

**Table S2.** List of the CNGC family genes in *Gossypium hirsutum*.

Gene Name	Gene ID	Chr:Location(strand)	AA	pI	D&M	Group	Subcellular Localization
<i>GhCNGC1</i>	Gh_A01G0520	A01:8277150..8284315(+)	709	9.02	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC2</i>	Gh_A01G1841	A01:98325294..98327741(+)	701	8.99	a,b,c,d	III	Plasma membrane
<i>GhCNGC3</i>	Gh_A03G0266	A03:4244529..4247150(+)	703	9.10	a,b,c,d	III	Plasma membrane
<i>GhCNGC4</i>	Gh_A05G0448	A05:4940335..4941778(-)	313	9.17	b,d,e	II	Nuclear
<i>GhCNGC5</i>	Gh_A05G0903	A05:8902041..8905061(-)	713	9.21	a,b,c,d	III	Plasma membrane
<i>GhCNGC6</i>	Gh_A05G1012	A05:10147786..10152216(+)	748	8.95	a,b,c,d,e	II	Plasma membrane
<i>GhCNGC7</i>	Gh_A05G3130	A05:80780849..80783618(-)	736	8.37	a,b,c,d	III	Plasma membrane
<i>GhCNGC8</i>	Gh_A05G3196	A05:83677517..83680754(-)	695	9.33	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC9</i>	Gh_A05G3588	A05:91763003..91768450(+)	695	9.30	a,b,c,d,e	I	Plasma membrane
<i>GhCNGC10</i>	Gh_NAU_A06*	A06:41590465..41594219(-)	709	9.11	a,b,c,d	III	Plasma membrane
<i>GhCNGC11</i>	Gh_A07G1267	A07:29283930..29286198(-)	599	9.23	a,b,c,d	I	Plasma membrane
<i>GhCNGC12</i>	Gh_A09G0110	A09:2549787..2554380(-)	524	9.35	a,b,d	IV-B	Plasma membrane
<i>GhCNGC13</i>	Gh_A09G0111	A09:2575761..2581410(+)	766	9.57	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC14</i>	Gh_A11G0014	A11:194792..217283(-)	786	8.84	a,b,c,d	IV-A	Plasma membrane
<i>GhCNGC15</i>	Gh_A12G1004	A12:61310236..61315344(+)	708	9.59	a,b,c,d,e	I	Plasma membrane
<i>GhCNGC16</i>	Gh_A13G1579	A13:74640085..74642700(+)	703	8.95	a,b,c,d	III	Plasma membrane
<i>GhCNGC17</i>	Gh_A13G1614	A13:74974260..74978836(+)	743	9.02	a,b,c,d,e	II	Plasma membrane
<i>GhCNGC18</i>	Gh_D01G0533	D01:6643589..6650779(+)	709	9.02	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC19</i>	Gh_D01G2082	D01:59853608..59856045(+)	726	8.92	a,b,c,d	III	Plasma membrane
<i>GhCNGC20</i>	Gh_D03G1301	D03:41182870..41185544(-)	721	9.01	a,b,c,d	III	Plasma membrane
<i>GhCNGC21</i>	Gh_D04G0016	D04:336247..341449(-)	729	9.00	a,b,c,d	I	Plasma membrane
<i>GhCNGC22</i>	Gh_D04G0409	D04:6457085..6464147(+)	631	9.48	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC23</i>	Gh_D04G0507	D04:8647485..8650049(+)	740	6.89	a,b,c,d	III	Plasma membrane
<i>GhCNGC24</i>	Gh_D04G0818	D04:18542044..18548380(-)	731	9.29	a,b,c,d	III	Plasma membrane
<i>GhCNGC25</i>	Gh_D05G0547	D05:4438080..4442575(+)	738	9.20	a,b,c,d,e	II	Plasma membrane
<i>GhCNGC26</i>	Gh_D05G0985	D05:8298111..8301011(-)	710	9.18	a,b,c,d	III	Plasma membrane
<i>GhCNGC27</i>	Gh_D05G1129	D05:9678476..9682896(+)	746	9.00	a,b,c,d,e	II	Plasma membrane
<i>GhCNGC28</i>	Gh_D06G1113	D06:25415590..25424220(-)	885	9.47	a,b,c,d	III	Plasma membrane
<i>GhCNGC29</i>	Gh_D07G1377	D07:22261532..22264949(-)	734	9.29	a,b,c,d	I	Plasma membrane
<i>GhCNGC30</i>	Gh_D08G1044	D08:29136722..29142273(-)	753	8.83	a,b,c,d	I	Plasma membrane
<i>GhCNGC31</i>	Gh_D09G0106	D09:2641533..2647632(-)	695	9.31	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC32</i>	Gh_D09G0107	D09:2667426..2672270(+)	766	9.57	a,b,c,d	IV-B	Plasma membrane
<i>GhCNGC33</i>	Gh_D09G1606	D09:43634992..43640328(-)	1057	9.06	a,b,c,d	III	Plasma membrane
<i>GhCNGC34</i>	Gh_D11G0011	D11:161114..174077(-)	770	9.20	a,b,c,d	IVA	Plasma membrane
<i>GhCNGC35</i>	Gh_D12G1124	D12:38003265..38008325(+)	719	9.51	a,b,c,d	I	Plasma membrane
<i>GhCNGC36</i>	Gh_D13G1938	D13:54757524..54759628(+)	586	9.12	a,b,c,d	III	Plasma membrane
<i>GhCNGC37</i>	Gh_D13G1974	D13:55088065..55092625(+)	743	8.97	a,b,c,d,e	II	Plasma membrane
<i>GhCNGC38</i>	Gh_A05G3666	scaffold1170_A05:953138..958831(+)	738	9.34	a,b,c,d	III	Plasma membrane
<i>GhCNGC39</i>	Gh_A09G2401	scaffold2299_A09:87921..90512(+)	692	9.06	a,b,c,d	III	Plasma membrane
<i>GhCNGC40</i>	Gh_Sca006927G01	scaffold6927:5643..9514(-)	513	8.72	a,b,c,d	I	Chloroplast

