Studying Salt-Induced Shifts in Gene Expression Patterns of Glucosinolate Transporters and Glucosinolate Accumulation in Two Contrasting *Brassica* Species

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Table S1: List of primers used for expression analysis in this study

Sr No	Primer Name	Sequence (5'— 3')
1	GTR2A2-F	GATTGCAACGGTACACAGGA
2	GTR2A2-R	CCATCTTGACATCACCAAGAA
3	GTR2B1/C2-F	CACAGGACGACGCAGAACT
4	GTR2B1/C2-R	AGCAAAATTAACCGCCAAGA
5	GTR2A1-F	TGATTGCAATGGTTCACAGG
6	GTR2A1-R	TTCCAGCAATCATGAAATAGAA
7	GTR1B1/A2-F	GAGCGGGGATCTTCTTTG
8	GTR1B1/A2-R	TCCATCCCTAGAGTCTGTTT
9	ACT-F	TGTGACAATGGAACTGGAAT
10	ACT-R	GACCCATCCCAACCATGA

Table S2: GTR genes and their respective protein properties. The table includes Gene IDs, Location of the gene on the chromosomes, transcript and protein length, molecular weight (Da), isoelectric point (pI), grand average of hydropathy values (GRAVY) and sub-cellular localization of proteins.

Gene ID	Gene Name	Chr. No.	Strand	Location	Transcript length	Protein length	Mol. Weight (Da)	pI	GRAVY	Sub-cellular localization
AT3G47960.1	*AtGTR1*	3	-	17697942-17700833	1911	636	71039.51	9.11	0.197	Plasma membrane
BolC3t18961H	*BolGTR1C1*	C3	+	45537027-45539805	1905	634	70460.97	8.71	0.247	Plasma membrane
BolC1t03184H	*BolGTR1C2*	C1	+	24730858-24733298	1926	641	71173.45	8.96	0.127	Plasma membrane
BolC8t51846H	*BolGTR1C3*	C8	-	45270014-45272334	1764	587	64966.96	9.22	0.282	Plasma membrane
BniB08g061180.2N	*BniGTR1B1*	B8	-	57886043 -57888835	1848	615	68205.34	8.61	0.239	Plasma membrane
BniB06g024230.2N	*BniGTR1B2*	B6	+	14337898-14340309	1905	634	70522.05	8.71	0.268	Plasma membrane
BniB05g052360.2N	*BniGTR1B3*	B5	-	44394313 -44396700	1854	617	68368.62	8.86	0.232	Plasma membrane
BraA06g019540.3.5C	*BraGTR1A1*	A6	+	10801141 -10804360	1848	615	68053.42	8.99	0.276	Plasma membrane
BraA06g025210.3.5C	*BraGTR1A2*	A6	-	16715892-16718716	1905	634	70567.02	8.79	0.211	Plasma membrane
BraA01g025200.3.5C	*BraGTR1A3*	A1	+	14570408- 14573089	1815	604	67112.62	9.33	0.307	Plasma membrane
A06p19700.1_BnaDAR	*BnaGTR1A1*	A6	+	11067707 -11070559	1848	615	68069.42	8.99	0.272	Plasma membrane
A06p27390.1_BnaDAR	*BnaGTR1A2*	A6	-	32634402- 32637103	1905	634	70552.05	8.86	0.22	Plasma membrane
A01p25730.1_BnaDAR	*BnaGTR1A3*	A1	+	14825160- 14827590	1926	641	71245.69	9.02	0.152	Plasma membrane
C03p72210.1_BnaDAR	*BnaGTR1C1*	C3	-	55171571 -55174464	1848	615	68172.52	8.92	0.254	Plasma membrane
C03p66900.1_BnaDAR	*BnaGTR1C2*	C3	+	45114907 -45117916	1905	634	70460.97	8.71	0.247	Plasma membrane
C01p32480.1_BnaDAR	*BnaGTR1C3*	C1	+	24863749 -24866191	1926	641	71310.64	8.9	0.13	Plasma membrane
BjuVA06G19500	*BjuGTR1A1*	A6	+	10676591 - 10679465	1848	615	68127.46	8.92	0.263	Plasma membrane
BjuVA06G26150	*BjuGTR1A2*	A6	-	28729916-28732684	1905	634	70567.02	8.79	0.211	Plasma membrane
BjuVA01G26580	*BjuGTR1A3*	A1	+	14804496- 14806848	1848	615	68053.21	9	0.228	Plasma membrane
BjuVB08G47510	*BjuGTR1B1*	B8	-	53659983-53663145	1848	615	68205.34	8.61	0.239	Plasma membrane
BjuVB06G23560	*BjuGTR1B2*	B6	+	15676902-15679502	1905	634	70544.01	8.61	0.26	Plasma membrane
BjuVB05G42900	*BjuGTR1B3*	B5	+	31049142-31051530	1854	617	68340.53	8.8	0.233	Plasma membrane
BcaB01g00859	*BcaGTR1B1*	B1	+	7365410-7368203	1848	615	68205.34	8.61	0.239	Plasma membrane
BcaB02g10681	*BcaGTR1B2*	B2	+	30683181-30685582	1905	634	70544.01	8.61	0.26	Plasma membrane
BcaB05g23096	*BcaGTR1B3*	B5	-	16137173-16139533	1854	617	68402.68	8.92	0.236	Plasma membrane
BcaC01g01757	*BcaGTR1C1*	C1	+	18324250 -18326854	1848	615	68226.55	8.86	0.253	Plasma membrane
BcaC01g02298	*BcaGTR1C2*	C1	-	29981307-29984085	1905	634	70460.97	8.71	0.247	Plasma membrane
BcaC09g49832	*BcaGTR1C3*	C9	-	25815759- 25818111	1836	611	67635.63	8.89	0.224	Plasma membrane
AT5G62680.1	*AtGTR2*	5	-	25165137-25167943	1851	616	67890.98	9.1	0.284	Plasma membrane
BolC2t12292H	*BolGTR2C1*	C2	-	61815970 -61818365	1839	612	67626.82	8.92	0.333	Plasma membrane
BolC3t18666H	*BolGTR2C2*	C3	+	42224839 -42227233	1839	612	67725.12	8.98	0.335	Plasma membrane
BolC9t53791H	*BolGTR2C3*	C9	-	5348144-5350524	1839	612	67447.53	8.87	0.348	Plasma membrane
BniB04g002130.2N	*BniGTR2B1*	B4	+	1022088 -1024566	1839	612	67716.02	9.01	0.329	Plasma membrane
BniB06g010940.2N	*BniGTR2B2*	B6	-	5574061-5576460	1839	612	67786.23	9.1	0.331	Plasma membrane
BniB07g041760.2N	*BniGTR2B3*	B7	-	47577010 -47579359	1821	606	66729.74	8.78	0.335	Plasma membrane

