

Potential of Inactivated *Bifidobacterium* Strain in Attenuating Benzo(A)Pyrene Exposure-Induced Damage in Colon Epithelial Cells In Vitro

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Table S1. GO classification of DEGs between Control and BI-04 (Cell Component) .

Gene Ontology Term	Cluster Frequency	Corrected P-value
nucleus	93 out of 264 genes, 35.2%	0.00042
intracellular membrane-bounded organelle	182 out of 264 genes, 68.9%	0.00863
membrane-bounded organelle	189 out of 264 genes, 71.6%	0.00997
extracellular space	10 out of 264 genes, 3.8%	0.03126
mitotic cohesin complex	2 out of 264 genes, 0.8%	0.04794

Table S2. GO classification of DEGs between Control and BI-04 (Biological Process) .

Gene Ontology Term	Cluster Frequency	Corrected P-value
RNA metabolic process	94 out of 249 genes, 37.8%	0.00046
organic cyclic compound metabolic process	118 out of 249 genes, 47.4%	0.00198
nucleic acid metabolic process	101 out of 249 genes, 40.6%	0.00226
RNA biosynthetic process	77 out of 249 genes, 30.9%	0.00305
nucleobase-containing compound biosynthetic process	81 out of 249 genes, 32.5%	0.00317
organic cyclic compound biosynthetic process	83 out of 249 genes, 33.3%	0.00408
aromatic compound biosynthetic process	81 out of 249 genes, 32.5%	0.00488
cellular nitrogen compound biosynthetic process	82 out of 249 genes, 32.9%	0.00541
heterocycle biosynthetic process	81 out of 249 genes, 32.5%	0.00565
nitrogen compound metabolic process	122 out of 249 genes, 49.0%	0.00658
cellular aromatic compound metabolic process	112 out of 249 genes, 45.0%	0.00955
transcription, DNA-templated	74 out of 249 genes, 29.7%	0.01589
cellular nitrogen compound metabolic process	112 out of 249 genes, 45.0%	0.02414
nucleobase-containing compound metabolic process	107 out of 249 genes, 43.0%	0.03089
heterocycle metabolic process	109 out of 249 genes, 43.8%	0.0341

Table S3. The up-regulated genes and down-regulated genes in cell components between Control and BI-04.

Up-regulated EDGs		Down-regulated EDGs	
GO:0005615	extracellular space	GO:0005794	Golgi apparatus
GO:0005886	plasma membrane	GO:0005813	centrosome
GO:0000922	spindle pole	GO:0000139	Golgi membrane

GO:0000932	cytoplasmic mRNA processing body	GO:0005887	integral component of plasma membrane
GO:0001725	stress fiber	GO:0030529	intracellular ribonucleoprotein complex
GO:0005578	proteinaceous extracellular matrix	GO:0043232	intracellular non-membrane-bounded organelle
GO:0005681	spliceosomal complex		
GO:0005764	lysosome		
GO:0005777	peroxisome		
GO:0005787	signal peptidase complex		

Table S4. The up-regulated genes and down-regulated genes in biological process between Control and BI-04.

Up-regulated EDGs		Down-regulated EDGs	
GO:0001666	response to hypoxia	GO:0007067	mitotic nuclear division
GO:0006412	translation	GO:0007154	Cell communication
GO:0009267	cellular response to starvation	GO:0015031	protein transport
GO:0009636	response to toxic substance	GO:0006468	protein phosphorylation
GO:0044093	positive regulation of molecular function	GO:0007155	cell adhesion
GO:0000209	protein polyubiquitination		

Table S5. GO classification of DEGs between Control and BaP (cell component) .