Note: *Gossypium hirsutum* ((AD)<sub>1</sub>) genome NAU-NBI Assembly v1.1 & Annotation v1.1.

Chr:Location(strand): chromosome & location (start..end) & strand.

AA: amino acids.

pI: isoelectric point.

D&M: domains & motif. a, transmembrane domains (TM); b, cyclic nucleotide-binding domain (CNBD) (InterPro: IPR000595, IPR018490); c, ion transport domain (ITP) (InterPro: IPR005821); d, plant CNGC-specific motif spanning the putative phosphate binding cassette (PBC) and the hinge within the CNBD (Zelman et al. *Front Plant Sci.* 2012, 3:95); e, IQ motif, EF-hand binding site (InterPro: IPR000048).

Group: phylogenetic classification in Figure 1.

**Table S3.** List of the CNGC family genes in *Gossypium barbadense*.

Gene Name	Gene ID	Chr:Location(strand)	AA	pI	D&M	Group	Subcellular Localization
<i>GbCNGC1</i>	Gbar_A01G006020	A01:8697293..8705568(+)	709	8.76	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC2</i>	Gbar_A01G021190	A01:113941390..113944341(+)	698	8.98	a,b,c,d	III	Plasma membrane
<i>GbCNGC3</i>	Gbar_A03G003890	A03:5102061..5105287(+)	686	9.35	a,b,c,d	III	Plasma membrane
<i>GbCNGC4</i>	Gbar_A05G005290	A05:5025709..5027152(-)	313	9.59	b,d,e	II	Nuclear
<i>GbCNGC5</i>	Gbar_A05G010100	A05:9148299..9152654(-)	713	9.33	a,b,c,d	III	Plasma membrane
<i>GbCNGC6</i>	Gbar_A05G034890	A05:83328986..83336012(+)	731	9.63	a,b,c,d	III	Plasma membrane
<i>GbCNGC7</i>	Gbar_A05G036490	A05:91999822..92002717(-)	719	7.64	a,b,c,d	III	Plasma membrane
<i>GbCNGC8</i>	Gbar_A05G037420	A05:94694789..94698128(-)	695	9.45	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC9</i>	Gbar_A05G041690	A05:102314038..102319578(+)	712	9.13	a,b,c,d	I	Plasma membrane
<i>GbCNGC10</i>	Gbar_A06G011120	A06:42300192..42307280(-)	709	9.11	a,b,c,d	III	Plasma membrane
<i>GbCNGC11</i>	Gbar_A07G014600	A07:29744624..29748343(-)	718	9.77	a,b,c,d,e	I	Plasma membrane
<i>GbCNGC12</i>	Gbar_A08G010210	A08:49311693..49318179(-)	708	9.16	a,b,c,d	I	Plasma membrane
<i>GbCNGC13</i>	Gbar_A09G001260	A09:2601895..2607487(-)	688	9.34	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC14</i>	Gbar_A09G001270	A09:2635374..2641554(+)	766	9.90	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC15</i>	Gbar_A09G018060	A09:70042981..70046031(-)	692	9.01	a,b,c,d	III	Plasma membrane
<i>GbCNGC16</i>	Gbar_A12G012100	A12:74687268..74693244(+)	708	10.06	a,b,c,d,e	I	Plasma membrane
<i>GbCNGC17</i>	Gbar_A13G019770	A13:103498649..103502436(+)	727	9.17	a,b,c,d	III	Plasma membrane
