

Supporting information

Enhancing Pulp Regeneration through Metabolic Reprogramming of Mature Dental Pulp Stem Cells Mediated by GLUT1/HK2 mRNA Delivery

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Results

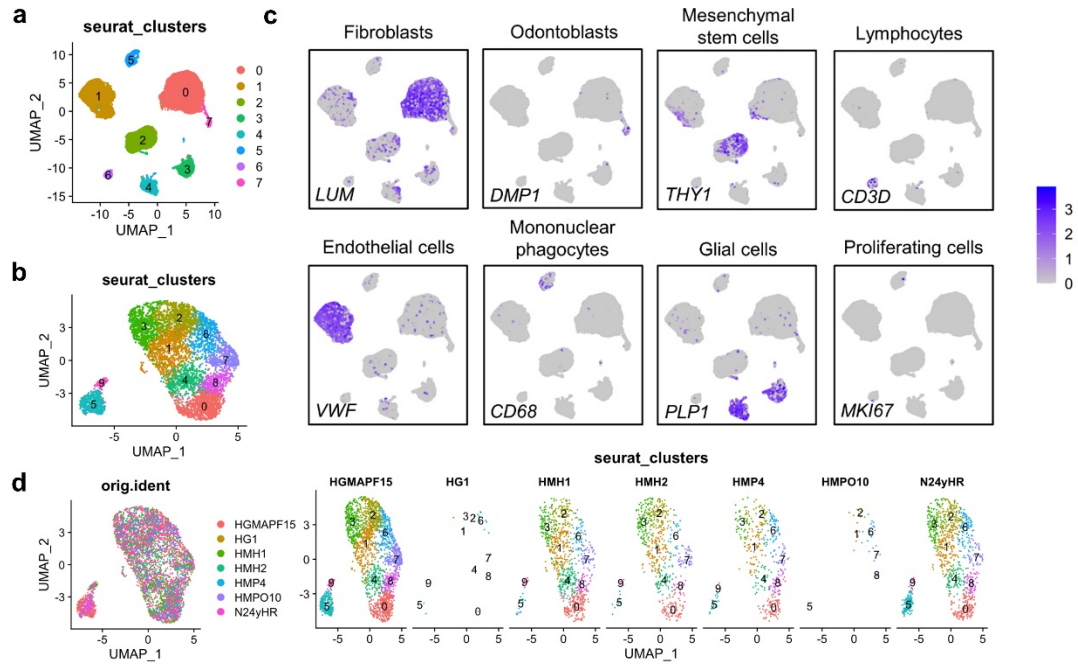


Figure S1. Gene expression landscape of scRNA-seq dataset (GEO: GSE146123). **(a-c)**: Unbiased identification of dental cell types and subpopulations. **(d)**: UMAP plots colored by sample origin.

