

**Table S1**

<b>STRING ID<sup>a</sup></b>	<b>Protein ID<sup>b</sup></b>	<b>Peptides<sup>c</sup></b>	<b>MW<sup>d</sup></b>	<b>UniProt<sup>e</sup></b>	<b>Location<sup>f</sup></b>	<b>Function<sup>g</sup></b>
ACTBL2	Actin, beta-like 2	4	42003	B2RPJ1	CSK	Structural
ACTG1	Gamma-actin	2	17136	P63261	CSK	Structural
FKSG30	Kappa-actin	2	42016	Q9BYX7	CSK	Actin turnover
ACTG1	Actin-like protein	2	11536	Q562M3	CSK	Actin turnover
ACTR2	Actin-related protein 2 isoform B	2	44760	P61160	CSK	Actin turnover
ARPC2	Actin related protein 2/3 complex	6	34333	O15144	CSK	Actin turnover
ARPC	Actin related protein 2/3 complex isoform A	5	19667	P59998	CSK	Actin turnover
ACTR1A	ARP1 actin-related protein 1 homolog A	2	42613	B2R6B0	CSK	Actin turnover
ACTR3	ARP3 actin-related protein 3 homolog	3	47357	Q59FV6	CSK	Actin turnover
ENSG00000206393	Phostensin	2	35379	Q6NYC8	CSK	Actin-binding
NA	Fimbrin	3	30499	157829993	CSK	Actin-binding
ANXA5	Annexin V	13	35804	P08758	PM	Actin-binding
TWF2	Twinfilin 2	3	39471	Q6IBS0	CSK	Actin-binding
LCP1	L-plastin 1	15	70289	P13796	C	Actin-binding
MARCKS	Myristoylated alanine-rich C-kinase substrate	2	31544	P29966	C/PM/CSK	Actin-binding
GSN	Gelsolin isoform A precursor	8	85697	P06396	S/CSK	Actin turnover
EPB41L3	Band 4.1-like protein 3	2	123704	Q9Y2J2	CSK	Actin turnover
CAPG	Macrophage Capping Protein Cap G	2	38524	P40121	CSK	Actin turnover
MSN	Moesin	3	67820	P26038	PM/CSK	Actin-PM cross-talk
VIL2	Ezrin	4	69398	P15311	PM	Actin-PM cross-talk
CORO1A	Coronin, actin binding protein, 1A	3	53249	P31146	CSK/EV	Actin-PM cross-talk
CYFIP1	Cytoplasmic FMR1-interacting protein 1	2	147134	Q7L576	PM/CSK	Actin-PM cross-talk
PFN1	Profilin 1	6	14852	P07737	CSK	Actin-binding
CFL1	Cofilin 1	4	18502	P23528	CSK	Actin-binding
GSN	Gelsolin	2	41704	P06396	PM/CSK	Actin-binding
GC	Vitamin D-Binding Protein	2	41816	P02774	S/CSK	Actin-binding
