOTERM_MF_FAT	GO:0004175-endopeptidase activity	3	4.41	0.495330504	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1455965_AT
	SP_PIR_KEYWORDS	Protease	3	4.41	0.63075561	1417870_X_AT, 1417868_A_AT, 1448591_AT, 1455965_AT
	Annotation Cluster 20	Enrichment Score: 0.7438319563573289				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0048754-branching morphogenesis of a tube	3	4.41	0.089454797	1452014_A_AT, 1448710_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0001763-morphogenesis of a branching structure	3	4.41	0.140041933	1452014_A_AT, 1448710_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0035239-tube morphogenesis	3	4.41	0.2177101	1452014_A_AT, 1448710_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0035295-tube development	3	4.41	0.388089477	1452014_A_AT, 1448710_AT, 1418910_AT
	Annotation Cluster 21	Enrichment Score: 0.7186851822773435				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0048770-pigment granule	3	4.41	0.114055629	1418028_AT, 1448303_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0042470-melanosome	3	4.41	0.114055629	1418028_AT, 1448303_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0031410-cytoplasmic vesicle	6	8.82	0.196237639	1418825_AT, 1420361_AT, 1418028_AT, 1448303_AT, 1438910_A_AT, 1419132_AT
	GOTERM_CC_FAT	GO:0031982-vesicle	6	8.82	0.207515257	1418825_AT, 1420361_AT, 1418028_AT, 1448303_AT, 1438910_A_AT, 1419132_AT
	GOTERM_CC_FAT	GO:0016023-cytoplasmic membrane-bounded vesicle	5	7.35	0.246291067	1418825_AT, 1420361_AT, 1418028_AT, 1448303_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0031988-membrane-bounded vesicle	5	7.35	0.255620839	1418825_AT, 1420361_AT, 1418028_AT, 1448303_AT, 1438910_A_AT
	SP_PIR_KEYWORDS	cytoplasmic vesicle	3	4.41	0.279314203	1418825_AT, 1448303_AT, 1419132_AT
	Annotation Cluster 22	Enrichment Score: 0.5211078231034835				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0007166-cell surface receptor linked signal transduction	10	14.71	0.098498028	1420699_AT, 1448710_AT, 1435477_S_AT, 1419483_AT, 1451161_A_AT, 1418910_AT, 1419132_AT, 1419482_AT, 1451941_A_AT, 1452014_A_AT, 1455332_X_AT, 1448606_AT, 1419128_AT
immune	SP_PIR_KEYWORDS	g-protein coupled receptor	4	5.88	0.226962037	1419482_AT, 1448710_AT, 1448606_AT, 1451161_A_AT, 1419483_AT
immune	SP_PIR_KEYWORDS	transducer	4	5.88	0.291676056	1419482_AT, 1448710_AT, 1448606_AT, 1451161_A_AT, 1419483_AT
immune	PIR_SUPERFAMILY	PIRSF800006:rhodopsin-like G protein-coupled receptors	3	4.41	0.414730487	1419482_AT, 1448710_AT, 1448606_AT, 1419483_AT
immune	INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	3	4.41	0.415416875	1419482_AT, 1448710_AT, 1448606_AT, 1419483_AT
immune	INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	3	4.41	0.427257576	1419482_AT, 1448710_AT, 1448606_AT, 1419483_AT
immune	GOTERM_BP_FAT	GO:0007186-G-protein coupled receptor protein signaling pathway	4	5.88	0.468839111	1419482_AT, 1448710_AT, 1448606_AT, 1451161_A_AT, 1419483_AT
