Supplementary table 18: Differential predicted KEGG pathways (level 1) between SG and GC in Inner Mongolia cohort

Predicted_function_level1	LogMaxMean	Class	LDA score	p value
Human_Diseases	4.034612314	SG	2.751932008	0.000808095
None	3.228250416	SG	2.474040184	0.027460154
Cellular_Processes	4.616929466	SG	3.630781178	0.000808095
Genetic_Information_Processing	5.268552471	GC	3.680194767	0.007634431
Unclassified	5.147473468	SG	2.872101032	0.196608197
Organismal_Systems	3.832498053	SG	2.420527812	0.32978478
Metabolism	5.680977114	GC	3.023944569	0.335865972
Environmental_Information_Processing	5.161875422	SG	3.23890648	0.788698891

Supplementary table 19: Differential predicted KEGG pathways (level 1) among SG, AG and GC in Inner Mongolia cohort

Predicted_function_level1	LogMaxMean	Class	LDA score	p value
Human_Diseases	4.034612314	SG	2.754418728	0.002828478
None	3.228250416	SG	2.47378945	0.058805837
Cellular_Processes	4.616929466	SG	3.637682616	0.005651568
Genetic_Information_Processing	5.268552471	GC	3.730838673	0.022417516
Unclassified	5.147473468	SG	2.936957482	0.053916224
Organismal_Systems	3.833489306	AG	2.493743094	0.383807805
Metabolism	5.680977114	GC	3.121040396	0.533818326
Environmental_Information_Processing	5.161875422	SG	3.152056569	0.901428312

Supplementary table 20: Differential predicted KEGG pathways (level 2) between SG and GC in Inner Mongolia cohort

Predicted_function_level2	LogMaxMean	Class	LDA score	p value
Carbohydrate_Metabolism	5.006487616	GC	3.342287521	0.002056104
Transcription	4.382635756	GC	2.777781523	0.009807292
Genetic_Information_Processing	4.451600245	GC	2.478087696	0.161240392
Energy_Metabolism	4.739622131	SG	2.885998392	0.278283196
Membrane_Transport	5.092649593	GC	3.205676782	0.479848086
Metabolism	4.378138888	GC	2.368559038	0.105192505
Neurodegenerative_Diseases	3.562320576	SG	2.675764845	0.000144267
Endocrine_System	3.432873267	SG	2.000977803	0.733034613
Cardiovascular_Diseases	1.868844255	SG	0.930499236	0.18423727
Nucleotide_Metabolism	4.599711544	GC	3.242270513	0.005687422
Metabolism_of_Terpenoids_and_Polyketides	4.274209172	SG	2.012128223	0.893402355
Translation	4.733581309	GC	3.303471433	0.008816305
Biosynthesis_of_Other_Secondary_Metabolites	3.860087132	SG	2.106956843	0.788698891
Signaling_Molecules_and_Interaction	3.340088105	GC	1.946113155	0.079398735
Amino_Acid_Metabolism	5.006486316	SG	3.325077865	0.002056104
Transport_and_Catabolism	3.420276345	SG	1.854500961	0.798090825
Metabolic_Diseases	2.971375732	GC	1.354886813	0.161240392
Immune_System_Diseases	2.70925312	SG	0.997407494	0.172452258
Folding	4.445232033	GC	3.106129625	0.373855535
Xenobiotics_Biodegradation_and_Metabolism	4.451141162	SG	2.64363666	0.835938527
Immune_System	2.772959221	SG	1.532785469	0.373855535
Cell_Motility	4.528753884	SG	3.624685076	0.00045086
Enzyme_Families	4.29177113	GC	2.595754102	0.000151527
Glycan_Biosynthesis_and_Metabolism	4.328644007	SG	2.670119746	0.566951697
Digestive_System	2.552765941	GC	1.683589153	0.000619118
Circulatory_System	2.773940811	SG	2.060721532	0.000283213

Cancers	3.138475639	SG	1.968615661	0.000212829
Metabolism_of_Cofactors_and_Vitamins	4.633581849	SG	2.511701969	0.116076349
Lipid_Metabolism	4.52152496	SG	2.573478693	0.534419348
Poorly_Characterized	4.702776192	SG	2.40338142	0.110528654
Metabolism_of_Other_Amino_Acids	4.27049416	SG	2.454948492	0.004892834
Replication_and_Repair	4.917870165	GC	3.256866255	0.03507782
Cellular_Processes_and_Signaling	4.590148673	SG	3.027249074	0.003597433
Nervous_System	2.951434282	GC	1.383419874	0.835938527
Cell_Communication	0	GC	1.547417414	0.35355848
Infectious_Diseases	3.648751145	GC	1.75980335	0.237349047
Cell_Growth_and_Death	3.723987228	GC	2.111683849	0.014343231
Sensory_System	0	GC	2.037947582	0.316266543
Environmental_Adaptation	3.184636454	SG	1.856396122	0.001475492
Signal_Transduction	4.327076416	SG	3.054117673	0.000565881
Excretory_System	2.424446308	GC	1.294654314	0.472308058

Supplementary table 21: Differential predicted KEGG pathways (level 2) among SG, AG and GC in Inner Mongolia cohort

Predicted_function_level2	LogMaxMean	Class	LDA score	p value
Carbohydrate_Metabolism	5.006487616	GC	3.33353087	0.009502424
Transcription	4.382635756	GC	2.846920595	0.014304444
Genetic_Information_Processing	4.451600245	GC	2.641205205	0.350351092
Energy_Metabolism	4.742810999	AG	2.880035101	0.231008434
Membrane_Transport	5.092649593	GC	3.188231398	0.783292637
Metabolism	4.378138888	GC	2.405637838	0.254975631
Neurodegenerative_Diseases	3.562320576	SG	2.666999171	0.000447982
Endocrine_System	3.4457923	AG	2.055489925	0.706918368
Cardiovascular_Diseases	1.90917605	AG	1.02352616	0.401422603
Nucleotide_Metabolism	4.599711544	GC	3.251699081	0.011666999
Metabolism_of_Terpenoids_and_Polyketides	4.276185508	AG	2.144904164	0.925731689
Translation	4.733581309	GC	3.3477182	0.018747437
Biosynthesis_of_Other_Secondary_Metabolites	3.860087132	SG	2.193594516	0.971110704
Signaling_Molecules_and_Interaction	3.340088105	GC	2.049849854	0.0906531
Amino_Acid_Metabolism	5.006486316	SG	3.351068437	0.003673348
Transport_and_Catabolism	3.434684943	AG	2.023149199	0.768735274
Metabolic_Diseases	2.971375732	GC	1.245791018	0.386478873
Immune_System_Diseases	2.70925312	SG	1.117013652	0.411177072
Folding	4.445232033	GC	3.076990601	0.655179885
Xenobiotics_Biodegradation_and_Metabolism	4.451141162	SG	2.798959724	0.411273117
Immune_System	2.778011476	AG	1.47372256	0.382471898
Cell_Motility	4.528753884	SG	3.607381036	0.002850415
Enzyme_Families	4.29177113	GC	2.61462747	0.000832517
Glycan_Biosynthesis_and_Metabolism	4.339194826	AG	2.746323444	0.244896111
Digestive_System	2.552765941	GC	1.672035623	0.001278294
Circulatory_System	2.773940811	SG	2.048046138	0.000782998
Cancers	3.138475639	SG	1.949881813	0.001500195
Metabolism_of_Cofactors_and_Vitamins	4.633581849	SG	2.510413261	0.333971008
Lipid_Metabolism	4.52152496	SG	2.676911868	0.251755295
Poorly_Characterized	4.702776192	SG	2.617709736	0.052036867
Metabolism_of_Other_Amino_Acids	4.27049416	SG	2.516753324	0.002405979
Replication_and_Repair	4.917870165	GC	3.32091774	0.082621477