Gene Ontology term	Cluster frequency	Corrected P-value
cell	818 out of 905 genes, 90.4%	1.21E-11
cell part	818 out of 905 genes, 90.4%	1.21E-11
intracellular	761 out of 905 genes, 84.1%	7.77E-10
intracellular part	753 out of 905 genes, 83.2%	9.92E-09
nucleus	284 out of 905 genes, 31.4%	1.67E-07
cytoplasm	422 out of 905 genes, 46.6%	2.36E-06
endomembrane system	177 out of 905 genes, 19.6%	2.38E-06
membrane-bounded organelle	624 out of 905 genes, 69.0%	2.62E-06
organelle	671 out of 905 genes, 74.1%	4.88E-06
intracellular organelle	651 out of 905 genes, 71.9%	7.67E-06
intracellular membrane-bounded organelle	595 out of 905 genes, 65.7%	1.14E-05
intracellular organelle part	392 out of 905 genes, 43.3%	0.00015
cytoplasmic part	375 out of 905 genes, 41.4%	0.00021
endoplasmic reticulum	64 out of 905 genes, 7.1%	0.00026
organelle part	422 out of 905 genes, 46.6%	0.00074
cell junction	56 out of 905 genes, 6.2%	0.0008
non-membrane-bounded organelle	219 out of 905 genes, 24.2%	0.00083
intracellular non-membrane-bounded organelle	219 out of 905 genes, 24.2%	0.00083
nuclear part	223 out of 905 genes, 24.6%	0.00213

cytoskeletal part	84 out of 905 genes, 9.3%	0.00215
cytoskeleton	125 out of 905 genes, 13.8%	0.0024
membrane region	49 out of 905 genes, 5.4%	0.00266
protein complex	196 out of 905 genes, 21.7%	0.00305
intracellular organelle lumen	211 out of 905 genes, 23.3%	0.01002
membrane-enclosed lumen	212 out of 905 genes, 23.4%	0.0107
organelle lumen	211 out of 905 genes, 23.3%	0.01222
cytosol	65 out of 905 genes, 7.2%	0.01571
Golgi apparatus	53 out of 905 genes, 5.9%	0.01996
postsynaptic membrane	9 out of 905 genes, 1.0%	0.02136
nuclear lumen	199 out of 905 genes, 22.0%	0.02563
chromosome	61 out of 905 genes, 6.7%	0.02663
cell-cell junction	29 out of 905 genes, 3.2%	0.03436
inclusion body	9 out of 905 genes, 1.0%	0.03531
centrosome	24 out of 905 genes, 2.7%	0.03838
microtubule cytoskeleton	77 out of 905 genes, 8.5%	0.03859
bounding membrane of organelle	78 out of 905 genes, 8.6%	0.04544

Table S6. GO classification of DEGs between Control and BaP (Molecular Function) .

Gene Ontology term	Cluster frequency	Corrected P-value
binding	753 out of 849 genes, 88.7%	2.81E-06
protein binding	392 out of 849 genes, 46.2%	0.00022
ion binding	321 out of 849 genes, 37.8%	0.00111
enzyme binding	98 out of 849 genes, 11.5%	0.00165
zinc ion binding	49 out of 849 genes, 5.8%	0.00398
metal ion binding	227 out of 849 genes, 26.7%	0.00444
DNA binding	107 out of 849 genes, 12.6%	0.00481
sequence-specific DNA binding RNA polymerase II transcription factor activity	31 out of 849 genes, 3.7%	0.01864
sequence-specific DNA binding transcription factor activity	45 out of 849 genes, 5.3%	0.01921
transition metal ion binding	156 out of 849 genes, 18.4%	0.0249
mannosyl-oligosaccharide mannosidase activity	5 out of 849 genes, 0.6%	0.03075
protein heterodimerization activity	14 out of 849 genes, 1.6%	0.03937
anion binding	87 out of 849 genes, 10.2%	0.04402

Table S7. GO classification of DEGs between Control and BaP (Biological Process) .