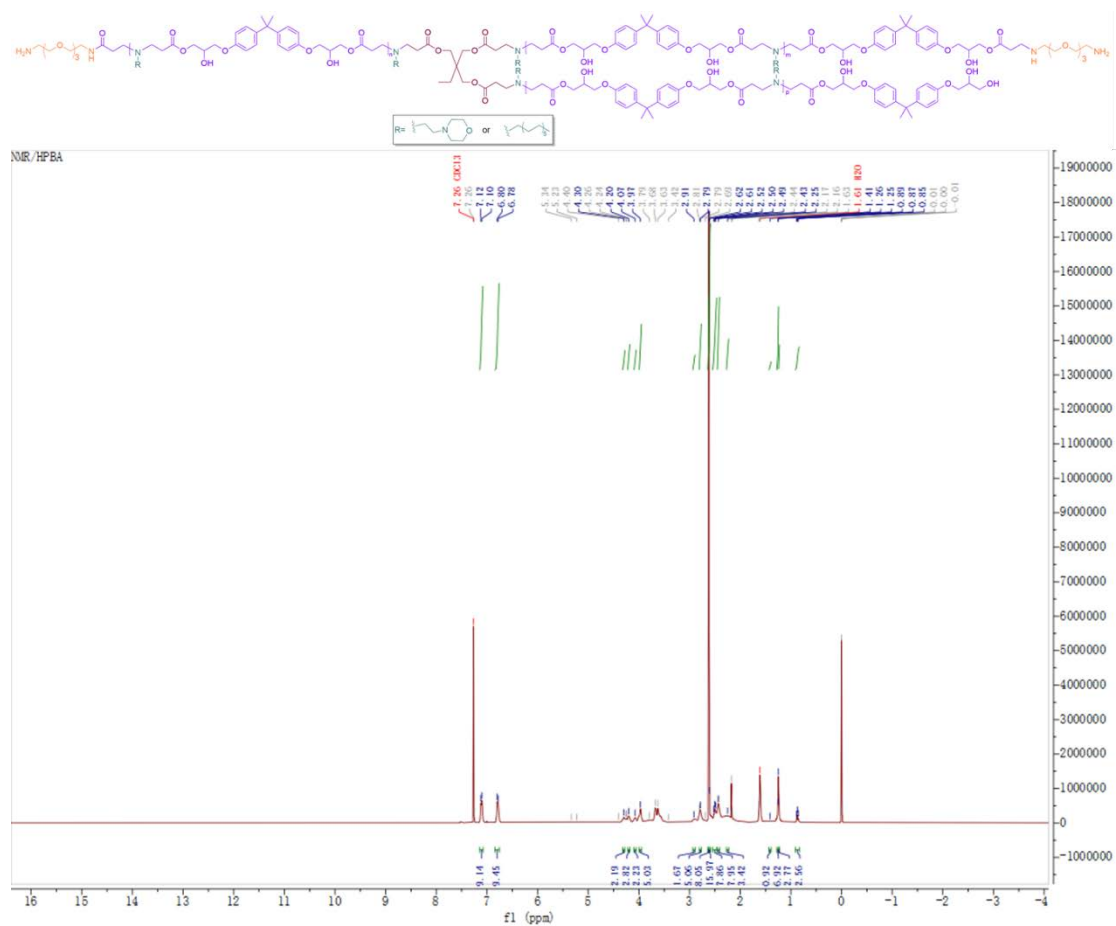


Figure S2. Analysis of HBPA ^1H NMR spectrum.

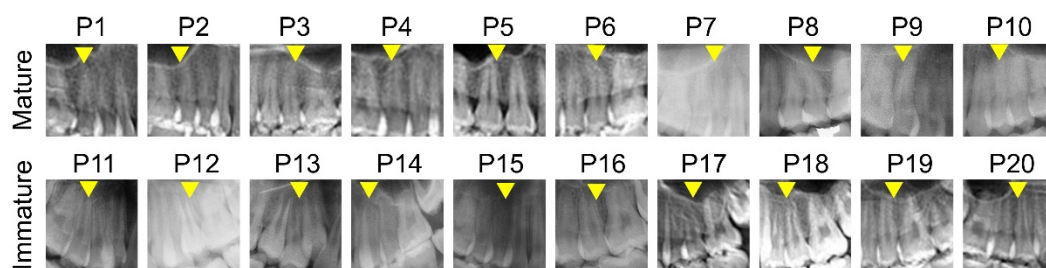


Figure S3. X-ray data of patients who are donors of human dental pulp tissue.