Cellular_Processes_and_Signaling	4.590148673	SG	2.989281777	0.003120761
Nervous_System	2.951434282	GC	1.423580208	0.388599989
Cell_Communication	0.045347806	AG	1.641962382	0.608086911
Infectious_Diseases	3.648751145	GC	1.875659224	0.29324321
Cell_Growth_and_Death	3.723987228	GC	2.156862318	0.010140886
Sensory_System	0	AG	2.104129319	0.585667313
Environmental_Adaptation	3.184636454	SG	1.79897194	0.007037681
Signal_Transduction	4.327076416	SG	3.063771419	0.00031389
Excretory_System	2.424446308	GC	1.347141791	0.516539301

Supplementary table 22: Differential predicted KEGG pathways (level 3) between SG and GC in Inner Mongolia cohort

Predicted_function_level3	LogMaxMean	Class	LDA score	p value
Cytokine_receptors	0	GC	1.690823817	0.002172288
Cysteine_and_methionine_metabolism	3.947926123	GC	2.36771006	0.004041362
Cytoskeleton_proteins	3.3798356	GC	2.031378197	0.008206346
Toxoplasmosis	1.699352737	SG	0.615987104	0.464833758
Prion_diseases	2.095171814	SG	1.228586559	0.002728892
ECM_receptor_interaction	0	GC	1.879477727	0.273216461
Ribosome	4.348265276	GC	3.030079117	0.009466452
Flavone_and_flavonol_biosynthesis	1.636020314	GC	0.619944285	0.816961322
Ubiquitin_system	2.348642133	GC	1.046715156	0.893402355
X_Alzheimer__s_disease_	3.124013459	SG	2.174232878	0.000565881
Lipopolysaccharide_biosynthesis_proteins	3.721191006	SG	2.802332849	0.003888145
Transcription_related_proteins	2.262898985	GC	1.412895706	0.760711888
Inorganic_ion_transport_and_metabolism	3.457959328	SG	2.171775758	0.022010504
Cardiac_muscle_contraction	2.774238712	SG	2.069363513	0.000270138
Protein_kinases	3.561720009	SG	1.58963547	0.526435998
Valine_leucine_and_isoleucine_degradation	3.896000557	SG	2.929390854	0.001414661
Benzoate_degradation	3.641609662	SG	2.072115298	0.393809583
Shigellosis	0	SG	0.373312173	0.335673418
Fatty_acid_metabolism	3.756231502	SG	2.58109169	0.051284087
Lipid_biosynthesis_proteins	3.836516627	SG	1.998640223	0.21856001
Ribosome_Biogenesis	4.132881029	GC	2.500963025	0.044430748
Cell_division	2.815310722	SG	1.545483492	0.348243411
Biosynthesis_of_12_14__and_16_membered_macrolides	1.092458457	SG	0.545709147	0.002518605
ErbB_signaling_pathway	0			-
Amino_acid_related_enzymes	4.146823709	GC	2.402496224	0.019979529
G_protein_coupled_receptors	0	GC	0.324660094	0.479848086
Chronic_myeloid_leukemia	0.111479813	SG	0.190174549	0.011282557
Vibrio_cholerae_pathogenic_cycle	3.039028264	SG	1.981981632	0.000357964
Glycerophospholipid_metabolism	3.746676713	SG	1.818997547	0.134037993
Cytokine_cytokine_receptor_interaction	0	GC	1.726378546	0.002172288
Non_homologous_end_joining	2.391877489	SG	1.277086885	0.262402981
Spliceosome	0			-
Glycosyltransferases	3.56630004	GC	2.339575146	0.000341677
Amino_acid_metabolism	3.289385858	GC	1.989472208	0.011680866
Cell_motility_and_secretion	3.384159316	SG	2.201988875	0.113275747
Mismatch_repair	3.86994726	GC	2.245615246	0.051284087
Pancreatic_secretion	0	SG	0.339652185	0.472308058
Renin_angiotensin_system	1.6274928	SG	0.79346082	0.026616566

Various_types_of_N_glycan_biosynthesis	0.26692447	GC	0.350138724	0.566951697
Restriction_enzyme	3.358976545	GC	2.140769431	0.10006288
Ethylbenzene_degradation	2.876645541	GC	1.92283399	0.003326627
Bacterial_toxins	3.095271072	GC	1.898029316	0.073336475
Tetracycline_biosynthesis	3.23595315	GC	1.853717272	0.317837729
Clavulanic_acid_biosynthesis	0	SG	0.746879739	0.760711888
Secretion_system	4.285217546	SG	3.111035214	0.000516932
Glycan_bindng_proteins	0	SG	1.446207104	0.836449558
Methane_metabolism	4.004195725	GC	1.86328028	0.059001021
Metabolism_of_cofactors_and_vitamins	3.305071873	SG	1.927180214	0.018114094
Endocytosis	0.599436038	GC	0.267728229	0.054262988
Fat_digestion_and_absorption	0			-
Glycosphingolipid_biosynthesis___globo_series	2.684207752	GC	1.793835256	0.005903447
Homologous_recombination	3.931225293	GC	2.394028048	0.021314405
Protein_export	3.764952979	GC	1.994185033	0.18423727
Membrane_and_intracellular_structural_molecules	3.857468102	SG	2.812103322	0.000112626
Alanine_aspartate_and_glutamate_metabolism	3.978769862	GC	1.789159136	0.855011718
Lipoic_acid_metabolism	2.766460939	GC	1.313419164	0.23254813
Toluene_degradation	3.28472551	SG	2.220319979	3.63324E-05
Folate_biosynthesis	3.678190401	GC	1.901037067	0.48745329
Cell_cycle	0	GC	1.936657308	0.432070076
Primary_bile_acid_biosynthesis	2.381143261	GC	1.254317505	0.526435998
Lysosome	2.747151123	GC	1.746060885	0.110528654
Secondary_bile_acid_biosynthesis	2.304230484	GC	1.286153722	0.617458472
Chagas_disease__American_trypanosomiasis_	2.220502907	SG	1.334007445	0.005687422
Penicillin_and_cephalosporin_biosynthesis	2.656096187	SG	1.659295914	0.007634431
Pantothenate_and_CoA_biosynthesis	3.755350311	SG	1.488087502	0.760711888
Phagosome	0	GC	0.221521876	0.328214495
Lipopolysaccharide_biosynthesis	3.636934338	SG	2.815969279	0.000565881
Type_I_diabetes_mellitus	2.721142	GC	0.74382636	0.742223888
Function_unknown	4.220737088	SG	2.600564291	0.02421876
Cytochrome_P450	0.407729209	SG	0.142511909	0.387087704
Energy_metabolism	3.908051963	SG	2.637652971	0.065847798
Signal_transduction_mechanisms	3.672829457	GC	2.173691753	0.196608197
Nicotinate_and_nicotinamide_metabolism	3.600657413	SG	1.354910363	0.130903502
Limonene_and_pinene_degradation	3.468186768	SG	2.196927759	0.137230221
Translation_proteins	3.921720962	GC	1.821425106	0.428465743
Carbon_fixation_pathways_in_prokaryotes	4.03778103	SG	2.623487811	0.00684342
Biosynthesis_and_biodegradation_of_secondary_metabolites	2.978289072	SG	2.005693895	0.000411285
Other_transporters	3.324733487	SG	1.406950643	0.696670401
Synthesis_and_degradation_of_ketone_bodies	3.203826987	SG	2.199176139	1.61512E-05
Proximal_tubule_bicarbonate_reclamation	2.419560604	GC	1.310025674	0.472308058
Starch_and_sucrose_metabolism	3.822574334	GC	2.839320913	7.5233E-05
Fc_epsilon_RI_signaling_pathway	0			-
Aldosterone_regulated_sodium_reabsorption	0	SG	0.722429554	0.407463622
Butanoate_metabolism	4.012188285	SG	2.699041293	0.002728892
Lysine_degradation	3.612306151	SG	2.600904845	0.000565881
Biosynthesis_of_ansamycins	2.834930862	GC	1.161822954	0.11893108
Glycerolipid_metabolism	3.597153972	GC	2.503641579	9.21542E-05
Galactose_metabolism	3.731209927	GC	2.845845831	6.45185E-05