BraA02g045700.3.5C	*BraGTR2A1*	A2	-	30298054-30300823	1839	612	67652.94	8.98	0.34	Plasma membrane
BraA06g027380.3.5C	*BraGTR2A2*	A6	-	18424905 -18427697	1839	612	67739.14	8.98	0.335	Plasma membrane
BraA09g007530.3.5C	*BraGTR2A3*	A9	-	4272215 -4274974	1839	612	67644.82	8.79	0.334	Plasma membrane
A02p42460.1_BnaDAR	*BnaGTR2A1*	A2	-	32205553 -32208391	1839	612	67640.89	8.98	0.332	Plasma membrane
A06p29420.1_BnaDAR	*BnaGTR2A2*	A6	-	34287866 -34290565	1839	612	67797.18	8.91	0.33	Plasma membrane
A09p07810.1_BnaDAR	*BnaGTR2A3*	A9	-	4463087 -4465822	1839	612	67644.82	8.79	0.334	Plasma membrane
C02p62380.1_BnaDAR	*BnaGTR2C1*	C2	-	60482227 -60490459	1839	612	67626.82	8.92	0.333	Plasma membrane
C03p64110.1_BnaDAR	*BnaGTR2C2*	C3	+	41808405 -41811139	1839	612	67725.12	8.98	0.335	Plasma membrane
C09p08780.1_BnaDAR	*BnaGTR2C3*	C9	-	5199813 -5202640	1836	611	67378.42	8.86	0.137	Plasma membrane
BjuVA02G47610	*BjuGTR2A1*	A2	-	31650239-31652620	1839	612	67656.89	8.98	0.328	Plasma membrane
BjuVA06G28410	*BjuGTR2A2*	A6	-	30414065-30416809	1839	612	67797.18	8.91	0.33	Plasma membrane
BjuVA09G07610	*BjuGTR2A3*	A9	-	4182819- 4194805	1581	526	57986.02	9	0.452	Plasma membrane
BjuVB04G01960	*BjuGTR2B1*	B4	+	1112996-1115472	1839	612	67625.89	9.02	0.326	Plasma membrane
BjuVB06G11810	*BjuGTR2B2*	B6	-	6701332-6704576	1839	612	67786.23	9.1	0.331	Plasma membrane
BjuVB07G18470	*BjuGTR2B3*	B7	+	10890421-10893018	1821	606	66694.69	8.78	0.333	Plasma membrane
BcaB02g09673	*BcaGTR2B1*	B2	-	21952429 -21954836	1839	612	67758.17	9.1	0.327	Plasma membrane
BcaNung01385	*BcaGTR2B2*	Contig503	+	38887-41234	1821	606	66694.69	8.78	0.333	Plasma membrane
BcaB07g29850	*BcaGTR2B3*	B7	-	1225649-1228114	1776	591	65345.13	8.64	0.361	Plasma membrane
BcaC01g02504	*BcaGTR2C1*	C1	-	32914562 -32924437	1836	611	67586.9	8.91	0.343	Plasma membrane
BcaC03g18168	*BcaGTR2C2*	C3	-	63135183-63154915	2223	740	81415.64	9.54	0.106	Plasma membrane
BcaC04g23397	*BcaGTR2C3*	C4	+	59044137-59046512	1836	611	67391.42	8.78	0.329	Plasma membrane

Table S3: K_a, K_s and K_a/K_s values of the *GTR* gene pairs

GTR 1	GTR 2	K_a	K_s	K_a/K_s
BnaGTR1A1	BjuGTR1A1	0.0007	0.0138	0.0514
BnaGTR1A3	BjuGTR1A3	0.0014	0.0068	0.2110
BnaGTR1C2	BjuGTR1A2	0.0052	0.0467	0.1112
BnaGTR2A1	BnaGTR2C1	0.0007	0.0762	0.0094
BnaGTR2A2	BnaGTR2C2	0.0007	0.0712	0.0100
BnaGTR2A3	BjuGTR2A3	0.0294	0.0638	0.4610

Table S4: Mean squares and levels of significance from ANOVA for (a) biochemical parameters, (b) non-enzymatic antioxidants, (c) GTR genes and (d) glucosinolates in *B. juncea* and *B. napus* under NaCl stress. (***, **, * at p = 0.0001, 0.001 and 0.01, respectively).

a) Response: Biochemical parameters

Source of variation	DF	H_2O_2	MDA	Phenolics	TFA	TSP
Species (Sp)	1	21.3942***	26.731*	0.0000445	0.00103397***	3.8068***
NaCl	2	6.4412***	77.217***	0.0038252***	0.00201673***	24.6687***
Sp x NaCl	2	0.4565*	0.873	0.0001121	0.00033979***	2.19***
Error	12	0.0972	2.902	0.0002278	0.00000442	0.0959

b) Response: Non-enzymatic antioxidants

Source of variation	DF	POD	CAT	APX	SOD
Species (Sp)	1	0.0001846*	18.76***	0.0047261***	2.041
NaCl	2	0.00197793***	4.3932*	0.0014783*	187.963***
Sp x NaCl	2	0.00021392*	0.9233g	0.0001319	21.086
Error	12	0.00003854	0.7102	0.0002205	7.936

c) Response: GTR genes

Source of variations	DF	GTR1A2/B1	GTR2A2	GTR2A1	GTR2B1/C2
Species (Sp)	1	53.125***	2.134	38.268.	37.270**
Plant part (PP)	4	34.32***	146.603**	27.604*	35.596***
Sp x PP	4	41.097***	272.908***	52.086***	65.552***
Error	80	2.457	34.9	10.121	4.966

d) Response: Glucosinolates

Source of variations	DF	Sum Sq	Mean Sq	*F* - Value	Pr (> *F*)	Significance
Species	1	37868	37868	1900.880	2×10^{-16}	***
NaCl	2	180	90	4.509	0.0145	*
Residuals	68	1355	20	—	—	—

Block 1:

