## **Supporting Information**

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Fig. S1. Splice junctions of exon 3/intron 3 and intron 3/exon 4 of the human and mouse  $\beta_i\beta_i$ -carotene-9', 10'-dioxygenase (BCO2) genes. The insertion of GKAA in the human gene is caused by a change in the donor splice site in the human gene. Intron sequences are in lowercase, 5' and 3'-ends are printed in red.



**Fig. S2.** Protein sequences of human BCO2 and mouse BCO2 used to design primers of mutagenesis experiments. Green underline shows the fragments switched between human BCO2 and mouse BCO2 and the vertical line shows the connection position. Blue underline shows the substituted amino acid positions between human BCO2 and mouse BCO2. These were numbered and the corresponding numbers are given to the primers in Table S1.



Fig. S3. SDS/PAGE (A) and Western blot (B) of recombinant human BCO2a (1), and mouse BCO2 (2) used for surface plasmon resonance (SPR).

DNAS



Fig. S4. SPR sensorgrams of carotenoids with human BCO2a, mouse BCO2, and human serum albumin.

DNAC

## Table S1. Primers used in the mutagenesis experiments to restore the carotenoid cleavage function of human BCO2

Primer	Sequence
1. T171M + k174R	5'-AAATTTGCTCCAATCTACCTTTTCTGTTCTTTCCAGCATTTCAATGTCCACTTTATTCATAAAGTTG-3' 5'-CAACTTTATGAATAAAGTGGACATTGAAATGCTGGAAAGAACAGAAAAGGTAGATTGGAGCAAATTT-3'
2. L197P	5'-CACATCCTCATTATGACCCGGATGGAACAGCATACAA-3'
3. F208Y, Y211R, F213S, S214C, K216N, V217I	5'-CCTTCTCTGGAGGAACCCGAATAATATTATAGCAGCTACCACGTGGCCCATAGGAGTTCCCCATATTGTATGCTG-3'
4. E223K, V225K, D226E, L227P	5'-CAGCATACAATATGGGGAACTCCTATGGGCCACGTGGTAGCTGCTATAATATTATTCGGGTTCCTCCAGAGAAGG-3' 5'-GGATTGTCTCCCCAGGCTCCTTCTTTTGGAGGAACCCGAATAACCTTATAGGA-3'
5 1/23/1 1/23/1	5'-TCCTATAAGGTTATTCGGGTTCCTCCAAAGAAGAAGAAGGAGCCTGGGGAGACAATCC-3'
J. V2J7, 12J7L	5'-GGAGACAATCCATGGAGCCCAGGTGTTATGTTCTATTGCTTCT-3'
6. G246M	5'-AAAGCTATGGTAGTAAGAAGGTTTCATTTTCTCTGTAGAAGCAATAGAACAT-3' 5'-ATGTTCTATTGCTTCTACAGAGAAAATGAAACCTTCTTACTACCATAGCTTT-3'
7. R258K	5'-GTTGTTCAATGAAAATTATATAGTTCTTTGTCATTCCAAAGCTATGGTAGTAA-3' 5'-TTACTACCATAGCTTTGGAATGACAAGAACTATATAATTTTCATTGAACAAC-3'
8. I264V, L268V, N271K, A276I	5'-CTTTCCCCGAATTTTAGAAGTGATAATTTTCCACAGGTTCATCTTAGAG-3'
	5'-GTTCATCTTTAGAGGTTGTTCAACGAAAATTATATAGTTCCTTGTCATTC-3' 5'-TAGAACTGGCAATTTTCCACAGCTTCATCTTTACAGGTTGTTCAATGAAAATTATA-3'
	5'-TATAATTTTCATTGAACAACCTGTAAAGATGAAGCTGTGGAAAATTGCCACTTCTA-3'
	5'-gaatgacaaggaactatataattttcgttgaacaacctctaaagatgaac-3'
