

Supplemental Table 1. Accession no. of nucleotide sequences registered in the DDBJ database

Name of cultivar/ Accession No.	Cluster No. ^a	<i>TrnK-MatK</i> CmCp1	<i>Rps16 intron1</i> CmCp2	<i>PsbK-PsbI</i> CmCp3	<i>AtpH-AtpI</i> CmCp5	<i>PsbC-TrnS</i> ccSSR 7	<i>PsaI-Ycf4</i> Cmcp15	<i>Rpl16-Rpl14</i> PS-ID	<i>NdhF-Rpl32</i> CmCp6	<i>NdhA intron1</i> CmCp11
Kinpyo	I a-1	AB716776	AB716781	AB716797	AB716813	AB716829	AB716845	AB716861	AB716877	AB716893
PI 614588	I a-2	AB716775	AB716782	AB716798	AB716814	AB716830	AB716846	AB716862	AB716878	AB716894
PI 482424	I a-3	AB716774	AB716783	AB716799	AB716815	AB716831	AB716847	AB716863	AB716879	AB716895
PI 525105	I b-1	AB716771	AB716784	AB716800	AB716816	AB716832	AB716848	AB716864	AB716880	AB716896
Earl's Favourite	I b-2	AB716772	AB716785	AB716801	AB716817	AB716833	AB716849	AB716865	AB716881	AB716897
Hami-gua 6	I b-3	AB716773	AB716786	AB716802	AB716818	AB716834	AB716850	AB716866	AB716882	AB716898
PI 185111	I c-1	AB716765	AB716787	AB716803	AB716819	AB716835	AB716851	AB716867	AB716883	AB716899
PI 436533	I c-2	AB716766	AB716788	AB716804	AB716820	AB716836	AB716852	AB716868	AB716884	AB716900
PI 490388	I c-3	AB716767	AB716789	AB716805	AB716821	AB716837	AB716853	AB716869	AB716885	AB716901
940112	I c-4	AB716768	AB716790	AB716806	AB716822	AB716838	AB716854	AB716870	AB716886	AB716902
940111	I c-5	AB716769	AB716791	AB716807	AB716823	AB716839	AB716855	AB716871	AB716887	AB716903
PI 482413	I c-6	AB716770	AB716792	AB716808	AB716824	AB716840	AB716856	AB716872	AB716888	AB716904
CYS68-1	II	AB716777	AB716793	AB716809	AB716825	AB716841	AB716857	AB716873	AB716889	AB716905
PI 282441	III	AB716778	AB716794	AB716810	AB716826	AB716842	AB716858	AB716874	AB716890	AB716906
PI 292190	III	AB716779	AB716795	AB716811	AB716827	AB716843	AB716859	AB716875	AB716891	AB716907
PI 482383	III	AB716780	AB716796	AB716812	AB716828	AB716844	AB716860	AB716876	AB716892	AB716908

^a Cluster number refers to Fig. 1.

Supplemental Table 2. Maximum and minimum values of sequence homology value (%) between 18 accessions of *Cucumis* across nine chloroplast genome regions

No.	Accession No.	Species	Cluster No.	No. ^b																		
				1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
1	PI 482424	<i>C. melo</i>	I a-1	-	100	100	100	100	100	100	100	100	100	100	100	100	98	98	98	98	99	98
2	PI 614588	<i>C. melo</i>	I a-2	100	-	100	100	100	100	100	100	100	100	100	100	100	98	98	98	98	99	98
3	Kinpyo	<i>C. melo</i>	I a-3	99	99	-	100	100	100	100	100	100	100	100	100	98	98	98	98	99	98	
4	PI 525105	<i>C. melo</i>	I b-1	99	99	99	-	100	100	100	100	100	100	99	99	99	98	99	98	99	98	
5	Earl's Favourite	<i>C. melo</i>	I b-2	99	99	99	100	-	100	100	100	100	100	99	99	98	98	98	98	99	98	
6	Hami-gua 6	<i>C. melo</i>	I b-3	99	99	99	100	100	-	100	100	100	100	99	99	99	98	99	98	99	98	
7	PI 185111	<i>C. melo</i>	I c-1	99	99	99	99	99	99	-	100	100	100	100	100	99	99	99	98	99	98	
8	PI 436533	<i>C. melo</i>	I c-2	99	99	99	99	99	99	99	-	100	100	100	100	99	99	99	98	99	98	
9	PI 490388	<i>C. melo</i>	I c-3	99	99	99	99	99	99	99	99	-	100	100	100	99	99	99	98	99	98	
10	940112	<i>C. melo</i>	I c-4	99	99	99	99	99	99	99	99	99	-	100	100	99	99	99	98	99	98	
11	940111	<i>C. melo</i>	I c-5	99	99	99	99	99	99	99	99	99	99	-	100	99	99	99	98	98	98	
12	PI 505602	<i>C. melo</i>	I c-6	99	99	99	99	99	99	99	99	99	99	100	-	99	99	99	98	98	98	
13	CYS68-2	<i>C. hystrix</i>	II	96	96	96	96	96	96	96	96	96	96	96	96	-	100	100	99	99	99	
14	Sm021-3	<i>C. hystrix</i>	II	96	96	95	96	96	96	96	96	96	96	95	95	95	-	100	99	99	98	
15	DQ865976 ^a	<i>C. sativus</i>	II	96	96	96	96	96	96	96	96	96	96	96	96	95	95	-	99	99	99	
16	PI 282441	<i>C. sagittatus</i>	III	96	96	96	96	96	96	96	95	95	95	96	96	95	96	95	-	99	98	
17	PI 292190	<i>C. metuliferus</i>	III	94	93	93	94	94	94	94	94	94	94	94	94	94	94	94	94	95	-	98
18	PI 482383	<i>C. anguria</i>	III	95	95	95	95	95	95	95	94	94	94	95	95	95	95	95	95	96	96	-

^aThe accession number of cucumber chloroplast genome sequence was indicated.

^bThe maximum and minimum of sequence homology were shown in the right upper side and the left lower side, respectively.