CAP1	Adenylyl cyclase-associated protein (CAP1) F-actin-capping protein subunit beta (CapZ beta)	8	51673	Q01518	PM/CSK	Actin turnover
CAPZB		2	31350	P47756	CSK	Actin turnover
CAPZA1	F-actin capping protein	3	32923	P52907	CSK	Actin turnover
CAPZA2	Capping protein (actin filament)	4	32949	Q53GC7	CSK	Actin turnover
ACTN1	Actinin, alpha 1	9	103057	P12814	CSK	Actin-anchoring and bundling
ACTN4	Alpha actinin 4	3	102268	O43707	CSK	Actin-anchoring and bundling
FLNA	Alpha-filamin	37	280757	P21333	CSK	Actin-anchoring and bundling
FLNB	Beta-filamin	7	278191	O75369	CSK	Actin-anchoring and bundling
DES	Desmin	2	53535	P17661	PM/CSK	Actin-anchoring to the PM
CAPNS1	Calpain	2	28316	P04632	PM	Actin arrangement
IQGAP2	Ras GTPase-activating-like protein IQGAP2	8	180611	Q13576	CSK	Actin arrangement
ARHGDIIB	Rho GDP dissociation inhibitor (GDI) beta	2	22988	P52566	CSK/EV	Actin arrangement
LSP1	Lymphocyte antigen (LSP1)	3	37235	P33241	PM/CSK	Actin arrangement
TLN1	Talin-1	32	269764	Q9Y490	PM/CSK	Actin-PM cross-talk
ZYX	Zyxin	2	61277	Q15942	PM/CSK	Adhesion plaque protein
PTPRC	Protein tyrosine phosphatase, receptor C (CD45)	2	147253	P08575	PM	Adhesion
ARHGAP4	Rho GTPase-activating protein 4	2	105055	P98171	PM/CSK	Adhesion
ARHGDI A	GDP dissociation inhibitor 1	3	50582	P52565	C/CSK	Adhesion
PLEK	Pleckstrin	4	40083	P08567	ECM	Adhesion
C20orf42	Kindlin-1	2	75634	Q9BQL6	PM	Adhesion
FERMT3	Kindlin-3	4	75952	Q86UX7	PM	Adhesion
LGALS3	Mac-2 antigen	5	26188	P17931	PM	Adhesion
ITGAX	Integrin alpha-X (CD11c)	4	127896	P20702	PM	Adhesion
ITGAM	Integrin alpha M precursor (CD11b)	3	127178	P11215	PM	Adhesion
ITGB1	Integrin beta 1 isoform 1A precursor (CD29)	2	88415	P05556	PM/EV	Adhesion
ITGB4	Integrin, beta 4 (CD104)	8	195013	A0AVL6	PM	Adhesion
VCL	Vinculin isoform VCL	5	116722	P18206	PM	Adhesion

