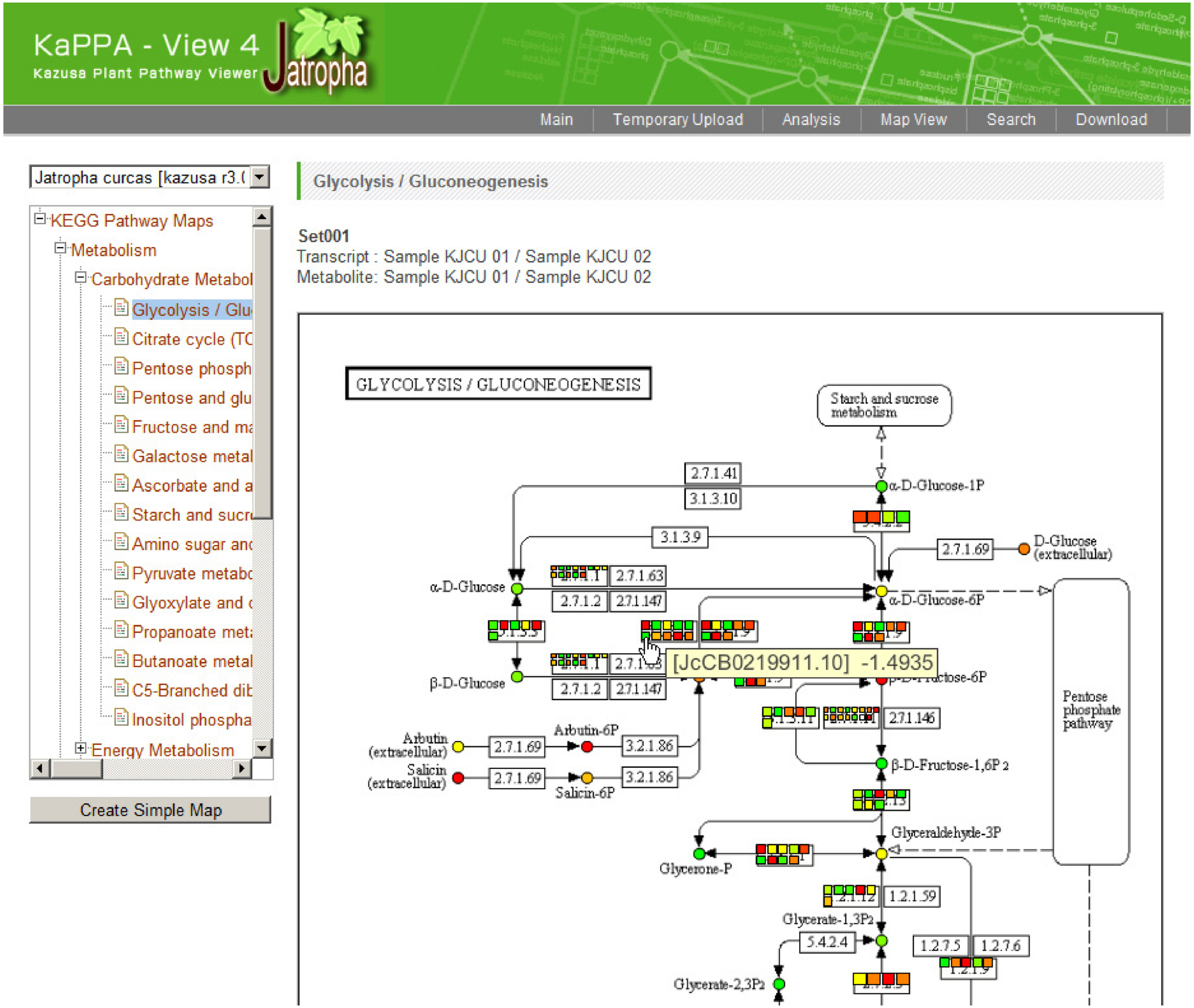


Glycolysis / Gluconeogenesis

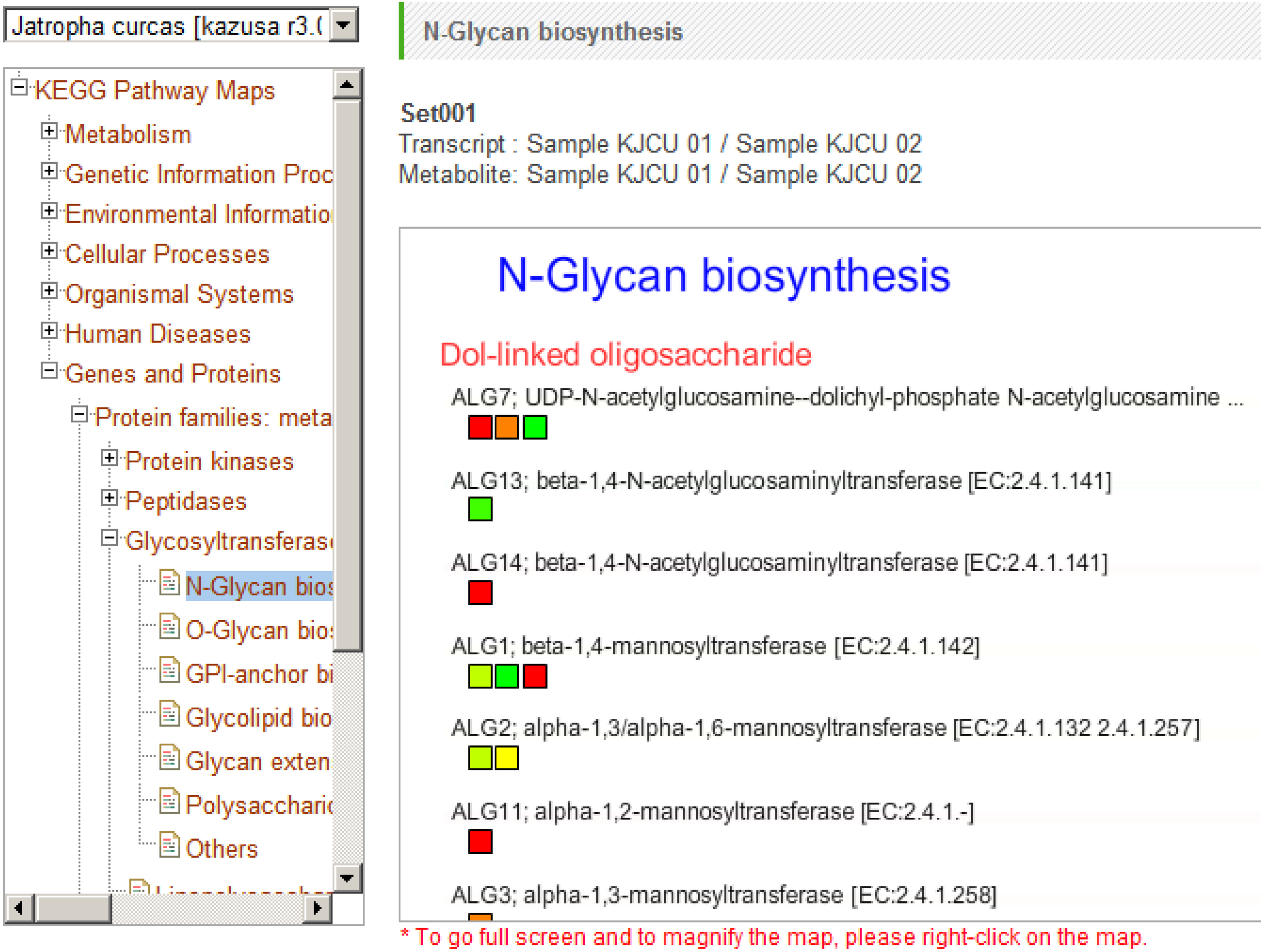
Set001

Transcript : Sample KJCU 01 / Sample KJCU 02

Metabolite: Sample KJCU 01 / Sample KJCU 02

[JcCB0219911.10] -1.4935

Supplemental Figure S1. A magnified image of Figure 1A.



Set001
Transcript : Sample KJCU 01 / Sample KJCU 02
Metabolite: Sample KJCU 01 / Sample KJCU 02

