

Table S1. Summary of enrolled subjects in this study

	Centenarians		Elderly	Adults
	Community-dwelling	Rehabilitation hospital		
Subjects (n)	20	10	17	9
Age	99.1 ± 3.5	98.7 ± 3.6	73.6 ± 3.6	34.3 ± 6.5
Male/Female	3/17	0/10	10/7	6/3

Table S2. The significance of pairwise differences of phylum between groups. L_C, centenarians in longevity villages; L_E, elderly in longevity villages; L_A, adults in longevity villages; U_E, elderly in urbanized town; U_A, adults in urbanized town.

	LC vs. LE	LC vs. LA	LC vs. UE	LC vs. UA	LE vs. LA	LE vs. UE	LE vs. UA	LA vs. UE	LA vs. UA	UE vs. UA
<i>Firmicutes</i>	0.1247	0.5661	0.04536	0.03957	0.5408	0.00164	0.003495	0.0363	0.0636	0.4706
<i>Bacteroidetes</i>	0.1547	0.2111	0.00152	0.00343	0.2416	0.00164	0.00186	0.0763	0.1703	0.3161
<i>Proteobacteria</i>	0.05863	0.00017	0.5927	0.3115	0.0612	0.7125	0.3194	0.0762	0.00475	0.9
<i>Tenericutes</i>	0.1355	0.3708	0.6013	0.9151	0.1776	0.3861	0.3365	0.258	0.7943	0.7647
<i>Actinobacteria</i>	0.5645	0.0521	0.0239	0.000663	0.271	0.0611	0.04911	0.1397	0.9201	0.05278
<i>Verrucomicrobia</i>	0.06523	0.03751	0.5822	0.0559	0.2688	0.1025	0.8454	0.1249	0.2206	0.1343

Table S3. The summary of diversity indices after normalized reads obtained from this study.

Group	Sample	Analyzed reads	Normalized reads	Observed OTUs	Estimated OTUs (Chao1)	Shannon diversity index	Good's coverage
Centenarians	C1	9,771	3,300	190	495.25	2.26	0.97
	C2	15,275	3,300	169	343.79	2.35	0.98
	C3	6,115	3,300	301	583.09	3.43	0.96
	C4	7,430	3,300	343	805.58	4.24	0.94
	C5	5,320	3,300	334	865.88	4.23	0.94
	C6	4,951	3,300	346	684.61	3.92	0.95
	C7	5,297	3,300	254	496.19	3.61	0.96
	C8	6,377	3,300	208	476.38	2.25	0.97
	C9	10,118	3,300	337	651.15	4.47	0.95
	C10	5,394	3,300	281	535.00	3.95	0.96
	C11	3,314	3,300	234	486.12	3.33	0.97
	C12	6,640	3,300	379	765.22	4.51	0.94
	C13	4,904	3,300	336	659.57	4.32	0.95
	C14	5,681	3,300	346	608.86	4.51	0.95
	C15	6,082	3,300	254	468.00	3.84	0.97
	C16	6,120	3,300	279	517.64	4.19	0.96
	C17	7,272	3,300	186	309.00	2.73	0.98
	C18	6,956	3,300	326	684.63	4.42	0.95
	C19	4,705	3,300	278	480.52	3.41	0.96
	C20	3,910	3,300	304	427.52	4.27	0.96
	C21	9,066	3,300	325	785.00	4.45	0.95
	C22	9,008	3,300	222	432.04	2.41	0.97
	C23	6,743	3,300	190	294.52	2.59	0.98

