Table S1. Ube2g2 Surface plot. The indicated residues are substituted with Alanine, and their phenotypes were shown as donor or accepter in Ub transfer.

Residue ID	Residue name	residue	Main chain	Side chain	Donor	Accepter
1	MET	12.4728	0.6138	24.3317	63%	100%
4	THR	8.5083	0.7721	18.8233	65%	65%
6	LEU	6.6487	0.0000	13.2975	65%	80%
7	LYS	16.4108	1.2085	28.5726	80%	80%
10	MET	10.3603	0.9218	19.7988	75%	93%
14	LYS	13.4109	0.8751	23.4395	97%	97%
15	GLN	9.8144	0.0000	17.6659	96%	98%
17	THR	9.9062	6.8016	14.0456	96%	100%
18	LEU	13.9217	6.3437	21.4997	100%	100%
19	ASN	11.7673	1.8172	21.7173	97%	100%
20	PRO	13.7280	6.0310	23.9906	78%	91%
22	GLU	18.0288	3.0348	30.0239	71%	75.5%
25	VAL	10.138	1.3983	21.7911	50%	90%
29	MET	10.5027	8.0315	12.9739	82%	97%
30	ASN	7.7358	1.6787	13.7928	77%	100%
31	GLU	15.0789	3.7810	24.1172	71%	93%
32	GLU	15.8253	9.6673	20.7518	100%	100%
33	ASN	7.6037	0.7836	14.4237	40%	60%
36	GLU	6.3676	0.0066	11.4564	59%	77%
38	GLU	9.8100	0.9117	16.9286	46%	100%
40	LEU	6.1963	0.0000	12.3927	59%	100%
45	GLU	15.6422	1.3261	27.0951	80%	96%
46	ASP	17.9081	9.7488	26.0674	85%	95%
48	CYS	2.4764	2.7476	1.9339	65%	0%
50	GLU	5.0434	1.0585	8.2313	95%	100%
51	PHE	14.4933	4.5361	20.1832	100%	100%
53	VAL	7.4934	0.3695	16.9920	64%	90%
59	SER	5.9672	0.8676	16.1665	78%	93%
62	LEU	15.5581	1.1298	29.9865	100%	93%
66	LEU	13.0181	4.8054	21.2307	0%	94%
67	SER	5.4040	0.1012	16.0096	65%	75%
70	LYS	13.6319	0.8460	23.8606	83%	100%
72	ARG	8.6006	0.0000	13.5152	61%	75%
74	THR	11.4828	8.4105	15.5790	67%	77%
75	CYS	5.6015	5.0682	6.6681	76%	59%
76	GLU	10.6153	4.2541	15.7043	71%	61%
81	ASN	0.8269	0.0000	1.6538	0%	92%
83	TYR	7.6841	1.3471	10.8526	0%	94%
84	PRO	17.9673	11.6024	26.4538	68%	70%

85	ASP	10.2882	3.8685	16.7078	0%	47%
87	ARG	7.2183	0.0001	11.3430	94%	87%
91	SER	8.1385	1.9748	20.4660	0%	80%
94	HIS	5.7924	0.0538	9.6181	0%	83%
96	PRO	11.5563	5.3132	19.8805	45%	100%
97	GLY	12.8797	12.8797	0.0000	0%	60%
98/99/ 104/108	ASP/ASP/ GLU/GLU	11.9102 12.7615	1.9860 2.6498	21.8344 20.8509	0%	25%
100	PRO	16.001	4.0498	31.9359	40%	100%
101	MET	23.8911	9.3826	38.3995	40%	100%
102	GLY	9.2395	9.2395	0	60%	100%
103	TYR	15.9691	1.8275	23.0399	0%	78%
105	SER	3.2078	1.0853	7.4529	40%	40%
106	SER	17.4492	11.259	29.8297	100%	100%
111	SER	5.6596	0.4863	16.0061	50%	100%
112	PRO	9.7874	2.3468	19.7081	68%	78%
115	SER	3.2144	0.0005	9.6422	0%	16%
117	GLU	6.4270	0.1331	11.4621	0%	100%
118	LYS	10.1417	1.0044	17.4516	0%	100%
121	LEU	10.5887	0.5161	20.6613	0%	98%
122	SER	6.5721	1.8279	16.0605	0%	80%
125	SER	10.1553	1.1233	28.2193	93%	100%
131	ASN	8.0487	1.3109	14.7865	0%	100%
134	SER	3.3683	2.8234	4.4581	0%	100%
138	VAL	13.3751	0.8544	30.0695	0%	100%
139	ASP	12.7040	0.8488	24.5593	0%	100%
142	LYS	11.4502	0.4151	20.2783	0%	100%
145	ARG	11.6227	5.8514	14.9206	0%	100%
146	ASP	10.5189	8.3880	12.6498	54%	74%
147	ASP	8.3641	1.7153	15.0129	100%	78%
148	ARG	7.9646	0.5627	12.1943	61%	78%
149	GLU	12.8595	0.7846	22.5193	53%	83%
150	GLN	7.5250	0.3682	13.2504	69%	90%
152	TYR	5.5125	0.0000	8.2688	60%	77%
153	LYS	14.5707	1.6230	24.9289	100%	100%
154	ILE	4.8688	0.0000	9.7377	100%	100%
156	LYS	12.4607	0.1165	22.3361	79%	100%
157	GLN	8.9279	0.2601	15.8622	100%	100%
160	GLN	9.4599	0.0000	17.0278	100%	100%
161	LYS	11.0239	5.2611	15.6341	96%	100%
163/165	LEU/LEU	9.5/17.3	7.3/8.1	11.7/24.6	0	95%

Ube2g2 mutants affect the accepter E2 function; Ube2g2 mutants affect the donor E2 function; Ube2g2 mutants affect both accepter and donor E2 function.