Data obtained during the analysis of sample FGFR3 KD which targeted m/z ratios potentially corresponding to Tyr- and pTyr-containing sequences of the kinase domain. In red is highlighted the peptide information presented in Table 2 of the manuscript.

Peptide	Tyr residue	z(PO4)	z(non-PO4)	Scores PO4		Score nonPO4	y_i			r_i			x_i (%)			Mean x
RPPGLD**Y**SFDTCKPPEEQLTFK	577	4	4	38	27	68 (MS2)	0.09 ?	0.21 ?	0.07 ?	3.44	3.60	3.59	>71	>72	>72	>72
RPPGLD**Y**SFDT	577	2	2	26	22	37 (MS2)	0.17 ?	0.35 ?	0.32 ?	2.40	2.64	2.63	>58	>62	>62	>61
DLVSCA**Y**QVAR	599	2 3	2 3	63 22	45 52	64 (MS2) 47 (MS2)	0.77 0.46	0.78 0.62	0.81 0.48	1.29 1.30	1.09 1.19	1.19 1.17	27 39	10 24	19 26	19 29
GME**Y**LASQK	607	2	2	37	37	54 (MS2)	0.86	0.88	0.85	1.18	1.28	1.36	17	24	29	23
DVHNLD**Y**YK	647	2 3	2 3	53 31	70 31	49 (MS2) 56 (MS2)	0.95 0.90	0.93 0.89	0.96 0.88	1.38 1.94	1.44 1.84	1.46 1.79				
DVHNLDY**Y**K	648	2	2	53	58	49 (MS2)	0.89	0.90	0.90	1.38	1.44	1.46				
DVHNLD**YY**K	647-648	2	2	29	26	49 (MS2)	0.90	0.92	0.92	1.38	1.44	1.46				
DVHNLD**Y**YKK	647	2 3 /	/ 3 4	44 28 /	27 22 /	/ 38 (MS2) 32 (MS2)	0.95 0.93 /	0.95 0.93 /	0.95 0.93 /	/ 5.56 5.14	/ 6.17 6.00	/ 5.37 5.90				
DVHNLDY**Y**KK	648	3	3	17	14	38 (MS2)	0.89	0.91	0.92	5.56	6.17	5.37				
DVHNLD**YY**KK	647-648	3	3	15	16	38 (MS2)	0.94	0.96	0.95							
CTHDL**Y**MIMR	724	/	3	/	/	42 (MSA)	/	/	/	1.82	1.58	1.93	>45	>37	>48	>43
MDKPANCTHDL**Y**M	724	/	2	/	/	24 (MS2)	/	/	/	1.59	1.79	1.55	>37	>44	>35	>38
MDKPANCTHDL**Y**MIMR	724	2 3 4	2 3 4	28 30 21	29 20 20	73 (MS2) 68 (MS2) 69 (MS2)	0.95 0.94 0.77	0.95 0.95 0.84	0.94 0.96 0.82	1.43 1.90 1.68	1.45 1.79 1.43	1.60 1.68 1.53	31 49 47	32 45 34	39 42 39	34 45 40
VLTVTSTDE**Y**LDLSAPF	760	/	2	/	/	39 (MSA)	/	/	/	2.68	2.41	2.90	>63	>58	>66	>62

?: the observed low yield of de-phosphorylation is in contradiction with the results obtained on peptide RPPGLD**Y**SFDTCKPPEEQLTFK in the second exploratory analysis (see third table below). The selected precursor must have been contaminated by another, non-phosphorylated species.

Data obtained during a first exploratory analysis of sample FGFR3 KD, which consisted of one FTMS scan followed by one MS2, one MSA and three HCD scans. In red is highlighted the peptide information presented in Table 2 of the manuscript.