	5'-CTCTAAAGATGAACCTGTGGAAAATTATCACTTCTAAAATTCGGGGAAAG-3'
9. A284P, S286A	5'-CCAGCTTATCCCATCTGCAAAGGGCTTTCCCCCGAATTTTAG-3'
10 52051/	5'-CTAAAATTCGGGGAAAGCCCTTTGCAGATGGGATAAGCTGG-3'
10. C295Y	5'-CATGAAACCGCGTATTATACTGGGGTTCCCCAGCTT-3'
11 F303D R305H	5 - AAGUTGGGAAUUUUAGTATAATAUGUGGTTTUATG-3 5'- Caaggagemeeroo acromememeeroo accaegaaacca-3'
11. 23052, 130511	5'-CGGTTTCATGTGGTGGATAAACACACTGGACAGCTCCTTC-3'
12. R313M, K317M, V320L, F322Y	5'-AAAGGCATTGATTTGATGATATGTAAGAAAAGGCATGCTGTAGTACATCCCTGGAAGGAGCTGTCCAGT-3'
13 \/3341 1335\/	5'-ACTGGACAGCTCCTTCCAGGGATGTACTACAGCATGCCTTTTCTTACATATCATCAAATCAATGCCTTT-3'
13. 000 11, 1000 0	5'-CCTTTGAGGACCAGGGCTGTATTGTAATTGAATTGATTTGTGCTGTCAA-3'
14. N343D, T346S, E348D, V349L	5'-CTGAGATTCTGTAACTGGTAAAGATCTAGGCTTCTTCCATCATCTTGACAGCACAAATCAATT-3'
	5'-AATTGATTTGTGCTGTCAAGATGATGGAAGAAGCCTAGATCTTTACCAGTTACAGAATCTCAG-3'
15. H366Y, N367E, S368L, A369K	
16. N382D, L385V, N386D, P388A, D391K	5'-TCGAAGGTTTGTTTTGCCTTTAGATGTCAGTGTGGGATGCCGCTGAGGGAAAGAACCTGAGTCCA-3'
	5'-tggactcaggttctttccctcagcggcatccacactgacatctaaaggcaaaacaaac
17. T399S	5'-CAGCACTGGCTGAAGAATAGGACAATGGACTCAGG-3'
	5'-CCTGAGTCCATTGTCCTATTCTTCAGCCAGTGCTG-3'
18. A407G, T410E, H415P, Q420H, K425E	5'-CAATGCCTCCTTCTTCTAGGTCCTCCTGATGT-3'
	5'-ACATCAGGAGGACCTAGAAGAGGAAGGAAGGAGGCATTG-3'
	5 - TUTUATGAAAATUTAUATUATGAGGAUUTAGAAAAGGAAGG
	5'-CAGTGCTGTGAAACAGGGTGATGGAGAGATCTGGTGCTCTCATG-3'
	5'-CATGAGAGCACCAGATCTCTCCCATCACCCTGTTTCACAGCACTG-3'
	5'-CCTTCCTTTTCTAGGTCCTCATGATGTAGATTTTCATGAGA-3'
	5'-TCCTGATGTAGATTTTCAGGAGAGCACCAGATCGTTC-3'
19. Y435N, D437G, S440N, H445S	5'-CCACAGCCATAAAAGAAACTATACTTTTTGCCACTGAATCGATCATAGTAGAT-3'
	5'-ATCTACTATGATCGATTCAGTGGCAAAAAGTATAGTTTCTTTTATGGCTGTGG-3'
	5'-AAAAGAAATGATACTTTTTGCCATTGAATCGACCATAGTTGATCTGAGGAAATTCAATGCCTC-3'
20 V466T K471B D476E	5 -GAGGCATIGATITCCTCAGATCACTATGGTCGATTCAATGGCAAAAAGTATCATTTCTTTT-5 5'-CACCCATTAAAAAGTATCATTCTCTCTCTCAATGCCAAAAAGTATCATTTCTTTT-5
20. 14001, 147 11, 04702	5'-CCAAACCTTCAGTGTCTTATTCGTCACATCAACCTTGATCAGAGAA-3'
	5'-TTCTCTCCAAACCCTCAGTGTCTTATTCACCACATCAAC-3'
	5'-TTCTCTGATCAAGGTTGATGTGACGAATAAGACACTGAAGGTTTGG-3'
	5'-CACTGAAGGTTTGGAGAGAGAGGGGCTTTTATCCCTC-3'
	5'-GTTGATGTGGTGAATAAGACACTGAGGGTTTGGAGAGAA-3'
21. A488V, T491A, N492D, G496S	5'-AGAATAACCCCACTATCTTCATTGGTTCCTGGTGC-3'
	5'-CUCACUATCTTCTTCATCGGCTCCTGGTACTGGAACAAAAACAGGT-3'
	J -GURUURAGURALURALGARGALAGIGUGUTTATTUT-3 5'-accmemmmmemmenaemacoaemaecaecoecameaacaacaacomecce-2'
22. N509S. I514L	5'-CATCCAAAACTAGGAGAAAATTGCTTTCATTCTGGTTGGGAGTGA-3'
	5'-GGATAAAATTGCTTTCACTCTGGTTGGGAGTGATCACCA-3'