	Annotation Cluster 23	Enrichment Score: 0.3647640030852192				
	Category	Term	Count	%	PValue	Genes
signaling	GOTERM_BP_FAT	GO:0042325-regulation of phosphorylation	3	4.41	0.421529239	1420361_AT, 1448606_AT, 1418910_AT
signaling	GOTERM_BP_FAT	GO:0019220-regulation of phosphate metabolic process	3	4.41	0.436958451	1420361_AT, 1448606_AT, 1418910_AT
signaling	GOTERM_BP_FAT	GO:0051174-regulation of phosphorus metabolic process	3	4.41	0.436958451	1420361_AT, 1448606_AT, 1418910_AT
	Annotation Cluster 24	Enrichment Score: 0.31694277192642684				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0005792-microsome	3	4.41	0.302373509	1421812_AT, 1418028_AT, 1416612_AT
	GOTERM_CC_FAT	GO:0042598-vesicular fraction	3	4.41	0.315465801	1421812_AT, 1418028_AT, 1416612_AT

	GOTERM_CC_FAT	GO:0005624-membrane fraction	4	5.88	0.605045042	1426509_S_AT, 1426508_AT, 1421812_AT, 1418028_AT, 1416612_AT
	GOTERM_CC_FAT	GO:0005626-insoluble fraction	4	5.88	0.631242357	1426509_S_AT, 1426508_AT, 1421812_AT, 1418028_AT, 1416612_AT
	GOTERM_CC_FAT	GO:0000267-cell fraction	4	5.88	0.714177684	1426509_S_AT, 1426508_AT, 1421812_AT, 1418028_AT, 1416612_AT
	Annotation Cluster 25	Enrichment Score: 0.2723631535154015				
	Category	Term	Count	%	PValue	Genes
	SP_PIR_KEYWORDS	iron	3	4.41	0.394711934	1454268_A_AT, 1420361_AT, 1416612_AT
	GOTERM_MF_FAT	GO:0005506-iron ion binding	3	4.41	0.408739369	1454268_A_AT, 1420361_AT, 1416612_AT
	GOTERM_MF_FAT	GO:0046914-transition metal ion binding	7	10.29	0.944460528	1454268_A_AT, 1416340_A_AT, 1420361_AT, 1418028_AT, 1416612_AT, 1455965_AT, 1460248_AT
	Annotation Cluster 26	Enrichment Score: 0.15449423971815338				
	Category	Term	Count	%	PValue	Genes
	GOTERM_BP_FAT	GO:0051173-positive regulation of nitrogen compound metabolic process	4	5.88	0.486259515	1452014_A_AT, 1420361_AT, 1418910_AT, 1419132_AT
	GOTERM_BP_FAT	GO:0031328-positive regulation of cellular biosynthetic process	4	5.88	0.51470792	1452014_A_AT, 1420361_AT, 1418910_AT, 1419132_AT
	GOTERM_BP_FAT	GO:0009891-positive regulation of biosynthetic process	4	5.88	0.520303373	1452014_A_AT, 1420361_AT, 1418910_AT, 1419132_AT
	GOTERM_BP_FAT	GO:0045944-positive regulation of transcription from RNA polymerase II promoter	3	4.41	0.536738344	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0045893-positive regulation of transcription, DNA-dependent	3	4.41	0.624129064	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0051254-positive regulation of RNA metabolic process	3	4.41	0.62852236	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0045941-positive regulation of transcription	3	4.41	0.694855856	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0010628-positive regulation of gene expression	3	4.41	0.708370506	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0045935-positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	3	4.41	0.728298171	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0010557-positive regulation of macromolecule biosynthetic