Gene Ontology term	Cluster frequency	Corrected P-value
nervous system development	131 out of 861 genes, 15.2%	2.02E-06
regulation of cellular macromolecule biosynthetic process	113 out of 861 genes, 13.1%	1.22E-05
multicellular organismal development	265 out of 861 genes, 30.8%	1.93E-05
regulation of transcription, DNA-templated	104 out of 861 genes, 12.1%	2.46E-05
regulation of nitrogen compound metabolic process	140 out of 861 genes, 16.3%	3.49E-05
regulation of nucleobase-containing compound metabolic process	138 out of 861 genes, 16.0%	3.93E-05
cardiovascular system development	68 out of 861 genes, 7.9%	4.38E-05

circulatory system development	68 out of 861 genes, 7.9%	4.38E-05
system development	241 out of 861 genes, 28.0%	5.03E-05
single-organism developmental process	305 out of 861 genes, 35.4%	8.00E-05
regulation of RNA biosynthetic process	105 out of 861 genes, 12.2%	9.04E-05
anatomical structure development	278 out of 861 genes, 32.3%	0.00015
regulation of RNA metabolic process	106 out of 861 genes, 12.3%	0.00015
regulation of macromolecule biosynthetic process	121 out of 861 genes, 14.1%	0.00016
regulation of biosynthetic process	127 out of 861 genes, 14.8%	0.00027
positive regulation of cellular process	163 out of 861 genes, 18.9%	0.00031
cell differentiation	175 out of 861 genes, 20.3%	0.00047
organic substance biosynthetic process	311 out of 861 genes, 36.1%	0.00056
regulation of cellular biosynthetic process	119 out of 861 genes, 13.8%	0.00063
neuron differentiation	65 out of 861 genes, 7.5%	0.00064
biosynthetic process	315 out of 861 genes, 36.6%	0.00088
macromolecule biosynthetic process	273 out of 861 genes, 31.7%	0.00091
regulation of cellular metabolic process	200 out of 861 genes, 23.2%	0.00098
cell development	86 out of 861 genes, 10.0%	0.00104
primary metabolic process	543 out of 861 genes, 63.1%	0.00134
positive regulation of cellular metabolic process	97 out of 861 genes, 11.3%	0.00153
cellular macromolecule biosynthetic process	268 out of 861 genes, 31.1%	0.00154
negative regulation of cell differentiation	34 out of 861 genes, 3.9%	0.00155
response to endogenous stimulus	87 out of 861 genes, 10.1%	0.00176
positive regulation of metabolic process	106 out of 861 genes, 12.3%	0.00184
anatomical structure morphogenesis	143 out of 861 genes, 16.6%	0.00197
transcription, DNA-templated	216 out of 861 genes, 25.1%	0.002
generation of neurons	78 out of 861 genes, 9.1%	0.00244
negative regulation of developmental process	38 out of 861 genes, 4.4%	0.00271
RNA biosynthetic process	217 out of 861 genes, 25.2%	0.00275
regulation of primary metabolic process	189 out of 861 genes, 22.0%	0.00304
cellular biosynthetic process	301 out of 861 genes, 35.0%	0.00325
cellular macromolecule metabolic process	415 out of 861 genes, 48.2%	0.00345
single-multicellular organism process	332 out of 861 genes, 38.6%	0.00355
regulation of metabolic process (view genes)	230 out of 861 genes, 26.7%	0.00415
neurogenesis	81 out of 861 genes, 9.4%	0.00432
developmental process	317 out of 861 genes, 36.8%	0.00433
cellular developmental process	194 out of 861 genes, 22.5%	0.00472
regulation of cell differentiation	63 out of 861 genes, 7.3%	0.0052
protein modification process	171 out of 861 genes, 19.9%	0.00613
cell cycle	110 out of 861 genes, 12.8%	0.0065
organic substance metabolic process	559 out of 861 genes, 64.9%	0.00685
macromolecule modification	177 out of 861 genes, 20.6%	0.00894
cellular protein modification process	168 out of 861 genes, 19.5%	0.00974
regulation of macromolecule metabolic process	182 out of 861 genes, 21.1%	0.01018
organic cyclic compound biosynthetic process	234 out of 861 genes, 27.2%	0.01179
negative regulation of cellular process	132 out of 861 genes, 15.3%	0.01228
positive regulation of gene expression	41 out of 861 genes, 4.8%	0.01263