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AtGTR1     MERKPLEVEPS-------TTTNTD---VVDSFEEEQRKIVYRGWKVMPFIIG
AtGTR2     MERKPLELESTHQNPSSAVYGGSVTAVDSVEEDVQNQKKVVYRGWKVMPFIIG
BjuGTR1A1  MERKPFEVETTDQKPYSAVDGGGSD---SVDSFDEDQKKLVYRGWKVMPFIIG
BjuGTR1A2  MERKPFDVETTDHKLYPSVDGGGSD---SVDSFEDEQKKLVYRGWKVMPFIIG
BjuGTR1A3  MERKPFEVETTDHKPYS--DGGASDLTSTVDSSGDEQKKLVYRGWKVMPYIIG
BjuGTR1B1  MERKPFEVETTDQKPYSAVDGGGSD---SVDSFDEDQKKLVYRGWKVMPFIIG
BjuGTR1B2  MERKPFDVETTDHKAYSSVDGGGSD---SVDSFEDEQKKLVYRGWKVMPFIIG
BjuGTR1B3  MERKPFEVETTDHKPYS-DGGGSDLTSTVDSSGDEQKKLVYRGWKVMPYIIG
BjuGTR2A1  MERKPLEVESTHQKPSSAVYDGSATAVDSVEEEVQ-ETKLVYRGWKVMPFIIG
BjuGTR2A2  MERKPLEVESTHQKPPSAVYDGSVMAVDSVEEEVE-ETKVVYRGWKVMPFIIG
BjuGTR2A3  MERKSLEVESMHQKLSSAVYDGSVTAVDSVKEDVQ-ETKVVYRGWKVMPYIIG
BjuGTR2B1  MERNPLEVESTHQKPSSAVYDGSATAVDSVEEEVQ-ETKVVYRGWKVMPFIIG
BjuGTR2B2  MERKPLEVESTHQKPPSAVYDGSVMAVDSVEEEVG-ETKVVYRGWKVMPFIIG
BjuGTR2B3  MERKSLEVESMHQKLS-SAYDGSVTAVDSVKEDVQ-ETKVVYRGWKVMPYIIG
BnaGTR1A1  MERKPFEVETTDQKPYSAVDGGGSD---SVDSFDEDQKKLVYRGWKVMPFIIG
BnaGTR1A2  MERKPFDVETTDHKPYSSVDGGGSD---SVDSFEDEQKKLVYRGWKVMPFIIG
BnaGTR1A3  MERKPFEVETTDHKPYS--DGGGSDLTSTVDSSGDEQKKLVYRGWKVMPYIIG
BnaGTR1C1  MERKPFEVETTDKKPYSAVDGGGSD---SVDSFDEDQEKLVYRGWKVMPFIIG
BnaGTR1C2  MERKPFDVETTDHKPYSSVVDGGSD---SVDSFDDEQTKLVYRGWKVMPFIIG
BnaGTR1C3  MERKPFEVETTDHKPYSAFDGGGSDLTSTVDSSDDEQKKLVYRGWKVMPYIIG
BnaGTR2A1  MERKPLEVESTHQKPSSAVYDGSATAVDSVEEEVE-ETKVVYRGWKVMPFIIG
BnaGTR2A2  MERKPLEVESTHQKPPSAVYDGSVMAVDSVEEEVE-ETKVVYRGWKVMPFIIG
BnaGTR2A3  MERKSLEVESMHQKLSSAVYDGSVTAVDSVKEDVQ-ETKVVYRGWKVMPYIIG
BnaGTR2C1  MERKPLEVESTHQKPSSAVYDGSATAVDSVQEEVQ-ETKVVYRGWKVMPFIIG
BnaGTR2C2  MERKPLEVESTHQKPSSAVYDGSPAVDSVEEVVE-ETKVVYRGWKVMPFIIG
BnaGTR2C3  MERKPLEVESTHQKLSSAVYDG------PVEEDVQ-ETKVVYRGWKVMPFIIG
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Block 2:

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AtGTR1     NETFEKLGIIGTLSNLLVYLTSVFNLKSYTAATIINAFSGTINFGTFIAAFLCD
AtGTR2     NETFEKLGIIGTLSNLLVYLTAVFNLKSITAATIINAFSGTINFGTFLAAFLCD
BjuGTR1A1  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIINAFSGTINFGTFLAAFLCD
BjuGTR1A2  NETFEKIGIIGTLSNLLVYLTSVFNLKSVTAATIINAFSGTINFGTFLAAFLCD
BjuGTR1A3  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIISAFSGTINFGTFFAAFLCD
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BjuGTR1B3  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIINAFAGTVNFGTFVAAFLCD
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BjuGTR2A2  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BjuGTR2A3  NETFEKLGIIGTLSNLLVYLTSVFNMKSITAATIITAFAGTVNFGTFVAAFLCD
BjuGTR2B1  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BjuGTR2B2  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFLAAFLCD
BjuGTR2B3  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFAGTVNFGTFVAAFLCD
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BnaGTR1A2  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIINAFSGTINFGTFLAAFLCD
BnaGTR1A3  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIISAFSGTINFGTFFAAFLCD
BnaGTR1C1  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIINAFSGTINFGTFLAAFLCD
BnaGTR1C2  NETFEKIGIIGTLSNLLVYLTSVFNLQSVTAATIINAFSGTINFGTFLAAFLCD
BnaGTR1C3  NETFEKIGIIGTLSNLLVYLTQVFNLKKYTAATIINAFSGTINFGTFFAAFLCD
BnaGTR2A1  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BnaGTR2A2  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BnaGTR2A3  NETFEKLGIIGTLSNLLVYLTSVFNMKSVTAATIITAFAGTVNFGTFVAAFLCD
BnaGTR2C1  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BnaGTR2C2  NETFEKLGIIGTLSNLLVYLTAVFNMKSITAATIINAFSGTINFGTFVAAFLCD
BnaGTR2C3  NETFEKLGIIGTLSNLLVYLTSVFNMKSVTAATIINAFAGTINFGTFVAAFLCD
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Block 3:

