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Diversity and validation of microsatellite markers in *Saltol*-QTL region in contrasting rice genotypes for salt tolerance at the early vegetative stage

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Supplementary Table 1. List of germplasm with plant growth, ion content in shoot, tolerance reaction (based on SES score) and their assignment to UPGMA clusters based on data on phenotypic traits under salt stress

Sl no	Common name *	Status of germplasm	Dry wt (mg)	Na^+ conc. (µg mg^{-1})	K^+ conc. (µg mg^{-1})	Shoot length (cm)	Increment of shoot (%)	Root length (cm)	Na^+-K^+ ratio in shoot	Salt-tolerance reaction	Cluster position
1	Rupshal	LR	46.40	91.52	236.67	31.51	48.35	16.19	0.39	MT	I
2	Matla	LR	38.18	70.52	218.67	24.05	33.68	14.09	0.33	MT	
3	Murishal	LR	36.00	79.52	238.92	26.25	40.57	16.05	0.33	MT	
4	Kumrogour (AC43233)	LR	28.04	85.52	198.42	24.90	36.64	11.66	0.44	MT	
5	Kanakchur (AC43231)	LR	43.10	93.77	205.17	29.35	59.54	10.93	0.46	MS	II
6	Kalomota (AC43216)	LR	29.20	102.77	243.42	28.17	43.76	12.81	0.43	MS	
7	Sadamota (AC43221)	LR	31.20	97.52	223.17	27.05	41.24	13.15	0.44	MS	
8	Nadashal (AC43225)	LR	32.20	117.77	214.17	26.51	40.32	11.52	0.56	MS	
9	Patnai (AC43220)	LR	59.10	54.77	252.42	33.79	51.37	13.43	0.22	MT	III
10	SR 26B	CV	52.00	70.52	270.42	31.55	52.64	14.95	0.26	MT	
11	Hasawi	LR	40.53	56.27	245.67	30.47	45.58	12.06	0.23	MT	
12	Kamini	LR	31.60	71.27	283.92	29.23	59.47	13.32	0.25	MT	
13	FL496	RIL	42.00	66.77	304.17	28.85	55.15	15.40	0.22	T	
14	FL478	RIL	58.64	58.52	297.42	29.44	59.80	10.74	0.20	T	

15	Kalodhan	LR	30.50	101.27	218.67	30.45	35.20	22.92	0.47	MS	IV
16	Talmugur (AC43228)	LR	52.70	66.02	268.17	39.81	50.95	22.67	0.25	MT	V
17	Chettivirippu (AC39388)	LR	76.70	63.77	337.92	42.87	57.39	17.31	0.19	MT	
18	Chettivirippu (AC39389)	LR	80.55	61.52	310.92	41.49	50.92	20.10	0.20	T	
19	Pokkali (AC39416)	LR	72.00	58.52	283.50	40.35	55.64	22.90	0.21	T	
20	Pokkali (AC41585)	LR	77.00	61.52	283.50	43.40	61.51	22.45	0.22	T	
21	Nona Bokra	LR	81.00	73.52	281.67	32.35	50.71	18.90	0.26	MT	
22	Rahspunjar	CV	67.00	99.77	308.67	35.55	51.48	20.10	0.32	MT	
23	Dhudheswar (AC43217)	LR	18.60	93.02	211.92	19.72	25.48	15.97	0.44	MS	VI
24	Mutishal	LR	17.50	89.27	189.42	22.99	27.90	14.19	0.48	S	
25	Salibahana	LR	19.00	87.02	171.42	14.76	31.94	14.39	0.51	S	
26	Jamainadu	LR	16.00	111.77	193.92	16.84	25.81	17.73	0.58	S	
27	Haynath	LR	11.00	110.27	121.92	13.92	14.34	13.03	0.93	S	
28	Latishal	LR	21.30	91.52	135.42	19.91	23.76	11.74	0.69	S	
29	Savitri	CV	35.00	96.77	139.92	19.15	26.68	13.65	0.69	S	
30	IR 29	CV	21.00	99.77	130.92	14.33	20.82	11.10	0.76	S	
	Mean	-	42.17	82.75	234.02	28.30	42.62	15.51	0.40	-	-
	C.V.	-	16.91	7.52	10.77	10.31	10.21	9.03	15.97	-	
	S.E.	-	5.04	4.40	11.82	2.06	3.08	0.99	0.05	-	
	C.D. (at 0.05)	-	14.59	12.73	31.54	5.97	8.90	2.87	0.13	-	

Note: *CRRI accession number in parenthesis

Note: LR: landrace, CV: cultivar; RIL: recombinant inbred line

Supplementary Table 2. Distance matrix derived from Euclidian coefficients among 30 rice germplasm based on morpho-physiological traits under salt-stress at seedling stage.