	C24	4,789	3,300	348	642.53	4.42	0.95
	C25	11,825	3,300	192	306.00	2.57	0.98
	C26	4,387	3,300	428	901.06	4.82	0.93
	C27	6,745	3,300	314	624.16	4.04	0.95
	C28	7,272	3,300	512	1064.55	5.03	0.92
	C29	3,882	3,300	324	679.68	4.63	0.95
	C30	7,264	3,300	273	527.09	4.03	0.96
Elderly	E1	7,409	3,300	189	480.83	3.09	0.97
	E2	6,423	3,300	193	371.14	3.57	0.97
	E3	9,350	3,300	230	497.24	3.42	0.96
	E4	6,257	3,300	256	482.62	3.46	0.96
	E5	3,395	3,300	355	626.69	4.54	0.95
	E6	10,501	3,300	177	486.38	3.42	0.97
	E7	5,504	3,300	334	604.95	4.54	0.96
	E8	3,994	3,300	408	733.52	4.86	0.94
	E9	4,203	3,300	288	489.92	3.81	0.96
	E10	4,827	3,300	327	605.32	4.23	0.95
	E11	3,942	3,300	308	572.63	4.22	0.96
	E12	4,188	3,300	336	694.14	4.29	0.95
	E13	4,281	3,300	315	520.50	4.23	0.96
	E14	7,291	3,300	225	432.20	3.32	0.97
	E15	8,030	3,300	383	804.98	4.66	0.94
	E16	4,626	3,300	332	600.28	4.34	0.96
	E17	7,801	3,300	220	383.90	3.40	0.97
	A1	3,894	3,300	397	668.73	4.64	0.94
	A2	5,625	3,300	182	329.96	3.39	0.97
	A3	6,807	3,300	233	375.50	3.45	0.97

Young	A4	10,244	3,300	143	356.46	2.63	0.98
Adults	A5	4,869	3,300	188	300.45	3.56	0.97
	A6	5,068	3,300	295	724.13	4.36	0.96
	A7	4,782	3,300	222	387.45	3.03	0.97
	A8	3,913	3,300	268	410.50	3.96	0.97
	A9	5,625	3,300	177	262.04	3.42	0.98

Table S4. Significantly different KEGG pathways among groups (Selected by Kruskal-Wallis H-test with Benjamini-Hochberg False discovery rate).

Level_1	Level_2	Level_3	<i>p</i> -values	<i>p</i> -values (corrected)
Metabolism	Metabolism of Cofactors and Vitamins	Lipoic acid metabolism	4.08E-05	0.003343599
Environmental Information Processing	Signal Transduction	Phosphatidylinositol signaling system	1.20E-05	0.003951783
Environmental Information Processing	Signaling Molecules and Interaction	Ion channels	3.94E-05	0.004304504
Human Diseases	Cancers	Bladder cancer	3.13E-05	0.005130009
Metabolism	Xenobiotics Biodegradation and Metabolism	Fluorobenzoate degradation	8.97E-05	0.005883103
Metabolism	Others	Others_Unclassified	0.000521704	0.024445545
Genetic Information Processing	Transcription related proteins	Transcription related proteins_Unclassified	0.000449989	0.02459942
Metabolism	Energy Metabolism	Photosynthesis proteins	0.000981397	0.026824858
Metabolism	Carbohydrate Metabolism	Ascorbate and aldarate metabolism	0.001160518	0.027189284
Human Diseases	Neurodegenerative Diseases	Parkinson's disease	0.001118965	0.028232354
Metabolism	Amino Acid Metabolism	Tyrosine metabolism	0.000965925	0.028802118
Poorly Characterized	Function unknown	Function unknown_Unclassified	0.000931466	0.030552087
Metabolism	Metabolism of Terpenoids and Polyketides	Terpenoid backbone biosynthesis	0.001640704	0.031655944
Human Diseases	Neurodegenerative Diseases	Huntington's disease	0.001458457	0.031891595
Metabolism	Metabolism of Terpenoids and Polyketides	Limonene and pinene degradation	0.001755805	0.031994672
Human Diseases	Infectious Diseases	Chagas disease (American trypanosomiasis)	0.001960953	0.032159628
Human Diseases	Infectious Diseases	Epithelial cell signaling in Helicobacter pylori infection	0.001572198	0.032230068
Human Diseases	Immune System Diseases	Systemic lupus erythematosus	0.00189287	0.032676921
Metabolism	Glycan Biosynthesis and Metabolism	Various types of N-glycan biosynthesis	0.002497459	0.032766661
Genetic Information Processing	Transcription	Basal transcription factors	0.002107434	0.032916119
Cellular Processes	Cell Motility	Cytoskeleton proteins	0.002450577	0.033491219

