

1 **Table S1.** Primers used in the study of gene expression in *E. coli* O157:H7.

Gene name	Primer	Primer sequence (5'-3')
<i>lpxC</i>	<i>lpxC</i> -F	ATTCCAGCAACCAGCGCTAT
	<i>lpxC</i> -R	CGATGGCACAATCGAAGCTG
<i>lpxH</i>	<i>lpxH</i> -F	GCGAACAGCAAAGAAGCCAA
	<i>lpxH</i> -R	GATAAGTTCATGCACCGCCG
<i>fabA</i>	<i>fabA</i> -F	GCAATTGCCAGCACCGAAC
	<i>fabB</i> -R	CGCGCGGCCTTTACCTTC
<i>accA</i>	<i>accA</i> -F	TTGCGCAACTGGCACGCCAT
	<i>accA</i> -R	GGCGCTGGCATAACCAAAGTT
<i>cyoA</i>	<i>cyoA</i> -F	CGGCACTTATGACGGTATCTC
	<i>cyoA</i> -R	TCCACCTGGTTGTATTCGCTA
<i>cyoC</i>	<i>cyoC</i> -F	GATGGCGGTGCTGATGGT
	<i>cyoC</i> -R	CACATCCAGGAAGTGCCAGA
<i>flgC</i>	<i>flgC</i> -F	CGTTGATGTTGTCTGGAGAGAT
	<i>flgC</i> -R	CGTAAGGGTTTTTCAGCATCAT
<i>flgD</i>	<i>flgD</i> -F	TCTGACTTTGTTGGTGGCG
	<i>flgD</i> -R	CGACTGGCTGTTATCAATCTGT
<i>pgaA</i>	<i>pgaA</i> -F	CGTCGCTTATCGTAACCTGC
	<i>pgaA</i> -R	CGCAGTATCATAGTGACCAGCA
<i>pgaB</i>	<i>pgaB</i> -F	TGTTCCACGATGATGCTTTG
	<i>pgaB</i> -R	TCGAATTTCTGCTCAGACTCC
<i>dnaE</i>	<i>dnaE</i> -F	ATGTCCGAGGCGTAAGGCT
	<i>dnaE</i> -R	TCCAGGGCGTCAGTAAACAA

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3 **Table S2.** KEGG enriched pathways of DEGs treated with RL.

KEGG ID	Pathway	Gene name	Count	p-adj
Up-regulated pathways				
eco03010	Ribosome	<i>rpsJ/rplC/rplW/rplD/rplI/rpsS/rplB/rpsF/rpsC/rplV/ykgO/rplF/rpsE/rplO/rpsH/rpmD/rpsR/rp mC/rpsQ/rplK/rpsN/rplP/rplA/rplR/rplJ/rplE/rpsM/rplQ/rpsI/rpsK/rplN/rplL/rpsD/rpsB/rpl M/rplX/rpsA/rpsG/rplS/rpmJ/rpmH/rpmB/rplU/rplY/rpmA/rpsT/rpsO/rpsL/rpsU/rplT/rpmI/ rpsP/rpmF/rpmG/rpmE</i>	55	2.31×10 ⁻³²
eco00540	Lipopolysaccharide biosynthesis	<i>lpxP/lpxK/waaA/lpxB/eptB/lpxM/arnT/eptA/waaG/rfaQ/kdsA/lpxH/lpxD/lpxA/eptC/rfaC/rfa P/waaO/lpxC/lpxT/gmhB/rfaF/kdsC/rfaD</i>	24	1.1×10 ⁻⁴
eco03070	Bacterial secretion system	<i>secY/yidC/secE/secG/secF/secA/secD/ffh/yajC/ftsY/gspK/secM/tatC/tatB/gspJ/tatE/tolC/gspL/e scC</i>	19	4.5×10 ⁻⁴
eco03440	Homologous recombination	<i>priB/dnaN/recO/dnaE/priA/ssb1/dnaX/hoI/recR/ruvC/recB/recA/hoI/recF/recG/recJ/dnaT/h olB/ruvB/recD</i>	20	4.5×10 ⁻⁴
eco00541	O-Antigen nucleotide sugar biosynthesis	<i>cpsG/ugd/galF/gmd/wecC/wecB/rffG/rffC/rfbA/rffA/galU</i>	14	4.5×10 ⁻⁴
eco03060	Protein export	<i>secY/yidC/secE/secG/secF/secA/secD/ffh/yajC/ftsY/secM/tatC/lepB/tatB/tatE</i>	15	6.0×10 ⁻⁴
eco00970	Aminoacyl-tRNA biosynthesis	<i>thrS/metG/glyS/hisS/aspS/lysS/glyQ/argS/cysS/proS/pheS/leuS/alaS/gltX/asnS/pheT/fmt</i>	17	0.01
eco03018	RNA degradation	<i>deaD/pnp/rhlE/rnr/rho/pcnB/recQ/rne/rhlB/eno</i>	10	0.02
eco00061	Fatty acid biosynthesis	<i>fabH/fabA/accC/fabD/fadD/accA/accD/accB</i>	8	0.02
eco00670	One carbon pool by folate	<i>purN/purH/glyA/folD/thyA/purU/fau/folA/gcvT/fmt</i>	10	0.02
eco00190	Oxidative phosphorylation	<i>yoA/cyoB/nuoN/sdhC/nuoM/cyoC/cyoE/ppa/cyoD/nuoL/nuoJ/atpH/atpB/atpC/atpG/atpF/atp A/atpD/sdhD/atpE/nuoI/nuoH/nuoK/nuoG</i>	24	0.04
Down-regulated pathways				
eco01120	Microbial metabolism in diverse environments	<i>sseA/napA/fucO/ldhA/pflB/frdB/frdA/hybO/frdC/narG/mgsA/hchA/agp/aldB/pdxI/kdgK/gapA /frdD/tdcE/fbaB/cysQ/nifJ/yeaD/fumB/pyk/lysA/fumC/fucA/adhE/allC/allD/ulaC/ulaE/hybC/p ta/narH/tkt/ackA/torA/ulaA/lysC/yihX/hemL/tkt/ydiF/fumB/torZ/rhaB/pfkB/torD/allB/tal/glk/</i>	93	2.13×10 ⁻⁸