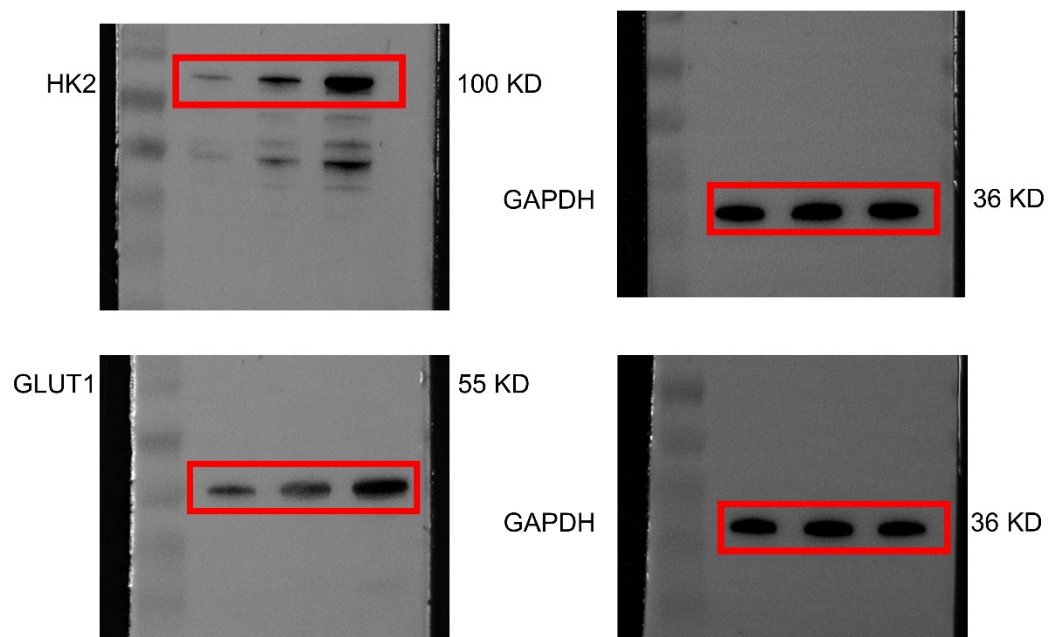


Figure S4. Uncropped images of the original Western blots used in this study.

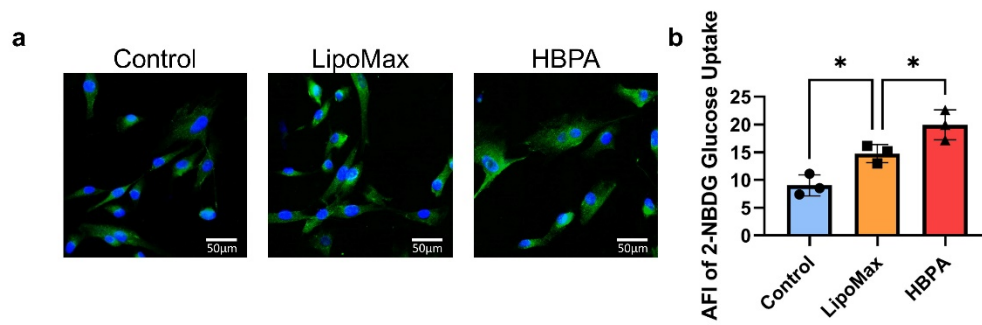


Figure S5. 2-NBDG glucose uptake of DPSCs.

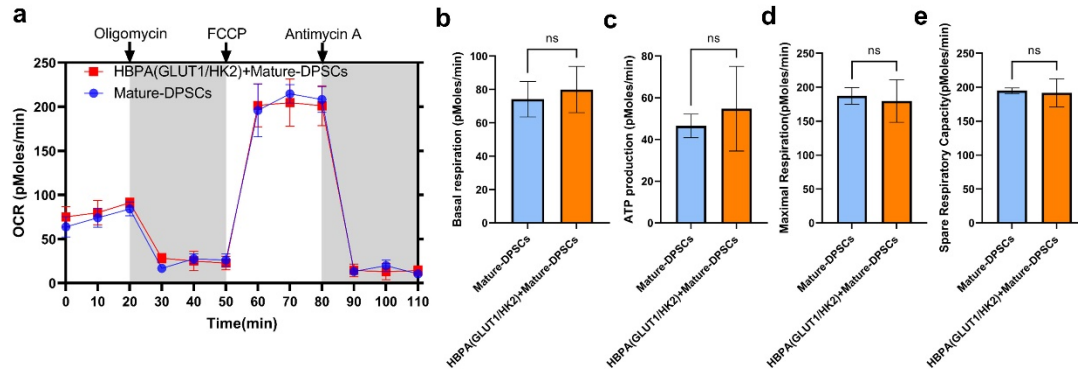


Figure S6. The mitochondrial oxidative phosphorylation in DPSCs post-transfection with HBPA was measured by Oxygen Consumption Rate, including **(a)** basal respiration, **(b)** ATP production, **(c)** maximal respiration and **(d)** spare respiratory capacity.