N-Glycan biosynthesis

Dol-linked oligosaccharide

ALG7; UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosamine ...
🟥🟧🟩

ALG13; beta-1,4-N-acetylglucosaminyltransferase [EC:2.4.1.141]
🟩

ALG14; beta-1,4-N-acetylglucosaminyltransferase [EC:2.4.1.141]
🟥

ALG1; beta-1,4-mannosyltransferase [EC:2.4.1.142]
🟩🟩🟥

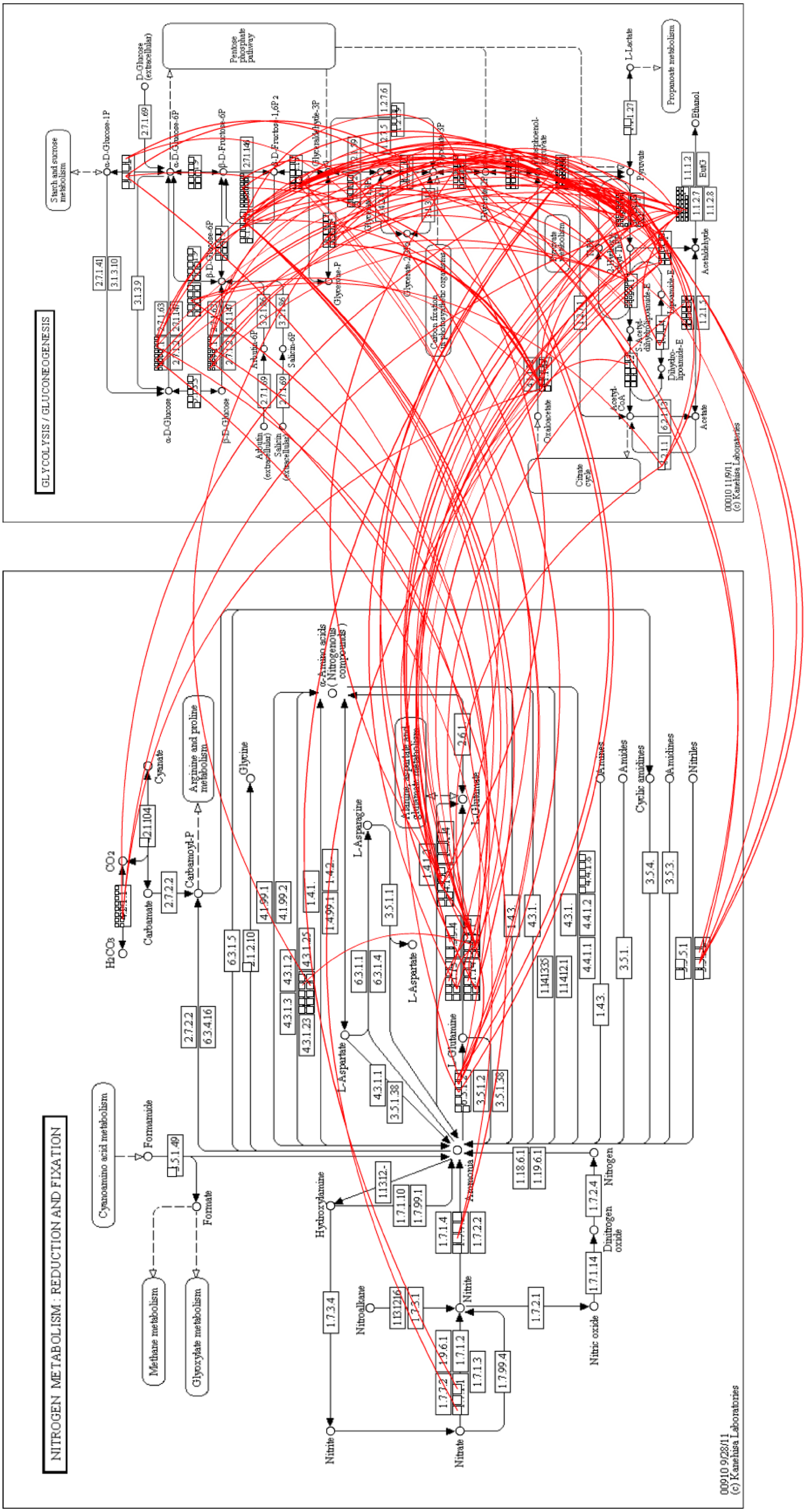
ALG2; alpha-1,3/alpha-1,6-mannosyltransferase [EC:2.4.1.132 2.4.1.257]
🟩🟨

ALG11; alpha-1,2-mannosyltransferase [EC:2.4.1.-]
🟥

ALG3; alpha-1,3-mannosyltransferase [EC:2.4.1.258]

* To go full screen and to magnify the map, please right-click on the map.

Supplemental Figure S2. A magnified image of Figure 1B.



Supplemental Figure S3. A magnified image of Figure 1C.

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map00010	Glycolysis/Gluconeogenesis	221	110	117	146	96
map00020	Citrate cycle (TCA cycle)	94	62	51	69	43
map00030	Pentose phosphate pathway	87	53	45	58	42
map00040	Pentose and glucuronate interconversions	104	62	30	54	48
map00051	Fructose and mannose metabolism	93	52	53	63	42
map00052	Galactose metabolism	99	44	46	49	39
map00053	Ascorbate and aldarate metabolism	49	34	33	36	25
map00061	Fatty acid biosynthesis	63	28	28	43	29
map00062	Fatty acid elongation	32	35	29	32	22
map00071	Fatty acid metabolism	88	43	43	54	33
map00072	Synthesis and degradation of ketone bodies	9	4	7	6	5
map00073	Cutin, suberine and wax biosynthesis	36	20	10	17	12
map00100	Steroid biosynthesis	49	33	24	37	24
map00120	Primary bile acid biosynthesis	0	0	0	1	0
map00130	Ubiquinone and other terpenoid-quinone biosynthesis	66	29	27	33	27
map00140	Steroid hormone biosynthesis	1	0	0	0	0
map00190	Oxidative phosphorylation	194	163	142	186	102
map00195	Photosynthesis	70	77	78	107	42
map00196	Photosynthesis - antenna proteins	15	22	15	23	16
map00230	Purine metabolism	266	140	109	149	116
map00232	Caffeine metabolism	8	3	2	2	2
map00240	Pyrimidine metabolism	204	102	90	111	81
map00250	Alanine, aspartate and glutamate metabolism	82	47	37	56	36
map00253	Tetracycline biosynthesis	22	6	0	11	7
map00260	Glycine, serine and threonine metabolism	76	47	37	53	35
map00270	Cysteine and methionine metabolism	120	83	74	100	68
map00280	Valine, leucine and isoleucine degradation	87	46	41	55	38
map00281	Geraniol degradation	7	1	2	1	1
map00290	Valine, leucine and isoleucine biosynthesis	50	24	16	19	17
map00300	Lysine biosynthesis	37	19	21	25	15
map00310	Lysine degradation	34	17	17	23	13
map00330	Arginine and proline metabolism	109	67	55	79	56
map00340	Histidine metabolism	33	19	17	25	16
map00350	Tyrosine metabolism	72	25	28	37	27
map00351	1-Trichloro-2,2-bis(4-chlorophenyl) ethane (DDT) degradation "	0	2	0	0	0
map00360	Phenylalanine metabolism	145	87	43	74	55
map00361	Chlorocyclohexane and chlorobenzene degradation	8	2	0	0	0
map00362	Benzoate degradation	17	6	8	8	7
map00363	Bisphenol degradation	5	58	9	0	0
map00364	Fluorobenzoate degradation	8	0	0	0	0
map00380	Tryptophan metabolism	44	38	22	31	21
map00400	Phenylalanine, tyrosine and tryptophan biosynthesis	73	43	31	40	33
map00401	Novobiocin biosynthesis	20	7	5	8	7
map00410	beta-Alanine metabolism	68	32	29	50	29
map00430	Taurine and hypotaurine metabolism	16	12	10	14	5
map00440	Phosphonate and phosphinate metabolism	6	2	6	4	3