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AtGTR1     TYFGRYKTLSVAVIACFLGSFVILLTAAIPSLHPVACGNKISCEGPSVGQILFL
AtGTR2     TYFGRYKTLSVAVIACFLGSFVILLTAAVPQLHPAACGTAADCNGPSGGQIAFL
BjuGTR1A1  TYFGRYKTLSVAVIACFLGSLVILLTAAVPGLHPTPCGTKSSCEGPGAGQILFL
BjuGTR1A2  TYFGRYKTLSVAVIACFLGSLVILLTAAVPGLHPIPCGTQSSCQGPSEGQIAFL
BjuGTR1A3  TYFGRYKTLSVAVIACFLGSLFILMTAAVPGLHPTPCGTKSSCQGPNGGQVLFL
BjuGTR1B1  TYFGRYKTLSVAVIACFLGSLAILLTAAVPGLHPTPCGTKSSCEGPDVGQIAFL
BjuGTR1B2  TYFGRYKTLTVAVIACFLGSLVILLTAAVPSLHPTPCGTQSSCQGPSEGQIAFL
BjuGTR1B3  TYFGRYKTLSVSVIACFLGSLCILLTAAVPGLHPTPCGTKSSCQGPNGGQIVFL
BjuGTR2A1  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPAPCGTALTCTGPSGGQIAFL
BjuGTR2A2  TYFGRYKTLTVAVIACFLGSLAILLTAAVPQLHPAPCGTALSCIGPSGGQIAFL
BjuGTR2A3  TYFGRYKTLTVAVIACFLGSLAILLTAAVPQLHPVPCGTASSCIGPSGGQIAFL
BjuGTR2B1  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPAPCGTALTCTGPSGGQIAFL
BjuGTR2B2  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPTPCGTAISCIGPSGGQIAFL
BjuGTR2B3  TYFGRYKTLTAAVIACFLGSLAILLTAAVPQLHPAPCGTASSCIGPSGGQIAFL
BnaGTR1A1  TYFGRYKTLSVAVIACFLGSLAILLTAAVPGLHPTPCGTKSSCEGPGAGQILFL
BnaGTR1A2  TYFGRYKTLSVAVIACFLGSLVILLTAAVPGLHPIPCGTQSSCQGPSEGQIAFL
BnaGTR1A3  TYFGRYKTLSVAVIACFLGSLFILMTAAVPGLHPTPCGTKSSCQGPNGGQVLFL
BnaGTR1C1  TYFGRYKTLSVAVVACFLGSLFILMTAAVPGLHPTPCGTKSSCEGPGACQILFL
BnaGTR1C2  TYFGRYKTLSVAVIACFLGSLVILLTAAVPGLHPIPCGTQSSCQGPSEGQIAFL
BnaGTR1C3  TYFGRYKTLSVAVIACFLGSVFILMTAAVPGLHPTPCGTKSSCQGPNGGQVLFL
BnaGTR2A1  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPAPCGTALTCTGPSGGQIAFL
BnaGTR2A2  TYFGRYKTLTVAVIACFLGSLAILLTAAVPQLHPAPCGTALSCIGPSGGQIAFL
BnaGTR2A3  TYFGRYKTLTVAVLACFLGSLAILLTAAVPQLHPAPCGTASSCIGPSGGQIAFL
BnaGTR2C1  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPAPCGTALTCTGPSGGQIAFL
BnaGTR2C2  TYFGRYKTLTVAVIACFLGSLVILLTAAVPQLHPAPCGTALSCIGPSGGQIAFL
BnaGTR2C3  TYFGRYKTLTVAVLACFLGSLAILLTAAVPQLHPAPCGTASSCSGPSGGQIAFL
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Multiple sequence alignment

Block 1:

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AtGTR1      LMGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
AtGTR2      LMGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BjuGTR1A1   MLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BjuGTR1A2   LMGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BjuGTR1A3   LLGLALLVVGAGGIRPCNLAFGADQFNPKSESGRKGINSFFNWYFFTFTFAQI
BjuGTR1B1   LLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BjuGTR1B2   LMGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BjuGTR1B3   LMGLSLLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BjuGTR2A1   LMGLAFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BjuGTR2A2   LLGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BjuGTR2A3   LMGLGILVVGAGGIRPCNLAFGADQFNPKSGSGKRGIDSFFNWYFFTFTFAQI
BjuGTR2B1   LMGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BjuGTR2B2   LLGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BjuGTR2B3   LMGLGILVVGAGGIRPCNLAFGADQFNPKSGSGKRGIDSFFNWYFFTFTFAQI
BnaGTR1A1   MLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR1A2   LMGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR1A3   LLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR1C1   MLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR1C2   LMGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR1C3   LLGLALLVVGAGGIRPCNLAFGADQFNPKSESGKKGINSFFNWYFFTFTFAQI
BnaGTR2A1   LMGLAFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BnaGTR2A2   LLGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BnaGTR2A3   LMGLGILVVGAGGIRPCNLAFGADQFNPKSGSGKRGIDSFFNWYFFTFTFAQI
BnaGTR2C1   LMGLAFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BnaGTR2C2   LLGLGFLVVGAGGIRPCNLAFGADQFNPKSESGKRGIDSFFNWYFFTFTFAQI
BnaGTR2C3   LMGLGILVVGAGGIRPCNLAFGADQFNPKSGSGKRGIDSFFNWYFFTFTFAQI
```

Block 2:

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AtGTR1      ISLTAVVYIQSNVSWTIGLIIPVALMFLACVIFFAGDRLYVKVKASGSPLAGIA
AtGTR2      LSLTLVVYVQSNVSWTIGLTIPAVLMFLACLIFFAGDKLYVKIKASGSPLAGIA
BjuGTR1A1   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIA
BjuGTR1A2   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIG
BjuGTR1A3   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIYFAGHNLYVKVKASGSPLAGIA
BjuGTR1B1   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIYFAGHKLYVKVKASGSPLAGIA
BjuGTR1B2   VSLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIG
BjuGTR1B3   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACIIYFAGHNLYVKVKASGSPLAGIA
BjuGTR2A1   LSLTLVVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLASIA
BjuGTR2A2   LSLTLIVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLAGIA
BjuGTR2A3   LSLTVVVYVQSNVSWTIGLTIPVVLMFLASVIFFAGASCMLRSKPQ------VV
BjuGTR2B1   LSLTLVVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLASIG
BjuGTR2B2   LSLTLIVYVQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLASIA
BjuGTR2B3   LSLTVVVYIQSNVSWTIGLTIPVVLMFLASVIFFAGAKLYVKIEASGSPLASIA
BnaGTR1A1   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIA
BnaGTR1A2   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIG
BnaGTR1A3   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIYFAGHNVYVKVKASGSPLAGIA
BnaGTR1C1   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIA
BnaGTR1C2   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIFFAGHKLYVKVKASGSPLAGIG
BnaGTR1C3   ISLTLVVYIQSNVSWTIGLSIPVGLMFLACVIYFAGHNLYVKVKASGSPLAGIA
BnaGTR2A1   LSLTLVVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLASIA
BnaGTR2A2   LSLTLIVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLAGIA
BnaGTR2A3   LSLTVVVYVQSNVSWTIGLTIPVVLMFLASVIFFAGAKLYVKIEASGSPLASIA
BnaGTR2C1   LSLTLVVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLASIA
BnaGTR2C2   LSLTLIVYIQSNVSWTIGLTIPVVLMFLACVIFFAGDKLYVKIKASGSPLAGIA
BnaGTR2C3   LSLTVVVYVQSNVSWTIGLTIPVVLMFLASVIFFAGAKLYVKIEASGSPLASIA
```