<i>GbCNGC18</i>	Gbar_A13G020140	A13:103833121..103839357(+)	743	9.04	a,b,c,d,e	II	Plasma membrane
<i>GbCNGC19</i>	Gbar_D01G006380	D01:8215486..8223064(+)	709	8.80	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC20</i>	Gbar_D03G014500	D03:46018646..46022630(-)	708	9.28	a,b,c,d	III	Plasma membrane
<i>GbCNGC21</i>	Gbar_D04G000200	D04:262035..268826(-)	712	9.13	a,b,c,d	I	Plasma membrane
<i>GbCNGC22</i>	Gbar_D04G004780	D04:6645898..6649036(+)	679	9.71	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC23</i>	Gbar_D04G005720	D04:8764155..8767091(+)	714	6.96	a,b,c,d	III	Plasma membrane
<i>GbCNGC24</i>	Gbar_D04G009040	D04:18371339..18378487(-)	731	9.57	a,b,c,d	III	Plasma membrane
<i>GbCNGC25</i>	Gbar_D05G005530	D05:4464122..4470130(+)	736	9.30	a,b,c,d,e	II	Plasma membrane
<i>GbCNGC26</i>	Gbar_D05G010670	D05:8644929..8649959(-)	713	9.26	a,b,c,d	III	Plasma membrane
<i>GbCNGC27</i>	Gbar_D05G012040	D05:10081285..10086992(+)	746	9.06	a,b,c,d,e	II	Plasma membrane
<i>GbCNGC28</i>	Gbar_D06G011530	D06:24826696..24831210(-)	588	9.24	a,b,c,d	III	Plasma membrane
<i>GbCNGC29</i>	Gbar_D07G015050	D07:22779814..22782638(-)	712	9.71	a,b,c,d,e	I	Plasma membrane
<i>GbCNGC30</i>	Gbar_D08G011030	D08:30426796..30433111(+)	708	9.22	a,b,c,d	I	Plasma membrane
<i>GbCNGC31</i>	Gbar_D09G001180	D09:2506003..2512155(-)	688	9.40	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC32</i>	Gbar_D09G001190	D09:2531299..2536464(+)	694	9.71	a,b,c,d	IV-B	Plasma membrane
<i>GbCNGC33</i>	Gbar_D09G017790	D09:44186045..44188613(-)	637	8.90	a,b,d	III	Plasma membrane
<i>GbCNGC34</i>	Gbar_D11G000120	D11:131979..146215(-)	770	9.24	a,b,c,d	IV-A	Plasma membrane
<i>GbCNGC35</i>	Gbar_D12G012180	D12:37968793..37974717(+)	719	10.04	a,b,c,d,e	I	Plasma membrane
<i>GbCNGC36</i>	Gbar_D13G019920	D13:54336903..54339837(+)	560	9.33	a,b,c,d	III	Plasma membrane
<i>GbCNGC37</i>	Gbar_D13G020320	D13:54643343..54649570(+)	743	8.96	a,b,c,d,e	II	Plasma membrane
<i>GbCNGC38</i>	Gbar_D01G024300	Scaffold2826:49768..52446(+)	706	8.81	a,b,c,d	III	Plasma membrane
<i>GbCNGC39</i>	Gbar_D11G035610	Scaffold2800:97663..116444(+)	738	9.24	a,b,c,d	IV-A	Plasma membrane
<i>GbCNGC40</i>	Gbar_Scaffold3324G000020	Scaffold3324:18011..22438(+)	748	8.89	a,b,c,d,e	II	Plasma membrane
<i>GbCNGC41</i>	Gbar_Scaffold863G000020	Scaffold863:4569..8992(+)	748	8.89	a,b,c,d,e	II	Plasma membrane

Note: *Gossypium barbadense* ((AD)<sub>2</sub>) genome HAU Assembly v2.0 & Annotation v1.0.

