Suppl. Fig. 1

cytosolic/ peroxisomal GR1 clade

AtGR1, TNL>
BrGR1, TSL>
PkGR1, SKI>
HvGR1, TNL>
VvGR1, TNL>
NtGR1(ESTs), TNL>
OsGR1, TNL>
RcGR1, TNL>
ZmGR1, TNL>
PtriGR1a, wo
PtriGR1b, TNL>
PpatGR1, LKV>
PsGR1, TNL>
GmGR1 (ESTs),
VuGR1, TNL>
PvGR1, TNL>
SoGR1, TNL>
McGR1, wo
OtGR, wo
OlGR, wo
CrGR1, SKL>
MpusGR, wo
MspecGR, AKM>
PpatGR2, wo
AtGR2, wo
NtGR2, wo
VvGR2, wo
PtriGR2, wo
RcGR2, wo
PsGR2, wo
GmGR2, wo
CrGR2(ESTs), wo
VuGR2, PvGR2, wo
wo
HvGR2, wo
OsGR2a, wo
OsGR2b, wo
UfGR, wo

1000
871
1000
681
973
1000
1000
1000
1000
1000
987
1000
990
984
1000
995
1000
473
905
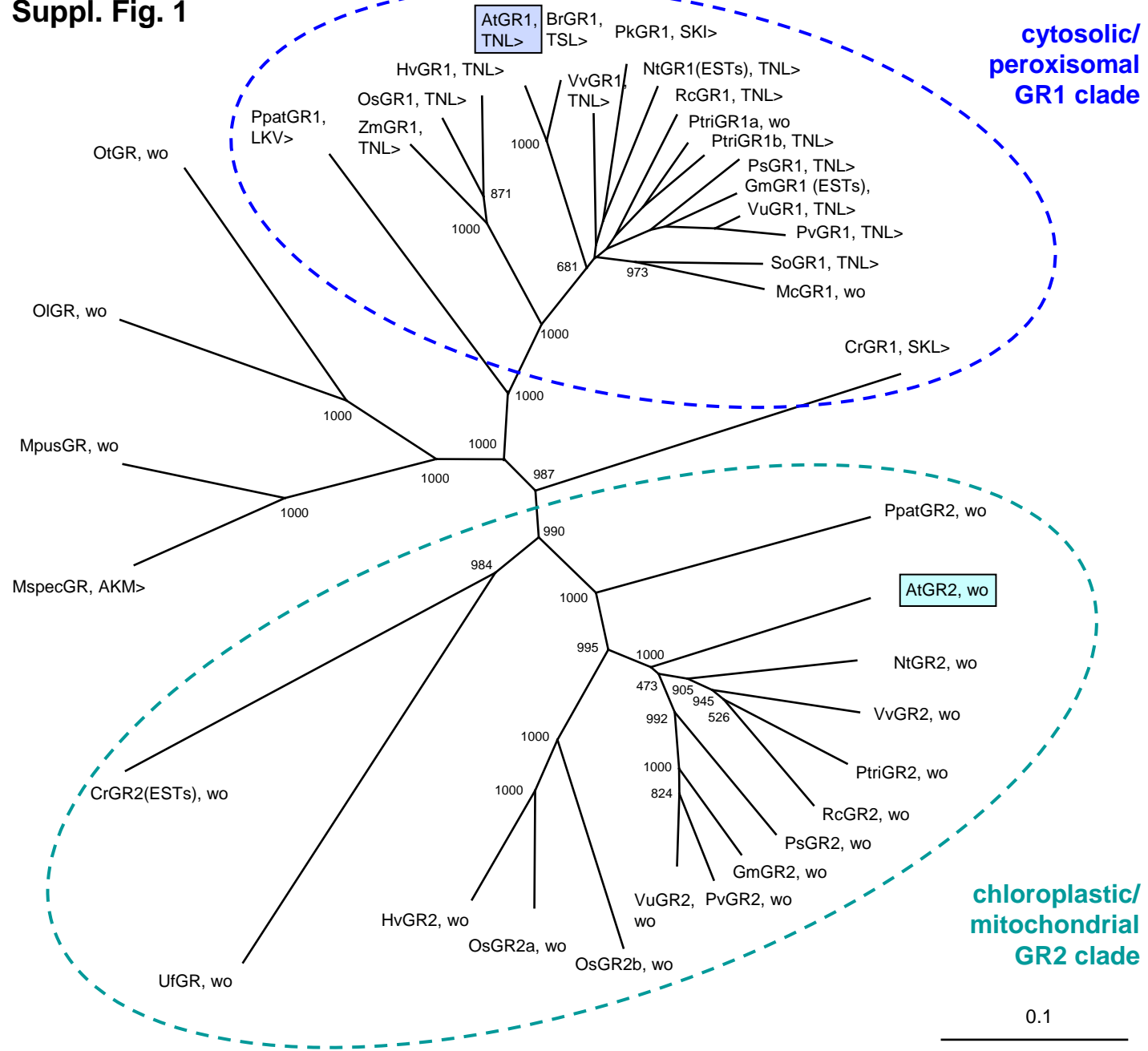945
992
526
1000
824
1000

chloroplastic/ mitochondrial GR2 clade

0.1

Suppl. Fig. 1. Phylogenetic analysis of GR homologs in Viridiplantae.

Sequences of full-length plant GR homologs or those assembled from overlapping ESTs (e.g., NtGR1(ESTs), GmGR1(ESTs), CrGR2(ESTs)) were identified by BLAST and aligned by ClustalX. The phylogenetic reconstruction was made by the neighbor-joining method using 1000 bootstraps. The tripeptide sequence of predicted PTS1 tripeptides is indicated. Additional species as compared to those mentioned in the legend of Fig. 1 are abbreviated as follows: Gm, *Glycine max*; Hv, *Hordeum vulgare* subsp. vulgare; Mc, *Mesembryanthemum crystallinum*; Mpus, *Micromonas pusilla* CCMP1545; Ol, *Ostreococcus lucimarinus* CCE9901; Ot, *Ostreococcus tauri*; Pv, *Phaseolus vulgaris*; So, *Spinacia oleracea*; Uf, *Ulva fasciata*; Vu, *Vigna unguiculata*.

Suppl. Table I: Arabidopsis gene models terminating with TNL>.

AGI code	Annotation	C-terminal 15 aa	Size (aa)
At1g80300.1	Nucleotide transporter 1	`ESPSSSPEKSAP`**`TNL`**	624
At1g80745.1	Unknown protein	`APLDNEDGVTKT`**`TNL`**	102
At3g24170.1/2/3	Glutathione-disulfide reductase	`VTRRIAHKPKPK`**`TNL`**	499
At3g31900.1	Unknown protein	`RKFLNVEADGPS`**`TNL`**	393
At4g01026.1	Unknown protein	`ASNGYREKNHTE`**`TNL`**	211
At4g09820.1	Transparent testa 8	`VKRAIHQVIIHD`**`TNL`**	518
At5g36700.3	2-Phosphoglycolate phosphatase 1	`GGCKTLLVLSGI`**`TNL`**	332
At5g41765.1	Unknown protein	`PQISFNNSEPKK`**`TNL`**	152