Block 3:

```
AtGTR1      RVIAAAIKKRGLKPVKQPWVNLYNHIPSNYANTTLKYTDQFRFLDKAAIMTPEE
AtGTR2      QVIAVAIKKRGLKPAKQPWLNLYNYYPPKYANSKLKYTDQFRFLDKAAILTPED
BjuGTR1A1   RVIAAAISKRGLKPVKQPWVDLYNHIPRNYANTTLKYTDQLRFLDKAAIMTPED
BjuGTR1A2   HVIAAAIKKRGLKPVKQPWIDLYNHIPHDYANSTLKYTDQLRFLDKAAIMTPED
BjuGTR1A3   RVIAAAIKKRGLKPVKKPCSDLYNHIPPNYANSTLKYSDQFRFLDKAAVMTPED
BjuGTR1B1   RVIAAAISKRGLKPVKQPWVDLYNHIPRNYANLTLKYTDQFRFLDKGAIMTPED
BjuGTR1B2   HVIAAAIKKRGLKPVKQPWIDLYNHIPHNYANSTLKYTDQLRFLDKAAIMTVDD
BjuGTR1B3   RVIAAAIKKRGLKPVNKPCSDLYNHIPLNYANSTLKYSDQFRFLDKAAIMTPED
BjuGTR2A1   QVITVAIKKRGLKAVKQPWLNLYNYYPLNYANSKLKYTDQFRFLDKAAILAPED
BjuGTR2A2   QVIAVAIKKRGLKPTKEPWLNLYNYYPPKYANSKLKYTDQFRFLDKAAILAPED
BjuGTR2A3   HWL-------------PWLNLYNYYPSKYANAKLKYTEQFRFLDKAAILTPED
BjuGTR2B1   QVITVAIKKRGLKPVKQPWLNLYNYYPLNYANSKLKYTDQFRFLDKAAIFAPED
BjuGTR2B2   QVIAVAIKKRGLKPTKQPWLNLYNYYPPKYANSKLKYTDQFRFLDKAAILAPED
BjuGTR2B3   HVITAAIKKHGLKSVEQPWLNLYNYYPAKYANAKLKYTDQFRFLDKAAILAPED
BnaGTR1A1   RVIAAAISKRGLKPVKQPWVDLYNHIPRNYANTTLKYTDQFRFLDKAAIMTPED
BnaGTR1A2   HVIAAAIKKRGLKPVKQPWIDLYNHIPHNYANSTLKYTDQLRFLDKAAIMTAED
BnaGTR1A3   RVIAAAIKKRGLKPVKKPCSDLYNHIPPNYANSTLKYSDQFRFLDKAAVMTPED
BnaGTR1C1   RVIAAAISKRGLKPVKQPWVDLYNHIPRNYANTTLKYTDQFRFLDKAAIMTPED
BnaGTR1C2   HVIAAAIKKRGLKPVKQPWIDLYNHIPPNYANSTLKYTDQLRFLDKAAIMTPED
BnaGTR1C3   RVIAAAIKKRGLKPVKKPCSDLYNHIPPNYANSTLKYSDQFRFLDKAAVMTPDD
BnaGTR2A1   QVITVAIKKRGLKAVKQPWVNLYNYYPLNYANSKLKYTDQFRFLDKAAILAPED
BnaGTR2A2   QVIAVAIKKRGLKPTKEPWLNLYNYYPPKYANSKLKYTDQFRFLDKAAILAPED
BnaGTR2A3   HVITAAIKKHRLEPVEQPWLNLYNYYPSKYANAKLKYTEQFRFLDKAAILTPED
BnaGTR2C1   QVITVAIKKRGLKAVKQPWVNLYNYYPLNYANSKLKYTDQFRFLDKAAILAPED
BnaGTR2C2   QVIAVAIKKRGLKPTKEPWLNLYNYYPPKYANSKLKYTDQFRFLDKAAILAPED
BnaGTR2C3   HVITAAIKKHGLKSVEQPWLNLYNYYPSKYANAKLKYTEQFRFLDKAANLTPED
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Block 1