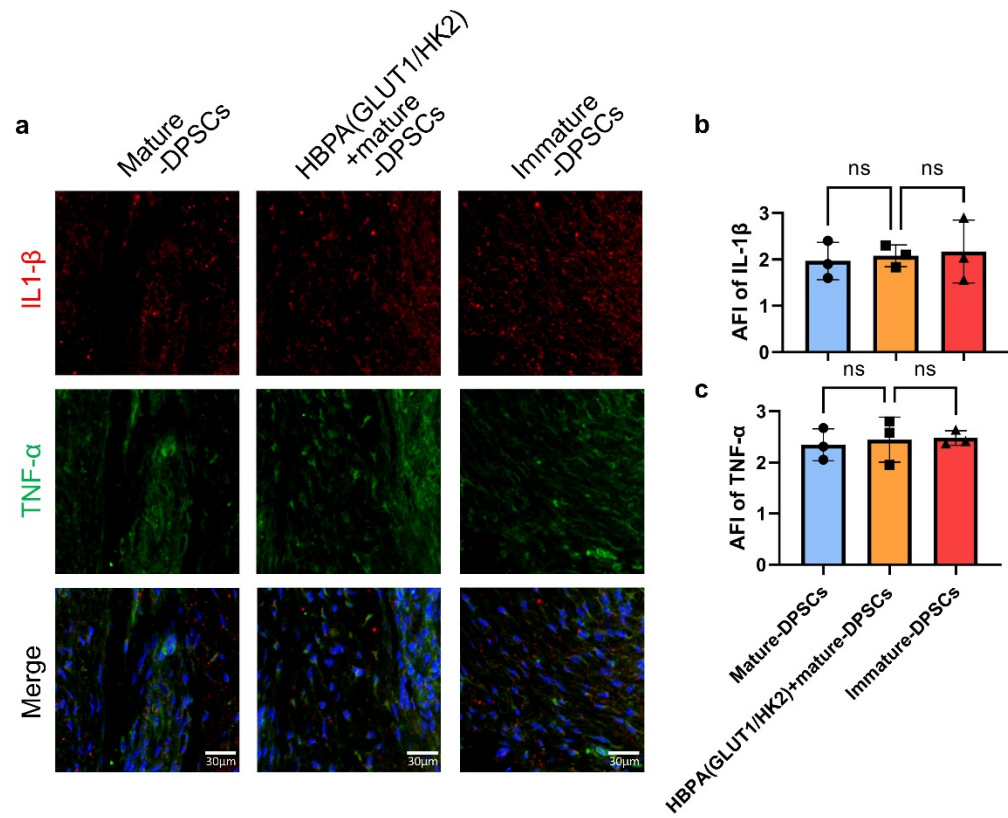


Figure S7. Expression of inflammatory factors in in vivo experiments of pulp regeneration, including IL-1 β and TNF- α .