Cellular Processes and Signaling	Inorganic ion transport and metabolism	Inorganic ion transport and metabolism_Unclassified	0.002351076	0.033528387
Metabolism	Energy Metabolism	Photosynthesis	0.000925261	0.033720641
Metabolism	Amino Acid Metabolism	Tryptophan metabolism	0.000847697	0.034755566
Metabolism	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - lacto and neolacto series	0.002334189	0.03480064
Genetic Information Processing	Folding, Sorting and Degradation	Ubiquitin system	0.003115423	0.039302254

Table S5. Significantly different KEGG pathway between community-dwelling and rehabilitation hospital-residing centenarians (Selected by Kruskal-Wallis H-test with Benjamini-Hochberg False discovery rate).

Level_1	Level_2	Level_3	<i>p</i>-values	<i>p</i>-values (corrected)
Metabolism	Carbohydrate metabolism	Carbohydrate metabolism_Unclassified	0.000509832	0.041806254
Genetic Information Processing	Transcription	Basal transcription factors	0.000219448	0.071979002

Table S6. Significantly different KEGG pathways between subjects of longevity villages and urbanized towns.

Level_1	Level_2	Level_3	Longevity (%)	Urban (%)	p-values	p-values (corrected)
Human Diseases	Infectious Diseases	Staphylococcus aureus infection	0.015093952	0.000650379	4.00E-11	1.31E-08
Metabolism	Energy Metabolism	Carbon fixation in photosynthetic organisms	0.641665726	0.706858555	1.08E-08	5.04E-07
Environmental Information Processing	Membrane Transport	Phosphotransferase system (PTS)	0.600163689	0.264248007	1.43E-08	5.86E-07
Organismal Systems	Endocrine System	Adipocytokine signaling pathway	0.055074668	0.097567337	1.79E-08	5.87E-07
Organismal Systems	Excretory System	Vasopressin-regulated water reabsorption	0.000879736	3.48E-05	1.07E-08	5.87E-07
Metabolism	Metabolism of Terpenoids and Polyketides	Tetracycline biosynthesis	0.158552085	0.109177548	9.06E-09	5.95E-07
Metabolism	Xenobiotics Biodegradation and Metabolism	Dioxin degradation	0.067993752	0.037562919	1.79E-08	6.52E-07
Cellular Processes	Transport and Catabolism	Peroxisome	0.148691268	0.204960408	8.08E-09	6.63E-07
Metabolism	Xenobiotics Biodegradation and Metabolism	1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation	1.30E-05	0.000648612	6.95E-09	7.60E-07
Metabolism	Xenobiotics Biodegradation and Metabolism	Xylene degradation	0.065518649	0.03662777	2.79E-08	8.33E-07
Metabolism	Carbohydrate Metabolism	Propanoate metabolism	0.520489713	0.45249071	6.80E-09	1.12E-06
Genetic Information Processing	Folding, Sorting and Degradation	RNA degradation	0.459222493	0.519840022	5.11E-08	1.20E-06
Human Diseases	Infectious Diseases	Bacterial invasion of epithelial cells	0.002608563	0.000449471	5.02E-08	1.27E-06
Genetic Information Processing	Folding, Sorting and Degradation	Chaperones and folding catalysts	0.978265519	1.117684757	4.84E-08	1.32E-06