```
AtGTR1    KLNSDGTASDPWKLCTLQQVEEVKCIVRVIPIWFASTIYYLAITIQMTYPVFQ
AtGTR2    KLQPDGKPADPWKLCTMQQVEEVKCIVRVLPIWFASSIYYLTITQQMTYPVFQ
BjuGTR1A1 KLNSDGTASDPWKLCTMQQVEEVKCIIRVIPIWFACAIYYLAISIQMTYPVFQ
BjuGTR1A2 KLNSDGTASDPWKLCTMQKVEEVKCILRVIPIWFACAIYYLAISMQMTYPVFQ
BjuGTR1A3 KLKPDGTASDPWNLCTMQQVEEVKCIVRVIPIWLACAVYYLAITLQMTYPVFQ
BjuGTR1B1 KLNSDGTASDPWKLCTMQQVEEVKCIVRVIPIWFACAIYYLAISIQMTYPVFQ
BjuGTR1B2 KLNSDGTASDPWKLCTMQQVEEVKCIVRVIPIWFACAIYYLAISMQMTYPVFQ
BjuGTR1B3 KLKPDGTASDPWNLCTMQQVEEVKCIVRVIPIWFACAVYYLAITLQMTYPVFQ
BjuGTR2A1 KLEADGKPTDPWKLCTMQQVEEVKCIVRVLPIWFASSIYYLTITQQMTYPVFQ
BjuGTR2A2 KLEADGKPADPWKLCTMQQVEEVKCIVRVLPIWFAASIYYLTITQQMTYPVFQ
BjuGTR2A3 KLEADGKPVNPWKLCTMQQVEEVKCIMRVLPIWFASSIYYLTIAQQMTYPVFQ
BjuGTR2B1 KLEADGKPVDPWKLCTMQQVEEVKCIVRVLPIWFASSIYYLTITQQMTYPVFQ
BjuGTR2B2 KLEADGKPADPWKLCTMQQVEEVKCIVRVLPIWFAASIYYLTITQQMTYPVFQ
BjuGTR2B3 KLEADGKPVNPWKLCTMQQVEEVKCIMRVLPISFASSIYYLTITQQMTYPVFQ
BnaGTR1A1 KLNSDGTASDPWKLCTMQQVEEVKCIIRVIPIWFACAIYYLAISIQMTYPVFQ
BnaGTR1A2 KLNSDGTASDPWKLCTMQKVEEVKCILRVIPIWFACAIYYLAISMQMTYPVFQ
BnaGTR1A3 KLKPDGTASDPWNLCTMQQVEEVKCIVRVIPIWLACAVYYLAITLQMTYPVFQ
BnaGTR1C1 KLNSDGTASDPWKLCTMQQVEEVKCIIRVIPIWFACAIYYLAISIQMTYPVFQ
BnaGTR1C2 KLNSDGTASDPWKLCTMQKVEEVKCILRVIPIWFACAIYYLAISMQMTYPVFQ
BnaGTR1C3 KLKPDGTASDPWNLCTMQQVEEVKCIVRVIPIWFACAVYYLAITLQMTYPVFQ
BnaGTR2A1 KLEADGKPTDPWKLCTMQQVEEVKCIVRVLPIWFASSIYYLTITQQMTYPVFQ
BnaGTR2A2 KLEADGKPADPWKLCTMQQVEEVKCIVRVLPIWFAASIYYLTITQQMTYPVFQ
BnaGTR2A3 KLEADGKPVNPWKLCTMQQVEEVKCIMRVLPIWFASSIYYLTMAQQMTYPVFQ
BnaGTR2C1 KLEADGKPTDPWKLCTMQQVEEVKCIVRVLPIWFASSIYYLTITQQMTYPVFQ
BnaGTR2C2 KLEADGKPADPWKLCTMQQVEEVKCIVRVLPIWFAASIYYLTITQQMTYPVFQ
BnaGTR2C3 KLDADGKPVNPWKLCTMQQVEEVKCIMRVLPIWFASSIYYLTIAQQMTYPVFQ
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Block 2

```
AtGTR1    ALQSDRRLGSGGFRIPAATYVVFLMTGMTVFIIFYDRVLVPSLRRVTGLETGI
AtGTR2    ALQSDRRLGSGGFVIPAATYVVFLMTGMTVFIVVYDRVLVPTMRRITGLDTGI
BjuGTR1A1 AQQSDRRLGTGGFKIPAATYVVFLMTGMTVFIIIYDRVLVPSLKRVTGLDTGI
BjuGTR1A2 ALQSDRRLGSGGFKIPAATYVVFLMSGMTVFIIIYDRVLVPSLRRVTGLDTGI
BjuGTR1A3 ALQSDRRLGSGGFKIPGATYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDNGI
BjuGTR1B1 AQQSDRRLGSGGFKIPAATYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDTGI
BjuGTR1B2 ALQSDRLLGSGGFKIPAATYVVFLMSGMTVFIIIYDRVLVPSLRRVTGLDTGI
BjuGTR1B3 ALQSDRRLGSGGFKIPSATYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDNGI
BjuGTR2A1 ALQSDRRLGSGGFVIPAATYVVFLMTGMTVFIIIYDRVLVPTLRRITGIDTGI
BjuGTR2A2 ALQSDRRLGSRGFVIPAATYVVFLMTGMTVFIIFYDRVLVPTLRRITGIDTGI
BjuGTR2A3 ALQSDRRLGSGGFMIPAATYVVFLMTGMTLFIIFYDRVLVPTFKRITGIETGI
BjuGTR2B1 ALQSDRRLGSGGFVIPAATYVVFLMTGMTVFIIIYDRVLVPTLRRITGIDTGI
BjuGTR2B2 ALQSDRRLGSRGFVIPAATYVVFLMTGMTVFIIFYDRVLVPTLRRITGIDTGI
BjuGTR2B3 ALQSDRRLGSGGFVIPAATYVVFLMTGMTLFIILYDRVLVPTLKRITGIETGI
BnaGTR1A1 AQQSDRRLGTGGFKIPAATYVVFLMTGMTVFIIIYDRVLVPSLKRVTGLDTGI
BnaGTR1A2 ALQSDRRLGSGGFKIPAATYVVFLMSGMTVFIIIYDRVLVPSLRRVTGLDTGI
BnaGTR1A3 ALQSDRRLGSGGFKIPGATYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDNGI
BnaGTR1C1 AQQSDRRLGTGGFKMPAATYVVFLMTGMTVFIIIYDRVLVPSLKRVTGLDTGI
BnaGTR1C2 ALQSDRLLGSGGFKIPAATYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDTGI
BnaGTR1C3 ALQSDRRLGSDGFKIPGGTYVVFLMSGMTVFIIFYDRVLVPSLRRVTGLDNGI
BnaGTR2A1 ALQSDRRLGSGGFVIPAATYVVFLMTGMTVFIIIYDRVLVPTLRRITGIDTGI
BnaGTR2A2 ALQSDRRLGSRGFVIPAATYVVFLMTGMTVFIIFYDRVLVPTLRRITGIDTGI
BnaGTR2A3 ALQSDRRLGSGGFMIPAATYVVFLMTGMTLFIIFYDRVLVPTLKRITGIETGI
BnaGTR2C1 ALQSDRRLGSGGFVIPAATYVVFLMTGMTVFIIIYDRVLVPTLRRITGIDTGI
BnaGTR2C2 ALQSDRRLGSRGFVIPAATYVVFLMTGMTVFIIFYDRVLVPTLRRITGIDTGI
BnaGTR2C3 ALQSDRRLGSGGFMIPAATYVVFLMTGMTLFIIFYDRVFVPTLKRITGIETGI
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Block 3

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AtGTR1    SLLQRIGAGFTFAIMSLLVSGFIEERRRNFALTKPTLGMAPRTGEISSMSALW
AtGTR2    TLLQRIGTGIFFATASLVVAGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BjuGTR1A1 TLLQRIGAGIFFAVLSLLVSGFIEERRRSIALTKQTLGMEPRTGEISSMSAMW
BjuGTR1A2 TLLQRIGAGIFFAVLSLLVSGFVEERRRAIALTKPTLGIEPRAGEISSMSAMW
BjuGTR1A3 TLLQRIGSGIFFALLSLLVSGFVEERRRAIALTKPTLGIEPRAGEISSMSAMW
BjuGTR1B1 TLLQRIGAGIFFAVLSLLVSGFIEERRRSIALTKQTLGMEPRAGEISSMSAMW