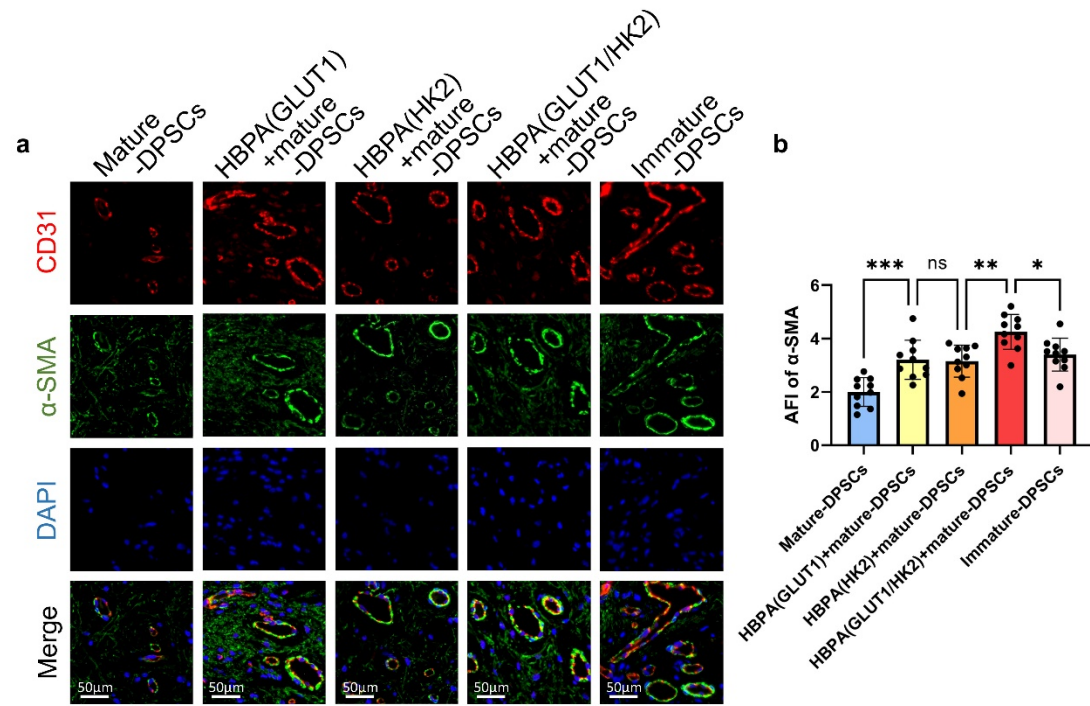


Figure S8. Expression of α -SMA and CD31 in in vivo experiments of dental pulp regeneration

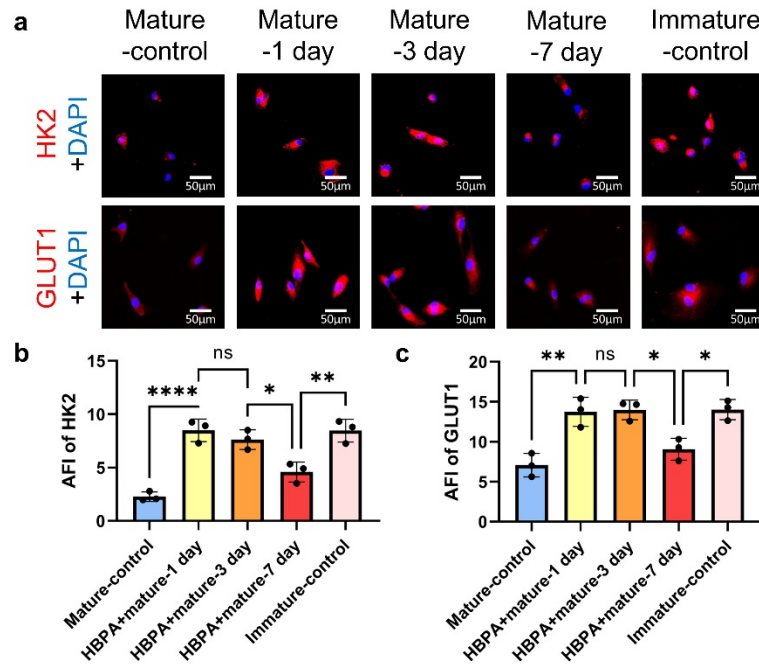


Figure S9. Dynamics of target protein expression at 1, 3, and 7 days post-transfection by HBPA(GLUT1/HK2).

Table S1. Sequences of primers for each molecular gene amplification.