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map00450	Selenocompound metabolism	35	18	16	20	14
map00460	Cyanoamino acid metabolism	57	28	19	24	20
map00471	D-Glutamine and D-glutamate metabolism	7	3	2	4	3
map00480	Glutathione metabolism	107	62	51	78	56
map00500	Starch and sucrose metabolism	276	117	96	124	103
map00510	N-Glycan biosynthesis	74	44	35	47	37
map00513	Various types of N-glycan biosynthesis	27	11	9	12	11
map00520	Amino sugar and nucleotide sugar metabolism	156	100	90	112	75
map00521	Streptomycin biosynthesis	21	12	13	12	8
map00523	Polyketide sugar unit biosynthesis	2	1	1	2	1
map00524	Butirosin and neomycin biosynthesis	13	6	9	6	5
map00531	Glycosaminoglycan degradation	20	7	7	12	7
map00540	Lipopolysaccharide biosynthesis	13	9	5	8	7
map00550	Peptidoglycan biosynthesis	3	0	0	0	0
map00561	Glycerolipid metabolism	87	44	40	59	41
map00562	Inositol phosphate metabolism	111	58	38	61	38
map00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	39	23	19	23	20
map00564	Glycerophospholipid metabolism	133	70	57	78	59
map00565	Ether lipid metabolism	49	26	20	26	16
map00590	Arachidonic acid metabolism	18	16	12	17	9
map00591	Linoleic acid metabolism	30	9	15	17	12
map00592	alpha-Linolenic acid metabolism	58	31	28	32	26
map00600	Sphingolipid metabolism	38	21	20	26	23
map00603	Glycosphingolipid biosynthesis - globo series	14	9	8	12	10
map00604	Glycosphingolipid biosynthesis - ganglio series	8	5	6	5	3
map00620	Pyruvate metabolism	159	80	72	100	69
map00623	Toluene degradation	8	0	0	0	0
map00624	Polycyclic aromatic hydrocarbon degradation	8	62	12	0	1
map00625	Chloroalkane and chloroalkene degradation	35	6	7	9	3
map00626	Naphthalene degradation	26	1	1	0	0
map00627	Aminobenzoate degradation	23	65	17	8	5
map00630	Glyoxylate and dicarboxylate metabolism	47	35	35	39	30
map00640	Propanoate metabolism	74	32	24	49	30
map00643	Styrene degradation	8	5	3	5	4
map00650	Butanoate metabolism	48	18	20	22	15
map00660	C5-Branched dibasic acid metabolism	9	6	4	6	5
map00670	One carbon pool by folate	38	19	15	22	16
map00680	Methane metabolism	187	45	41	45	35
map00710	Carbon fixation in photosynthetic organisms	138	79	79	100	68
map00720	Carbon fixation pathways in prokaryotes	79	36	27	45	31
map00730	Thiamine metabolism	11	7	7	9	7
map00740	Riboflavin metabolism	15	8	7	10	6
map00750	Vitamin B6 metabolism	15	9	7	9	9
map00760	Nicotinate and nicotinamide metabolism	23	11	10	17	14
map00770	Pantothenate and CoA biosynthesis	46	27	24	28	24
map00780	Biotin metabolism	8	3	4	4	3
map00785	Lipoic acid metabolism	6	4	5	5	4
map00790	Folate biosynthesis	27	21	13	20	17
map00791	Atrazine degradation	4	1	0	1	1
map00830	Retinol metabolism	27	0	0	0	0