ITGB2	Cell surface adhesion glycoprotein LFA-1(CD18)	3	83881	P05107	PM	Adhesion
MYLCLB	Myosin regulatory light chain MRCL2	3	19779	O14950	CSK	Cell contraction
MYL6	Myosin, light polypeptide 6	2	16961	P60660	CSK	Cell contraction
DPYSL2	Dihydropyrimidinase-like 2	3	62293	Q16555	CSK	Cell contraction
TUBA1A	Alpha tubulin	2	49698	Q71U36	CSK	Structural
TUBA1C	tubulin alpha 6	7	49895	Q53GA7	CSK	Structural
ENSG00000137379	Beta-tubulin	7	48880	Q6LC01	CSK	Structural
NA	Diff6,H5,CDC10 homologue	4	46585	Q15019	CSK	Microtubule assembly
MAP4	Microtubule-associated protein 4	2	103328	P27816	CSK	Microtubule assembly
TCP1	T-complex protein 1 isoform A	3	60343	P17987	CSK	Microtubule assembly
ALDOA	Aldolase	6	39289	P04075	C/CSK/EV	Actin and microtubule organization
HSPB1	Heat shock 27kDa protein 1	2	22782	P04792	C/CSK	Actin and microtubule organization
VIM	Vimentin	20	52438	P08670	C/S	Structural/Intermediate filaments
PLEC1	Plectin	12	518488	Q15149	CSK	Structural/Intermediate filaments
LMNB1	Lamin B1	6	66408	P20700	CSK/N	Structural/Intermediate filaments
CT5	Chaperonin containing TCP1	3	59671	A8JZY8	C	Chaperone
ENSG00000187978	Heat shock protein 60	5	61054	P10809	M	Chaperone
HSPA1L	Heat shock 70 kDa protein 1L	3	70405	P34931	C/PM	Chaperone
HSPA6	Heat shock 70kDa protein 6	3	71028	P17066	C/PM	Chaperone
HSPA2	Heat shock 70kDa protein 2	3	70021	P54652	C/PM	Chaperone
HSPA1B	Heat shock 70kDa protein 1A	3	70052	A8K510	C/PM	Chaperone
HSPA8	Heat shock 70kDa protein 8	4	53517	P11142	C/PM	Chaperone
PARK7	Parkinson disease protein 7	3	19891	Q99497	C	Chaperone
RNH1	Ribonuclease inhibitor	2	49905	P13489	C	Protein biosynthesis
HNRPA1	Heterogeneous ribonucleoprotein A1	2	20037	P09651	C	Protein biosynthesis
BACH1	Transcription regulator BACH1	2	73258	O14867	N	Protein biosynthesis
HNRPN	RNA-Recognition Motif Domain Of Hnmp A1	2	22263	P09651	C	Protein biosynthesis
NA	Prohibitin 2	4	33296	Q99623	M	Protein biosynthesis
NA	Glutamyl-tRNA synthetase	3	163025	CAA38224	C	Protein biosynthesis
KPNB1	Importin 1	2	97170	Q14974	C/N	Protein biosynthesis
ENSG00000096171	Valyl-tRNA synthetase (VAR5)	2	140475	P26640	C	Protein biosynthesis
MATR3	Matrin 3	3	94623	P43243	N	Protein biosynthesis
SFPQ	Splicing factor proline/glutamine rich	2	76149	P23246	N	Protein biosynthesis
DDX3X	DEAD/H (Asp-Glu-Ala-Asp/His) box	4	73243	O00571	PM/C	Protein biosynthesis
DUSP3	Dual specificity phosphatase 3	2	20478	P51452	C	Protein metabolism
ABHD10	Abhydrolase domain containing 10	3	33932	Q9NUJ1	M	Protein metabolism
GARS	Glycyl-tRNA synthetase	2	77530	P41250	S	Protein metabolism
CNDP2	Glutamate carboxypeptidase	5	52852	Q96KP4	C	Protein metabolism
SHMT2	Serine hydroxymethyltransferase 2	2	55993	P34897	M	Protein metabolism
WARS	Tryptophanyl-tRNA synthetase isoform A	3	53165	P23381	C	Protein metabolism
PSMD2	Proteasome 26S non-ATPase subunit 2	3	100199	Q13200	C	Protein transport/Turnover
PSMD3	Proteasome beta 3 subunit	2	22949	P49720	C	Protein transport/Turnover
PSMB8	Proteasome subunit beta-5i	3	30354	P28062	C	Protein transport/Turnover
OTUB1	Ubiquitin thioesterase OTUB1	2	31312	Q96FW1	C	Protein transport/Turnover
HERC6	E3 ubiquitin-protein ligase HERC6	2	44541	Q81VU3	C	Protein transport/Turnover
UBE2L3	Ubiquitin-conjugating enzyme E2L 3 isoform 1	2	17861	P68036	C	Protein transport/Turnover
PSMA2	Proteasome alpha 2 subunit	3	25898	P25787	C	Protein transport/Turnover
PSMB2	Proteasome beta 2 subunit	2	22836	P49721	C	Protein transport/Turnover
UBE1	Ubiquitin-activating enzyme E1 Ubiquitin-like, containing PHD and RING finger domain	8	117848	P22314	C	Protein transport/Turnover
UHRF1		2	89813	Q96T88	N	Protein transport/Turnover
FTL	Ferritin	4	20020	Q96AU9	C	Redox
SQRDL	Sulfide dehydrogenase like	7	49960	Q9Y6N5	M	Redox
CSTB	Stefin B	3	11158	P04080	C	Redox
BLVR1	Biliverdin reductase A	3	33428	P53004	C/PM	Redox
BLVRB2	Biliverdin reductase B	5	22119	P30043	C/PM	Redox