Metabolism	Xenobiotics Biodegradation and Metabolism	Chloroalkane and chloroalkene degradation	0.196960029	0.144333785	7.07E-08	1.55E-06
Metabolism	Lipid Metabolism	Ether lipid metabolism	0.00353774	0.000783153	9.24E-08	1.90E-06
Organismal Systems	Endocrine System	PPAR signaling pathway	0.094642643	0.128600949	1.14E-07	2.21E-06
Human Diseases	Neurodegenerative Diseases	Prion diseases	0.007577196	0.002103645	1.34E-07	2.44E-06
Genetic Information Processing	Restriction enzyme	Restriction enzyme_Unclassified	0.201982645	0.264251607	1.74E-07	3.01E-06
Metabolism	Lipid Metabolism	Sphingolipid metabolism	0.182492231	0.311103614	1.84E-07	3.01E-06
Genetic Information Processing	Transcription	Transcription factors	1.822073106	1.417438667	3.24E-07	5.06E-06
Metabolism	Xenobiotics Biodegradation and Metabolism	Nitrotoluene degradation	0.093392661	0.052975968	3.59E-07	5.35E-06
Metabolism	Glycan Biosynthesis and Metabolism	Other glycan degradation	0.236651699	0.441268286	8.03E-07	1.15E-05
Organismal Systems	Digestive System	Protein digestion and absorption	0.013583826	0.038348864	1.08E-06	1.48E-05
Cellular Processes and Signaling	Signal transduction mechanisms	Signal transduction mechanisms_Unclassified	0.500883212	0.429264965	1.19E-06	1.56E-05
Metabolism	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism	1.043781546	1.160524243	1.38E-06	1.74E-05
Metabolism	Metabolism of Terpenoids and Polyketides	Zeatin biosynthesis	0.050637449	0.06316787	1.59E-06	1.80E-05
Metabolism	Metabolism of Terpenoids and Polyketides	Polyketide sugar unit biosynthesis	0.180538944	0.229048314	1.52E-06	1.84E-05
Metabolism	Lipid Metabolism	Glycerolipid metabolism	0.409338449	0.341139472	1.59E-06	1.87E-05
Metabolism	Lipid Metabolism	Steroid biosynthesis	0.0029158	0.000297703	1.82E-06	1.99E-05
Metabolism	Biosynthesis of Other Secondary Metabolites	Streptomycin biosynthesis	0.291119782	0.356258033	2.45E-06	2.59E-05
Metabolism	Xenobiotics Biodegradation and Metabolism	Benzoate degradation	0.231192641	0.186215215	3.11E-06	3.18E-05

Environmental Information Processing	Membrane Transport	ABC transporters	3.353897919	2.685102156	3.93E-06	3.90E-05
Environmental Information Processing	Membrane Transport	Transporters	6.804091509	5.475459769	4.95E-06	4.77E-05
Genetic Information Processing	Folding, Sorting and Degradation	Protein export	0.594139134	0.648264045	5.43E-06	5.09E-05
Metabolism	Biosynthesis of Other Secondary Metabolites	Phenylpropanoid biosynthesis	0.137420359	0.214570166	7.82E-06	7.12E-05
Genetic Information Processing	Replication and Repair	Non-homologous end-joining	0.010629821	0.003234389	9.79E-06	8.68E-05
Metabolism	Amino Acid Metabolism	Tyrosine metabolism	0.365137979	0.317427035	1.02E-05	8.84E-05
Metabolism	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - ganglio series	0.040188017	0.098638141	1.17E-05	9.59E-05
Metabolism	Glycan Biosynthesis and Metabolism	Glycosaminoglycan degradation	0.061744496	0.129261964	1.22E-05	9.79E-05
Metabolism	Metabolism of Cofactors and Vitamins	Vitamin B6 metabolism	0.18762829	0.218081535	1.17E-05	9.84E-05
Cellular Processes	Transport and Catabolism	Lysosome	0.091931253	0.182508898	1.53E-05	0.000119098
Environmental Information Processing	Signaling Molecules and Interaction	G protein-coupled receptors	0.000798329	2.89E-06	1.62E-05	0.000123355
Genetic Information Processing	Folding, Sorting and Degradation	Protein processing in endoplasmic reticulum	0.061301567	0.08056406	2.35E-05	0.000157628
Metabolism	Metabolism of Other Amino Acids	Cyanoamino acid metabolism	0.268880548	0.347765985	2.26E-05	0.000160834
Metabolism	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - globo series	0.098120426	0.163921707	2.35E-05	0.000160912
Cellular Processes and Signaling	Pores ion channels	Pores ion channels_Unclassified	0.293742038	0.43885303	2.16E-05	0.000161047
Metabolism	Lipid metabolism	Lipid metabolism_Unclassified	0.141364149	0.122548806	2.46E-05	0.000161255
Metabolism	Lipid Metabolism	Biosynthesis of unsaturated fatty acids	0.124138225	0.098046731	2.35E-05	0.000164335