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map00860	Porphyrin and chlorophyll metabolism	82	47	36	54	39
map00900	Terpenoid backbone biosynthesis	69	48	37	58	38
map00901	Indole alkaloid biosynthesis	1	7	0	1	3
map00902	Monoterpenoid biosynthesis	10	6	0	2	2
map00903	Limonene and pinene degradation	17	67	18	12	5
map00904	Diterpenoid biosynthesis	31	16	15	11	10
map00905	Brassinosteroid biosynthesis	8	8	7	9	5
map00906	Carotenoid biosynthesis	51	23	22	36	25
map00908	Zeatin biosynthesis	28	19	12	22	15
map00909	Sesquiterpenoid biosynthesis	2	1	0	0	0
map00910	Nitrogen metabolism	76	44	33	48	34
map00920	Sulfur metabolism	36	34	29	33	25
map00930	Caprolactam degradation	3	0	1	0	0
map00940	Phenylpropanoid biosynthesis	164	109	53	79	59
map00941	Flavonoid biosynthesis	47	17	16	31	16
map00942	Anthocyanin biosynthesis	2	1	0	0	0
map00944	Flavone and flavonol biosynthesis	15	3	2	4	2
map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	19	62	15	8	6
map00950	Isoquinoline alkaloid biosynthesis	34	8	12	15	13
map00960	Tropane, piperidine and pyridine alkaloid biosynthesis	39	21	8	19	12
map00965	Betalain biosynthesis	1	0	0	1	3
map00970	Aminoacyl-tRNA biosynthesis	152	107	86	90	47
map00980	Metabolism of xenobiotics by cytochrome P450	56	0	0	0	0
map00982	Drug metabolism - cytochrome P450	56	0	0	0	0
map00983	Drug metabolism - other enzymes	35	17	12	19	13
map01040	Biosynthesis of unsaturated fatty acids	0	2	0	0	0
map01051	Biosynthesis of ansamycins	2	2	2	3	2
map01053	Biosynthesis of siderophore group nonribosomal peptides	7	3	0	1	2
map02010	ABC transporters	61	24	9	26	21
map02020	Two-component system	19	9	8	12	7
map02030	Bacterial chemotaxis	1	0	0	0	0
map03008	Ribosome biogenesis in eukaryotes	168	91	85	109	74
map03010	Ribosome	241	311	257	365	193
map03013	RNA transport	264	129	105	160	113
map03015	mRNA surveillance pathway	189	87	78	107	85
map03018	RNA degradation	129	58	58	82	59
map03020	RNA polymerase	87	35	34	36	29
map03022	Basal transcription factors	85	47	32	49	32
map03030	DNA replication	87	47	40	43	38
map03040	Spliceosome	233	117	106	150	113
map03050	Proteasome	83	58	61	70	40
map03060	Protein export	71	46	46	58	36
map03070	Bacterial secretion system	27	14	12	14	12
map03320	PPAR signaling pathway	56	18	15	17	11
map03410	Base excision repair	59	39	33	34	26
map03420	Nucleotide excision repair	101	61	50	58	42
map03430	Mismatch repair	75	35	31	34	27
map03440	Homologous recombination	78	44	33	39	35
map03450	Non-homologous end-joining	18	8	7	6	7
map03460	Fanconi anemia pathway	121	45	34	45	36
map04010	MAPK signaling pathway	64	28	16	19	15
map04011	MAPK signaling pathway - yeast	15	4	4	7	5
map04012	ErbB signaling pathway	46	15	9	13	8

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map04013	MAPK signaling pathway - fly	22	12	6	10	6
map04020	Calcium signaling pathway	60	14	10	11	8
map04062	Chemokine signaling pathway	37	13	6	10	7
map04070	Phosphatidylinositol signaling system	93	53	35	47	32
map04075	Plant hormone signal transduction	259	232	131	265	138
map04110	Cell cycle	196	92	62	65	49
map04111	Cell cycle - yeast	189	68	51	52	43
map04112	Cell cycle - Caulobacter	22	10	13	13	13
map04113	Meiosis - yeast	132	44	39	43	36
map04114	Oocyte meiosis	145	66	44	47	31
map04115	p53 signaling pathway	65	28	15	32	22
map04120	Ubiquitin mediated proteolysis	204	105	75	104	72
map04122	Sulfur relay system	20	14	11	12	10
map04130	SNARE interactions in vesicular transport	37	48	23	28	22
map04140	Regulation of autophagy	26	12	12	18	12
map04141	Protein processing in endoplasmic reticulum	305	137	109	167	121
map04142	Lysosome	178	19	14	19	11
map04144	Endocytosis	166	72	56	77	51
map04145	Phagosome	125	66	62	77	58
map04146	Peroxisome	143	69	66	86	58
map04150	mTOR signaling pathway	65	21	11	22	14
map04210	Apoptosis	24	6	4	5	4
map04260	Cardiac muscle contraction	10	0	0	0	0
map04270	Vascular smooth muscle contraction	36	19	11	13	9
map04310	Wnt signaling pathway	91	43	33	29	23
map04320	Dorso-ventral axis formation	22	12	6	10	6
map04330	Notch signaling pathway	24	6	7	6	4
map04340	Hedgehog signaling pathway	15	4	3	1	2
map04350	TGF-beta signaling pathway	61	36	20	18	11
map04360	Axon guidance	40	19	20	23	17
map04370	VEGF signaling pathway	42	18	16	21	16
map04380	Osteoclast differentiation	31	12	12	15	12
map04510	Focal adhesion	49	19	16	21	17
map04512	ECM-receptor interaction	1	0	0	0	0
map04520	Adherens junction	44	15	14	15	12
map04530	Tight junction	49	6	2	6	6
map04540	Gap junction	48	28	17	22	17
map04612	Antigen processing and presentation	69	11	11	16	8
map04614	Renin-angiotensin system	46	10	5	8	11
map04620	Toll-like receptor signaling pathway	31	13	12	15	12
map04621	NOD-like receptor signaling pathway	41	16	10	17	10
map04622	RIG-I-like receptor signaling pathway	13	7	5	7	4
map04623	Cytosolic DNA-sensing pathway	37	0	0	0	0
map04626	Plant-pathogen interaction	205	148	68	116	85
map04630	Jak-STAT signaling pathway	7	5	3	2	1
map04650	Natural killer cell mediated cytotoxicity	38	17	15	20	15
map04660	T cell receptor signaling pathway	30	14	8	10	6
map04662	B cell receptor signaling pathway	39	19	17	20	15
map04664	Fc epsilon RI signaling pathway	33	12	12	15	12
map04666	Fc gamma R-mediated phagocytosis	103	41	29	36	25
map04670	Leukocyte transendothelial migration	10	0	6	6	7
map04710	Circadian rhythm - mammal	22	24	13	9	6
map04711	Circadian rhythm - fly	3	4	2	1	0
map04712	Circadian rhythm - plant	43	31	19	28	8
map04720	Long-term potentiation	47	29	17	20	13