AKR1C3	Aldo-keto reductase family 1, member A1	2	36573	P42330	C	Redox
SOD2	Manganese superoxide dismutase	3	24710	P04179	M	Redox
GPX1	Glutathione peroxidase	3	21899	P07203	C	Redox
GSTO1	Glutathione-S-transferase omega 1	2	27566	P78417	C	Redox
GSTA1	Glutathione transferase	6	23356	P08263	C	Redox
SPR	Sepiapterin reductase	3	28048	P35270	C	Redox
GLUD2	Glutamate dehydrogenase (NAD(P)+)	2	61433	P49448	M	Redox
CYP27A1	Cytochrome P450 27	2	60263	Q02318	M	Redox
CBR1	Carbonyl reductase 1	4	30375	P16152	C	Redox
HEBP1	Heme binding protein 1	2	21097	Q9NRV9	C	Redox
SH3BGR3	SH3 domain binding glutamic acid-rich protein like 3	2	10438	Q9H299	C	Redox
RNPEP	Aminopeptidase B	8	72623	Q9H4A4	PM/S	Leukotriene biosynthesis
ACAA2	Acetyl-coenzyme A acyltransferase 2	4	41924	P42765	M	Lipid metabolism
AADACL1	Arylacamide deacetylase-like 1	3	48072	Q6PIU2	PM	Lipid metabolism
ACADVL	Acyl-CoA dehydrogenase	7	70436	P49748	PM/M	Lipid metabolism
TPI1	Triosephosphate isomerase 1	6	26669	P60174	C	Lipid metabolism
LTA4H	Leukotriene A4 hydrolase	7	69285	P09960	C/PM	Lipid metabolism
HADHA	Enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	4	82959	P40939	M	Lipid metabolism
EHHADH	Peroxisomal enoyl-coenzyme A hydratase-like protein	4	35816	Q58EZ5	C	Lipid metabolism
PPAH1B2	Acetylhydrolase, isoform Ib	2	25569	P68402	C	Lipid metabolism
HADHB	Acetyl-CoA acyltransferase	3	51294	P55084	M	Lipid metabolism
ACLY	ACLY variant protein	2	124556	Q4LE36	C	Carbohydrate metabolism
PCK2	Phosphoenolpyruvate carboxykinase S62599 UTP-glucose-1-phosphate uridylyltransferase	6	70637	Q16822	C	Carbohydrate metabolism
UGP2	Pyruvate kinase, muscle isoform M2	3	56965	Q16851	C	Carbohydrate metabolism
PKM2	Pyruvate kinase, muscle isoform M2	18	57937	P14618	C	Carbohydrate metabolism
GPI	Glucose phosphate isomerase	6	63147	P06744	C	Carbohydrate metabolism
GALM	Galactose mutarotase (aldose 1-epimerase)	3	37765	Q96C23	C	Carbohydrate metabolism
PGK1	Phosphoglycerate kinase 1	7	44614	P00558	C	Carbohydrate metabolism
PGD	Phosphogluconate dehydrogenase	6	53140	P52209	C	Carbohydrate metabolism
ALDH2	Aldehyde Dehydrogenase	2	54445	P05091	M	Carbohydrate metabolism
MDH2	Malate dehydrogenase	4	35531	P40926	M	Carbohydrate metabolism
DLST	Dihydrolipoyllysine-residue succinyltransferase	3	48640	P36957	M	Carbohydrate metabolism
HK3	Hexokinase 3	3	98919	P52790	C	Carbohydrate metabolism
ENO1	Enolase 1	7	47169	P06733	C/PM	Carbohydrate metabolism
ENO3	Enolase 3	2	46987	P13929	C	Carbohydrate metabolism
TALDO1	Transaldolase 1	6	37540	P37837	C	Carbohydrate metabolism
G6PD	Glucose-6-phosphate 1-dehydrogenase	5	59265	P11413	C	Carbohydrate metabolism
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	7	36053	P04406	C/PM	Carbohydrate metabolism
PGK2	Phosphoglycerate kinase 2	2	44895	P07205	C	Carbohydrate metabolism
LHDB	L-Lactate Dehydrogenase	2	36507	P07195	C	Carbohydrate metabolism
FBP1	Fructose-1,6-bisphosphatase 1	8	36842	P09467	C	Carbohydrate metabolism
FBP2	Fructose-1,6-bisphosphatase 2	2	36743	O00757	C	Carbohydrate metabolism
APOB	Apolipoprotein B-100 precursor (Apo B-100)	8	515561	P04114	S	Lipid metabolism
APOE	Apolipoprotein E precursor	2	36154	P02649	S	Lipid metabolism
MDH1	Malate dehydrogenase	2	36426	P40925	C	Carbohydrate metabolism
NAGK	N-Acetylglucosamine kinase	2	37416	Q9UJ70	C	Carbohydrate metabolism
ACO2	Aconitase 2 precursor	3	85425	Q99798	M	Carbohydrate metabolism
TKT	Transketolase	6	67877	P29401	C	Carbohydrate metabolism
ATP5B	ATP synthase	8	57955	P06576	M	ADP/ATP exchange
ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex	2	17490	P30049	M	ADP/ATP exchange
SLC25A5	ADP/ATP translocase 2	2	32895	P05141	PM/M	ADP/ATP exchange
ATP5O	ATP synthase, O subunit precursor	4	23277	P48047	PM/M	Proton transport
KCTD7	Potassium channel tetramerisation domain	3	35701	A4D2M4	PM	PM voltage
VDAC1	Voltage-dependent anion channel 1 (VDAC1)	10	30772	P21796	PM	Cell volume
VDAC2	VDAC2	3	30412	P45880	PM	Membrane potential