Carotenoid_biosynthesis	2.396679631	GC	1.358747423	0.051284087
DNA_replication	3.805952054	GC	2.268884462	0.073336475
Biosynthesis_of_type_II_polyketide_backbone	0.191254553	SG	0.262329713	0.113275747
Phosphotransferase_system__PTS_	3.695722149	GC	3.017912917	0.000619118
Amino_sugar_and_nucleotide_sugar_metabolism	4.088930371	GC	2.958728665	0.00016709
Glycosaminoglycan_biosynthesis___chondroitin_sulfate	0	GC	2.059677152	0.900831209
Cell_cycle___yeast	0			-
X_Huntington__s_disease_	3.046281941	SG	2.168870755	0.00025763
Electron_transfer_carriers	2.579641766	GC	1.345442048	0.414395187
Meiosis___yeast	2.264018425	GC	0.96096673	0.534419348
Cholinergic_synapse	0			-
Ether_lipid_metabolism	1.816348994	SG	0.692891419	0.751450055
Chlorocyclohexane_and_chlorobenzene_degradation	2.815176194	SG	1.711455862	0.14379021
General_function_prediction_only	4.536635062	GC	2.421902799	0.075313709
Proteasome	2.506906936	SG	1.221606629	0.387087704
Biotin_metabolism	3.220431643	SG	2.159071696	0.019979529
Replication_recombination_and_repair_proteins	3.941758654	GC	2.589510352	0.010521946
Hedgehog_signaling_pathway	0			-
Xylene_degradation	2.791988272	GC	1.802982323	0.021314405
Tyrosine_metabolism	3.655333862	GC	2.276713855	0.116076349
African_trypanosomiasis	2.216998403	SG	1.2865882	0.010521946
Sesquiterpenoid_biosynthesis	0.093445298	SG	0.214970499	0.039519963
Transcription_factors	4.181611726	GC	2.684972115	0.102602193
Phosphonate_and_phosphinate_metabolism	2.779917089	GC	1.32187946	0.011282557
Tuberculosis	3.156264502	GC	1.798113796	8.32884E-05
Plant_pathogen_interaction	3.174877879	SG	1.82607481	0.00436435
Nitrogen_metabolism	3.867520271	SG	2.022503554	0.192418704
Germination	1.688770203	GC	0.773295819	0.180244442
Isoquinoline_alkaloid_biosynthesis	2.687157454	SG	1.265631725	0.91269759
Streptomycin_biosynthesis	3.405893852	GC	2.041094631	0.021314405
RNA_transport	3.089056936	GC	1.93939161	0.043157139
Pyrimidine_metabolism	4.234841902	GC	2.928805514	0.003888145
Citrate_cycle__TCA_cycle_	3.8553165	SG	2.519537804	0.002230854
D_Glutamine_and_D_glutamate_metabolism	3.159348297	GC	1.836619656	0.026616566
Photosynthesis___antenna_proteins	1.000592097	GC	0.598774387	0.002056104
Sphingolipid_metabolism	2.996471052	GC	2.115558229	0.002141846
PPAR_signaling_pathway	3.127101452	SG	1.665061767	0.669842251
Long_term_depression	0			-
Phenylalanine_tyrosine_and_tryptophan_biosynthesis	3.860022334	SG	2.271373062	0.826437252
VEGF_signaling_pathway	0	GC	0.509860175	0.223153929
Glycan_biosynthesis_and_metabolism	2.825993808	SG	1.972905356	0.000565881
Phenylalanine_metabolism	3.47297394	SG	2.404331635	0.003740222
Other_glycan_degradation	3.114645046	GC	2.227727551	0.005276633
Vasopressin_regulated_water_reabsorption	0.624088968	GC	0.194250422	0.770008145
Progesterone_mediated_oocyte_maturation	2.427815884	SG	1.443872292	0.048443333
MAPK_signaling_pathway___yeast	2.616456109	SG	1.444825712	0.097573932
Retinol_metabolism	2.858823729	GC	1.411032729	0.951431509
One_carbon_pool_by_folate	3.735847512	GC	2.341675013	4.72689E-05
Valine_leucine_and_isoleucine_biosynthesis	3.819160571	GC	2.029226968	0.360906957
Chaperones_and_folding_catalysts	3.988443231	SG	2.045424124	0.407463622

DNA_replication_proteins	4.03723184	GC	2.314323723	0.134037993
Photosynthesis	3.544031656	GC	2.189600146	0.009136217
Glycosphingolipid_biosynthesis___lacto_and_neolacto_series	0	SG	1.067426463	0.15535945
GTP_binding_proteins	0	GC	1.820329231	0.432070076
Linoleic_acid_metabolism	2.822008925	GC	1.821806818	0.040702318
Bacterial_secretion_system	3.88799858	SG	2.623795625	0.001143736
Leishmaniasis	0	GC	0.510309387	0.223153929
Fatty_acid_biosynthesis	3.734362448	GC	2.196247355	0.038366891
Drug_metabolism___other_enzymes	3.449888964	GC	2.177625166	0.001604445
Biosynthesis_of_type_II_polyketide_products	1.075706183	GC	0.718845028	0.289226324
Oxidative_phosphorylation	4.102767036	SG	2.841330702	0.007098505
Fatty_acid_elongation_in_mitochondria	0	SG	0.402392632	0.164914823
NOD_like_receptor_signaling_pathway	2.453454456	SG	1.207067592	0.414395187
Insulin_signaling_pathway	2.69885736	GC	1.4214227	0.069509362
Ion_channels	2.615966528	GC	1.840755623	0.021314405
Indole_alkaloid_biosynthesis	1.046391476	SG	0.266022206	0.348243411
Peptidoglycan_biosynthesis	3.882626183	GC	2.648942266	0.000619118
Glutathione_metabolism	3.60125535	SG	2.153684045	0.001893995
Apoptosis	2.201634049	GC	1.528457228	0.001743702
X_Parkinson__s_disease_	2.809583712	SG	2.079596757	0.000212829
Salivary_secretion	0	GC	0.548688808	0.35453948
Purine_metabolism	4.357279709	GC	3.008919686	0.009136217
mRNA_surveillance_pathway	0.392427248	SG	0.167268934	0.380436275
Adipocytokine_signaling_pathway	2.781756076	SG	1.430859147	0.835938527
Fc_gamma_R_mediated_phagocytosis	0.599436038	GC	0.267398354	0.054262988
Glycolysis___Gluconeogenesis	4.057881375	GC	2.883459564	0.000374974
Pancreatic_cancer	0			-
Antigen_processing_and_presentation	2.427815884	SG	1.443872292	0.048443333
Prenyltransferases	3.511993464	GC	2.059239624	0.011680866
Histidine_metabolism	3.692961864	SG	2.004270174	0.845463801
Drug_metabolism___cytochrome_P450	3.131456534	SG	1.845518388	0.062346699
Hypertrophic_cardiomyopathy__HCM_	1.366828356	SG	0.646846279	0.011680866
Vitamin_B6_metabolism	3.245978717	SG	1.719474679	0.237349047
C5_Branched_dibasic_acid_metabolism	3.415585709	GC	1.805972604	0.407463622
Complement_and_coagulation_cascades	0			-
Long_term_potentiation	0			-
Caffeine_metabolism	1.166063139	SG	0.284740371	0.464833758
Oocyte_meiosis	0			-
Peroxisome	3.339631187	SG	2.031569592	0.140480769
Systemic_lupus_erythematosus	0.817335226	SG	0.19787307	0.733034613
Ubiquinone_and_other_terpenoid_quinone_biosynthesis	3.522713268	SG	2.238918154	0.001672741
Peptidases	4.205231305	GC	2.642583907	7.91639E-05
Tight_junction	0	GC	0.221521876	0.328214495
Glycosylphosphatidylinositol_GPI__anchor_biosynthesis	0	SG	1.584647397	0.345551511
Naphthalene_degradation	3.383124135	GC	2.072458695	0.030130689
Vascular_smooth_muscle_contraction	0			-
Sulfur_relay_system	3.567306232	SG	2.142494453	0.002141846
Protein_processing_in_endoplasmic_reticulum	2.664660395	SG	1.22097395	0.591957783
Measles	0			-
Renal_cell_carcinoma	2.445565069	SG	0.951440311	0.450084421