Variety	**Savitri**	**FL496**	**SR26B**	**IR29**	**Matla**	**Rahspunjar**	**Nonabokra**	**FL478**	**PokAC39416**	**Kamini**	**Mutisal**	**Kalomota**	**Sadamota**	**CheAC39388**	**Murisal**	**Kanakchur**	**Kalodhan**	**Talmugur**	**Kumargaur**	**Nadasal**	**Patnai**	**Dhudeswar**	**Jamainadu**	**Rupsal**	**Latisal**	**Salibahana**	**Haynath**	**PokAC41585**	**Hasawi**	**CheAC39389**
Savitri	0																													
FL496	2.83	0																												

SR26B	3.93	1.77	0																											
IR29	3.42	1.33	1.84	0																										
Matla	2.33	2.5	2.97	3.35	0																									
Rashpunjar	5.66	3.6	2.72	3.08	5.03	0																								
Nonabokra	2.58	4.5	5.56	5.16	3.11	7.53	0																							
FL478	2.4	4.22	5.62	4.55	4.25	7.13	2.62	0																						
PokAC39416	2.04	3.68	4.99	4.06	3.86	6.71	3.01	1.87	0																					
Kamini	4.02	2.23	2.34	1.6	3.97	2.08	5.92	5.19	4.92	0																				
Mutisal	1.84	3.33	4.15	3.32	3.69	5.37	4.05	2.92	2.33	3.68	0																			
Kalomota	1.81	2.09	2.89	2.54	2.81	4.6	4.22	3.44	2.6	3.07	1.75	0																		
Sadamota	3.33	5.7	6.9	6.33	4.84	8.69	2.33	2.41	3.13	6.97	4.35	4.66	0																	
CheAC39388	2.6	2.41	2.66	2.64	3.22	3.85	4.99	4.41	3.71	2.65	2.17	1.27	5.61	0																
Murisal	2.05	1.97	3.54	2.37	3.05	5.03	3.45	2.4	2.43	3.15	2.63	2.21	4.27	3.02	0															
Kanakchur	2.1	1.74	3.08	1.95	3.15	4.25	4.21	3.14	2.71	2.36	1.99	1.51	4.95	1.98	1.34	0														
Kalodhan	3.39	5.67	6.9	6.36	4.58	8.67	2.01	2.68	3.57	6.99	4.71	4.97	1.6	5.84	4.27	5.07	0													
Talmugur	3.09	5.02	6.46	5.36	5.19	7.9	3.65	1.72	1.96	6.04	3.34	4.03	2.67	4.92	3.35	3.8	3.1	0												
Kumargaur	4.65	2.72	2.47	2.04	4.51	1.46	6.66	5.92	5.57	0.94	4.25	3.63	7.66	2.99	3.83	3.02	7.67	6.63	0											
Nadasal	3	0.96	1.86	1.09	2.91	3.31	4.7	4.2	3.76	1.66	3.1	1.99	5.86	2.24	2.06	1.55	5.92	5.14	2.36	0										
Patnai	2.37	3.55	5.1	3.88	4.09	6.52	3.13	1.13	1.58	4.54	2.74	2.99	3.29	3.99	1.73	2.42	3.52	1.99	5.27	3.52	0									
Dhudeswar	3.68	2.15	2.05	1.6	3.54	2.24	5.59	5.03	4.84	0.9	3.47	2.9	6.67	2.42	3.06	2.4	6.64	5.91	1.26	1.76	4.54	0								
Jamainadu	2.03	4.27	5.06	5.03	2.94	7.09	2.26	3.21	3.09	5.71	3.46	3.27	2.55	3.98	3.63	3.99	2.6	3.68	6.26	4.59	3.67	5.22	0							
Rupsal	1.53	3.63	4.95	4.1	3.47	6.68	2.25	1.1	1.23	4.87	2.41	2.69	2.37	3.72	2.12	2.72	2.65	1.88	5.55	3.74	1.4	4.63	2.36	0						
Latisal	1.34	4.22	5.66	4.7	4.0	7.39	2.68	1.9	1.41	5.6	3.2	3.4	2.5	4.5	2.8	3.43	2.7	1.5	6.2	4.5	1.9	5.49	2.87	1.4	0					