process	3	4.41	0.746017186	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0006357-regulation of transcription from RNA polymerase II promoter	3	4.41	0.814198901	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0010604-positive regulation of macromolecule metabolic process	3	4.41	0.826992857	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0006355-regulation of transcription, DNA-dependent	3	4.41	0.988133938	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0051252-regulation of RNA metabolic process	3	4.41	0.989472578	1452014_A_AT, 1420361_AT, 1418910_AT
	GOTERM_BP_FAT	GO:0045449-regulation of transcription	4	5.88	0.997419705	1452014_A_AT, 1420361_AT, 1418910_AT, 1419132_AT
	Annotation Cluster 27	Enrichment Score: 0.11532949597072797				
	Category	Term	Count	%	PValue	Genes
apoptosis	GOTERM_BP_FAT	GO:0042981-regulation of apoptosis	3	4.41	0.762762843	1452014_A_AT, 1419004_S_AT, 1418910_AT
apoptosis	GOTERM_BP_FAT	GO:0043067-regulation of programmed cell death	3	4.41	0.767801444	1452014_A_AT, 1419004_S_AT, 1418910_AT
apoptosis	GOTERM_BP_FAT	GO:0010941-regulation of cell death	3	4.41	0.769791407	1452014_A_AT, 1419004_S_AT, 1418910_AT
	Annotation Cluster 28	Enrichment Score: 0.008719633323897162				
	Category	Term	Count	%	PValue	Genes
	GOTERM_MF_FAT	GO:0046914-transition metal ion binding	7	10.29	0.944460528	1454268_A_AT, 1416340_A_AT, 1420361_AT, 1418028_AT, 1416612_AT, 1455965_AT, 1460248_AT
	GOTERM_MF_FAT	GO:0046872-metal ion binding	10	14.71	0.979505533	1454268_A_AT, 1416340_A_AT, 1420361_AT, 1418028_AT, 1421223_A_AT, 1416612_AT, 1455965_AT, 1460248_AT, 1451161_A_AT, 1419128_AT
	GOTERM_MF_FAT	GO:0043169-cation binding	10	14.71	0.981612539	1454268_A_AT, 1416340_A_AT, 1420361_AT, 1418028_AT, 1421223_A_AT, 1416612_AT, 1455965_AT, 1460248_AT, 1451161_A_AT, 1419128_AT
	GOTERM_MF_FAT	GO:0043167-ion binding	10	14.71	0.984353291	1454268_A_AT, 1416340_A_AT, 1420361_AT, 1418028_AT, 1421223_A_AT, 1416612_AT, 1455965_AT, 1460248_AT, 1451161_A_AT, 1419128_AT
	SP_PIR_KEYWORDS	metal-binding	6	8.82	0.987425401	1454268_A_AT, 1419298_AT, 1416340_A_AT, 1418028_AT, 1416612_AT, 1455965_AT
	GOTERM_MF_FAT	GO:0008270-zinc ion binding	4	5.88	0.988338271	1416340_A_AT, 1418028_AT, 1455965_AT, 1460248_AT

	SP_PIR_KEYWORDS	zinc	3	4.41	0.996026421	1416340_A_AT, 1418028_AT, 1455965_AT
	Annotation Cluster 29	Enrichment Score: 0.0021074596656234946				
	Category	Term	Count	%	PValue	Genes
	GOTERM_CC_FAT	GO:0005856-cytoskeleton	3	4.41	0.985804132	1426509_S_AT, 1426508_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0043228-non-membrane-bounded organelle	3	4.41	0.999869897	1426509_S_AT, 1426508_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1438910_A_AT
	GOTERM_CC_FAT	GO:0043232-intracellular non-membrane-bounded organelle	3	4.41	0.999869897	1426509_S_AT, 1426508_AT, 1451941_A_AT, 1455332_X_AT, 1435477_S_AT, 1438910_A_AT
	Unclustered terms					
	INTERPRO	IPR015631:Signalling lymphocyte activation molecule	4	5.88	2.05E-05	1419315_AT, 1422875_AT, 1427301_AT, 1449156_AT