D_Alanine_metabolism	3.127532866	GC	2.104469722	0.004200041
Small_cell_lung_cancer	1.701490437	SG	0.611099325	0.464833758
Rheumatoid_arthritis	0			-
Phototransduction___fly	0	GC	0.221521876	0.328214495
Butirosin_and_neomycin_biosynthesis	2.735999941	GC	1.541137323	0.001538725
Influenza_A	1.703304771	SG	0.619842938	0.442810364
Nitrotoluene_degradation	2.923502713	SG	1.885626666	0.283719035
Pores_ion_channels	3.683451794	SG	2.644999065	0.000676984
Mineral_absorption	2.026194013	GC	0.772188676	0.188295207
Colorectal_cancer	1.69919692	SG	0.615855004	0.464833758
Protein_digestion_and_absorption	1.84769731	SG	0.72523605	0.387087704
Pathways_in_cancer	2.776963863	SG	1.544951987	0.013401631
Terpenoid_backbone_biosynthesis	3.747894117	GC	2.326378044	0.008816305
Amyotrophic_lateral_sclerosis__ALS_	2.644224986	SG	1.710161242	4.03823E-05
Primary_immunodeficiency	2.704165855	SG	1.029664269	0.242219569
RIG_I_like_receptor_signaling_pathway	1.743290802	GC	0.994889159	0.015865064
Neuroactive_ligand_receptor_interaction	0	SG	0.488944679	0.040702318
Bladder_cancer	2.1139078	SG	1.352998411	0.001299878
Nucleotide_excision_repair	3.56398508	GC	2.112395488	0.03614637
Olfactory_transduction	0			-
Others	4.003865213	GC	2.873114901	5.52594E-05
Geraniol_degradation	3.442765596	SG	2.515855999	0.010159025
N_Glycan_biosynthesis	2.265352152	GC	1.015647462	0.705700166
ABC_transporters	4.53348587	SG	2.634766648	0.380436275
Bacterial_motility_proteins	4.232253076	SG	3.372710503	0.00029688
Lysine_biosynthesis	3.826162922	GC	2.374947513	0.000540891
Type_II_diabetes_mellitus	2.61670772	GC	1.276527866	0.11893108
Vibrio_cholerae_infection	1.346168478	SG	0.604729227	0.015865064
Pertussis	2.369509666	SG	1.292664639	0.110528654
Other_ion_coupled_transporters	4.116931588	GC	2.113070057	0.922365269
X111_Trichloro_22_bis_4_chlorophenyl_ethane__DDT__degradation	1.285762914	SG	0.437560852	0.057384899
Neurotrophin_signaling_pathway	0			-
alpha_Linolenic_acid_metabolism	2.617841161	SG	1.835431626	1.80282E-05
Fluorobenzoate_degradation	2.368966233	SG	1.280151251	0.237349047
Sulfur_metabolism	3.473819031	GC	1.656585143	0.116076349
Riboflavin_metabolism	3.429264805	SG	1.783623309	0.028326707
Base_excision_repair	3.667201862	GC	2.005780959	0.11893108
Phototransduction	0			-
Viral_myocarditis	1.701211623	SG	0.615302379	0.457425711
Focal_adhesion	0	GC	0.245778083	0.399641193
Cyanoamino_acid_metabolism	3.328749887	GC	1.342581347	0.534419348
CAM_ligands	0	GC	1.500218923	0.273216461
Flagellar_assembly	3.91803541	SG	3.120975326	0.000184148
Tropanepiperidine_and_pyridine_alkaloid_biosynthesis	2.992671028	SG	1.37596952	0.566951697
GnRH_signaling_pathway	0.599436038	GC	0.267728229	0.054262988
Pyruvate_metabolism	4.05880538	GC	2.188277331	0.591957783
Carbon_fixation_in_photosynthetic_organisms	3.704783662	GC	2.27671014	3.63324E-05
Arginine_and_proline_metabolism	4.089008474	SG	2.791312816	0.000184148
Cell_cycle___Caulobacter	3.692665691	GC	2.034494522	0.013865375
Chloroalkane_and_chloroalkene_degradation	3.40060282	GC	1.975173242	0.196608197

Hepatitis_C	0			-
Leukocyte_transendothelial_migration	0	GC	0.221521876	0.328214495
Zeatin_biosynthesis	2.634667663	GC	1.330274327	0.007915763
Betalain_biosynthesis	1.17138243	SG	0.35266155	0.342018875
Metabolism_of_xenobiotics_by_cytochrome_P450	3.111865468	SG	1.833296947	0.052755966
RNA_degradation	3.655580987	SG	1.657340364	0.893402355
Calcium_signaling_pathway	0	GC	0.454039292	0.77933757
Adherens_junction	0	GC	0.221521876	0.328214495
Glycosaminoglycan_degradation	2.420822568	GC	1.419584729	0.161240392
TGF_beta_signaling_pathway	0			-
Dioxin_degradation	2.904953396	GC	1.678978129	0.21856001
Regulation_of_actin_cytoskeleton	0	GC	0.221521876	0.328214495
Protein_folding_and_associated_processing	3.924534567	SG	2.594715225	0.004200041
Bisphenol_degradation	3.025038381	GC	1.715482335	0.116076349
Sporulation	3.203381213	GC	2.40780098	0.000392738
Steroid_biosynthesis	1.882198075	SG	0.886576699	0.107834449
Hematopoietic_cell_lineage	0.17611235	GC	0.194177901	0.961136561
Melanogenesis	0.661677567	SG	0.204163491	0.373855535
Steroid_hormone_biosynthesis	2.104086935	SG	0.857788599	0.575230638
Isoflavonoid_biosynthesis	0.586277042	SG	0.212428562	0.311971919
Arachidonic_acid_metabolism	2.816101016	SG	1.752942954	0.000270138
Inositol_phosphate_metabolism	3.32888535	SG	2.267727788	0.004200041
Carbohydrate_digestion_and_absorption	2.251783442	GC	1.695559663	0.000540891
Porphyrin_and_chlorophyll_metabolism	3.952692848	SG	2.397506893	0.11893108
Translation_factors	3.683076406	GC	2.327114859	0.001538725
Selenocompound_metabolism	3.587826464	GC	2.08996203	0.002839943
Arrhythmogenic_right_ventricular_cardiomyopathy__ARVC	0	GC	0.221521876	0.328214495
Notch_signaling_pathway	0.111479813	SG	0.190174549	0.011282557
Carbohydrate_metabolism	3.068129326	GC	2.006347878	0.003888145
mTOR_signaling_pathway	0			-
Bacterial_invasion_of_epithelial_cells	1.656459133	GC	1.124453984	0.00135615
Basal_transcription_factors	1.457690595	GC	0.697822963	0.335865972
Taurine_and_hypotaurine_metabolism	3.2055418	SG	1.578175828	0.205186859
p53_signaling_pathway	1.713233019	SG	0.61194534	0.479848086
Tryptophan_metabolism	3.696617051	SG	2.688380698	0.000493966
Flavonoid_biosynthesis	1.991022514	SG	0.813112591	0.442810364
Wnt_signaling_pathway	0.111479813	SG	0.190174549	0.011282557
Aminoacyl_tRNA_biosynthesis	4.073513091	GC	2.715978361	0.011680866
Other_types_of_O_glycan_biosynthesis	0	SG	1.581888514	0.63678001
Nucleotide_metabolism	2.821403391	GC	1.813094802	0.242219569
Two_component_system	4.296755411	SG	3.060691325	0.000921488
Bile_secretion	0.868158957	SG	0.23526965	0.479848086
Lipid_metabolism	3.047987344	GC	1.822202891	0.001005091
Ribosome_biogenesis_in_eukaryotes	2.787994555	SG	1.280423929	0.02421876
Stilbenoid_diarylheptanoid_and_gingerol_biosynthesis	2.100106959	GC	0.963984692	0.300455682
Pentose_and_glucuronate_interconversions	3.575360125	GC	1.987743597	0.034036353
beta_Alanine_metabolism	3.63955766	SG	2.659313906	0.001005091
D_Arginine_and_D_ornithine_metabolism	1.945591823	GC	1.169699639	0.000808095
Propanoate_metabolism	3.958747936	SG	2.680382337	0.000844369
Circadian_rhythm___plant	1.553412899	SG	0.658288362	0.407463622