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with “map” are derived from the KEGG PATHWAY database. The maps whose map IDs start with “CAT” are derived from the “Genes and Proteins” of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map04721	Synaptic vesicle cycle	88	8	4	9	5
map04722	Neurotrophin signaling pathway	48	20	19	18	14
map04724	Glutamatergic synapse	69	33	22	28	16
map04725	Cholinergic synapse	27	13	6	10	7
map04726	Serotonergic synapse	29	13	6	11	10
map04727	GABAergic synapse	48	13	12	19	9
map04728	Dopaminergic synapse	53	33	24	31	22
map04730	Long-term depression	36	12	6	10	6
map04740	Olfactory transduction	4	7	5	3	3
map04742	Taste transduction	4	1	0	0	1
map04744	Phototransduction	4	6	5	3	2
map04745	Phototransduction - fly	3	6	5	4	3
map04810	Regulation of actin cytoskeleton	82	17	19	28	22
map04910	Insulin signaling pathway	147	25	16	25	17
map04912	GnRH signaling pathway	59	31	21	21	15
map04914	Progesterone-mediated oocyte maturation	98	36	18	32	22
map04916	Melanogenesis	33	26	16	15	10
map04920	Adipocytokine signaling pathway	58	1	1	2	1
map04930	Type II diabetes mellitus	73	11	6	9	5
map04940	Type I diabetes mellitus	12	7	8	8	5
map04960	Aldosterone-regulated sodium reabsorption	20	12	6	8	5
map04961	Endocrine and other factor-regulated calcium reabsorption	23	9	4	9	6
map04962	Vasopressin-regulated water reabsorption	19	1	1	0	1
map04964	Proximal tubule bicarbonate reclamation	10	3	2	4	3
map04966	Collecting duct acid secretion	34	0	0	0	0
map04970	Salivary secretion	4	7	5	3	3
map04971	Gastric acid secretion	4	7	5	3	3
map04972	Pancreatic secretion	20	0	6	5	6
map04973	Carbohydrate digestion and absorption	16	6	9	6	5
map04974	Protein digestion and absorption	19	0	0	0	0
map04975	Fat digestion and absorption	12	1	2	2	2
map04976	Bile secretion	66	24	10	31	24
map04977	Vitamin digestion and absorption	3	0	0	0	0
map04978	Mineral absorption	22	2	1	2	1
map05010	Alzheimer's disease	132	27	20	18	12
map05012	Parkinson's disease	97	6	4	7	3
map05014	Amyotrophic lateral sclerosis (ALS)	32	8	13	13	11
map05016	Huntington's disease	164	20	16	16	11
map05020	Prion diseases	32	16	11	15	9
map05100	Bacterial invasion of epithelial cells	30	5	8	10	10
map05110	Vibrio cholerae infection	57	10	10	10	7
map05120	Epithelial cell signaling in Helicobacter pylori infection	47	0	6	5	6
map05130	Pathogenic Escherichia coli infection	32	17	13	15	12
map05131	Shigellosis	43	14	15	21	19
map05132	Salmonella infection	41	13	14	21	16
map05133	Pertussis	25	19	14	16	11
map05134	Legionellosis	60	24	21	26	19
map05140	Leishmaniasis	20	11	6	8	5
map05142	Chagas disease (American trypanosomiasis)	43	12	9	9	7
map05143	African trypanosomiasis	10	2	3	2	3
map05145	Toxoplasmosis	67	44	20	31	23