Chr:Location(strand): chromosome & location (start..end) & strand.

AA: amino acids.

pI: isoelectric point.

D&M: domains & motif. a, transmembrane domains (TM); b, cyclic nucleotide-binding domain (CNBD) (InterPro: IPR000595, IPR018490); c, ion transport domain (ITP) (InterPro: IPR005821); d, plant CNGC-specific motif spanning the putative phosphate binding cassette (PBC) and the hinge within the CNBD (Zelman et al. *Front Plant Sci.* 2012, 3:95); e, IQ motif, EF-hand binding site (InterPro: IPR000048).

Group: phylogenetic classification in Figure 1.

**Table S4.** List of the CNGC family genes in *Gossypium arboreum*.

Gene Name	Gene ID	Chr:Location(strand)	AA	pI	D&M	Group	Subcellular Localization
<i>GaCNGC1</i>	Ga01G0732	Chr01:9914558..9921711(+)	709	8.93	a,b,c,d	IVB	Plasma membrane
<i>GaCNGC2</i>	Ga01G2411	Chr01:107207852..107210607(+)	708	9.16	a,b,c,d	III	Plasma membrane
<i>GaCNGC3</i>	Ga02G1657	Chr02:97749586..97752188(+)	715	8.96	a,b,c,d	III	Plasma membrane
<i>GaCNGC4</i>	Ga04G0852	Chr04:23568369..23572259(-)	709	9.21	a,b,c,d,e	I	Plasma membrane
<i>GaCNGC5</i>	Ga04G1517	Chr04:86898684..86901259(-)	717	7.52	a,b,c,d	III	Plasma membrane
<i>GaCNGC6</i>	Ga04G1626	Chr04:90143417..90146638(-)	695	9.37	a,b,c,d	IVB	Plasma membrane
<i>GaCNGC7</i>	Ga04G2110	Chr04:98071052..98076588(+)	712	9.10	a,b,c,d	I	Plasma membrane
<i>GaCNGC8</i>	Ga05G0572	Chr05:5145230..5149709(+)	738	9.11	a,b,c,d,e	II	Plasma membrane
<i>GaCNGC9</i>	Ga05G1104	Chr05:9506677..9509703(-)	713	9.19	a,b,c,d	III	Plasma membrane
<i>GaCNGC10</i>	Ga05G1255	Chr05:11108037..11112466(+)	748	8.90	a,b,c,d,e	II	Plasma membrane
<i>GaCNGC11</i>	Ga06G1223	Chr06:47404847..47410039(-)	714	8.93	a,b,c,d	III	Plasma membrane
<i>GaCNGC12</i>	Ga08G1175	Chr08:65285350..65290913(-)	753	8.89	a,b,c,d	I	Plasma membrane
<i>GaCNGC13</i>	Ga09G0093	Chr09:2006369..2013520(+)	712	9.45	a,b,c,d	IVB	Plasma membrane
<i>GaCNGC14</i>	Ga09G0167	Chr09:3622561..3627663(-)	695	9.22	a,b,c,d	IVB	Plasma membrane
<i>GaCNGC15</i>	Ga09G1844	Chr09:76172097..76174688(-)	692	9.06	a,b,c,d	III	Plasma membrane
<i>GaCNGC16</i>	Ga11G4114	Chr11:124328652..124350352(+)	770	9.22	a,b,c,d	IVA	Plasma membrane
<i>GaCNGC17</i>	Ga12G1804	Chr12:29109060..29114159(-)	708	9.58	a,b,c,d,e	I	Plasma membrane
<i>GaCNGC18</i>	Ga13G2256	Chr13:117824620..117828265(+)	705	9.05	a,b,c,d	III	Plasma membrane
<i>GaCNGC19</i>	Ga13G2293	Chr13:118190385..118194964(+)	743	9.06	a,b,c,d,e	II	Plasma membrane
<i>GaCNGC20</i>	Ga14G2437	Tig00021276:18324..24625(+)	731	9.32	a,b,c,d	III	Plasma membrane

Note: *Gossypium arboreum* (A<sub>2</sub>) genome CRI Assembly v1.0 & Annotation v1.0.

Chr:Location(strand): chromosome & location (start..end) & strand.

AA: amino acids.

pI: isoelectric point.