Peptide	Tyr residue	z(PO4)	z(non-PO4)	Scores PO4		Score nonPO4	y_i			r_i			x_i (%)			Mean x
DLVSCA**Y**QVAR	599	2	2	63	53	50 (MS2)	0.88	0.92	0.87	1.15	1.17	1.18	15	16	17	16
		2	3			42 (MS2)	0.88	0.92	0.87	1.30	1.03	1.11	25	3	12	13
GME**Y**LASQK	607	/	2	/	/	53 (MSA)	-	-	-	1.24	1.28	1.30	19	22	23	>22
GME**Y**LASQK + Metox			2			46 (MSA)				1.94	1.58	1.70	48	37	41	>42
DVHNLD**YY**K	647	2	2	57	59	47 (MS2)	0.94	0.95	0.94	1.72	1.54	1.70				
		2	3			42 (MS2)	0.94	0.95	0.94	1.89	1.72	1.70				
DVHNLD**YY**KK	647-648	2	2	26	9	52 (MSA)	0.95	0.95	0.97	10.16	9.33	8.99				
		3	3	16	10	40 (MSA)	0.95	0.93	0.95	10.27	9.43	8.62				
MDKPANCTHDL**Y**MIMR	724	2	2	34	28	72 (MS2)	0.94	0.95	0.94	1.77	1.60	1.71	45	39	43	42
		3	3	52	50	51 (MSA)	0.96	0.94	0.93	1.78	1.76	1.70	45	45	43	45
		4	4	22	21	43 (MSA)	0.94	0.94	0.97	1.55	1.94	1.47	37	50	33	40
MDKPANCTHDL**Y**MIMR + Metox	724	/	2	/	/	62 (MS2)	/	/	/	2.83	2.30	2.70	>65	>57	>63	>61
			3			49 (MS2)				2.74	2.47	2.66	>63	>59	>62	>61
RPPGLD**Y**SFDTCKPPEEQLTFK	577	/	2	/	/	50 (MS2)	-	-	-	6.03	4.50	4.94	83	78	80	>80
		/	4	/	/	55 (MS2)	-	-	-	3.90	4.46	4.07	74	78	75	>75
VLTVTSTDE**Y**LDLSAPF	760	/	2	/	/	77 (MS2)	-	-	-	5.82	5.20	4.48	83	81	78	>81
VLTVTSTDEYLDLSAPFEQ**Y**SPGGQDTP SSSSSGDDSVFAHDLLPPAPPSSGGSR	770	4	5	/	63	36 (MSA)	1	1	1	inf	inf	inf	100	100	100	100
VLTVTSTDE**Y**LDLSAPFEQ**Y**SPGGQDTP SSSSSGDDSVFAHDLLPPAPPSSGGSR	760, 770	4	5	/	77		1	1	1							

Data obtained during a second exploratory analysis of sample FGFR3 KD, which consisted of one FTMS scan followed by one MS2, one MSA and three HCD scans. In red is highlighted the peptide information presented in Table 2 of the manuscript.

Peptide	Tyr residue	z(PO4)	z(non-PO4)	Scores PO4		Score nonPO4	y_i			r_i			x_i (%)			Mean x
RPPGLD**Y**SFDTCKPPEEQLTFK	577	5	4 5	17	16	54 (MS2) 37 (MSA)	0.92	0.94	0.94	3.72 2.65	2.17 ***inf.***	2.40 3.86	75 64	55 ***100***	60 75	63 80
DLVSCA**Y**QVAR	599	2	2 3	65	46	65 (MS2) 51 (MSA)	0.84	0.85	0.80	1.07 0.94	1.02 1.23	1.19 1.09	7 0	2 21	19 10	9 10
GME**Y**LASQK GME**Y**LASQK + Metox	607	/	2 2	/	/	54 (MS2) 53 (MSA)	/	/	/	1.26 1.21	1.28 1.17	1.17 1.23	>21 >17	>22 >15	>15 >19	>19 >17
DVHNLD**Y**YK	647	2 3	2 3	56 32	54 26	48 (MSA) 45 (MS2)	0.94 0.92	0.94 0.93	0.95 0.93	1.49 1.79	1.40 1.96	1.39 1.84				
DVHNLDY**Y**K	648	2	2	51	52	48 (MSA)	0.88	0.86	0.86	1.49	1.40	1.39				
DVHNLD**YY**KK	647	3	2 3 4	15	20	53 (MSA) 39 (MSA) 20 (MSA)	0.94	0.94	0.94	7.77 7.46 9.42	9.93 8.74 8.13	7.76 7.34 8.31				
MDKPANCTHDL**Y**MIMR	724	2 3 4	2 3 4	34 31 29	32 34 22	67 (MS2) 50 (MSA) 47 (MSA)	0.97 0.94 0.95	1.00 0.94 0.94	0.96 0.93 0.96	1.54 1.55 1.43	1.37 1.44 1.59	1.61 1.67 1.48	36 37 31	27 32 39	39 42 33	34 37 34
MDKPANCTHDL**Y**MIMR + Metox	724	/	2 3	/	/	50 (MSA) 46 (MS2)	/	/	/	2.12 1.93	1.74 1.67	1.97 1.89	>53 >48	>43 >40	>49 >47	>48 >45
PANCTHDL**Y**MIMR	724	/	3	**/**	**/**	53 (MSA)	/	/	/	1.15	1.37	1.31	>13	>27	>23	>21
VLTVTSTDE**Y**LDLSAPF	760	2	2	49	38	73 (MS2)	1.00	1.00	1.00	inf	7.36	3.75	100	86	73	86
VLTVTSTDE**Y**LDLSAPFE	760	/	2	/	/	44 (MSA)	/	/	/	inf	4.10	3.88	100	>76	>74	>83