Environmental Information Processing	Membrane Transport	Secretion system	1.227789749	1.040706222	2.26E-05	0.000164409
Genetic Information Processing	Replication, recombination and repair proteins	Replication, recombination and repair proteins_Unclassified	0.858211685	0.738189836	2.68E-05	0.000172227
Metabolism	Xenobiotics Biodegradation and Metabolism	Styrene degradation	0.019128746	0.011399271	2.92E-05	0.000183952
Metabolism	Xenobiotics Biodegradation and Metabolism	Drug metabolism - other enzymes	0.336538936	0.376894017	3.04E-05	0.000188317
Metabolism	Metabolism of Terpenoids and Polyketides	Limonene and pinene degradation	0.099447825	0.070388346	3.17E-05	0.000189332
Metabolism	Lipid Metabolism	Fatty acid biosynthesis	0.494227037	0.447244295	3.17E-05	0.000192838
Metabolism	Metabolism of Terpenoids and Polyketides	Carotenoid biosynthesis	0.007342797	0.001980194	3.31E-05	0.00019399
Metabolism	Xenobiotics Biodegradation and Metabolism	Toluene degradation	0.06957133	0.112731212	3.45E-05	0.000198808
Metabolism	Metabolism of Other Amino Acids	D-Alanine metabolism	0.113792979	0.100340122	4.83E-05	0.000273037
Metabolism	Lipid Metabolism	Steroid hormone biosynthesis	0.013433594	0.034331272	5.03E-05	0.000279763
Metabolism	Energy Metabolism	Sulfur metabolism	0.249939255	0.292560451	5.47E-05	0.000298786
Metabolism	Others	Others_Unclassified	0.961076661	0.830767134	6.99E-05	0.000363787
Metabolism	Xenobiotics Biodegradation and Metabolism	Atrazine degradation	0.017688348	0.008220562	7.28E-05	0.000367213
Metabolism	Amino acid metabolism	Amino acid metabolism_Unclassified	0.219445138	0.181535888	6.99E-05	0.000369654
Metabolism	Glycan Biosynthesis and Metabolism	Lipopolysaccharide biosynthesis	0.187780926	0.342769933	7.28E-05	0.000372951
Metabolism	Metabolism of Cofactors and Vitamins	One carbon pool by folate	0.639259552	0.708518515	6.99E-05	0.000375714