BjuGTR1B2 TLLQRIGAGIFFAVLSLLVSGFIEERRRTFALTRPTLGSEPRTGEISSMSAMW
BjuGTR1B3 TLLQRIGSGIFFALLSLLVSGFIEERRRTIALTKPTLGIEPRAGEISSMSAMW
BjuGTR2A1 TLLQRIGTGIFFAFLSLVVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BjuGTR2A2 TLLQRIGTGIFFAFVSLIVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BjuGTR2A3 TLLQRIGAGILFALLSLIVSGFVEERRRTLALTKPTLGLAPRKGEISSMSAMW
BjuGTR2B1 TLLQRIGTGIFFAFLSLVVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BjuGTR2B2 TLLQRIGTGIFFAFLSLIVSGFVEERRRTFALTKPTLGLAPRKGEISSMSAMW
BjuGTR2B3 TLLQRIGTGIFFALLSLIVSGFVEEHRRNLALTKPTLGLAPRKGEISSMSAMW
BnaGTR1A1 TLLQRIGAGIFFAVLSLLVSGFIEERRRSIALTKQTLGMEPRTGEISSMSAMW
BnaGTR1A2 TLLQRIGAGIFFAVLSLLVSGFIEERRRTFALTRPTLGSEPRTGEISSMSGMW
BnaGTR1A3 TLLQRIGSGIFFALLSLLVSGFVEERRRAIALTKPTLGIEPRAGEISSMSAMW
BnaGTR1C1 TLLQRIGAGIFFAVLSLLVSGFIEERRRSIALTKQTLGMEPRTGEISSMSAMW
BnaGTR1C2 TLLQRIGAGIFFAVLSLLVSGFIEERRRTFALTRPTLGSEPRTGEISSMSAMW
BnaGTR1C3 TLLQRIGSGIFFALLSMLISGFVEERRRAIALTKPTLGIEPRAGEISSMSAMW
BnaGTR2A1 TLLQRIGTGIFFAFLSLVVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BnaGTR2A2 TLLQRIGTGIFFAFVSLIVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BnaGTR2A3 TLLQRIGAGIFFALLSLIVSGFVEERRRTLALTQPTLGLAPRKGEISSMSAMW
BnaGTR2C1 TLLQRIGTGIFFAFLSLVVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BnaGTR2C2 TLLQRIGTGIFFAFVSLIVSGFVEERRRTFALTKPTLGMAPRKGEISSMSAMW
BnaGTR2C3 TLLQRIGAGIFFALLSLIVSGFVEERRRTLALTKPTLGLAPRKGEISSMSAMW
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          * *  * ***    **  *   *         *        *         *      * *
AtGTR1    LIPQLTLAGIAEAFAAIGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
AtGTR2    LIPQLSLAGVAEAFAAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYLGSFL
BjuGTR1A1 LIPQLVLAGIAEAFTAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLASFL
BjuGTR1A2 LIPQLVLAGVAEAFAAIGQMEFYYKQFPENMKSFAGSIFYVGGGVSSYLASFL
BjuGTR1A3 LIPQLVLAGIAEAFAAVGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
BjuGTR1B1 LIPQLVLAGIAEAFTAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLASFL
BjuGTR1B2 LIPQLVLAGIAEAFAAIGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
BjuGTR1B3 LIPQLLLAGIAEAFAAIGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
BjuGTR2A1 LIPQLTLAGVAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYLGSFL
BjuGTR2A2 LIPQLALAGIAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLGSFL
BjuGTR2A3 LIPQLVLAGIADAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYISSFL
BjuGTR2B1 LIPQLTLAGVAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYLASFL
BjuGTR2B2 LIPQLALAGIAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLGSFL
BjuGTR2B3 LVPQLVLAGIGDAFGAIGQMEFYYKQFPENMRSFAGSLFYVGAGVSSYISSFL
BnaGTR1A1 LIPQLVLAGIAEAFTAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLASFL
BnaGTR1A2 LIPQLVLAGVAEAFAAIGQMEFYYKQFPENMKSFAGSIFYVGGGVSSYLASFL
BnaGTR1A3 LIPQLVLAGIAEAFAAVGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
BnaGTR1C1 LIPQLVLAGIAEAFTAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLASFL
BnaGTR1C2 LIPQLVLAGVAEAFVAIGQMEFYYKQFPENMKSFAGSIFYVGGGVSSYLASFL
BnaGTR1C3 LIPQLTLAGIAEAFAAVGQMEFYYKQFPENMKSFAGSIFYVGAGVSSYLASFL
BnaGTR2A1 LIPQLTLAGVAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYLGSFL
BnaGTR2A2 LIPQLALAGIAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLGSFL
BnaGTR2A3 LIPQLVLAGIADAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYISSFL
BnaGTR2C1 LIPQLTLAGVAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGGGVSSYLGSFL
BnaGTR2C2 LIPQLALAGIAEAFGAIGQMEFYYKQFPENMRSFAGSIFYVGAGVSSYLGSFL
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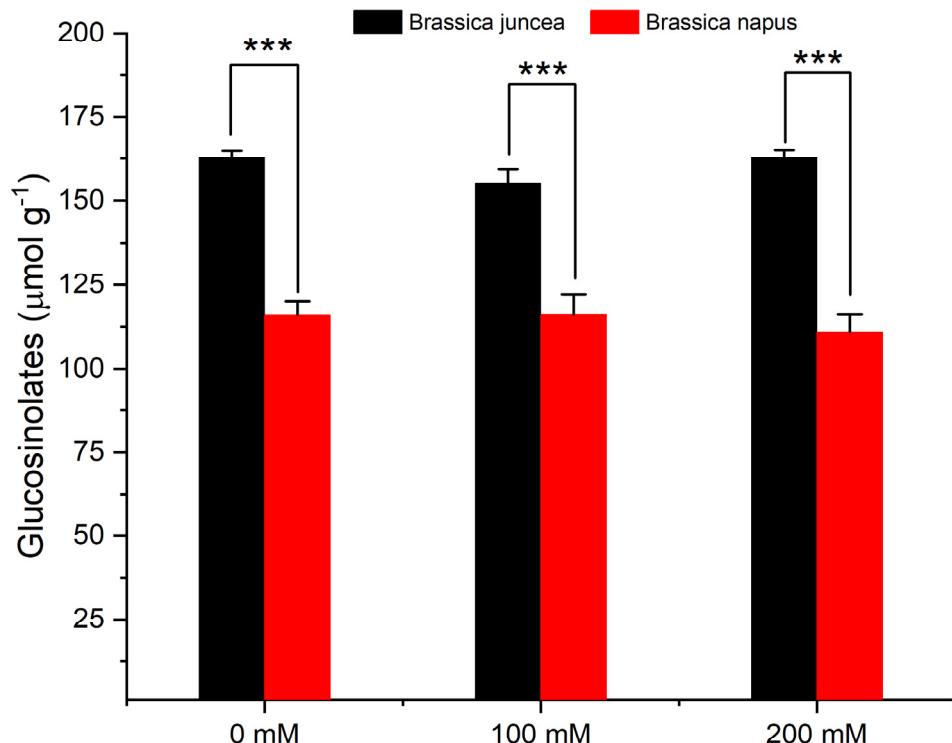
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          *  * *   *          * *
AtGTR1    ISTVHRTTAHSPSGNWLAEDLNKAKLDYFYFMLTGLMVVNMAYFLLMARWYRYK
AtGTR2    IATVHRTTQNSSGGNWLAEDLNKGRLDLFYFMIAGILAVNFAYFLVMSRWYRYK
BjuGTR1A1 ISTVHRTTEHSPSGNWLAEDLNKAKLDYFYFMLTGLMFVNMVYFLIMAKFYRYK
BjuGTR1A2 ISTVHRTTEHSPTGNWLAEDLNKAKLDYFYFMLTGLMFVNFLYFLLMARWYRYK
BjuGTR1A3 ISTVHKTTEHSRSGNWLAEDLNKGKLDYFYFMLTGLMFVNMVYFLLMAKFYRYK
