Supplemental Table 1: Primers Used for Quantitative Real-Time PCR

Target Gene		Primer Sequence
BMP2	Forward	5’-CTGTATCGCAGGCACTCA-3’
	Reverse	5’-CTCCGTGGGGATAGAACTT-3’
OPN	Forward	5’-GATGGCCGAGGTGATAGTGT-3’
	Reverse	5’-CCATTCAACTCCTCGCTTTC-3’
GAPDH	Forward	5’-AACGTGTCAGTGGTGGACCTG-3’
	Reverse	5’-AGTGGGTGTCGCTGTTGAAGT-3’

Supplemental Table 2: Predicted Impact of the Three Replicated PhosSNPs on Protein Phosphorylation

Position of Effect Residue	Code of Effect Residue	Protein Kinase	*Effect Peptide(7,7)	Nucleotide Accession No.	Type of phosSNP
rs16861032 | pos=275 | CTA->GTA | L->V				NM_144718	II (+)
279	Y	TK/Fer	TETVDSSYVVGHVLN		
279	Y	TK/Met/Met	TETVDSSYVVGHVLN		
279	Y	TK/Tec/BTK	TETVDSSYVVGHVLN		
279	Y	TK/VEGFR/FLT4	TETVDSSYVVGHVLN		
rs16861032 | pos=275 | CTA->GTA | L->V				NM_144718	II (-)
278	S	TKL/STKR	STETLDSSYVVGHVL		
rs16861032 | pos=275 | CTA->GTA | L->V				NM_144718	III (-)
271	S	TKL/STKR	TRLQPEESTETLDSS		
271	S	AGC/GRK/GRK/GRK-4	TRLQPEESTETLDSS		
rs2657879 | pos=581 | CTC->CCC | L->P				NM_013267	II (+)
582	S	AGC/GRK	YQDSYTPSETQAEAA		
582	S	CMGC/DYRK/Dyrk1	YQDSYTPSETQAEAA		
582	S	STE/STE-Unique/NIK	YQDSYTPSETQAEAA		
582	S	AGC/GRK/BARK/GRK-2	YQDSYTPSETQAEAA		
rs2657879 | pos=581 | CTC->CCC | L->P				NM_013267	III (+)
575	Y	TK/FGFR	VVKLLQDYQDSYTPS		
578	S	TKL/RAF	LLQDYQDSYTPSETQ		
578	S	STE/STE-Unique/COT	LLQDYQDSYTPSETQ		
578	S	Other/AUR/AUR-A	LLQDYQDSYTPSETQ		
578	S	AGC/RSK/RSK/RSK1	LLQDYQDSYTPSETQ		
579	Y	TK/Csk	LQDYQDSYTPSETQA		
579	Y	TK/EGFR	LQDYQDSYTPSETQA		
579	Y	TK/Syk	LQDYQDSYTPSETQA		
579	Y	TK/Src/Lyn	LQDYQDSYTPSETQA		
579	Y	TK/Syk/Syk	LQDYQDSYTPSETQA		

<table>
<tr><td>580</td><td>T</td><td>CMGC</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>CMGC/CDK</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>CMGC/GSK</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>Other/CK2</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>Other/PLK</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
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<tr><td>580</td><td>T</td><td>CMGC/MAPK/ERK</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>CMGC/MAPK/JNK</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>CMGC/MAPK/p38</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>Other/CK2/CK2a</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
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<tr><td>580</td><td>T</td><td>CMGC/MAPK/ERK/MAPK3</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
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<tr><td>580</td><td>T</td><td>CMGC/MAPK/p38/MAPK14</td><td>QDYQDSYTPSETQAE</td><td></td><td></td></tr>
<tr><td colspan="4">rs2657879 | pos=581 | CTC->CCC | L->P</td><td>NM_013267</td><td>III (-)</td></tr>
<tr><td>575</td><td>Y</td><td>TK/Eph</td><td>VVKLLQDYQDSYTLS</td><td></td><td></td></tr>
<tr><td>575</td><td>Y</td><td>TK/VEGFR/FLT1</td><td>VVKLLQDYQDSYTLS</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>AGC/GRK</td><td>QDYQDSYTLSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>TKL/MLK</td><td>QDYQDSYTLSETQAE</td><td></td><td></td></tr>
<tr><td>580</td><td>T</td><td>TKL/MLK/ILK</td><td>QDYQDSYTLSETQAE</td><td></td><td></td></tr>
<tr><td colspan="4">rs6265 | pos=66 | GTG->ATG | V->M</td><td>NM_001709</td><td>II (-)</td></tr>
<tr><td>62</td><td>T</td><td>CAMK/RAD53</td><td>GLTSLADTFEHVIEE</td><td></td><td></td></tr>
</table>

Note: The impacts of the identified phosSNPs on protein phosphorylation were predicted by GPS2.0 (12).
*Underlined residues are encoded by phosSNP-harboring codon. Residues right in the middle are affected phosphorylation sites.

Type II phosSNP: a nsSNP that creates (+) or removes (-) one or multiple phosphorylation site(s) adjacent to the SNP.

Type III phosSNP: a nsSNP that changes the type of protein kinase for one or multiple phosphorylation site (s) adjacent to the SNP.