Metabolism	Amino Acid Metabolism	Glycine, serine and threonine metabolism	0.782842841	0.835584619	7.89E-05	0.000392156
Environmental Information Processing	Signaling Molecules and Interaction	Cellular antigens	0.034707339	0.062035326	8.22E-05	0.000402213
Cellular Processes and Signaling	Membrane and intracellular structural molecules	Membrane and intracellular structural molecules_Unclassified	0.452286178	0.632541188	8.55E-05	0.000406603
Cellular Processes and Signaling	Electron transfer carriers	Electron transfer carriers_Unclassified	0.025627908	0.011436611	8.55E-05	0.000412582
Metabolism	Metabolism of cofactors and vitamins	Metabolism of cofactors and vitamins_Unclassified	0.117951542	0.09629872	9.65E-05	0.000452018
Metabolism	Metabolism of Terpenoids and Polyketides	Prenyltransferases	0.313052158	0.353528052	0.00010447	0.000482642
Organismal Systems	Immune System	NOD-like receptor signaling pathway	0.040986238	0.047685778	0.00011311	0.000515259
Metabolism	Glycan Biosynthesis and Metabolism	N-Glycan biosynthesis	0.017463825	0.028000683	0.00012732	0.000572082
Metabolism	Metabolism of Terpenoids and Polyketides	Biosynthesis of vancomycin group antibiotics	0.056132068	0.069640339	0.00014321	0.000634781
Metabolism	Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - lacto and neolacto series	6.17E-05	0.00054434	0.00015785	0.00069031
Metabolism	Metabolism of Cofactors and Vitamins	Biotin metabolism	0.132709202	0.161231808	0.00016096	0.000694655
Cellular Processes	Cell Motility	Bacterial motility proteins	0.936610418	0.639916435	0.00021892	0.000920585
Environmental Information Processing	Signaling Molecules and Interaction	Ion channels	0.019127789	0.009954262	0.00021892	0.000932541
Metabolism	Glycan Biosynthesis and Metabolism	Lipopolysaccharide biosynthesis proteins	0.289481796	0.457776411	0.00023621	0.000980709
Cellular Processes and Signaling	Sporulation	Sporulation_Unclassified	0.84249665	0.58904795	0.00026456	0.001084679
Metabolism	Energy Metabolism	Oxidative phosphorylation	1.057946406	1.180721178	0.00027469	0.001112339
Human Diseases	Infectious Diseases	African trypanosomiasis	0.002666897	0.000734711	0.00029534	0.00118135

Genetic Information Processing	Transcription	Transcription machinery	0.987673641	1.072278987	0.000319	0.001260618
Cellular Processes	Cell Motility	Bacterial chemotaxis	0.431508405	0.315094351	0.00039815	0.001554672
Genetic Information Processing	Folding, Sorting and Degradation	Sulfur relay system	0.265727757	0.226911726	0.000413	0.001575172
Cellular Processes and Signaling	Other ion-coupled transporters	Other ion-coupled transporters_Unclassified	1.245801799	1.372102083	0.000413	0.001593703
Metabolism	Amino Acid Metabolism	Amino acid related enzymes	1.494165356	1.585098602	0.00044428	0.001674976
Human Diseases	Metabolic Diseases	Type I diabetes mellitus	0.052557211	0.059522355	0.00046073	0.001697974
Metabolism	Carbohydrate Metabolism	Butanoate metabolism	0.645014406	0.597918384	0.00046073	0.001717269
Metabolism	Lipid Metabolism	Lipid biosynthesis proteins	0.580291971	0.615374543	0.00061435	0.002238953
Metabolism	Metabolism of Cofactors and Vitamins	Pantothenate and CoA biosynthesis	0.605554963	0.649333882	0.00070791	0.002551587
Metabolism	Carbohydrate Metabolism	Pyruvate metabolism	1.070516939	1.014785876	0.00073329	0.002614324
Cellular Processes	Cell Motility	Flagellar assembly	0.390861291	0.261292207	0.00090416	0.003188856
Human Diseases	Cancers	Prostate cancer	0.042275251	0.048294468	0.00096886	0.003345125
Metabolism	Energy Metabolism	Carbon fixation pathways in prokaryotes	0.982023214	1.064964733	0.00096886	0.003380711
Genetic Information Processing	Folding, Sorting and Degradation	Ubiquitin system	0.003946542	0.010100526	0.00111132	0.003797024
Metabolism	Metabolism of Cofactors and Vitamins	Nicotinate and nicotinamide metabolism	0.433375527	0.460312225	0.00114985	0.003848469
Metabolism	Metabolism of Other Amino Acids	D-Glutamine and D-glutamate metabolism	0.147396605	0.157950454	0.00114985	0.003888144
Genetic Information Processing	Translation	Translation factors	0.548362337	0.592788063	0.00160894	0.005330645
Metabolism	Carbohydrate Metabolism	Galactose metabolism	0.743385672	0.840382018	0.00166311	0.005401005
Metabolism	Biosynthesis of Other Secondary Metabolites	Penicillin and cephalosporin biosynthesis	0.01851142	0.026753236	0.00166311	0.005455015
Metabolism	Nucleotide metabolism	Nucleotide metabolism_Unclassified	0.055915167	0.039018877	0.00202494	0.006448341
Organismal Systems	Nervous System	Glutamatergic synapse	0.102242629	0.113308157	0.00202494	0.00651156