Genes	Primers
<i>PTK2</i>	F: CGGCACCATCCCTAACCAT R: CACCAAACATCCATACGTCACTAGC
<i>SRC</i>	F: GGACCATGGGTAGCAACAAG R: AGGGAATTCGCCTGGATGGAGTCG
<i>RAS</i>	F: ACGACTTCCCCGTTGTGTTG R: AAAGCCTCGTCCACGTTGAG
<i>RAF1</i>	F: CACCTCCAGTCCCTCATCTG R: CTCAATCATCCTGCTGCTCA
<i>MAPK1</i>	F: TGATCACACAGGGTTCCTGA R: TGGAAAGATGGGCCTGTTAG
<i>MAPK3</i>	F: TCCGCCATGAGAATGTTATAGGC R: GGTGGTGTGATAAGCAGATTGG
<i>PIK3CA</i>	F: CCTGATCTTCCTCGTGCTGCTC R: ATGCCAATGGACAGTGTTCTCTT
<i>PIK3CB</i>	F: CGCTTGATGGATTTACTCTGGA R: GAGGTGCTCACAACCTTCAATG
<i>AKT1</i>	F: GTGCTGGAGGACAACGACT R: GTGTAGGGTCCTTCTTGAGCA
<i>AKT2</i>	F: ACATCATCTCGTACATGACCAC R: CTCTGCAAAGAGGGCATCAG
<i>MTOR</i>	F: CCCAGCTGCTGGAACAAAAA R: GTCATGCCCACGTTCTTAAC
<i>RPS6KB1</i>	F: ATGAGGCGACGAAGGAGG R: CTCCAGCTCATCCTCAGA
<i>RHOA</i>	F: ACGGGAAGCAGGTAGAGTTG R: CTAGGATGATGGGCACATTTGG
<i>RAC1</i>	F: CCAAAGTGTTGGGATTACGG R: CGGAGTTTCTCTGGACTTCG
<i>CDC42</i>	F: TAACTCACCCTGTCCAAAGACTCC R: CCTCATCAAACACATTCTTCAGACC
<i>ROCK1</i>	F: GGTATCGTCACAAGTAGCAGCATCA R: TAAACCAGGGCATCCAATCCA
<i>ROCK2</i>	F: AGGTATCTGTACATGGTAAT R: AGCATGTTGTCAGGCTTCAC
<i>HRAS</i>	F: GGGGCAGGAGACCCTGTAG R: TTTTCAAGACCATCCAATAATTT
<i>KRAS</i>	F: GGACTGGGGAGGGCTTTCT R: GCCTGTTTTGTGTCTACTGTTCT
<i>NFKB1</i>	F: GGCAGCACTACTTCTTGACC R: CAGCAAACATGGCAGGCTAT
<i>RELA</i>	F: GCCTGTCCTTTCTCATCCCA

<i>CHUK</i>	R: CTGCCAGAGTTTCGGTTCAC F: GACCGTGAACATCCTCTGACATGTG
<i>IKBKB</i>	R: GCTCTGGTCCTCATTGCTTCACG F: AACCAGCATCCAGATTGACC R: CTCAGGTCGTCCAGCGTTC

Table S2. Molecular weight and molecular weight distribution of reaction mixture and HPBA.

Reaction Time (hours)	M_n (g/mol)	M_w (g/mol)	$\bar{D}$
12	4,300	10,400	2.45
13	4,400	11,000	2.49
18	4,800	13,200	2.74
20	5,100	14,900	2.92
After end-capping	4,500	12,400	2.77
After purification	5,100	11,300	2.22

