

Table 2. Accession numbers and characteristics of *Arabidopsis* LCR proteins.

Gene name	Genomic sequence accession number	Coordinates of coding region (bp) ^a		EST accession N ^o	Previous or alternative gene name	intron size (bp)	Predicted cleavage site ^b	Protein mass (Da) ^c	pI
<i>LCR1</i>	AB020745.1	69811-69871	70503-70708	-	-	631	VVG/NV	9177	9.32
<i>LCR2</i>	AL161517.2	177572-177632	178425-178630	-	-	792	VIG/NL	7692	9.13
<i>LCR3</i>	AB018117.1	8754-8709	8598-8411	-	-	110	IEG/QQ	6073	8.06
<i>LCR4</i>	AB026647.1	72545-72485	71986-71805	-	-	498	VVG/NV	6620	8.51
<i>LCR5</i>	AC006283.5	42007-42067	42533-42702	-	-	465	VVA/NE	5850	8.65
<i>LCR6</i>	AB025609.1	6619-6574	6527-6349	-	-	46	IQG/QH	5627	6.29
<i>LCR7</i>	AL161550.2	12421-12481	12937-13127	-	-	455	-	6299	7.88
<i>LCR8</i>	AL137898.1	30245-30200	30077-29902	-	-	122	TQG/QH	5682	7.89
<i>LCR9</i>	AC007154.3	3842-3782	3514-3341	-	-	267	VMG/NV	6113	8.85
<i>LCR10</i>	AC006248.3	28255-28316	28443-28624	-	-	126	SGA/MV	5840	9.06
<i>LCR11</i>	AL050399.1	48232-48172	47816-47572	-	-	643	TVG/KG	7862	9.04
<i>LCR12</i>	AB017061.1	7348-7399	7649-7848	-	-	249	TEA/QK	6454	8.67
<i>LCR13</i>	AL049482.1	67951-67999	68147-68328	-	-	147	TQG/DT	5982	4.57
<i>LCR14</i>	AC006300.3	383-443	1109-1284	-	-	665	VVG/NM	6258	8.68
<i>LCR15</i>	AL161550.2	15023-14963	14331-14141	-	-	631	AKG/QP	6317	5.82
<i>LCR16</i>	AC007504.3	44047-44095	44248-44412	-	-	152	TQG/AN	5295	4.92
<i>LCR17</i>	AL161532.2	130261-130321	130840-131069	F15145	<i>ATg11760</i>	518	TLG/QA	7091	8.49
<i>LCR18</i>	AC009465.5	35413-35473	35662-35828	-	-	188	SSG/NK	6240	7.00
<i>LCR19</i>	AL161576.2	40212-40154	39817-39498	-	-	336	VEN/KV	10945	8.12
<i>LCR20</i>	AB025609.1	5666-5621	5524-5346	-	-	96	IQG/QN	5610	7.53
<i>LCR21</i>	AL161574.2	158681-158630	158499-158306	-	-	130	TKG/KR	6063	6.29
<i>LCR22</i>	AL161574.2	156346-156294	156162-155984	-	<i>AT4g29280</i>	131	VFS/LV	6163	6.84
<i>LCR23</i>	AL161574.2	153894-153842	153703-153524	-	-	138	GKG/DQ	5843	7.50
<i>LCR24</i>	AL161574.2	159692-159744	160075-160250	-	-	330	AEG/AD	5477	8.12
<i>LCR25</i>	AL161574.2	164711-164660	164524-164367	-	-	135	AEG/KR	5338	7.88
<i>LCR26</i>	AL161574.2	161165-161113	161002-160824	-	<i>AT4g29290</i>	110	VEC/DE	5812	6.83
<i>LCR27</i>	AL161574.2	162448-162219	-	-	<i>AT4g29300</i>	0	VEG/EE	5505	4.28
<i>LCR28</i>	AB033294.1	5283-5235	5035-4908	-	-	199	(CEI/DQ)	4195	4.49
<i>LCR29</i>	AC007188.6	58460-58529	58602-58774	-	-	72	TQG/HI	5581	4.85
<i>LCR30</i>	AL138644.1	42572-42523	42366-42187	-	-	156	TQG/QE	5634	6.29
<i>LCR31</i>	AF053747.1	3176-3236	3493-3674	-	-	256	VQG/KV	6401	8.68
<i>LCR32</i>	AC006283.5	76705-76645	76097-75913	-	-	547	AVG/DV	6559	8.68
<i>LCR33</i>	AL138643.1	45705-45645	44499-44327	-	-	1145	VMG/ND	6771	8.66
<i>LCR34</i>	AL161516.2	80716-80656	79858-79665	-	-	797	VAP/EK	6298	8.83
<i>LCR35</i>	AC007232.5	26653-26704	26864-27045	-	-	159	AKG/DG	5412	3.93
<i>LCR36</i>	AL161514.2	47464-47515	47603-47778	-	-	87	AKG/DK	5476	4.51
<i>LCR37</i>	AL079349.2	86640-86692	86974-87128	-	-	281	(EGG/AT)	5355	7.50
<i>LCR38</i>	AL161551.2	184442-184391	184027-183852	-	-	363	SSA/KQ	5788	7.53
<i>LCR39</i>	AB025608.1	25346-25289	25154-24982	-	-	134	GEA/KT	6220	5.00
<i>LCR40</i>	AC005396.2	51963-52020	52152-52315	-	-	867	GEA/KT	5685	6.83
<i>LCR41</i>	AC009465.5	36267-36324	36510-36694	-	-	185	SEN/GI	6813	5.76