				9	3			3		5	7	9	4		5		1	6	6	2	5									
Salibahana	2.35	4.6	5.74	5.18	3.74	7.52	2.02	2.18	2.91	5.89	3.64	3.92	1.84	4.72	3.28	4.03	1.53	2.71	6.49	4.89	2.94	5.44	1.82	1.83	2.27	0				
Haynath	2.43	5.64	6.81	6.28	4.31	8.64	1.55	2.94	3.66	7	4.81	5.1	1.88	5.99	4.35	5.16	1.04	3.5	7.69	5.91	3.71	6.63	2.77	2.83	2.84	1.83	0			
PokAC41585	3.6	6	7.11	6.6	4.61	8.92	1.85	3.11	3.82	7.27	4.84	5.26	1.76	6.13	4.7	5.41	1.14	3.6	7.97	6.22	3.97	6.89	2.81	3.02	3.09	2.01	0.65	0		
Hasawi	1.21	2.18	3.66	2.84	2.44	5.41	2.79	2.3	1.9	3.68	2.38	1.97	3.72	2.89	1.12	1.65	3.69	3.03	4.22	2.49	1.84	3.48	2.8	1.59	2.15	2.7	3.69	4.03	0	
CheAC39389	1.76	1.77	2.69	2.15	2.68	4.33	3.96	3.31	2.66	2.68	1.74	0.53	4.73	1.34	1.84	1.12	4.95	4.04	3.29	1.61	2.84	2.5	3.39	2.65	3.51	3.85	5.04	5.24	1.76	0

Supplementary Table 3. Primers in the *Saltol* QTL region tested for polymorphism in rice genotypes

Primer name	Marker position on Chromosome 1 (Mb)/ gene bank accession	Motif	Forward (5’-3’)	Reverse (5’-3’)	Polymorphism (%)/ reaction	Number of alleles	Size range of alleles (bp)	PIC	MI
RM10682	10.8	$(AG)_{17}$	CCATTTGCAGTATGAACCATGC	ATCATGCAATAGCCGGTAGAGG	100	4	180-220	0.37	0.43
RM8094	11.2	$(AT)_{31}$	AAGTTTGTACACATCGTATACA	CGCGACCAGTACTACTACTA	66	2	170-210	0.17	0.13
RM10719	11.35	$(CCG)_{8}$	GAGGACGAAGGAGAAGGACAAGG	CGAGCCCATCTGATGTGAGACC	100	3	160-490	0.30	0.38
RM10720	11.4	$(TA)_{34}$	GCAAACGTCTACGTGAGAAACAAGC	GCATGTGGTGCCTTAACATTTGG	100	4	185-250	0.30	0.30
RM10745	11.7	$(TATG)_{9}$	TGACGAATTGACACACCGAGTACG	ACTTCACCGTCGGCAACATGG	100	4	190-205	0.34	0.34
RM10772	12.1	$(AAG)_{16}$	GCACACCATGCAAATCAATGC	CAGAAACCTCATCTCCACCTTCC	100	4	385-430	0.26	0.28
RM10777	12.25	$(AAG)_{9}$	GTACGTAAACGCGGAAGGTGACG	CGACGTACGAGATGCCGATCC	100	5	180-230	0.30	0.30
RM3412	11.5	$(CT)_{17}$	AAAGCAGGTTTTCCTCCTCC	CCCATGTGCAATGTGTCTTC	100	6	200-270	0.29	0.32
RM23	10.7	-	CATTGGAGTGGAGGCTGG	GTCAGGCTTCTGCCATTCTC	NCR	-	-	-	-
RM10711	11.15	$(GAG)_{9}$	GCTTCGATCGATGAGAAAGTAGAGG	GAATCTCCCATCCTTCCCTTCC	NCR	-	-	-	-