	SP_PIR_KEYWORDS	receptor	17	25.00	3.86E-05	1420394_S_AT, 1422875_AT, 1420699_AT, 1448710_AT, 1421792_S_AT, 1428018_A_AT, 1435477_S_AT, 1451161_A_AT, 1419483_AT, 1419132_AT, 1419599_S_AT, 1419482_AT, 1418826_AT, 1419455_AT, 1451941_A_AT, 1419598_AT, 1455332_X_AT, 1435903_AT, 1448606_AT, 1448891_AT, 1419128_AT
	UP_SEQ_FEATURE	sequence variant	9	13.24	4.81E-04	1451683_X_AT, 1451784_X_AT, 1422875_AT, 1448591_AT, 1420361_AT, 1437540_AT, 1421792_S_AT, 1435477_S_AT, 1449156_AT, 1425545_X_AT, 1451941_A_AT, 1455332_X_AT, 1418028_AT
immune	GOTERM_BP_FAT	GO:0048002-antigen processing and presentation of peptide antigen	4	5.88	6.57E-04	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1421812_AT, 1451941_A_AT, 1420361_AT, 1455332_X_AT, 1435477_S_AT
	INTERPRO	IPR007237:CD20/IgE Fc receptor beta subunit	3	4.41	0.002025329	1419599_S_AT, 1418826_AT, 1419598_AT, 1424754_AT
	GOTERM_MF_FAT	GO:0005044-scavenger receptor activity	3	4.41	0.010980001	1448380_AT, 1449195_S_AT, 1448891_AT
	SP_PIR_KEYWORDS	sulfation	3	4.41	0.013052052	1418021_AT, 1419482_AT, 1448710_AT, 1419483_AT
	SP_PIR_KEYWORDS	glycosidase	3	4.41	0.037284712	1416340_A_AT, 1436996_X_AT, 1423547_AT, 1439426_X_AT
immune	GOTERM_MF_FAT	GO:0032403-protein complex binding	3	4.41	0.050623651	1451941_A_AT, 1455332_X_AT, 1448303_AT, 1426808_AT, 1435477_S_AT
	UP_SEQ_FEATURE	short sequence motif:Cell attachment site	3	4.41	0.053720887	1424067_AT, 1448303_AT, 1451161_A_AT
immune	UP_SEQ_FEATURE	domain:Ig-like V-type	3	4.41	0.062520649	1421792_S_AT, 1428018_A_AT, 1435903_AT
	SP_PIR_KEYWORDS	polymorphism	4	5.88	0.075869107	1418021_AT, 1451941_A_AT, 1422875_AT, 1455332_X_AT, 1435477_S_AT, 1449156_AT
immune	KEGG_PATHWAY	mmu04612:Antigen processing and presentation	3	4.41	0.077093483	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1421812_AT, 1448591_AT
	GOTERM_BP_FAT	GO:0001655-urogenital system development	3	4.41	0.16526476	1452014_A_AT, 1421223_A_AT, 1418910_AT
	KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	3	4.41	0.175657176	1454268_A_AT, 1424067_AT, 1448710_AT
	KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	3	4.41	0.175657176	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1424067_AT, 1427301_AT
	SP_PIR_KEYWORDS	hydrolase	9	13.24	0.295622672	1418021_AT, 1419298_AT, 1417870_X_AT, 1416340_A_AT, 1418825_AT, 1417868_A_AT, 1448591_AT, 1455965_AT, 1436996_X_AT, 1423547_AT, 1439426_X_AT
	KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	3	4.41	0.323759014	1448710_AT, 1449195_S_AT, 1419561_AT
signaling	GOTERM_BP_FAT	GO:0044093-positive regulation of molecular function	3	4.41	0.413738129	1420361_AT, 1448606_AT, 1419132_AT
development	GOTERM_BP_FAT	GO:0030030-cell projection organization	3	4.41	0.433120767	1448710_AT, 1448606_AT, 1418910_AT
	SP_PIR_KEYWORDS	lipoprotein	4	5.88	0.502756052	1416527_AT, 1427301_AT, 1448606_AT, 1438910_A_AT