Glutamatergic_synapse	2.953240572	GC	1.344468456	0.903042814
Gastric_acid_secretion	0	GC	0.548688808	0.35453948
Fructose_and_mannose_metabolism	3.912277962	GC	2.958633115	0.000234227
Pathogenic_Escherichia_coli_infection	0	GC	0.221521876	0.328214495
Dilated_cardiomyopathy__DCM_	0	GC	0.221521876	0.328214495
Staphylococcus_aureus_infection	2.904609462	GC	2.335010013	0.001604445
Ascorbate_and_aldarate_metabolism	3.084353435	GC	1.535801366	0.367345699
Glycine_serine_and_threonine_metabolism	3.963001186	SG	2.466898287	0.002230854
Cytosolic_DNA_sensing_pathway	0			-
MAPK_signaling_pathway	0			-
Transcription_machinery	3.862615522	GC	1.824405898	0.652185451
Polycyclic_aromatic_hydrocarbon_degradation	3.190528571	GC	1.83766193	0.044430748
Styrene_degradation	2.936577131	SG	2.086377814	0.000234227
Glyoxylate_and_dicarboxylate_metabolism	3.864890869	SG	2.885281654	0.000112626
Biosynthesis_of_unsaturated_fatty_acids	3.347941402	SG	2.284570224	0.003198307
Polyketide_sugar_unit_biosynthesis	3.124537971	GC	1.801373777	0.092744582
Prostate_cancer	2.428013925	SG	1.443373278	0.048443333
Phosphatidylinositol_signaling_system	3.048645195	GC	1.575258713	0.116076349
Thiamine_metabolism	3.660600364	GC	2.373807465	0.015865064
Epithelial_cell_signaling_in_Helicobacter_pylori_infection	2.864078297	SG	1.761432745	0.380436275
Novobiocin_biosynthesis	3.045622449	SG	1.37140793	0.172452258
Glioma	0			-
Glycosphingolipid_biosynthesis___ganglio_series	2.265252038	GC	1.412772571	0.064077506
Transporters	4.795186229	GC	3.345469593	0.021314405
Photosynthesis_proteins	3.562056155	GC	2.151075804	0.007915763
Phenylpropanoid_biosynthesis	2.902622848	SG	1.40775928	0.495123096
Endocrine_and_other_factor_regulated_calcium_reabsorption	0	GC	0.548688808	0.35453948
Bacterial_chemotaxis	3.799934829	SG	2.88513076	0.008206346
Biosynthesis_of_vancomycin_group_antibiotics	2.644838268	GC	1.428791598	0.073336475
Pentose_phosphate_pathway	3.890585346	GC	2.468649395	0.002056104
DNA_repair_and_recombination_proteins	4.433769465	GC	2.926373884	0.007915763
Biosynthesis_of_siderophore_group_nonribosomal_peptides	2.711231584	SG	1.383088767	0.054262988
Amoebiasis	2.149720418	SG	1.247994998	0.209576838
Aminobenzoate_degradation	3.46439492	GC	1.867992234	0.687683413
RNA_polymerase	3.236896702	GC	2.123509844	0.002518605
Caprolactam_degradation	3.300199586	SG	2.348928029	0.004200041
beta_Lactam_resistance	2.498655459	SG	1.664123939	0.000619118
Cellular_antigens	2.787676373	SG	1.586032814	0.008206346
Chromosome	4.151424023	GC	2.285365285	0.088109024
Atrazine_degradation	2.823893071	SG	1.915659364	0.00232324

Supplementary table 23: Differential predicted KEGG pathways (level 3) among SG, AG and GC in Inner Mongolia cohort

Predicted_function_level3	LogMaxMean	Class	LDA score	p value
Cytokine_receptors	0	GC	1.775086744	0.00321421
Cysteine_and_methionine_metabolism	3.947926123	GC	2.395509929	0.006365014
Cytoskeleton_proteins	3.3798356	GC	2.051901671	0.014748109
Toxoplasmosis	1.785166233	AG	0.983445468	0.663800325
Prion_diseases	2.095171814	SG	1.279629442	0.002579845
ECM_receptor_interaction	0	GC	2.11914417	0.448216518
Ribosome	4.348265276	GC	3.085004557	0.016031322

Flavone_and_flavonol_biosynthesis	1.636020314	GC	0.619449107	0.71595628
Ubiquitin_system	2.348642133	GC	1.179350215	0.302027083
X_Alzheimer__s_disease_	3.124013459	SG	2.140317926	0.001453219
Lipopolysaccharide_biosynthesis_proteins	3.721191006	SG	2.759812861	0.019254913
Transcription_related_proteins	2.262898985	GC	1.51612994	0.030146589
Inorganic_ion_transport_and_metabolism	3.457959328	SG	2.227483077	0.052243837
Cardiac_muscle_contraction	2.774238712	SG	2.041879466	0.00077964
Protein_kinases	3.561720009	SG	1.592238842	0.654574535
Valine_leucine_and_isoleucine_degradation	3.896000557	SG	2.965541606	0.002237051
Benzoate_degradation	3.641609662	SG	2.190462	0.372757185
Shigellosis	0	AG	0.765171996	0.582938689
Fatty_acid_metabolism	3.756231502	SG	2.641676516	0.107081496
Lipid_biosynthesis_proteins	3.836516627	SG	2.084037269	0.386716425
Ribosome_Biogenesis	4.132881029	GC	2.511187327	0.106951138
Cell_division	2.817128547	AG	1.573899384	0.471239566
Biosynthesis_of_12_14__and_16_membered_macrolides	1.092458457	SG	0.604303744	0.002770415
ErbB_signaling_pathway	0			-
Amino_acid_related_enzymes	4.146823709	GC	2.463113069	0.049900477
G_protein_coupled_receptors	0	GC	0.594229067	0.222989434
Chronic_myeloid_leukemia	0.111479813	SG	0.326505859	0.053309772
Vibrio_cholerae_pathogenic_cycle	3.039028264	SG	1.964066922	0.002231817
Glycerophospholipid_metabolism	3.746676713	SG	1.741009995	0.379887572
Cytokine_cytokine_receptor_interaction	0	GC	1.777516453	0.00321421
Non_homologous_end_joining	2.391877489	SG	1.346694588	0.477454227
Spliceosome	0			-
Glycosyltransferases	3.56630004	GC	2.346744815	0.00041375
Amino_acid_metabolism	3.289385858	GC	1.957779209	0.038864384
Cell_motility_and_secretion	3.390146491	AG	2.193889912	0.144575775
Mismatch_repair	3.86994726	GC	2.323242381	0.122313026
Pancreatic_secretion	0	AG	0.601435091	0.739377886
Renin_angiotensin_system	1.6274928	SG	0.851808378	0.076917535
Various_types_of_N_glycan_biosynthesis	0.279069829	AG	0.514707956	0.284344441
Restriction_enzyme	3.358976545	GC	2.206339803	0.219053815
Ethylbenzene_degradation	2.876645541	GC	1.908166364	0.013234457
Bacterial_toxins	3.098188996	AG	1.965074884	0.095246791
Tetracycline_biosynthesis	3.23595315	GC	1.929053769	0.563433318
Clavulanic_acid_biosynthesis	0	AG	0.895857324	0.940742186
Secretion_system	4.285217546	SG	3.081861773	0.002640055
Glycan_bindng_proteins	0	AG	1.523252256	0.933522435
Methane_metabolism	4.004195725	GC	1.824289969	0.123647267
Metabolism_of_cofactors_and_vitamins	3.305071873	SG	1.997160737	0.014921641
Endocytosis	0.599436038	GC	0.252840718	0.181024137
Fat_digestion_and_absorption	0			-
Glycosphingolipid_biosynthesis___globo_series	2.684207752	GC	1.784124712	0.01959978
Homologous_recombination	3.931225293	GC	2.43501324	0.045145685
Protein_export	3.766674663	AG	2.128430412	0.210577797
Membrane_and_intracellular_structural_molecules	3.857468102	SG	2.820720082	0.000133013
Alanine_aspartate_and_glutamate_metabolism	3.978769862	GC	1.859749921	0.223742266
Lipoic_acid_metabolism	2.766460939	GC	1.272617119	0.4581801
Toluene_degradation	3.28472551	SG	2.229658323	4.95145E-06