BjuGTR1B1 ISTVHRTTEHSPSGNWLAEDLNKAKLDYFYFMLTGLMFVNMVYFLIMAKFYRYK
BjuGTR1B2 ISTVHRTTEHSPTGNWLAEDLNKAKLDYFYFMLTGLMFVNFLYFLLMARWYRYK
BjuGTR1B3 ISTVHKTTEHSPSGNWLAEDLNKGKLDYFYFMLTGLMFVNMGYFLLIAKFYRYK
BjuGTR2A1 IATVHRTTQNSAGGNWLAEDLNKGRLDLFYFMIAGILAVNFAYFLVMSRWYRYK
BjuGTR2A2 IAMVHRTTQNSAGGNWLAEDLNKGRLDYFYFMIAGILAVNFAYFLVMSRWYRYK
BjuGTR2A3 ITTVHRMTQN---------DL--------------------------------
BjuGTR2B1 IATVHRTTQNSAGGNWLAEDLNKGRLDLFYFMIAGILAVNFAYFLVMSRWYRYK
BjuGTR2B2 IAMVHRTTQNSAGGNWLAEDLNKGRLDYFYFMIAGILAVNFAYFLVMSRWYRYK
BjuGTR2B3 ITTVHRTTQNSAGGNWLAEDLNKGRLDYFYFLLAGISAVNFAYFLVMARWYRYK
BnaGTR1A1 ISTVHRTTEHSPSGNWLAEDLNKAKLDYFYFMLTGLMFVNMVYFLIMAKFYRYK
BnaGTR1A2 ISTVHRTTEHSPTGNWLAEDLNKAKLDYFYFMLTGLMFVNFLYFLLMARWYRYK
BnaGTR1A3 ISTVHKTTEHSPSGNWLAEDLNKGKLDYFYFMLTGLMFVNMVYFLIMAKFYRYK
BnaGTR1C1 ISTVHRTTEHSPSGNWLAEDLNKAKLDYFYFMLTGLMFVNMVYFLIMAKFYRYK
BnaGTR1C2 ISTVHRTTEHSPTGNWLAEDLNKAKLDYFYFMLTGLMFVNFLYFLLMARWYRYK
BnaGTR1C3 ISTVHKTTEHSRSGNWLAEDLNKGKLDYFYFMITGLMFVNMGYFLLMAKFYRYK
BnaGTR2A1 IATVHRTTQNSAGGNWLAEDLNKGRLDLFYFMIAGILAVNFAYFLVMSRWYRYK
BnaGTR2A2 IAMVHRTTQNSAGGNWLAEDLNKGRLDYFYFMIAGILAVNFAYFLVMSRWYRYK
BnaGTR2A3 ITTVHRMTQNSAGGNWLAEDLNKGRLDYFYFLLAGILAVNFAYFLVMARWYRYK
BnaGTR2C1 IATVHRTTQNSAGGNWLAEDLNKGRLDLFYFMIAGILAVNFAYFLVMSRWYRYK
BnaGTR2C2 IAMVHRTTQNSAGGNWLAEDLNKGRLDYFYFMIAGILAVNFAYFLVMSRWYRYK
BnaGTR2C3 ITTVHRMTQNSAGGNWLAEDLNKGRLDYFYFLLAGILAVNFAYFLVMARWYKYK
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AtGTR1    GGNDEDITEIETNEEETKLQDKNSV
AtGTR2    GSDDE-VTTYETNENIIKQQDKNVA
BjuGTR1A1 GSDDKVISAIETSEDETKKQEKNSV
BjuGTR1A2 GTHDEVSYVVDTVDEETKQQDKNSV
BjuGTR1A3 VTNDEANSVIKTNEEETKQHDKSYV
BjuGTR1B1 DSDDKGISAIETSEEETKKEEKNSV
BjuGTR1B2 GTHDEVSYVVETVEEETKQQDKNSV
BjuGTR1B3 VTDDEENSVIKINEEEAKQQNKNHV
BjuGTR2A1 GSDDE-VTSYETNGDVIKQQDKNKV
BjuGTR2A2 GSDDE-VTTYETNGDAIKQQDKNTV
BjuGTR2A3 -------------------------
BjuGTR2B1 GSDDD-VTTCETNGDVIKQQDKNNV
BjuGTR2B2 GSDDE-VKTYETNGDIIKQQDKNKV
BjuGTR2B3 GSDDE-EISYETNGDIIKEQDKNKV
BnaGTR1A1 GSDDKVISAIETSEDETKKQAKNSV
BnaGTR1A2 GTHDEVSYVVDTVDEETKQQDKNSV
BnaGTR1A3 VTNDEANSVIKTNEEETKQHDKSYV
BnaGTR1C1 GSDDKVISAIETNEDETKKQEKNSV
BnaGTR1C2 GTHDEVSYVVDTVDEETKQQDKNSV
BnaGTR1C3 VTNDEANSVIKTYEEETKQQDKSYV
BnaGTR2A1 GSDDE-VTAYETNGDVIKQQDKNKV
BnaGTR2A2 GSDDE-VTTYETNGDAIKQQDKNTV
BnaGTR2A3 GSDDE-ETSYETSGDIIKEQDKNKV
BnaGTR2C1 GSDDE-VTAYETNGDVIKQQDKNKV
BnaGTR2C2 GSDDE-VTTYETNGDAIKQQDKNTV
BnaGTR2C3 GSDDE-ETSYETSGDIIKEQDKNKV
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Figure S1: Multiple sequence alignment of GTR proteins from Arabidopsis*, B. juncea* and *B. napus.* Multiple sequence alignment was performed by submitting the protein sequences into online available MUSCLE alignment tool using default settings. Different conserved amino acids are represented by different color codes in the picture. The accession number of the query proteins are given as under: AtGTR1 (AT3G47960.1), BnaGTR1A1 (A06p19700.1_BnaDAR), BnaGTR1A2 (A06p27390.1_BnaDAR), BnaGTR1A3 (A01p25730.1_BnaDAR), BnaGTR1C1 (C03p72210.1_BnaDAR), BnaGTR1C2 (C03p66900.1_BnaDAR), BnaGTR1C3(C01p32480.1_BnaDAR), BjuGTR1A1 (BjuVA06G19500), BjuGTR1A2 (BjuVA06G26150), BjuGTR1A3 (BjuVA01G26580), BjuGTR1B1 (BjuVB08G47510), BjuGTR1B2 (BjuVB06G23560), BjuGTR1B3 (BjuVB05G42900), BnaGTR2A1 (A02p42460.1_BnaDAR), BnaGTR2A2 (A06p29420.1_BnaDAR), BnaGTR2A3 (A09p07810.1_BnaDAR), BnaGTR2C1 (C02p62380.1_BnaDAR), BnaGTR2C2 (C03p64110.1_BnaDAR), BnaGTR2C3 (C09p08780.1_BnaDAR), BjuGTR2A1 (BjuVA02G47610), BjuGTR2A2 (BjuVA06G28410), BjuGTR2A3 (BjuVA09G07610), BjuGTR2B1 (BjuVB04G01960), BjuGTR2B2 (BjuVB06G11810), BjuGTR2B3 (BjuVB07G18470).

Figure S2: Concentration of overall glucosinolates content in seed. Plants of *B. juncea* (blue lines) and *B. napus* (orange) were grown under 0, 100 and 200 mM NaCl concentrations. Values represent means ± SD from three biological replicates per treatment. Data points represent the means ± SD of three biological replicates. Significant differences are shown with different asterisks (Tukey's HSD, *p* = 0.05).) Significant codes: ***, **, * at *p* = 0.0001, 0.001 and 0.01, respectively.)