extracellular matrix/adhesion	GOTERM_CC_FAT	GO:0005578-proteinaceous extracellular matrix	3	4.41	0.509463423	1448380_AT, 1426808_AT, 1455965_AT
extracellular matrix/adhesion	GOTERM_CC_FAT	GO:0031012-extracellular matrix	3	4.41	0.527172974	1448380_AT, 1426808_AT, 1455965_AT
myelination	GOTERM_BP_FAT	GO:0048878-chemical homeostasis	3	4.41	0.529882946	1452014_A_AT, 1419064_A_AT, 1420361_AT
myelination	GOTERM_BP_FAT	GO:0042592-homeostatic process	4	5.88	0.530015865	1452014_A_AT, 1419064_A_AT, 1420361_AT, 1419004_S_AT
	GOTERM_BP_FAT	GO:0042127-regulation of cell proliferation	4	5.88	0.536889914	1448148_AT, 1451941_A_AT, 1452014_A_AT, 1455332_X_AT, 1456567_X_AT, 1435477_S_AT, 1418910_AT
development	GOTERM_BP_FAT	GO:0030182-neuron differentiation	3	4.41	0.555247068	1448710_AT, 1437540_AT, 1418910_AT
	SP_PIR_KEYWORDS	transmembrane protein	3	4.41	0.563170642	1425545_X_AT, 1451683_X_AT, 1451784_X_AT, 1451941_A_AT, 1455332_X_AT, 1449164_AT, 1435477_S_AT
	SP_PIR_KEYWORDS	calcium	4	5.88	0.588065553	1419298_AT, 1421223_A_AT, 1451161_A_AT, 1419128_AT
ion transport/channels	SP_PIR_KEYWORDS	transport	7	10.29	0.698992751	1454268_A_AT, 1426025_S_AT, 1428114_AT, 1420361_AT, 1427221_AT, 1437540_AT, 1448640_AT, 1417963_AT
	SP_PIR_KEYWORDS	oxidoreductase	3	4.41	0.717341002	1454268_A_AT, 1416612_AT, 1418808_AT
	GOTERM_BP_FAT	GO:0008219-cell death	3	4.41	0.717891715	1419004_S_AT, 1436996_X_AT, 1423547_AT, 1439426_X_AT
	GOTERM_BP_FAT	GO:0016265-death	3	4.41	0.727157692	1419004_S_AT, 1436996_X_AT, 1423547_AT, 1439426_X_AT
myelination	GOTERM_BP_FAT	GO:0050877-neurological system process	3	4.41	0.736172056	1416340_A_AT, 1419064_A_AT, 1437540_AT
	GOTERM_BP_FAT	GO:0055114-oxidation reduction	3	4.41	0.805791109	1454268_A_AT, 1416612_AT, 1418808_AT
	GOTERM_MF_FAT	GO:0005509-calcium ion binding	3	4.41	0.862082527	1421223_A_AT, 1451161_A_AT, 1419128_AT
	GOTERM_CC_FAT	GO:0005783-endoplasmic reticulum	4	5.88	0.883113724	1421812_AT, 1418825_AT, 1416612_AT, 1418808_AT

	GOTERM_BP_FAT	GO:0007242-intracellular signaling cascade	3	4.41	0.92974142	1416527_AT, 1420361_AT, 1448606_AT
	GOTERM_CC_FAT	GO:0031090-organelle membrane	3	4.41	0.959984749	1426025_S_AT, 1418825_AT, 1420361_AT
	SP_PIR_KEYWORDS	phosphoprotein	22	32.35	0.96868323	1426025_S_AT, 1454268_A_AT, 1451683_X_AT, 1419298_AT, 1420394_S_AT, 1418825_AT, 1422875_AT, 1420361_AT, 1418808_AT, 1438910_A_AT, 1416527_AT, 1422660_AT, 1426808_AT, 1435903_AT, 1427301_AT, 1451784_X_AT, 1448710_AT, 1420699_AT, 1421223_A_AT, 1435477_S_AT, 1417963_AT, 1426509_S_AT, 1425545_X_AT, 1426508_AT, 1451941_A_AT, 1455332_X_AT, 1448303_AT
	GOTERM_CC_FAT	GO:0005739-mitochondrion	4	5.88	0.985725559	1454268_A_AT, 1448148_AT, 1416527_AT, 1456567_X_AT, 1418808_AT
signaling	GOTERM_MF_FAT	GO:0000166-nucleotide binding	3	4.41	0.999512242	1418825_AT, 1416527_AT, 1422660_AT
	SP_PIR_KEYWORDS	acetylation	3	4.41	0.999940469	1416527_AT, 1421223_A_AT, 1426808_AT
	SP_PIR_KEYWORDS	cytoplasm	4	5.88	0.999949456	1426509_S_AT, 1426508_AT, 1451941_A_AT, 1455332_X_AT, 1419004_S_AT, 1422660_AT, 1435477_S_AT