Folate_biosynthesis	3.682236404	AG	1.951903131	0.492034627
Cell_cycle	0	GC	2.093959487	0.297371656
Primary_bile_acid_biosynthesis	2.381143261	GC	1.464429648	0.029085505
Lysosome	2.747151123	GC	1.73757898	0.338562847
Secondary_bile_acid_biosynthesis	2.304230484	GC	1.51270551	0.019475609
Chagas_disease__American_trypanosomiasis_	2.220502907	SG	1.383389338	0.011129894
Penicillin_and_cephalosporin_biosynthesis	2.656096187	SG	1.717937718	0.017559239
Pantothenate_and_CoA_biosynthesis	3.761825975	AG	1.752132875	0.224232679
Phagosome	0	AG	0.223152946	0.592453473
Lipopolysaccharide_biosynthesis	3.636934338	SG	2.782528349	0.003875597
Type_I_diabetes_mellitus	2.723715648	AG	0.748608102	0.630315442
Function_unknown	4.220737088	SG	2.665702787	0.021543603
Cytochrome_P450	0.434662923	AG	0.382364829	0.506086646
Energy_metabolism	3.908051963	SG	2.666624414	0.150839576
Signal_transduction_mechanisms	3.672829457	GC	2.300854523	0.065004341
Nicotinate_and_nicotinamide_metabolism	3.600657413	SG	1.278092839	0.310853329
Limonene_and_pinene_degradation	3.468186768	SG	2.264272739	0.217109786
Translation_proteins	3.921720962	GC	1.858221386	0.66648157
Carbon_fixation_pathways_in_prokaryotes	4.03778103	SG	2.592410551	0.026356568
Biosynthesis_and_biodegradation_of_secondary_metabolites	2.978289072	SG	1.993011214	0.001083325
Other_transporters	3.324733487	SG	1.347259483	0.90368412
Synthesis_and_degradation_of_ketone_bodies	3.203826987	SG	2.209810831	4.73668E-05
Proximal_tubule_bicarbonate_reclamation	2.419560604	GC	1.334908561	0.489375922
Starch_and_sucrose_metabolism	3.822574334	GC	2.8327886	0.000498276
Fc_epsilon_RI_signaling_pathway	0			-
Aldosterone_regulated_sodium_reabsorption	0	AG	1.222875675	0.337262024
Butanoate_metabolism	4.012188285	SG	2.746859423	0.005222019
Lysine_degradation	3.612306151	SG	2.628770387	0.002648912
Biosynthesis_of_ansamycins	2.837944273	AG	1.185279183	0.286902684
Glycerolipid_metabolism	3.597153972	GC	2.506180008	0.000104563
Galactose_metabolism	3.731209927	GC	2.846729296	0.000321322
Carotenoid_biosynthesis	2.396679631	GC	1.359374454	0.086823908
DNA_replication	3.805952054	GC	2.328340267	0.141774666
Biosynthesis_of_type_II_polyketide_backbone	0.191254553	SG	0.64179916	0.203459596
Phosphotransferase_system__PTS_	3.695722149	GC	3.021763994	0.002602072
Amino_sugar_and_nucleotide_sugar_metabolism	4.088930371	GC	2.975857263	0.00022108
Glycosaminoglycan_biosynthesis___chondroitin_sulfate	0	GC	1.949941131	0.742545535
Cell_cycle___yeast	0			-
X_Huntington__s_disease_	3.046281941	SG	2.145053829	0.00091471
Electron_transfer_carriers	2.60899202	AG	1.391235528	0.21236673
Meiosis___yeast	2.317020041	AG	1.19776677	0.553581386
Cholinergic_synapse	0			-
Ether_lipid_metabolism	1.872463077	AG	0.872718031	0.378213051
Chlorocyclohexane_and_chlorobenzene_degradation	2.815176194	SG	1.759047466	0.261995538
General_function_prediction_only	4.536635062	GC	2.436877023	0.127077252
Proteasome	2.53112116	AG	1.418538345	0.077255013
Biotin_metabolism	3.229029872	AG	2.155411082	0.051933642
Replication_recombination_and_repair_proteins	3.941758654	GC	2.635750755	0.030355392
Hedgehog_signaling_pathway	0			-
Xylene_degradation	2.791988272	GC	1.837585118	0.04104418

Tyrosine_metabolism	3.655333862	GC	2.309113353	0.184947669
African_trypanosomiasis	2.216998403	SG	1.339037854	0.016992945
Sesquiterpenoid_biosynthesis	0.093445298	SG	0.418079381	0.070977333
Transcription_factors	4.181611726	GC	2.778567635	0.047955756
Phosphonate_and_phosphinate_metabolism	2.779917089	GC	1.314773828	0.055830534
Tuberculosis	3.156264502	GC	1.78963844	7.50142E-05
Plant_pathogen_interaction	3.174877879	SG	1.794486791	0.021803986
Nitrogen_metabolism	3.867520271	SG	2.056185988	0.240723683
Germination	1.688770203	GC	0.75397501	0.370211639
Isoquinoline_alkaloid_biosynthesis	2.689817528	AG	1.307386382	0.611394911
Streptomycin_biosynthesis	3.405893852	GC	1.983154748	0.068294576
RNA_transport	3.089056936	GC	1.955971706	0.049963512
Pyrimidine_metabolism	4.234841902	GC	2.966246299	0.008554326
Citrate_cycle__TCA_cycle_	3.8553165	SG	2.488524658	0.006073785
D_Glutamine_and_D_glutamate_metabolism	3.159348297	GC	1.863331679	0.030905775
Photosynthesis___antenna_proteins	1.000592097	GC	0.549552042	0.006884302
Sphingolipid_metabolism	2.996471052	GC	2.104789505	0.005915512
PPAR_signaling_pathway	3.130737781	AG	1.74067942	0.87500402
Long_term_depression	0			-
Phenylalanine_tyrosine_and_tryptophan_biosynthesis	3.882887431	AG	2.489494121	0.090978599
VEGF_signaling_pathway	0	GC	0.651970406	0.296639211
Glycan_biosynthesis_and_metabolism	2.825993808	SG	1.962670394	0.003866328
Phenylalanine_metabolism	3.47297394	SG	2.441904165	0.009173474
Other_glycan_degradation	3.114645046	GC	2.225093588	0.018610732
Vasopressin_regulated_water_reabsorption	0.624088968	GC	0.340710519	0.878238455
Progesterone_mediated_oocyte_maturation	2.427815884	SG	1.417028106	0.136042356
MAPK_signaling_pathway___yeast	2.616456109	SG	1.518619796	0.163440664
Retinol_metabolism	2.858823729	GC	1.529796561	0.380913399
One_carbon_pool_by_folate	3.735847512	GC	2.321121226	0.00072088
Valine_leucine_and_isoleucine_biosynthesis	3.820230691	AG	2.052041069	0.425914455
Chaperones_and_folding_catalysts	3.990602602	AG	2.067703253	0.2465279
DNA_replication_proteins	4.03723184	GC	2.424973345	0.295397418
Photosynthesis	3.544031656	GC	2.250845536	0.010654233
Glycosphingolipid_biosynthesis___lacto_and_neolacto_series	0	AG	1.038114684	0.337435189
GTP_binding_proteins	0	GC	1.95836263	0.297371656
Linoleic_acid_metabolism	2.822008925	GC	1.834872531	0.076443591
Bacterial_secretion_system	3.88799858	SG	2.593525764	0.003747569
Leishmaniasis	0	GC	0.638336642	0.296639211
Fatty_acid_biosynthesis	3.734362448	GC	2.251528987	0.077983882
Drug_metabolism___other_enzymes	3.449888964	GC	2.155770516	0.006595727
Biosynthesis_of_type_II_polyketide_products	1.077415818	AG	0.702733426	0.261364997
Oxidative_phosphorylation	4.105202445	AG	2.816462455	0.016423059
Fatty_acid_elongation_in_mitochondria	0.121123591	AG	0.507341134	0.381742781
NOD_like_receptor_signaling_pathway	2.464125229	AG	1.2724883	0.472987403
Insulin_signaling_pathway	2.69885736	GC	1.45711148	0.085221184
Ion_channels	2.615966528	GC	1.835305079	0.057563103
Indole_alkaloid_biosynthesis	1.046391476	SG	0.349840202	0.49491893
Peptidoglycan_biosynthesis	3.882626183	GC	2.671082565	0.000530203
Glutathione_metabolism	3.60125535	SG	2.175812585	0.003709166
Apoptosis	2.201634049	GC	1.52177222	0.00547594