RM10725	11.45	$(GT)_{25}$	TGAGGCTACTTACCTACGATGTGC	GTCTGACCGCACACATAACACC	NCR	-	-	-	-
RM10740	11.6	$(AG)_{17}$	TGATGGATCTCTGAGGTGTAAAGAG	TGCACTAATCTTTCTGCCACAGC	NCR	-	-	-	-
SAL-1	OS01g0756700		TTGAGAAGGACATCCGGTTC	AAGAGGGTGACCTGGTGTTG	NP	-	-	-	-
SAL-2	GenBank: DQ148410.1		CCTGCCACCTTACACCACTT	GCTGTAGTTGATGGGGTCGT	NP	-	-	-	-
SAL-3	GenBank: EF611740.1		CGGTATTGCTGTTGATGACG	ACTTCCAGATCAAGGCGATG	NP	-	-	-	-
SAL-4	GenBank: EF611739.1		ATGGTGTCAATGATGCTCCA	ATATCCAGATGAGCGCGAGT	NP	-	-	-	-
SAL-5	GenBank: AY137590.1		CGTCTTTTCCGTCCTCTCTG	CGTAGTTTGTTGCCCGATTT	NP	-	-	-	-

NCR: Not clear reaction in all the genotypes, NP: Non-polymorphic, blank (-) indices unavailability of data

Supplementary Table 4. Jaccard's coefficients matrix among 30 rice germplasm based on SSR primers in the *Saltol* QTL region.

Variety	**Savitri**	**FL496**	**SR26B**	**IR29**	**Matla**	**Rashpunjar**	**Nonabokra**	**FL478**	**PokAC39416**	**Kamini**	**Mutisal**	**Kalomota**	**Sadamota**	**CheAC39388**	**Murisal**	**Kanakchur**	**Kalodhan**	**Talmugur**	**Kumargaur**	**Nadasal**	**Patnai**	**Dudeswar**	**Jamainadu**	**Rupsal**	**Latisal**	**Salibahana**	**Haynath**	**PokAC41585**	**Hasawi**	**CheAC39389**
Savitri	1																													
FL496	0.33	1																												
SR26B	0.31	0.24	1																											
IR29	0.25	0.25	0.62	1																										
Matla	0.54	0.18	0.5	0.3	1																									
Rashpunjar	0.5	0.5	0.47	0.6	0.3	1																								
Nonabokra	0.62	0.31	0.29	0.2	0.3	0.47	1																							
FL478	0.27	0.36	0.33	0.5	0.3	0.43	0.18	1																						
PokAC39416	0.29	0.38	0.27	0.4	0.2	0.46	0.19	0.89	1																					
Kamini	0.27	0.19	0.33	0.4	0.4	0.18	0.18	0.2	0.21	1																				