Cellular Processes and Signaling	Cell motility and secretion	Cell motility and secretion_Unclassified	0.156012914	0.177172443	0.00238018	0.007506727
Genetic Information Processing	Transcription related proteins	Transcription related proteins_Unclassified	0.008996014	0.003207203	0.00270451	0.008368661
Metabolism	Metabolism of Cofactors and Vitamins	Folate biosynthesis	0.368411336	0.408440404	0.00270451	0.008448362
Genetic Information Processing	Replication and Repair	DNA replication proteins	1.268856506	1.369339111	0.00279166	0.00855762
Metabolism	Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	1.430317136	1.533075532	0.00288138	0.00875085
Metabolism	Nucleotide Metabolism	Purine metabolism	2.210420262	2.310734929	0.00297372	0.008948431
Metabolism	Energy Metabolism	Nitrogen metabolism	0.671722678	0.718368631	0.00306875	0.009150448
Cellular Processes and Signaling	Cell division	Cell division_Unclassified	0.073248891	0.084431444	0.00393457	0.011626472
Metabolism	Carbohydrate Metabolism	Citrate cycle (TCA cycle)	0.577708482	0.659750922	0.00418316	0.012250681
Genetic Information Processing	Translation	RNA transport	0.139695272	0.124445051	0.00431272	0.01251835
Poorly Characterized	General function prediction only	General function prediction only_Unclassified	3.633374312	3.708688084	0.00444592	0.012791761
Metabolism	Carbohydrate Metabolism	Pentose and glucuronate interconversions	0.51601371	0.597678548	0.00458283	0.012958337
Metabolism	Carbohydrate Metabolism	Starch and sucrose metabolism	1.022160883	1.129995831	0.00458283	0.013071018
Metabolism	Carbohydrate Metabolism	Glyoxylate and dicarboxylate metabolism	0.480186381	0.53117868	0.00472354	0.013242071
Metabolism	Amino Acid Metabolism	Tryptophan metabolism	0.142340727	0.119116853	0.00501677	0.013944924
Metabolism	Metabolism of Terpenoids and Polyketides	Geraniol degradation	0.035050084	0.045860171	0.00516947	0.014248629
Metabolism	Metabolism of Cofactors and Vitamins	Riboflavin metabolism	0.241171707	0.265082582	0.00548754	0.014999268
Genetic Information Processing	Replication and Repair	Chromosome	1.594254415	1.673155919	0.00636136	0.017244015
Metabolism	Glycan Biosynthesis and Metabolism	Various types of N-glycan biosynthesis	3.81E-05	0	0.00666901	0.017929798