D&M: domains & motif. a, transmembrane domains (TM); b, cyclic nucleotide-binding domain (CNBD) (InterPro: IPR000595, IPR018490); c, ion transport domain (ITP) (InterPro: IPR005821); d, plant CNGC-specific motif spanning the putative phosphate binding cassette (PBC) and the hinge within the CNBD (Zelman et al. *Front Plant Sci.* 2012, 3:95); e, IQ motif, EF-hand binding site (InterPro: IPR000048).

Group: phylogenetic classification in Figure 1.

**Table S5.** List of the CNGC family genes in *Gossypium herbaceum*.

Gene Name	Gene ID	Chr:Location(strand)	AA	pI	D&M	Group	Subcellular Localization
<i>GheCNGC1</i>	Ghe01G07250	Chr01:8894127..8901253(+)	709	8.73	a,b,c,d	IV-B	Plasma membrane
<i>GheCNGC2</i>	Ghe01G27300	Chr01:121183440..121185977(+)	627	8.62	a,b,c,d	III	Plasma membrane
<i>GheCNGC3</i>	Ghe02G04280	Chr02:5055948..5058703(+)	496	8.23	a,b,c,d	III	Chloroplast
<i>GheCNGC4</i>	Ghe04G00530	Chr04:619194..620813(-)	313	9.66	b,d	I	Mitochondrial inner membrane
<i>GheCNGC5</i>	Ghe04G05860	Chr04:8878635..8881856(+)	695	6.20	a,b,c,d	IV-B	Plasma membrane
<i>GheCNGC6</i>	Ghe04G06950	Chr04:11684349..11686924(+)	579	6.20	a,b,c,d	III	Chloroplast
<i>GheCNGC7</i>	Ghe04G10960	Chr04:29417675..29423996(-)	394	9.10	a,b,d	III	Chloroplast
<i>GheCNGC8</i>	Ghe05G05920	Chr05:5479046..5495297(+)	1445	7.50	a,b,c,d	II	Plasma membrane
<i>GheCNGC9</i>	Ghe05G11250	Chr05:10302915..10305938(-)	510	8.66	a,b,c,d	III	Chloroplast
<i>GheCNGC10</i>	Ghe05G12750	Chr05:11861550..11865985(+)	713	8.54	a,b,c,d,e	II	Plasma membrane
<i>GheCNGC11</i>	Ghe06G13600	Chr06:46711807..46713030(-)	348	9.60	a,b,d	III	Chloroplast
<i>GheCNGC12</i>	Ghe07G16730	Chr07:31265588..31268395(-)	517	9.59	a,b,c,d,e	I	Mitochondrial inner membrane
<i>GheCNGC13</i>	Ghe08G12560	Chr08:55213223..55361119(-)	524	7.42	a,b,c,d	I	Chloroplast
<i>GheCNGC14</i>	Ghe09G01380	Chr09:2706335..2713663(-)	714	8.80	a,b,c,d	IV-B	Plasma membrane
<i>GheCNGC15</i>	Ghe09G01390	Chr09:2758562..2764089(+)	686	9.99	a,b,c,d	IV-B	Plasma membrane
<i>GheCNGC16</i>	Ghe09G21870	Chr09:76207315..76208906(-)	446	8.16	a,b,c,d	III	Chloroplast
<i>GheCNGC17</i>	Ghe11G00200	Chr11:208294..230215(-)	786	8.42	a,b,c,d	IV-A	Plasma membrane
<i>GheCNGC18</i>	Ghe12G15190	Chr12:80976907..80982067(+)	731	10.11	a,b,c,d,e	I	Plasma membrane
<i>GheCNGC19</i>	Ghe13G24840	Chr13:111635813..111637449(+)	355	9.28	a,b,d	III	Chloroplast
<i>GheCNGC20</i>	Ghe13G25210	Chr13:111969677..111974253(+)	541	8.62	a,b,c,d,e	II	Nuclear

Note: *Gossypium herbaceum* (A<sub>1</sub>) genome WHU Assembly v1.0 & Annotation v1.0.

Chr:Location(strand): chromosome & location (start..end) & strand.

AA: amino acids.

pI: isoelectric point.

D&M: domains & motif. a, transmembrane domains (TM); b, cyclic nucleotide-binding domain (CNBD) (InterPro: IPR000595, IPR018490); c, ion transport domain (ITP) (InterPro: IPR005821); d, plant CNGC-specific motif spanning the putative phosphate binding cassette (PBC) and the hinge within the CNBD (Zelman et al. *Front Plant Sci.* 2012, 3:95); e, IQ motif, EF-hand binding site (InterPro: IPR000048).