positive regulation of nitrogen compound metabolic process	47 out of 861 genes, 5.5%	0.01325
cellular component organization	266 out of 861 genes, 30.9%	0.01638
cell cycle process	96 out of 861 genes, 11.1%	0.01677
positive regulation of biological process	182 out of 861 genes, 21.1%	0.01906
positive regulation of nucleobase-containing compound metabolic process	46 out of 861 genes, 5.3%	0.01986
vasculature development	44 out of 861 genes, 5.1%	0.02144
positive regulation of transcription, DNA-templated	38 out of 861 genes, 4.4%	0.02295
cellular component morphogenesis	62 out of 861 genes, 7.2%	0.02363
positive regulation of macromolecule metabolic process	88 out of 861 genes, 10.2%	0.02569
regulation of transcription from RNA polymerase II promoter	51 out of 861 genes, 5.9%	0.0279
cellular component organization or biogenesis	272 out of 861 genes, 31.6%	0.02807
cellular metabolic process	526 out of 861 genes, 61.1%	0.02819
nucleic acid metabolic process	287 out of 861 genes, 33.3%	0.02979
positive regulation of RNA biosynthetic process	38 out of 861 genes, 4.4%	0.0386
nucleobase-containing compound biosynthetic process	223 out of 861 genes, 25.9%	0.04117
aromatic compound biosynthetic process	225 out of 861 genes, 26.1%	0.04186
axon guidance	18 out of 861 genes, 2.1%	0.04192
neuron projection guidance	18 out of 861 genes, 2.1%	0.04192

Table S8. The up-regulated genes and down-regulated genes in cell components between Control and BaP.

Up-regulated EDGs		Down-regulated EDGs	
GO:0000932	cytoplasmic mRNA processing body	GO:0005813	centrosome
GO:0005669	transcription factor TFIID complex	GO:0005794	Golgi apparatus
GO:0005776	autophagosome	GO:0097060	synaptic membrane
GO:0005844	polysome	GO:0030054	cell junction
GO:0005849	mRNA cleavage factor complex	GO:0005764	lysosome
GO:0005891	voltage-gated calcium channel complex	GO:0005769	early endosome
GO:0031074	nucleocytoplasmic shuttling complex	GO:0016323	basolateral plasma membrane
GO:0031201	SNARE complex	GO:0031965	nuclear membrane
GO:0031225	anchored component of membrane		
GO:0034704	calcium channel complex		

Table S9. The up-regulated genes and down-regulated genes in molecular function between Control and BaP.

Up-regulated EDGs	Down-regulated EDGs
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GO:0016209	antioxidant activity	GO:0008092	cytoskeletal protein binding
GO:0003729	mRNA binding	GO:0005543	phospholipid binding
GO:000495	dopamine neurotransmitter receptor activity	GO:0017016	Ras GTPase binding
GO:0008106	alcohol dehydrogenase (NADP+) activity	GO:0003774	motor activity
GO:0008408	3'-5' exonuclease activity	GO:0005509	calcium ion binding
GO:0009055	electron carrier activity	GO:0005539	glycosaminoglycan binding
GO:0003684	damaged DNA binding	GO:0000287	magnesium ion binding
GO:0005035	death receptor activity		

Table S10. The up-regulated genes and down-regulated genes in biological process between Control and BaP.

Up-regulated EDGs		Down-regulated EDGs	
GO:0001523	retinoid metabolic process	GO:0007599	hemostasis
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	GO:0007067	mitotic nuclear division
GO:0009267	cellular response to starvation	GO:0019538	protein metabolic process
GO:0009812	flavonoid metabolic process	GO:0000087	mitotic M phase
GO:0030647	aminoglycoside antibiotic metabolic process	GO:0006886	intracellular protein transport
GO:0000060	protein import into nucleus, translocation	GO:0019827	stem cell population maintenance
GO:0048167	regulation of synaptic plasticity	GO:0006928	movement of cell or subcellular component
GO:0006304	DNA modification	GO:0016337	single organismal cell-cell adhesion
GO:0009753	response to jasmonic acid	GO:0040007	growth
GO:0072331	signal transduction by p53 class mediator	GO:0001935	endothelial cell proliferation

Table S11. GO classification of DEGs between BaP and BI-04+BaP (Cell Component) .