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
map05146	Amoebiasis	15	3	1	1	2
map05152	Tuberculosis	74	34	26	26	17
map05160	Hepatitis C	40	14	11	12	7
map05162	Measles	42	16	13	13	8
map05164	Influenza A	72	36	27	32	25
map05166	HTLV-I infection	134	34	25	22	15
map05168	Herpes simplex infection	101	34	25	25	14
map05200	Pathways in cancer	134	45	34	44	30
map05202	Transcriptional misregulation in cancers	41	23	19	14	10
map05210	Colorectal cancer	58	18	12	14	10
map05211	Renal cell carcinoma	41	20	17	22	16
map05212	Pancreatic cancer	36	15	14	17	14
map05213	Endometrial cancer	37	20	11	16	11
map05214	Glioma	44	22	13	19	12
map05215	Prostate cancer	73	30	20	28	18
map05216	Thyroid cancer	31	12	6	10	6
map05217	Basal cell carcinoma	6	3	3	1	1
map05218	Melanoma	26	15	7	14	9
map05219	Bladder cancer	22	12	6	10	6
map05220	Chronic myeloid leukemia	25	17	12	14	9
map05221	Acute myeloid leukemia	45	13	7	13	8
map05222	Small cell lung cancer	13	6	4	7	5
map05223	Non-small cell lung cancer	26	15	8	12	8
map05322	Systemic lupus erythematosus	37	48	41	31	23
map05323	Rheumatoid arthritis	57	0	0	7	6
map05340	Primary immunodeficiency	3	2	2	2	2
map05410	Hypertrophic cardiomyopathy (HCM)	8	0	0	2	2
map05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	1	0	0	1	1
map05414	Dilated cardiomyopathy (DCM)	3	1	0	1	2
map05416	Viral myocarditis	25	2	7	9	9
CAT30003	Serine/threonine protein kinases: AGC group	17	3	1	5	4
CAT30004	Serine/threonine protein kinases: CAMK group	40	35	20	32	21
CAT30005	Serine/threonine protein kinases: CK1 group	9	9	6	7	5
CAT30006	Serine/threonine protein kinases: CMGC group	47	27	19	22	17
CAT30007	Serine/threonine protein kinases: STE group	23	5	3	6	4
CAT30008	Serine/threonine protein kinases: TKL group	25	12	5	10	9
CAT30009	Serine/threonine protein kinases: Others	172	54	37	60	41
CAT30010	Tyrosine protein kinases	1	0	0	0	0
CAT30013	Aspartic Peptidases	13	7	9	13	10
CAT30014	Cysteine Peptidases	124	48	38	72	43
CAT30015	Metallo Peptidases	139	59	55	72	48
CAT30016	Serine Peptidases	101	47	43	65	47
CAT30017	Threonine Peptidases	36	29	26	34	20
CAT30018	Peptidases of Unknown Catalytic Type	3	1	0	1	1
CAT30020	N-Glycan biosynthesis	28	17	15	20	15
CAT30021	O-Glycan biosynthesis	6	4	1	3	2
CAT30022	GPI-anchor biosynthesis	11	4	3	4	4
CAT30023	Glycolipid biosynthesis	3	3	3	4	2
CAT30024	Glycan extension	28	19	16	19	15
CAT30026	Polysaccharide	162	68	50	70	47
CAT30027	Others	71	43	16	22	19

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with "map" are derived from the KEGG PATHWAY database. The maps whose map IDs start with "CAT" are derived from the "Genes and Proteins" of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
CAT30029	Lipopolysaccharide biosynthesis proteins	13	9	5	8	7
CAT30031	Fatty acid synthase	38	25	29	33	23
CAT30032	Desaturase	18	15	16	18	12
CAT30035	Acyl-CoA synthetase	31	13	13	12	10
CAT30036	Phospholipid acyltransferase	2	21	17	25	18
CAT30055	CYP39 family	0	0	0	1	0
CAT30057	CYP51 family	2	1	5	2	1
CAT30068	CYP71 family	4	1	0	0	0
CAT30069	CYP72 family	0	1	0	0	0
CAT30070	CYP73 family	3	1	3	3	2
CAT30071	CYP74 family	4	2	2	2	2
CAT30072	CYP75 family	3	1	1	3	1
CAT30074	CYP77 family	0	1	0	0	0
CAT30075	CYP79 family	2	5	0	0	0
CAT30079	CYP83 family	0	2	0	0	0
CAT30080	CYP84 family	6	2	2	2	1
CAT30081	CYP85 family	2	2	1	1	1
CAT30082	CYP86 family	4	6	2	4	3
CAT30083	CYP88 family	6	2	1	2	1
CAT30084	CYP90 family	2	4	4	4	2
CAT30086	CYP94 family	2	0	0	1	1
CAT30087	CYP96 family	0	1	0	0	0
CAT30088	CYP98 family	2	3	1	1	1
CAT30089	CYP701 family	1	1	2	0	1
CAT30090	CYP707 family	8	4	2	4	4
CAT30091	CYP710 family	1	4	1	1	0
CAT30094	CYP724 family	0	0	1	1	1
CAT30096	CYP734 family	0	1	0	0	0
CAT30097	CYP735 family	1	2	1	2	1
CAT30104	Extracellular matrix (ECM) proteoglycans	6	1	1	1	1
CAT30106	Photosystem and electron transport system	72	78	79	108	43
CAT30114	Basic leucine zipper (bZIP)	35	26	24	35	20
CAT30115	Basic helix-loop-helix (bHLH)	2	2	1	2	1
CAT30118	Zinc finger	16	11	9	12	9
CAT30119	Helix-turn-helix	158	171	81	179	66
CAT30120	beta-Scaffold factors with minor groove contacts	32	13	12	14	9
CAT30121	Other transcription factors	46	61	21	31	27
CAT30124	Other transcription factors	0	0	1	0	1
CAT30128	Eukaryotes	170	232	179	281	153
CAT30129	Bacteria	68	71	69	78	40
CAT30130	Archaea	116	142	127	174	94
CAT30131	Ribosomal RNAs	0	10	11	8	0
CAT30133	Eukaryotic Type	47	27	31	37	24
CAT30134	Prokaryotic Type	35	16	16	21	15
CAT30136	Heat shock proteins	134	45	64	97	72
CAT30137	Other chaperones and cochaperones	32	16	16	21	11
CAT30138	Intramolecular chaperones	78	16	11	24	21
CAT30139	Protein folding catalysts	8	8	14	19	12
CAT30141	Syntaxin (Qa)	8	18	7	5	4
CAT30142	SNAP-25[N] (Qb)	8	11	7	7	7
CAT30143	SNAP-25[C] (Qc)	4	10	5	5	4
CAT30144	SNAP-25 (Qb,c)	2	3	0	1	2
CAT30145	VAMP, Ykt6, Sec22 (R)	22	15	9	12	6
CAT30147	Ubiquitins and Ubiquitin-like proteins	16	18	12	19	9

Supplemental Table S1. The number of genes assigned on the maps. The maps whose Map ID starts with “map” are derived from the KEGG PATHWAY database. The maps whose map IDs start with “CAT” are derived from the “Genes and Proteins” of the KEGG BRITE database.

Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
CAT30148	Ubiquitin-activating enzymes (E1)	20	10	10	10	9
CAT30149	Ubiquitin-conjugating enzymes (E2)	43	34	23	42	24
CAT30150	Ubiquitin ligases (E3)	44	11	9	15	11
CAT30151	Deubiquitinating enzyme (DUB)	7	2	3	4	3
CAT30153	Eukaryotic Type	19	5	3	5	4
CAT30154	Prokaryotic Type	9	3	2	3	3
CAT30157	Sister chromatid cohesion proteins	56	18	15	17	18
CAT30158	Nucleosome assembly factors	33	50	46	33	24
CAT30159	Histone modification proteins	39	16	12	17	12
CAT30160	Chromosome condensation proteins	42	10	7	10	10
CAT30162	Kinetochore proteins	15	27	14	10	9
CAT30163	SAC (spindle assembly checkpoint) factors	44	22	12	22	14
CAT30164	Other centromeric chromatin formation proteins	16	25	17	22	14
CAT30165	Heterochromatin formation proteins	38	21	16	19	15
CAT30166	Sister chromatid separation proteins	43	20	15	18	15
CAT30167	Chromatin remodeling factors	65	36	30	38	34
CAT30170	Chromosome partitioning proteins	11	5	4	6	7
CAT30173	SSBR (single strand breaks repair)	6	3	2	3	4
CAT30175	HR (homologous recombination)	71	47	35	40	39
CAT30176	NHEJ (non-homologous end-joining)	19	8	6	7	7
CAT30177	FA (Fanconi anemia) pathway	45	22	16	21	20
CAT30178	Other DSBR factors	10	3	2	3	3
CAT30179	TLS (translesion DNA synthesis) factors	21	14	13	16	11
CAT30180	Check point factors	41	11	11	11	12
CAT30181	Other factors with a suspected DNA repair function	24	13	8	16	13
CAT30183	SSBR (single strand breaks repair)	4	2	2	4	3
CAT30185	HR (homologous recombination)	5	2	2	4	3
CAT30187	TLS (translesion DNA synthesis) factors	4	2	3	4	3
CAT30188	Other factors with a suspected DNA repair function	1	1	1	1	0
CAT30193	ABCB (MDR/TAP) subfamily	61	24	9	26	21
CAT30197	Other subfamilies	2	1	1	1	1
CAT30199	Mineral and organic ion transporters	0	0	0	0	1
CAT30200	Oligosaccharide and polyol transporters	3	2	2	5	2
CAT30203	Peptide and nickel transporters	1	0	0	0	0
CAT30205	ABC-2 type and other transporters	2	1	1	1	1
CAT30207	Sugar transporters	9	5	5	8	8
CAT30209	Phosphate and organophosphate transporters	6	11	8	7	5
CAT30210	Nitrate/nitrite transporters	3	0	0	0	2
CAT30220	OmpR family	0	0	0	0	1
CAT30234	Pilus system	0	0	0	0	1
CAT30241	Type II toxins: Membrane damaging toxins	8	6	3	7	4
CAT30246	Type I secretion system	0	0	0	0	1
CAT30247	Type II secretion system	2	2	3	4	3
CAT30254	Sec (secretion) system	55	32	30	36	24
CAT30255	Twin-arginine translocation (Tat) system	1	2	2	2	2
CAT30259	Actins	3	9	8	1	1
CAT30260	Actin-binding proteins	13	14	13	20	15
CAT30263	Tubulins	30	18	14	16	14
CAT30264	Tubulin-binding proteins	50	14	7	19	14
CAT30265	Prokaryotic cytoskeleton proteins	1	1	1	1	1
CAT30269	Alpha Subunits	2	1	1	1	1

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Map ID	Map Name	*Jatropha curcas*	*Arabidopsis thaliana*	*Oryza sativa*	*Populus trichocarpa*	*Ricinus communis*
CAT30270	Beta Subunits	0	1	1	2	1
CAT30274	Rho Family	16	12	7	8	8
CAT30275	Rab Family	21	56	27	15	9
CAT30276	Ran Family	2	4	3	4	1
CAT30277	Arf/Sar Family	18	22	16	11	6
CAT30420	VLA-1	0	0	0	1	0
CAT30421	VLA-2	0	0	0	1	0
CAT30430	alpha 11 beta 1	0	0	0	1	0
CAT30439	VNR	0	0	0	1	0
CAT30453	4. Link Protein Family	0	0	0	1	0
CAT30460	7. Others	0	0	0	1	0
CAT30461	Cellular antigens	61	30	13	32	23
CAT30462	Glycan binding proteins	6	6	6	8	6