Group: phylogenetic classification in Figure 1.

**Table S6.** List of the CNGC family genes in *Gossypium raimondii*

Gene name	Gene ID	Chr:Location(strand)	AA	pI	D&M <sup>s</sup>	Group	Subcellular localization
<i>GrCNGC1</i>	Gorai.001G155300	Chr01:21774055..21777693(-)	712	9.34	a,b,c,d,e	I	Plasma membrane
<i>GrCNGC2</i>	Gorai.002G076600	Chr02:9066932..9074583(+)	709	9.02	a,b,c,d	IVB	Plasma membrane
<i>GrCNGC3</i>	Gorai.002G248200	Chr02:61219773..61222311(+)	698	9.10	a,b,c,d	III	Plasma membrane
<i>GrCNGC4</i>	Gorai.003G143300	Chr03:40840047..40843299(-)	708	9.16	a,b,c,d	III	Plasma membrane
<i>GrCNGC5</i>	Gorai.004G115300	Chr04:27570395..27576917(-)	582	8.78	a,b,c,d	I	Plasma membrane
<i>GrCNGC6</i>	Gorai.006G012500	Chr06:2655669..2661881(-)	688	9.34	a,b,c,d	IVB	Plasma membrane
<i>GrCNGC7</i>	Gorai.006G012600	Chr06:2689723..2695126(+)	766	9.53	a,b,c,d	IVB	Plasma membrane
<i>GrCNGC8</i>	Gorai.006G187100	Chr06:44397567..44400915(-)	692	9.07	a,b,c,d	III	Plasma membrane
<i>GrCNGC9</i>	Gorai.007G002000	Chr07:201004..215206(-)	770	9.29	a,b,c,d	IVA	Plasma membrane
<i>GrCNGC10</i>	Gorai.008G124800	Chr08:36428101..36434147(+)	719	9.54	a,b,c,d,e	I	Plasma membrane
<i>GrCNGC11</i>	Gorai.009G056700	Chr09:4097678..4103911(+)	745	9.19	a,b,c,d,e	II	Plasma membrane
<i>GrCNGC12</i>	Gorai.009G108500	Chr09:7879763..7884030(-)	715	9.21	a,b,c,d	III	Plasma membrane
<i>GrCNGC13</i>	Gorai.009G123300	Chr09:9200673..9206164(+)	746	9.00	a,b,c,d,e	II	Plasma membrane
<i>GrCNGC14</i>	Gorai.010G121000	Chr10:24503137..24509026(-)	709	9.13	a,b,c,d	III	Plasma membrane
<i>GrCNGC15</i>	Gorai.010G245300	Chr10:61428605..61431508(-)	641	9.25	a,b,c,d	III	Plasma membrane
<i>GrCNGC16</i>	Gorai.012G003500	Chr12:416603..423954(-)	712	9.10	a,b,c,d	I	Plasma membrane
<i>GrCNGC17</i>	Gorai.012G050600	Chr12:6577438..6580915(+)	695	9.41	a,b,c,d	IVB	Plasma membrane
<i>GrCNGC18</i>	Gorai.012G060800	Chr12:8516862..8519426(+)	714	6.53	a,b,c,d	III	Plasma membrane
<i>GrCNGC19</i>	Gorai.012G095800	Chr12:17638792..17646002(-)	738	9.25	a,b,c,d	III	Plasma membrane
<i>GrCNGC20</i>	Gorai.013G215800	Chr13:53579111..53585314(+)	743	9.01	a,b,c,d,e	II	Plasma membrane

Note: *Gossypium raimondii* (D<sub>5</sub>) genome JGI Assembly v2.0 & Annotation v2.1.

Chr:Location(strand): chromosome & location (start..end) & strand.

AA: amino acids.

pI: isoelectric point.

D&M: domains & motif. a, transmembrane domains (TM); b, cyclic nucleotide-binding domain (CNBD) (InterPro: IPR000595, IPR018490); c, ion transport domain (ITP) (InterPro: IPR005821); d, plant CNGC-specific motif spanning the putative phosphate binding cassette (PBC) and the hinge within the CNBD (Zelman et al. *Front Plant Sci.* 2012, 3:95); e, IQ motif, EF-hand binding site (InterPro: IPR000048).

Group: phylogenetic classification in Figure 1.