Gene Ontology term	Cluster frequency	Corrected P-value
nucleus	28 out of 62 genes, 45.2%	0.00686
nucleoplasm	11 out of 62 genes, 17.7%	0.02477

Table S12. GO classification of DEGs between BaP and BI-04+BaP (Molecular Function) .

Gene Ontology term	Cluster frequency	Corrected P-value
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metal ion bindin	24 out of 57 genes, 42.1%	0.01861
ion binding	30 out of 57 genes, 52.6%	0.03843

Table 13. GO classification of DEGs between BaP and BI-04+BaP (Biological Process) .

Gene Ontology term	Cluster frequency	Corrected P-value
cellular macromolecule metabolic process	38 out of 54 genes, 70.4%	0.00381
macromolecule metabolic process	41 out of 54 genes, 75.9%	0.00484
cellular metabolic process	44 out of 54 genes, 81.5%	0.0108
nitrogen compound metabolic process	34 out of 54 genes, 63.0%	0.01454
metabolic process	47 out of 54 genes, 87.0%	0.01676
primary metabolic process	44 out of 54 genes, 81.5%	0.0192
organic substance metabolic process	45 out of 54 genes, 83.3%	0.02231
organic cyclic compound metabolic process	32 out of 54 genes, 59.3%	0.03169
heterocycle metabolic process	31 out of 54 genes, 57.4%	0.03385
nucleic acid metabolic process	28 out of 54 genes, 51.9%	0.04035
cellular aromatic compound metabolic process	31 out of 54 genes, 57.4%	0.0411

Table S14. The up-regulated genes and down-regulated genes in cell components between BaP and BI-04+BaP.

Up-regulated EDGs		Down-regulated EDGs	
GO:0016020	membrane		mitochondrial proton-transporting
GO:0005681	spliceosomal complex	GO:0000276	ATP synthase complex, coupling factor F(o)
GO:0000812	Swr1 complex	GO:0000139	Golgi membrane
		GO:0000777	condensed chromosome kinetochore
		GO:0005769	early endosome
		GO:0030529	intracellular ribonucleoprotein complex
		GO:0043232	intracellular non-membrane-bounded organelle
		GO:0019866	organelle inner membrane

Table S15. The up-regulated genes and down-regulated genes in molecular function between BaP and BI-04+BaP.

Up-regulated EDGs		Down-regulated EDGs	
GO:0008270	zinc ion binding	GO:0004623	phospholipase A2 activity protein
GO:0016859	cis-trans isomerase activity	GO:0004661	geranylgeranyltransferase activity
GO:0019904	protein domain specific binding	GO:0005506	iron ion binding
GO:0042802	identical protein binding	GO:0043168	phospholipid binding
GO:0001071	nucleic acid binding transcription factor activity	GO:0008135	translation factor activity, RNA binding
GO:0003824	catalytic activity	GO:0008417	fucosyltransferase activity
GO:0019900	kinase binding	GO:0008757	

GO:0032550	purine ribonucleoside binding		S-adenosylmethionine-dependent methyltransferase activity
GO:0036094	small molecule binding	GO:0016702	oxidoreductase activity
		GO:0016811	hydrolase activity

Table S16. The up-regulated genes and down-regulated genes in biological process between BaP and BI-04+BaP.

Up-regulated EDGs		Down-regulated EDGs	
GO:0006355	regulation of transcription, DNA-templated	GO:0000723	telomere maintenance
GO:0006366	transcription from RNA polymerase II promoter	GO:0001501	skeletal system development
GO:0006915	apoptotic process	GO:0001558	regulation of cell growth
GO:0000377	RNA splicing	GO:0006468	protein phosphorylation
GO:0008283	cell proliferation	GO:0007155	cell adhesion
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	GO:0001666	response to hypoxia
		GO:0001676	long-chain fatty acid metabolic process
		GO:0002761	regulation of myeloid leukocyte differentiation
		GO:0006658	phosphatidylserine metabolic process
		GO:0006952	defense response