								9																						
Mutisal	0.18	0.43	0.31	0.4	0.3	0.31	0.17	0.46	0.38	0.36	1																			
Kalomota	0.27	0.46	0.25	0.5	0.2	0.54	0.25	0.38	0.42	0.29	0.46	1																		
Sadamota	0.19	0.27	0.43	0.3	0.3	0.25	0.25	0.38	0.31	0.29	0.46	0.29	1																	
CheAC39388	0.18	0.43	0.24	0.3	0.2	0.31	0.17	0.73	0.64	0.27	0.33	0.27	0.27	1																
Murisal	0.27	0.46	0.25	0.4	0.2	0.43	0.18	0.5	0.55	0.29	0.46	0.64	0.29	0.36	1															
Kanakchur	0.2	0.38	0.36	0.5	0.3	0.36	0.12	0.55	0.45	0.42	0.64	0.55	0.42	0.38	0.7	1														
Kalodhan	0.36	0.27	0.25	0.4	0.4	0.33	0.25	0.29	0.31	0.29	0.36	0.38	0.13	0.19	0.29	0.31	1													
Talmugur	0.29	0.22	0.53	0.5	0.3	0.53	0.35	0.24	0.25	0.31	0.29	0.4	0.31	0.22	0.31	0.25	0.24	1												
Kumargaur	0.25	0.25	0.5	0.4	0.3	0.4	0.31	0.27	0.2	0.19	0.33	0.27	0.36	0.25	0.36	0.38	0.19	0.57	1											
Nadasal	0.27	0.36	0.43	0.6	0.4	0.43	0.18	0.5	0.42	0.29	0.58	0.38	0.29	0.36	0.5	0.7	0.5	0.31	0.46	1										
Patnai	0.36	0.27	0.43	0.5	0.3	0.54	0.25	0.29	0.31	0.29	0.27	0.38	0.2	0.19	0.5	0.42	0.29	0.5	0.58	0.5	1									
Dhudeswar	0.25	0.33	0.4	0.3	0.2	0.4	0.24	0.27	0.29	0.36	0.33	0.46	0.36	0.18	0.58	0.5	0.19	0.38	0.43	0.36	0.73	1								
Jamainadu	0.19	0.36	0.33	0.4	0.19	0.25	0.11	0.29	0.31	0.5	0.46	0.38	0.29	0.19	0.38	0.42	0.38	0.31	0.19	0.38	0.38	0.46	1							
Rupsal	0.36	0.27	0.33	0.3	0.36	0.33	0.25	0.2	0.21	0.38	0.27	0.38	0.29	0.12	0.5	0.42	0.29	0.4	0.46	**0.29**	**0.5**	**0.58**	0.29	1						
Latisal	0.46	0.27	0.25	0.3	0.46	0.25	0.25	0.38	0.31	0.64	0.36	0.29	0.38	0.27	0.29	0.42	0.29	0.17	0.19	**0.29**	**0.29**	**0.36**	0.38	0.38	1					
Salibahana	0.29	0.64	0.19	0.3	0.2	0.36	0.19	0.42	0.45	0.21	0.38	0.42	0.31	0.5	0.42	0.45	0.21	0.18	0.2	0.31	0.21	0.29	0.31	0.21	0.42	1				
Haynath	0.27	0.27	0.11	0.2	0.36	0.18	0.18	0.29	0.31	0.2	0.27	0.2	0.06	0.36	0.2	0.21	0.38	0.11	0.12	0.2	0.13	0.12	0.2	0.2	0.29	0.42	1			
PokAC41585	0.19	0.19	0.25	0.3	0.27	0.18	0.25	0.38	0.31	0.29	0.27	0.29	0.2	0.36	0.29	0.31	0.38	0.11	0.19	0.29	0.13	0.19	0.13	0.2	0.29	0.21	0.29	1		
Hasawi	0.46	0.46	0.11	0.2	0.27	0.33	0.33	0.38	0.42	0.2	0.19	0.29	0.13	0.46	0.29	0.21	0.29	0.17	0.19	0.2	0.2	0.19	0.13	0.29	0.38	0.55	0.64	0.29	1	
CheAC39389	0.12	0.27	0.25	0.4	0.19	0.25	0.11	0.5	0.42	0.2	0.36	0.38	0.2	0.46	0.38	0.42	0.29	0.17	0.27	0.38	0.2	0.19	0.2	0.13	0.2	0.31	0.2	0.64	0.2	1

Supplementary Table 5. Allelic diversity using microsatellite markers at the *Saltol* QTL region (and the region adjacent to it) of parents and derived lines from Annapurna × FL 478.

	Microsatellite primers												
	RM6515	RM1287	RM8094	RM3412	RM10740	RM10772	RM10773	RM10777	RM10780	RM140	RM7075	RM11008	RM24
	Position on short arm of chromosome 1 (Mb)												
	3.1	10.8	11.2	11.5	11.6	12.1	12.15	12.25	12.25	12.4	15.1	18	18.9
	Band position (bp) in agarose gel												
A allele (Annapurna)	220	22	280	220	240	490	400	190	360	310	180	220	160
B allele (FL478)	200	200	190	200	220	390	450	200	310	295	150	240	140
Breeding lines													
AF1	A	B	B	B	B	B	B	B	B	B	B	B	B
AF2	A	A	A	A	A	C	A	A	A	A	A	A	A
AF3	A	B	B	B	B	B	B	B	B	B	B	B	B
AF4	B	A	A	A	A	C	A	C	A	A	A	A	A
AF5	A	B	C	C	A	C	B	C	C	A	C	B	B
AF6	A	A	A	B	B	B	B	B	B	B	B	B	B
AF7	A	A	C	C	A	B	B	C	B	B	C	A	A
AF8	A	B	B	B	B	B	B	C	B	B	B	B	B
AF9	C	A	A	A	A	A	A	A	A	A	A	A	A
AF10	A	A	A	A	C	C	C	A	C	C	C	A	A
AF11	B	B	B	B	B	B	B	B	B	B	B	B	B
AF12	C	B	B	B	B	B	C	B	B	B	B	B	B
AF13	C	A	A	A	A	A	A	A	A	U	A	A	A
AF14	C	A	A	B	A	C	B	A	C	B	C	B	A
AF15	C	C	C	B	B	C	B	C	C	B	C	B	C
AF16	A	C	C	A	B	B	B	B	B	B	C	B	B
AF17	B	B	B	B	B	B	B	B	B	B	B	B	B
AF18	C	A	A	A	A	C	A	A	A	A	A	A	A