X_Parkinson__s_disease_	2.809583712	SG	2.054103074	0.000947004
Salivary_secretion	0	AG	0.793693219	0.338741248
Purine_metabolism	4.357279709	GC	3.01704351	0.014373427
mRNA_surveillance_pathway	0.455387029	AG	0.414758807	0.68146038
Adipocytokine_signaling_pathway	2.809374159	AG	1.564493648	0.64782425
Fc_gamma_R_mediated_phagocytosis	0.599436038	GC	0.2512504	0.184535315
Glycolysis___Gluconeogenesis	4.057881375	GC	2.891323894	0.000309616
Pancreatic_cancer	0			-
Antigen_processing_and_presentation	2.427815884	SG	1.417028106	0.136042356
Prenyltransferases	3.511993464	GC	2.086304753	0.023524977
Histidine_metabolism	3.692961864	SG	2.012898493	0.718208931
Drug_metabolism___cytochrome_P450	3.131456534	SG	1.933121586	0.107882939
Hypertrophic_cardiomyopathy__HCM_	1.366828356	SG	0.701079651	0.018117778
Vitamin_B6_metabolism	3.25075284	AG	1.794696352	0.486439992
C5_Branched_dibasic_acid_metabolism	3.415585709	GC	1.754332038	0.353465359
Complement_and_coagulation_cascades	0			-
Long_term_potentiation	0			-
Caffeine_metabolism	1.166063139	SG	0.36189721	0.639402712
Oocyte_meiosis	0			-
Peroxisome	3.346790078	AG	2.130922166	0.259281103
Systemic_lupus_erythematosus	0.869123192	AG	0.291534289	0.255362277
Ubiquinone_and_other_terpenoid_quinone_biosynthesis	3.522713268	SG	2.260692426	0.00172267
Peptidases	4.205231305	GC	2.629318643	0.000333826
Tight_junction	0	AG	0.22292014	0.592453473
Glycosylphosphatidylinositol_GPI__anchor_biosynthesis	0	SG	1.796065301	0.296518234
Naphthalene_degradation	3.383124135	GC	2.059988451	0.087823347
Vascular_smooth_muscle_contraction	0			-
Sulfur_relay_system	3.567306232	SG	2.122945359	0.010355961
Protein_processing_in_endoplasmic_reticulum	2.664660395	SG	1.224212144	0.814066061
Measles	0			-
Renal_cell_carcinoma	2.445565069	SG	0.946301624	0.760872179
D_Alanine_metabolism	3.127532866	GC	2.12711805	0.007583738
Small_cell_lung_cancer	1.787428194	AG	0.981255627	0.664446854
Rheumatoid_arthritis	0			-
Phototransduction___fly	0	AG	0.223152946	0.592453473
Butirosin_and_neomycin_biosynthesis	2.735999941	GC	1.565225109	0.002706881
Influenza_A	1.789133194	AG	0.988111089	0.645225005
Nitrotoluene_degradation	2.950227389	AG	1.962263464	0.332069135
Pores_ion_channels	3.683451794	SG	2.653135168	0.000884126
Mineral_absorption	2.052879737	AG	0.872862448	0.199923523
Colorectal_cancer	1.785104268	AG	0.983535669	0.658495008
Protein_digestion_and_absorption	1.853228926	AG	0.801696506	0.628941587
Pathways_in_cancer	2.77967827	AG	1.500224693	0.041027031
Terpenoid_backbone_biosynthesis	3.747894117	GC	2.365307978	0.014502851
Amyotrophic_lateral_sclerosis__ALS_	2.644224986	SG	1.708982193	0.000185109
Primary_immunodeficiency	2.704165855	SG	0.964112601	0.522987872
RIG_I_like_receptor_signaling_pathway	1.743290802	GC	1.000989471	0.043544346
Neuroactive_ligand_receptor_interaction	0	SG	0.903185735	0.075557477
Bladder_cancer	2.1139078	SG	1.38752149	0.001654269
Nucleotide_excision_repair	3.56398508	GC	2.167017268	0.062859382

Olfactory_transduction	0			-
Others	4.003865213	GC	2.875284752	9.76106E-05
Geraniol_degradation	3.442765596	SG	2.563622279	0.035132402
N_Glycan_biosynthesis	2.300767782	AG	1.20819171	0.503822325
ABC_transporters	4.53348587	SG	2.717478247	0.697004566
Bacterial_motility_proteins	4.232253076	SG	3.369763233	0.001444925
Lysine_biosynthesis	3.826162922	GC	2.395898821	0.001156304
Type_II_diabetes_mellitus	2.61670772	GC	1.22666565	0.223937173
Vibrio_cholerae_infection	1.346168478	SG	0.655852374	0.036912558
Pertussis	2.369509666	SG	1.331050816	0.285631981
Other_ion_coupled_transporters	4.116931588	GC	2.499694485	0.067328258
X111_Trichloro_22_bis_4_chlorophenyl_ethane__DDT__degradation	1.285762914	SG	0.508188888	0.063516232
Neurotrophin_signaling_pathway	0			-
alpha_Linolenic_acid_metabolism	2.617841161	SG	1.838590971	1.66859E-05
Fluorobenzoate_degradation	2.373668597	AG	1.369515079	0.440238883
Sulfur_metabolism	3.473819031	GC	1.654489283	0.204037039
Riboflavin_metabolism	3.429264805	SG	1.718862381	0.10443576
Base_excision_repair	3.667201862	GC	2.019404741	0.244111008
Phototransduction	0			-
Viral_myocarditis	1.787713642	AG	0.986165739	0.661150684
Focal_adhesion	0	AG	0.565236109	0.635439421
Cyanoamino_acid_metabolism	3.329621085	AG	1.444526727	0.504726409
CAM_ligands	0	GC	2.11491155	0.448216518
Flagellar_assembly	3.91803541	SG	3.101633339	0.001129506
Tropanepiperidine_and_pyridine_alkaloid_biosynthesis	2.999331723	AG	1.47650137	0.839321286
GnRH_signaling_pathway	0.599436038	GC	0.252840718	0.181024137
Pyruvate_metabolism	4.05880538	GC	2.355455462	0.134710757
Carbon_fixation_in_photosynthetic_organisms	3.704783662	GC	2.291776923	1.51052E-05
Arginine_and_proline_metabolism	4.089008474	SG	2.81705793	0.000111039
Cell_cycle___Caulobacter	3.692665691	GC	2.111338968	0.008654601
Chloroalkane_and_chloroalkene_degradation	3.40060282	GC	2.051346599	0.199849604
Hepatitis_C	0			-
Leukocyte_transendothelial_migration	0	AG	0.223152946	0.592453473
Zeatin_biosynthesis	2.634667663	GC	1.383018761	0.01048744
Betalain_biosynthesis	1.17138243	SG	0.436410282	0.481369394
Metabolism_of_xenobiotics_by_cytochrome_P450	3.111865468	SG	1.91818238	0.082218465
RNA_degradation	3.660558732	AG	1.709932777	0.747421841
Calcium_signaling_pathway	0	GC	0.633286478	0.618589432
Adherens_junction	0	AG	0.223152946	0.592453473
Glycosaminoglycan_degradation	2.420822568	GC	1.404794466	0.382901978
TGF_beta_signaling_pathway	0			-
Dioxin_degradation	2.904953396	GC	1.701795135	0.318631801
Regulation_of_actin_cytoskeleton	0	AG	0.223152946	0.592453473
Protein_folding_and_associated_processing	3.924534567	SG	2.566238485	0.01609191
Bisphenol_degradation	3.025038381	GC	1.744416067	0.152696808
Sporulation	3.203381213	GC	2.412411379	0.00081055
Steroid_biosynthesis	1.891209282	AG	0.984390703	0.206450439
Hematopoietic_cell_lineage	0.17611235	GC	0.355704711	0.785635222
Melanogenesis	0.661677567	SG	0.347805309	0.405314496
Steroid_hormone_biosynthesis	2.114493747	AG	0.935280321	0.856964077