ENSG00000096238	Chloride intracellular channel protein 1	2	23543	O00299	PM	Chloride ion transporter
ATP1A2	Na <sup>+</sup> /K <sup>+</sup> -ATPase alpha 2 subunit proprotein	2	112265	P50993	PM	Na <sup>+</sup> /K <sup>+</sup> transport
ATP1A1	Na <sup>+</sup> /K <sup>+</sup> -ATPase alpha 1 subunit isoform a	2	112895	P05023	PM	Na <sup>+</sup> /K <sup>+</sup> transport
PTPN6	Protein tyrosine phosphatase, non-receptor type 6	4	67719	P29350	PM/C	Cell signaling
PTPRE	Protein tyrosine phosphatase receptor type E	2	80641	P23469	PM	Cell signaling
PPP2R5A	Pp2a, Pr65alpha	2	65177	Q15172	C	Cell signaling
PBEF1	Nicotinamide phosphoribosyltransferase precursor	4	55521	P43490	C	Cell signaling
NA	14-3-3 protein gamma	3	28302	P61983	C	Signaling Scaffold
YWHAZ	14-3-3 protein zeta/delta	3	27745	P63104	C	Signaling Scaffold
RHOT2	Ras homolog gene family, member G	3	21308	A2IDC2	C	Calcium signaling
SLC25A24	Calcium-binding transporter	3	45819	Q6NUK1	M	Calcium regulation
IGAP1	IQ motif containing GTPase activating protein 1	29	189250	A7MBM3	C	GTPase activating
C3	Complement Component C3c	3	21496	P01024	S	Immune response
ILF2	Interleukin enhancer binding factor 2	2	43062	Q12905	N	Immune response
IL1RN	Interleukin 1 receptor antagonist isoform 1 precursor	2	20055	P18510	S/C	Immune response
ECGF1	Platelet-derived endothelial cell growth factor	5	49981	P19971	M	Immune response
C1QBP	Hyaluronan-binding protein 1	2	23801	Q07021	M	Immune response
SERPING1	Complement component 1 inhibitor precursor	3	55154	P05155	S	Immune response
CD14	CD14 protein precursor	2	40136	P08571	PM	Immune response
A2M	Alpha-2-macroglobulin precursor (Alpha-2-M)	20	163277	P01023	S	Immune response
SAMHD1	Monocyte protein 5	4	72200	Q9Y3Z3	C	Immune response
PYCARD	PYD and CARD domain containing isoform A	2	21627	Q9ULZ3	C	Cellular survival
PRKAR1A	cAMP-dependent protein kinase	2	42981	P10644	C	Cellular survival

<sup>a</sup> STRING database accession number (accessible at <http://string-db.org/>)

<sup>b</sup> Protein ID

<sup>c</sup> Number of unique significant ( $P < 0.05$ ) peptides identified for each protein

<sup>d</sup> Theoretical molecular mass for the primary translation product calculated from DNA sequences protein

<sup>e</sup> Accession numbers for UniProt (accessible at <http://www.uniprot.org/>)

<sup>f</sup> Postulated subcellular localization (accessible at <http://locate.imb.uq.edu.au> and

<http://www.uniprot.org/>) as follows: Plasma membrane (PM); secreted (S); cytoskeleton (CSK); cytosol

(C); mitochondria (M); nucleus (N); not available (NA, in this group are included proteins with no

postulated localization)

## Figure Legends

**Figure S1.** (A) Functional connectivity map of BC proteome generated on known and predicted protein-protein functional interactions of STRING database. Line thickness indicates level of interaction based on a confidence score. STRING map protein ID abbreviations are included in Table 1.