AF19	A	B	B	B	B	B	B	B	B	B	B	B	B
AF20	A	B	A	A	B	B	B	B	B	B	B	B	B
AF21	B	C	B	C	B	C	C	B	C	B	C	A	A
AF22	A	A	A	A	A	B	B	B	B	B	B	B	B
AF23	A	B	A	A	A	B	B	B	B	B	B	A	B
AF24	A	B	C	A	A	B	B	C	B	B	B	B	A
AF25	A	B	B	A	A	B	B	B	B	B	B	B	B
AF26	A	A	A	A	A	A	A	A	A	A	C	B	C
AF27	A	C	A	A	A	B	B	B	B	B	B	B	B
AF28	B	B	B	B	B	B	B	B	B	B	B	B	B
AF29	C	B	B	B	B	B	B	B	B	B	B	B	B
AF30	C	C	B	A	B	B	B	B	B	B	B	B	B
AF31	A	B	B	B	B	B	B	B	B	B	B	B	B
AF32	A	B	B	B	C	B	B	B	B	B	B	B	B
AF33	B	A	A	A	A	C	B	A	A	A	A	B	A
AF34	A	A	A	A	A	B	B	B	B	B	B	A	B
AF35	C	A	A	A	A	B	B	B	B	B	B	B	B
AF36	B	A	A	A	A	B	B	C	B	B	B	B	B
AF37	A	A	A	A	A	B	B	B	B	B	B	B	B

Footnote: A: Annapurna allele, B: FL478 allele, C: heterozygote for both the alleles, U: unidentified /no reaction

Supplementary Table 6. Phenotypic description of derived lines from Annapurna × FL478 cross under salinity stress (at 6-8 dSm^{-1}).

	Genotypes	SES score	Survival (%)	Plant height (cm)	Maturity duration (days)	Yield under stress (g sq. m^{-1})
ANN	Annapurna	9	30	81	105	130
FL478	FL 478	3	80	98	115	190
AF1	CR 2815-4-23-5-S-2-1-1	3	90	84.3	102	662
AF2	CR 2815-2-4-2-1-1-1	3	95	85.3	103	685
AF3	CR 2815-4-23-5-S-1-1-1	3	92	85.3	104	650

AF4	CR 2815-5-1-3-5-1-2-1	3	100	86	109	695
AF5	CR 2815-4-27-4-S-1-1-1	3	100	82.3	110	632
AF6	CR 2815-5-6-1-S-1-1-1	5	80	73.7	111	174
AF7	AC35319	3	80	135	113	315
AF8	CR 2815-5-6-1-S-1-1-1	5	80	73.7	111	174
AF9	CR 2815-4-23-1-S-2-1-1	5	99	75.7	109	446
AF10	CR 2815-5-1-3-S-1-2-1	3	100	86	109	737
AF11	CR 2815-4-3-1-1-1-1	5	100	82.7	107	425
AF12	CR 2815-4-26-1-S-5-2-1	3	86	75.7	103	507
AF13	CR 2815-2-4-2-1-1-1	3	95	85.3	103	690
AF14	CR 2815-2-4-2-2-1-1	3	93	82.3	105	680
AF15	CR 2815-4-25-1-S-4-1-1	5	98	73.7	106	443
AF16	CR 2815-4-27-4-S-2-1-1	3	100	82.3	108	595
AF17	CR 2815-4-26-5-S-2-1-1	3	98	85.3	105	535
AF18	CR 2815-5-1-3-S-1-2-2	3	95	88	108	683
AF19	CR 2815-4-23-8-S-4-2-1	5	78	70	105	203
AF20	CR 2815-3-12-1-1-1-1	5	92	67.3	111	229
AF21	CR 2815-2-3-2-2-1-1	5	82	82.6	103	135
AF22	CR 2815-4-23-7-S-1-2-1	5	100	71.3	107	371
AF23	CR 2815-4-23-7-S-1-1-1	5	91	75	105	275
AF24	CR 2815-4-3-1-1-1-2	5	100	82.7	107	425
AF25	CR 2815-4-23-5-1-1-1	5	86	72	112	345
AF26	CR 2815-4-26-1-S-2-2-1	3	87	91	110	568
AF27	CR 2815-4-27-4-1-1-1	3	100	84.7	107	511
AF28	CR-2815-4-7-1-1-1-1	3	97	81.7	105	641
AF29	CR 2815-4-7-2-1-1-1	3	95	84.3	107	622
AF30	CR 2815-4-23-1-S-2-1-1	5	99	75.7	109	446
AF31	CR 2815-4-23-1-S-3-1-1	5	88	75.3	111	402
AF32	CR 2815-4-23-7-S-2-1-1	5	95	73.5	107	426
AF33	CR 2815- 4-26-2-1-1-1	3	97	84.3	110	722