PNAS PNAS

## Table S1. Cont.

PNAS PNAS

5'-TGGTGATCACTCCCAACCAGAGTGAAAGCAATTTTAT	FCC-3'
5'-TCACTCCCAACCAGAATGAAAGCAATTTTCTCCTAGT	TTTTGGATG-3'
5'-ACCTCTGCTCGGCCCAGCTCCGTAAAGCTCTTGGCAT	FCCAAAACTAGG-3'
5'-cctagttttggatgccaagagctttacggagctgggc	CCGAGCAGAGGT-3'
5'-CTCGAGCTAGATGGGTACGAAGGTACCATGGAACC-3	3'
5'-GGTTCCATGGTACCTTCGTACCCATCTAGCTCGAG-3	3'
5'-ATGTCAAGGTTTGAGCCACCTGGTAAAGCTGCAACTA	ATGACTGACAACAC-3'
5'-GTGTTGTCAGTCATAGTTGCAGCTTTACCAGGTGGCT	FCAAACCTTGACAT-3'
5'-gtccaggtttgagctgcctatgactgacaatactaat	rg-3'
5'-cattagtattgtcagtcataggcagctcaaacctgga	AC-3'
5'-TCCAGGTTTGAGCTGCCTACCATGACTGACAATA-3'	
5'-TATTGTCAGTCATGGTAGGCAGCTCAAACCTGGA-3'	
5'-ATGAATAAGGTGGACATTGAGATGC-3'	
5'-CCCCGGGCTCTTTCTTTTTG-3'	
5'-TTCGAAGGAATTCGGTACCATGGGAAATACTCCTCAG	GAAAAAGC-3'
5'-AGCATCTCAATGTCCACCTTATTCATAAAGTTGGTCT	rcagtgcag-3'
5'-AAAACCTGTATTTTCAGGGCGAAGGAGTTCGAACCAT	IGTTGGGACCGAAGCAAAG-3'
5'-TCTGTTTTTTCCAGAGTTTCAATGTCCACTTTATTCA	ATAAAATTAGTCTCTGTGCTC-3'
J122S 5'-TCTCCCGGATCCATGCAAGAGTATTTTTGAACGTTTC	CATGTCC-3'
5'-ggacatgaaacgttcaaaaatactcttgcatggatcc	CGGGAGA-3'
.133P 5'-ATGTCCAGGTTTGAGCCGCCTACCATGACTGAC-3'	
5'-gtcagtcatggtaggcggctcaaacctggacat-3'	
5'-ggcattgaatttcctcagatcaactatggtcgattca	AGTGGCAAAAAGTA-3'
5'-TACTTTTTGCCACTGAATCGACCATAGTTGATCTGAG	GGAAATTCAATGCC-3'
440N 5'-TTCCTCAGATCAACTATGGTCGATTCAATGGCAAAAA	AGTATC-3'
5'-gatactttttgccattgaatcgaccatagttgatctg	GAGGAA-3'
5'-ATGTCCAGGTTTGAGCCGCCTACCATGACTGAC-3'	
5'-gtcagtcatggtaggcggctcaaacctggacat-3'	
5'-TTCCTCAGATCAACTATGGTCGATTCAATGGCAAAAA	AGTATC-3'
5'-gatactttttgccattgaatcgaccatagttgatctg	GAGGAA-3'
5'-CCTAGTTTTGGATGCCAAGAGCTTTACGGAGCTGGGC   5'-CTCGAGCTAGATGGTACGAAGGTACCATGGAACC-3   5'-GGTTCCATGGTACCTTCGTACCATCTAGCTCGAG-3   5'-ATGTCAAGGTTTGAGCCACCTGGTAAAGCTGCAACTA   5'-GTCCAGGTTTGAGCTGCCTATGACTGACAATACTAAT   5'-CATTAGTATTGTCAGTCATAGGCAGCTCAAACCTGGA   5'-TCCAGGTTTGAGCTGCCTACCATGACTGACAATACTAAT   5'-CCTGGGTTTGAGCTGCCTACCATGACTGACAATACTAAT   5'-TCCAGGTTTGAGCTGCCTACCATGACTGACAATACTAAT   5'-TCCAGGTTTGAGCTGCCTACCATGACAACCTGGA-3'   5'-TCCAGGCTCTTTCTTTTTTG-3'   5'-TCCGGACCTGTATTCCACGTGGAAATACTCCTCAG   5'-ATGCATCTCAATGTCCACCTTATTCATAAAGTTGGTCT   5'-AGCATCTCAATGTCCACCTTATTCATATAGTTGGACCAT   5'-TCCGGACCTGTTTTTTCAGGGCGAAGGAGTTCGAACCAT   5'-TCTCCCGGATCCATGCAACGTGGAAGAGTTCGAACCAT   5'-TCTCCCGGATCCATGCAAGAGTATTTTTGAACGTTTC   5'-GGACATGAAACGTTCAAAATACTCTTGCATGGATCC   5'-GGCATTGAACTGTGAGCGGCCTACACTAGACTGACGACA-3'   5'-TACTTTTTGCCACTGAATCGACCATAGTTGATCTGAG   5'-GGCATTGAATTTCCTCAGATCAACTATGGTCGATTCAA   5'-TACTTTTTGCCACTGAATCGACCATAGTTGATCTGAG   5'-GCCAGGTTTGAGCCGCCTACAACTAGGCGAAAAA   5'-TACTTTTTGCCACTGAATCGACCATAGTGAACTGG   5'-TACTTTTTGCCACTGAATCGACCATAGTGACTGAG   5'-TACTTTTTGCCACTGAATCGACCATAGTGACTGAGCAAAAA   5'-GCCAGGCTCAAACTATGGTCAATGGCCAACATAGCTGAACACAGCAACACACTGGCAAACA	CCGAGCAGAGGT-3' 3' 3' ATGACTGACAACAC-3' TCAAACCTTGACAT-3' TGAAACCTTGACAT-3' TGAAACCTTGACAT-3' AC-3' GAAAAAAGC-3' TCAGTGGCAG-3' TGTTGGGACCGAAGCAAAG-3' ATAAAATTAGTCTCTGTGCTC-3' CAGTGCC-3' CGGGAGA-3' AGTATC-3' GAGAATTCAATGCC-3' GAGGAA-3'