Isoflavonoid_biosynthesis	0.588585903	AG	0.359619028	0.635788512
Arachidonic_acid_metabolism	2.816101016	SG	1.76968805	0.000786193
Inositol_phosphate_metabolism	3.32888535	SG	2.321395885	0.003051809
Carbohydrate_digestion_and_absorption	2.251783442	GC	1.690179096	0.000874223
Porphyrin_and_chlorophyll_metabolism	3.952692848	SG	2.41669448	0.097248449
Translation_factors	3.683076406	GC	2.367786772	0.001848717
Selenocompound_metabolism	3.587826464	GC	2.069294652	0.009963434
Arrhythmogenic_right_ventricular_cardiomyopathy__ARVC	0	AG	0.223152946	0.592453473
Notch_signaling_pathway	0.111479813	SG	0.326505859	0.053309772
Carbohydrate_metabolism	3.068129326	GC	2.013447513	0.012048524
mTOR_signaling_pathway	0			-
Bacterial_invasion_of_epithelial_cells	1.656459133	GC	1.118145	0.002206114
Basal_transcription_factors	1.457690595	GC	0.646159217	0.672457301
Taurine_and_hypotaurine_metabolism	3.2055418	SG	1.519446384	0.280721834
p53_signaling_pathway	1.798995537	AG	0.98742924	0.683012912
Tryptophan_metabolism	3.696617051	SG	2.717159262	0.001733867
Flavonoid_biosynthesis	1.991022514	SG	0.810904629	0.74051892
Wnt_signaling_pathway	0.111479813	SG	0.32769618	0.053309772
Aminoacyl_tRNA_biosynthesis	4.073513091	GC	2.772064328	0.017736799
Other_types_of_O_glycan_biosynthesis	0	SG	1.849067066	0.525614084
Nucleotide_metabolism	2.821403391	GC	1.850494515	0.198838409
Two_component_system	4.296755411	SG	3.072522799	0.000602963
Bile_secretion	0.868158957	SG	0.361777752	0.711345208
Lipid_metabolism	3.047987344	GC	1.844786809	0.002031964
Ribosome_biogenesis_in_eukaryotes	2.787994555	SG	1.291044621	0.063760312
Stilbenoid_diarylheptanoid_and_gingerol_biosynthesis	2.118847454	AG	0.985194826	0.541319515
Pentose_and_glucuronate_interconversions	3.575360125	GC	1.963690368	0.113865055
beta_Alanine_metabolism	3.63955766	SG	2.696099604	0.002212267
D_Arginine_and_D_ornithine_metabolism	1.945591823	GC	1.19856594	0.001786566
Propanoate_metabolism	3.958747936	SG	2.713041371	0.001520405
Circadian_rhythm___plant	1.553412899	SG	0.712041175	0.660127202
Glutamatergic_synapse	2.953240572	GC	1.405584983	0.375472818
Gastric_acid_secretion	0	AG	0.793693219	0.338741248
Fructose_and_mannose_metabolism	3.912277962	GC	2.97082958	0.000150801
Pathogenic_Escherichia_coli_infection	0	AG	0.223152946	0.592453473
Dilated_cardiomyopathy__DCM_	0	AG	0.223152946	0.592453473
Staphylococcus_aureus_infection	2.904609462	GC	2.34574709	0.00442767
Ascorbate_and_aldarate_metabolism	3.085665085	AG	1.493285033	0.486820373
Glycine_serine_and_threonine_metabolism	3.963001186	SG	2.492833236	0.003603375
Cytosolic_DNA_sensing_pathway	0			-
MAPK_signaling_pathway	0			-
Transcription_machinery	3.862957117	AG	1.783425177	0.846369613
Polycyclic_aromatic_hydrocarbon_degradation	3.190528571	GC	1.88742066	0.069631294
Styrene_degradation	2.936577131	SG	2.112445415	0.00033391
Glyoxylate_and_dicarboxylate_metabolism	3.864890869	SG	2.905029672	0.000105129
Biosynthesis_of_unsaturated_fatty_acids	3.347941402	SG	2.326808793	0.00825589
Polyketide_sugar_unit_biosynthesis	3.124537971	GC	1.738937133	0.257838066
Prostate_cancer	2.428013925	SG	1.416504951	0.137595265
Phosphatidylinositol_signaling_system	3.048645195	GC	1.597232723	0.177776374
Thiamine_metabolism	3.660600364	GC	2.377888928	0.040403482

Epithelial_cell_signaling_in_Helicobacter_pylori_infection	2.886085054	AG	1.796570244	0.32592829
Novobiocin_biosynthesis	3.063758884	AG	1.497199893	0.102701163
Glioma	0			-
Glycosphingolipid_biosynthesis___ganglio_series	2.265252038	GC	1.400958044	0.167766115
Transporters	4.795186229	GC	3.299399119	0.083329728
Photosynthesis_proteins	3.562056155	GC	2.214263331	0.008844945
Phenylpropanoid_biosynthesis	2.902622848	SG	1.447732597	0.641759494
Endocrine_and_other_factor_regulated_calcium_reabsorption	0	AG	0.793693219	0.338741248
Bacterial_chemotaxis	3.799934829	SG	2.880283917	0.021095866
Biosynthesis_of_vancomycin_group_antibiotics	2.644838268	GC	1.374717664	0.193729412
Pentose_phosphate_pathway	3.890585346	GC	2.494724392	0.004490386
DNA_repair_and_recombination_proteins	4.433769465	GC	2.948427681	0.014068278
Biosynthesis_of_siderophore_group_nonribosomal_peptides	2.711231584	SG	1.473469547	0.124355729
Amoebiasis	2.195565715	AG	1.339396591	0.133859594
Aminobenzoate_degradation	3.46439492	GC	1.84817987	0.839602976
RNA_polymerase	3.236896702	GC	2.145445483	0.003812898
Caprolactam_degradation	3.300199586	SG	2.40144435	0.019678735
beta_Lactam_resistance	2.498655459	SG	1.701057733	0.000553866
Cellular_antigens	2.787676373	SG	1.601124975	0.031459264
Chromosome	4.151424023	GC	2.360347233	0.239684414
Atrazine_degradation	2.826157947	AG	1.868379524	0.008420346

LDA: Linear discriminant analysis

KEGG: Kyoto Encyclopedia of genes and Genomes

SG: Superficial gastritis

AG: Atrophic gastritis

GC: Gastric cancer