AF34	CR 2815-4-26-1-S-4-1-1	3	100	77	107	672
AF35	CR 2815-4-27-4-S-2-1-1	3	100	82.3	108	595
AF36	CR 2815-4-23-1-S-4-1-1	5	95	72.7	107	435
AF37	CR 2815-4-23-5-1-1-2	5	88	68	110	237

upplementary Table 7. List of microsatellite primers located inside and adjacent to the *Saltol* QTL region (1.0 Mb-25 Mb) on the short arm of chromosome 1, tested for polymorphism between Annapurna and FL 478.

	Primer	Forward (5’-3’)	Reverse (5’-3’)
1	RM10715	GTAATCCATGCGATGGGACACG	AGCGCGCATAATCCCTACTTTGG
2	RM10716	CCTTCTTGCCGCCAACCTAGTCC	TTTGGCTGACATGACGCCTACG
3	RM10718	TAACTCGCCACCGATGATTTCG	CGACCAACGTGCAATAGTACAAGC
4	RM10719	GAGGACGAAGGAGAAGGACAAGG	CGAGCCCATCTGATGTGAGACC
5	RM10720	GCAAACGTCTACGTGAGAAACAAGC	GCATGTGGTGCCTTAACATTTGG
6	RM10724	ACATTTCCCAGGTTTGACTACGC	TGTAAGTCTGGTCAAGCATTGAGG
7	RM10725	TGAGGCTACTTACCTACGATGTGC	GTCTGACCGCACACATAACACC
8	RM10726	TGAGGCTACTTACCTACGATGTGC	GTCTGACCGCACACATAACACC
9	RM10727	GCCACTTATCAAAGGACGGTTCC	CGTGACGCCTTGGCAAATAGG
10	RM10738	CGTGCGAATGCGTGAGCTACC	CAATGCCCTAAGCAACCAGATACTCC
11	RM10739	CGTGCGAATGCGTGAGCTACC	CAATGCCCTAAGCAACCAGATACTCC
12	RM10740	TGATGGATCTCTGAGGTGTAAAGAGC	TGCACTAATCTTTCTGCCACAGC
13	RM10741	AGGTCGCCTGAGTTTCATACCC	TGTGCGGTTTAAGATAGAGTGAGC
14	RM10742	GTAGGAGCTCCACGCTAGTTTCC	ACAACTTGGAAGGTACGGACAGG
15	RM10744	CCACGCACCCAGTATATCACACC	ACATGCGCCCTCACTCTACG
16	RM10745	TGACGAATTGACACACCGAGTACG	ACTTCACCGTCGGCAACATGG
17	RM10746	ATGACTCTTCGCCATTCCATAGC	ACCATGGTCAGCCATCACTAGG
18	RM10747	TTTCACCATTTCGTCGGCATTGG	CAAACGCATCAAGCCATGAGACC
19	RM10748	CATCGGTGACCACCTTCTCC	CCTGTCATCTATCTCCCTCAAGC
20	RM10749	CGATGTAGTCGATGTGGATCAGG	TATGGTCGGATCAGCGTAAGTCC
21	RM10750	GTACGTAAATCGGGCGCTGACG	GCTTGTGAGGCCTAATTTGAGTTGC
22	RM10754	GCAGTAGCAGCGGTAGGAGTAGC	CCTGCTGCCTTGAATTGAACC
23	RM10757	GGCGCTAGTTATGGTAGAGATTTCG	AACAAATCTAGCGGCTGTTTCC
24	RM10763	AGATGTCGCCTGATCTTGCATCG	GATCGACCAGGTTGCATTAACAGC
25	RM10764	AGATGTCGCCTGATCTTGCATCG	GATCGACCAGGTTGCATTAACAGC
26	RM10765	AACCTGGTCGATCCGATAGC	GGTTCCCAACCAGGATTAAAGC
27	RM10766	CCGACCGACCAAAGATGATTTATCC	ACGTGCCAGCTGCAAGCTAATCC
28	RM10770	AATTTGCAGTTGGCATGGTTGG	ATGGATGGGAATCCACGTATAGAGC
29	RM10771	AGCATCGTCTCGATGTTCACG	CGAGTAGTTGTTGTCAGTTTGTCACC
30	RM10772	GCACACCATGCAAATCAATGC	CAGAAACCTCATCTCCACCTTCC
31	RM10773	CCACCTATAGAAATAGGTCCATGC	TAGAACATGTCACCATCCAAGG