Environmental Information Processing	Signal Transduction	Two-component system	1.374206397	1.230958198	0.00674461	0.017985629
Metabolism	Biosynthesis of Other Secondary Metabolites	Isoquinoline alkaloid biosynthesis	0.054711653	0.063245923	0.00802197	0.021219412
Human Diseases	Infectious Diseases	Pertussis	0.026869741	0.033017479	0.00825476	0.021660499
Metabolism	Lipid Metabolism	Arachidonic acid metabolism	0.03503018	0.024033843	0.00924753	0.024072935
Environmental Information Processing	Signal Transduction	MAPK signaling pathway - yeast	0.045348535	0.055969122	0.01006064	0.025983396
Genetic Information Processing	Replication and Repair	Homologous recombination	0.962618154	1.027911781	0.01063751	0.027047311
Metabolism	Lipid Metabolism	Fatty acid metabolism	0.231738391	0.216530704	0.01063751	0.027258618
Cellular Processes	Cell Growth and Death	Cell cycle - Caulobacter	0.505273594	0.534135043	0.011558	0.029161728
Human Diseases	Infectious Diseases	Chagas disease (American trypanosomiasis)	0.002197771	0.000483442	0.0123694	0.030970723
Organismal Systems	Immune System	RIG-I-like receptor signaling pathway	0.002649388	0.000865093	0.01303269	0.03238426
Metabolism	Xenobiotics Biodegradation and Metabolism	Polycyclic aromatic hydrocarbon degradation	0.110603077	0.118869447	0.01398574	0.034491146
Metabolism	Lipid Metabolism	Synthesis and degradation of ketone bodies	0.033189959	0.025365424	0.01515715	0.037101075
Human Diseases	Immune System Diseases	Primary immunodeficiency	0.042635702	0.048135814	0.0159853	0.038271382
Metabolism	Lipid Metabolism	Secondary bile acid biosynthesis	0.031326436	0.038333618	0.0159853	0.03855279
Metabolism	Metabolism of Cofactors and Vitamins	Ubiquinone and other terpenoid-quinone biosynthesis	0.144230428	0.190214997	0.0159853	0.038838366
Metabolism	Glycan Biosynthesis and Metabolism	Glycosyltransferases	0.316660925	0.339206435	0.01641411	0.03901324
Metabolism	Lipid Metabolism	Primary bile acid biosynthesis	0.031566202	0.038367135	0.018232	0.042714978
Metabolism	Xenobiotics Biodegradation and Metabolism	Naphthalene degradation	0.156466359	0.127935702	0.018232	0.04302228
Metabolism	Enzyme Families	Protein kinases	0.280972645	0.252174517	0.01871314	0.043531274

Metabolism	Nucleotide Metabolism	Pyrimidine metabolism	1.88636841	1.992525764	0.01970883	0.045524627
Environmental Information Processing	Signal Transduction	Phosphatidylinositol signaling system	0.084355738	0.092563825	0.02022381	0.046387473
Cellular Processes and Signaling	Germination	Germination_Unclassified	0.046703617	0.033567269	0.02128908	0.048157359
Metabolism	Amino Acid Metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	0.785584291	0.83916953	0.02128908	0.048491785
Environmental Information Processing	Membrane Transport	Bacterial secretion system	0.586756878	0.609760756	0.02183981	0.049064768

Table S7. Comparison of dietary habits of centenarians from community-dwelling and rehabilitation hospital.

	Community-dwelling	Rehabilitation hospital	<i>p</i> value
Subjects (n)	18	7	
Number of meals (per day)	2.78 ± 0.43	3.00 ± 0.00	0.182
Number of snacks (per day)	0.81 ± 0.79	1.71 ± 0.49	0.012
Frequency of intake (per month)	Community-dwelling	Rehabilitation hospital	<i>p</i> value
Subjects (n)	18	4	
Meat	8.2 ± 20.8	37.5 ± 15.0	0.005
Eggs	7.0 ± 7.2	12.9 ± 12.1	0.345
Fish	6.7 ± 7.6	18.2 ± 13.7	0.086
Bean curds	8.9 ± 9.8	29.5 ± 13.1	0.012
Fermented soybean pastes	23.2 ± 25.0	53.0 ± 25.0	0.054
Dairy products	6.7 ± 9.7	4.3 ± 8.6	0.395
Fruits	14.6 ± 13.4	4.3 ± 8.6	0.073
Eat protein	30.9 ± 28.2	98.0 ± 17.2	0.005

Figure S2. Frequently detected genera among groups. Genera that comprised more than 0.5% of all subjects were selected and compared. The significance of the differences between groups was tested using the Mann-Whitney test. L_C, centenarians in longevity villages; L_E, elderly in longevity villages; L_A, adults in longevity villages; U_E, elderly in urbanized town; U_A, adults in urbanized town. (***) $p < 0.001$; ** $p < 0.01$; * $p < 0.05$).