Table S3. Nucleotide Sequences of HK2 and GLUT1

Genes	Nucleotide Sequence
<i>HK2</i>	ATGATTGCCTCGCATCTGCTTGCCTACTTCTTCACGGAGCTCAACCATGACCAAGTGCAGAAGGT TGACCAGTATCTCTACCACATGCGCCTCTCTGATGAGACCCTCTTGAGATCTCTAAGCGGTTCC GCAAGGAGATGGAGAAAGGGCTTGGAGCCACCACTCACCTACTGCAGCAGTGAAGATGCTGC CCACCTTTGTGAGGTCCACTCCAGATGGGACAGAACACGGAGAGTTCTTGCTCTGGATCTTGG AGGGACCAACTTCCGTGTGCTTTGGGTGAAAGTAACGGACAATGGGCTCCAGAAGGTGGAGAT GGAGAATCAGATCTATGCCATCCCTGAGGACATCATGCGAGGCAGTGGCACCCAGCTGTTTGAC CACATTGCCGAATGCCTGGCTAACTTCATGGATAAGCTACAAATCAAAGACAAGAAGCTCCCAC TGGGTTTTACCTTCTCGTTCCCCTGCCACCAGACTAACTAGACGAGAGTTTCTTGCTCTCATGG ACCAAGGGATTCAAGTCCAGTGGAGTGGGAAGGCAGAGACGTTGTGGCTCTGATCCGGAAGGCC ATCCAGAGGAGAGGGGACTTTGATATCGACATTGTGGCTGTGGTGAATGACACAGTTGGGACCA TGATGACCTGTGGTTATGATGACCACAACCTGTGAGATTGGTCTCATTGTGGGACGCGGCAGCAA CGCCTGCTACATGGAAGAGATGCGCCACATCGACATGGTGGGAAGGCGATGAGGGGCGGATGTG TATCAATATGGAGTGGGGGGCCTTCGGGGACGATGGCTCGCTCAACGACATTCGCACTGAGTTT GACCAGGAGATTGACATGGGCTCACTGAACCCGGGAAAGCAACTGTTTGAGAAGATGATCAGT GGGATGTACATGGGGGAGCTGGTGAGGCTTATCCTGGTGAAGATGGCCAAGGAGGAGCTGCTCT TTGGGGGGAAGCTCAGCCCAGAGCTTCTCAACACCGGTCGCTTTGAGACCAAAGACATCTCAGA CATTGAAGGGGAGAAGGATGGCATCCGGAAGGCCCGTGAGGTCCTGATGCGGTTGGGCCTGGA CCCGACTCAGGAGGACTGCGTGGCCACTCACCGGATCTGCCAGATCGTGTCCACACGCTCCGCC AGCCTGTGCGCAGCCACCCTGGCCGCGCTGCTGCAGCGCATCAAGGAGAACAAAGGCGAGGAG CGGCTGCGCTCTACTATTGGGGTCGACGGTTCCGTCTACAAGAAACACCCCCATTTTGCCAAGCG TCTACATAAGACCGTGCGGCGGCTGGTGCCCGGCTGCGATGTCCGCTTCTCCGCTCCGAGGAT GGCAGTGGCAAAGGTGCAGCCATGGTGACAGCAGTGGCTTACCGGCTGGCCGATCAACACCGT GCCCCGCCAGAAGACATTAGAGCATCTGCAGCTGAGCCATGACCAGCTGCTGGAGGTCAAGAGG AGGATGAAGGTAGAAATGGAGCGAGGTCTGAGCAAGGAGACTCATGCCAGTGCCCCCGTCAAG ATGCTGCCACCTACGTGTGTGCTACCCCGGACGGCACAGAGAAAGGGGACTTCTTGCCCTTGG ACCTTGAGGAACAAATTTCCGGGTCTGCTGGTCCGTGTTCCGGAATGGGAAGTGGGGTGGAGT GGAGATGCACAACAAGATCTACGCCATCCCGCAGGAGGTCATGCACGGCACCGGGGACGAGCT CTTTGACCACATTGTCCAGTGCATCGCGGACTTCCTCGAGTACATGGGCATGAAGGGCGTGTCCC TGCTCTGGGTTTTACCTTCTCCTTCCCCTGCCAGCAGAACAGCCTGGACGAGAGCATCCTCCTC AAGTGGACAAAAGGCTTCAAGGCATCTGGCTGCGAGGGCGAGGACGTGGTGACCCTGCTGAAG GAAGCGATCCACCGGCGAGAGGAGTTTGACCTGGATGTGGTTGCTGTGGTGAACGACACAGTCG GAACTATGATGACCTGTGGCTTTGAAGACCCTCACTGTGAAGTTGGCCTCATTGTTGGCACGGGC AGCAATGCCTGCTACATGGAGGAGATGCGCAACGTGGAACCTGGTGGGAAGGAGAAGAGGGGCGG ATGTGTGTGAACATGGAATGGGGGGCCTTCGGGGACAATGGATGCCTAGATGACTTCCGCACAG AATTTGATGTGGCTGTGGATGAGCTTTCCTCAACCCCGGCAAGCAGAGGTTTCGAGAAAATGAT CAGTGGAATGTACCTGGGTGAGATTGTCCGTAACATTCTCATCGATTTCACCAAGCGTGGACTAC TCTTCCGAGGCCGCATCTCAGAGCGGCTCAAGACAAGGGGCATCTTTGAAACCAAGTTCTTGTC TCAGATTGAGAGTGAAGTGCCTGGCCCTGCTGCAAGTCCGAGCCATCCTGCAACACTTAGGGCTT GAGAGCACCTGTGACGACAGCATCATTGTTAAGGAGGTGTGCACTGTGGTGGCCCGGCGGGCAG CCCAGCTCTGTGGCGCAGGCATGGCCGCTGTGGTGGACAGGATACGAGAAAACCGTGGGCTGG ACGCTCTCAAAGTGACAGTGGGTGTGGATGGGACCCTCTACAAGCTACATCCTCACTTTGCCAA

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AGCGATAG

GLUT1 ATGGAGCCCAGCAGCAAGAAGCTGACGGGTCGCCTCATGCTGGCCGTGGGAGGAGCAGTGCTT
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