32	RM10774	GGTCTAGCAGCTCTCCCTTCG	GCGATTTAGGAGCGTTTGTAAGG
33	RM10776	CCACGGTCAACAGAGAGATTCC	TTTCACCGACGAGGCTATCG
34	RM10777	GTACGTAAACGCGGAAGGTGACG	CGACGTACGAGATGCCGATCC
35	RM10778	CCTATATTACGCATGGCAACAACC	AAAGAGGTGCATATCCTTCCATGC
36	RM10779	TATGTTGTCGCCCTTCAGAAAGC	AGGAAGACTCCTTCGACGTTGC
37	RM10780	CTTGCACAAGAGATGATGATGAGC	CATGCTGAGAAATAGTACGCTTGG
38	RM10782	CTACTGATATGCCCGTACCAACG	CCAAACTGGAGTAGTATTAGGTGTGG
39	RM10791	TCTTCAAGAACCGTGAACGTTTGG	CTAATCGTCCCATTCGCCTACACC
40	RM10793	GACTTGCCAACTCCTTCAATTCG	TCGTCGAGTAGCTTCCCTCTCTACC
41	RM8115	TATATAGTAAATTTGTTTGGTGTAGG	ACAGATGGATATTATAAGAAGTAACA
42	RM10800	CGTACGCCCTCACATCACCTTTCC	CTCTCCGGGAGCTCACTTGTCG
43	RM10825	GGACACAAGTCCATGATCCTATCC	GTTTCCTTTCCATCCTTGTTGC
44	RM10843	CACCTCTTCTGCCTCCTATCATGC	GTTTCTTCGCGAAATCGTGTGG
45	RM10884	CAGGCTTGACGGACGACTCC	ACGAACGTGAACGAGCTAGGG
46	RM10871	TGAGGCTGTAACGTAGACGATGAACC	AAGCCTGCTAGAGAGGCCCAACC
47	RM10927	TGGATCCCACTAATCCAAATGC	GAAAGACTCCTTCCAATGTTAGGC
48	RM6711	TAGTGATAGGGGTGGTGTGG	TTACAAGCATGGGAGTTGGG
49	RM3252	GGTAACTTTGTTCCCATGCC	GGTCAATCATGCATGCAAGC
50	RM10115	ACAAGACGAGGTAACACGCAAGC	GCGAAGGATCAACGATGATATGG
51	RM575	CAATTTCCATAGGCTGCATG	GCTTGGGTTAGCGACGAC
52	RM3412 b	TCATGATGGATCTCTGAGGTG	GGGAGGATGCACTAATCTTTC
53	RM10287	GTATTCCTTGCTGCTGCTGATGG	GACTGGAGATGTGATCGGAAACC
54	RM11008	TTTGGATGGTCATTAGCCTCTGG	ATCAACCTTGCATGCTGTCTTCC
55	RM11300	GGTGAGGGAGGTACCGAACTAGG	AACTAGGGCGCTGGGAGAGG
56	RM1349	CGTTCCAATATTCAGACACAG	TTTCCATCTCGAGAAGCTC
57	RM7643	TCCTCCTATTCGGTCGAAAC	ACCAACGAAATACCGGCAC
56	RM11757	GCTTGTTGCCTGTGAACAGTAGC	TGTCAGCATGCAACATCAATCC
59	RM11874	CCACTAGCAGATGATCACAGACG	GAGCACCTCATAAGGGTTTCAGC
60	RM472	CCATGGCCTGAGAGAGAGAG	AGCTAAATGGCCATACGGTG
61	RM3482	TTGTTGTCAAGCTACGGTGG	CTGCTTCGTGATGTTGTTGG