		<i>ulaF/ulaD/narI/patD/xdhA/cadA/dmpG/maeB/narZ/glxK/ulaG/ahr/nrfA/yggF/ulaB/nfsA/csiD/hcaE/mhpD/eutG/ltaE/yihR/hyaA/cysN/gpmM/ybhJ/cysC/mhpB/galM/aceF/ppsA/thrB/narI/gabD/hcaD/eutE/asd/mhpC/hyaB/rhmD</i>		
eco00040	Pentose and glucuronate interconversions	<i>uxuB/uxuA/uxaC/araA/uxaB/xylA/uxaA/fucA/ulaE/araB/xylB/rhaB/kduI/ulaF/ulaD/kduD</i>	16	2.2×10 ⁻⁴
eco00620	Pyruvate metabolism	<i>ldhA/pflB/frdB/frdA/frdC/hchA/aldB/frdD/tdcE/nifJ/fumB/pyk/fumC/adhE/pta/ackA/fumB/pta/poxB/maeB/ahr/eutG/aceF/ppsA/maeA/eutE</i>	26	3.0×10 ⁻³
eco00053	Ascorbate and aldarate metabolism	<i>garD/ulaC/ulaE/ulaA/gudD/ulaF/ulaD/lgoD/ulaG/ulaB</i>	10	3.0×10 ⁻³
eco00052	Galactose metabolism	<i>agaV/kbaZ/melA/galT/pfkB/glk/agaI/galK/gatZ/yihR/gatY/galM</i>	12	3.0×10 ⁻³
eco00010	Glycolysis / Gluconeogenesis	<i>malX/agp/aldB/gapA/fbaB/nifJ/yeaD/pyk/adhE/yihX/pfkB/glk/ascF/ahr/yggF/eutG/yihR/ascB/gpmM/galM/aceF/ppsA</i>	22	3.0×10 ⁻³
eco02060	Phosphotransferase system (PTS)	<i>malX/mtlA/cmtA/agaV/ulaC/murP/treB/ulaA/nagE/ascF/ulaB/srIE/cmtB</i>	13	0.01
eco00650	Butanoate metabolism	<i>pflB/frdB/frdA/frdC/frdD/tdcE/nifJ/adhE/ydiF/ilvM/yihU/dmlA/ilvN/gabD</i>	14	0.01
eco00051	Fructose and mannose metabolism	<i>mtlA/fbaB/mak/xylA/cmtA/fucA/rhaB/pfkB/mtlD/sorE/hxpA/yggF/srIE/cmtB/rhmD</i>	15	0.05

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