LCR42	AB025608.1	23821-23764	23586-23414	-	-	177	SEN/QK	6326	6.31
LCR43	AC016827.5	51156-51225	51349-51502	-	-	123	AQK/EC	5358	4.65
LCR44	AC016827.5	44505-44557	44660-44796	-	-	103	VEA/EP	4532	4.63
LCR45	AL035708.2	52799-52862	53004-53185	-	-	142	ATA/IT	6299	7.54
LCR46	AB017061.1	20842-20919	21386-21579	-	-	532	ISG/QI	6639	7.51
LCR47	AL138653.1	63731-63809	64301-64452	-	-	507	CSA/FT	5420	7.10
LCR48	AL096856.1	92536-92452	92249-92095	-	-	202	AIA/SE	5868	5.65
LCR49	AC002334.2	74072-73998	73795-73641	-	-	202	SSS/QN	6391	5.61
LCR50	AC007268.4	23305-23218	23121-22961	-	-	96	VHC/SD	6519	6.25
LCR51	AC004261.2	10644-10728	10839-11020	-	-	110	VHC/RM	9691	8.25
LCR52	AL137898.1	31444-31396	31302-31121	-	-	93	TQG/QE	5991	8.31
LCR53	AL137898.1	32926-32878	32783-32608	-	-	94	TKG/QE	5727	8.51
LCR54	AL137898.1	36273-36225	36087-35909	-	-	137	TQG/EE	5610	3.96
LCR55	AP000604	8637-8586	8477-8302	-	-	108	TRG/QE	5682	5.58
LCR56	AP000604	6453-6402	6296-6118	-	-	105	TQG/QE	5598	6.83
LCR57	AB023032.1	30453-30393	30033-29735	-	-	359	IRA/QT	9934	7.56
LCR58	AB011481.1	13816-13873	14653-14979	-	-	779	TRA/DS	10694	4.84
LCR59	AL161576.2	37200-37257	37635-37963	-	-	377	ARG/DT	11014	5.62
LCR60	AC006569.4	5008-5068	5251-5441	-	-	182	VEQ/NM	6419	6.04
LCR61	AL078464.1	31124-31184	31290-31462	-	-	105	VEQ/NM	5677	5.51
LCR62	AC005315.2	56107-56168	56668-56840	-	-	499	VEQ/NM	5650	5.30
LCR63	AL161576.2	35725-35785	35954-36126	-	-	168	NMG/CI	5579	7.56
LCR64	AC012679.3	2304-2364	2644-2852	-	-	279	NMG/CN	7517	8.50
LCR65	AC012679.3	4205-4265	4494-4693	-	-	228	TGC/FD	7076	8.18
LCR66	AC018908.6	87555-87495	87274-87108	-	-	220	VEA/RT	5175	7.89
LCR67	AF049870.1	16602-16666	16774-16249	Z27258.1	PDF1.1	107	VEA/QK	5666	8.33
LCR68	AC005936.2	37573-37695	37799-38180	AA712928.1	At2g02130	103	ATG/MG	6132	8.92
LCR69	AC005936.2	25958-26021	26277-26446	AA712693.1	At2g02100	255	ATG/MG	6068	8.54
LCR70	AC005936.2	35880-35943	36234-36403	Z17665.1	At2g02120	290	ATG/MG	6120	8.34
LCR71	AC005936.2	39513-39731	-	-	-	0	(SLG/GS)	8083	6.20
LCR72	AC005936.2	42316-42379	42573-42730	-	At2g02140	193	VEA/RT	4741	8.33
LCR73	AC005936.2	44225-44294	44415-44584	-	-	120	TTA/EV	6450	7.00
LCR74	AB005234.1	38818-38873	39023-39186	-	-	149	IIG/GE	5740	8.72
LCR75	AC006223.3	4752-4824	5055-5227	-	-	230	LLA/SP	6864	8.32
LCR76	AC006223.3	473-536	867-1060	-	-	330	APG/MK	7305	8.86
LCR77	AB017065.1	20995-20932	20839-20664	T04323	PDF1.2	92	VEA/QK	5491	8.12
LCR78	AC025808.8	115221-115157	115042-114873	-	-	114	MMA/VE	6069	8.34
LCR79	AC006223.3	4773-4824	5049-5223	-	-	224	VEG/QQ	6134	8.70
LCR80	AB011481.1	17523-17580	17933-18198	-	-	352	GLC/DG	9220	5.58
LCR81	AC007070.4	39111-39177	39427-39596	-	-	249	(VKP/EV)	8490	6.84
LCR82	AC006951.1	35067-34989	34764-34541	-	-	224	ISG/QF	8183	5.91
LCR83	AB010695.1	16640-16718	16914-17080	-	-	195	VSG/NF	5918	7.87
LCR84	AC006304.3	61207-61285	61425-61573	-	-	139	SNA/LP	5856	5.54
LCR85	AL021712.2	23080-23155	23244-23425	-	-	88	TDG/RR	6336	4.94
LCR86	AB017061.1	24314-24248	23965-23778	-	-	716	INA/ID	6575	7.58

a: coordinates correspond to the genomic sequences whose accession numbers are given in the column to the left. b: the slash marks the predicted cleavage site according to signalP; brackets indicate cleavage sites that are poorly predicted, "-": no predicted cleavage site. c: predicted mass of mature, cleaved polypeptide in Daltons.

