Electronic Supplementary Material (ESI) for Analyst.

forward (FW) and reverse (RV) primers	target gene	sequence	amplicon size (bp)
*h*PTPRG FW *h*PTPRG RV	*human PTPRG*	5'-GTTTCAAGCTAATACCACTCG-3' 5'-TGGAAACAAATGAGAATGGG-3'	155
*h*BACT FW *h*BACT RV	*human β-actin*	5'-TGACCCAGATCATGTTTGAG-3' 5'-CTTCTCCTTAATGTCACGCAC-3'	290
BCR/ABL FW BCR/ABL RV	*Bcr/Abl*	5'-GATGCTGACCAACTCGTGTG-3' 5'-AGCAGATACTCAGCGGCATT-3'	411-486
BCR/ABL FW BCR/ABL RV	*Bcr/Abl*	5'-GTTCCTGATCTCCTCTGACTATGAGCGTG-3' 5'-TGTGATTATAGCCTAAGACCCGGAG-3'	411-486
(external round nested PCR) *m*PTPRGex FW *m*PTPRGex RV	*mouse Ptprg*	5'-ATCCTATTATCCACGGGCTG-3' 5'-TGTAAATGTCTTCTCCTTCTCGTC-3'	483
(internal round nested PCR) *m*PTPRGin FW *m*PTPRGin RV	*mouse PTPRG*	5'-GTACCTGAGAAATAACTTCCGAC-3' 5'-AGAGCTGCAAACTTTAGAGG-3'	144
*m*βACT FW *m*βACT RV	*mouse β-actin*	5'-GTACCTGAGAAATAACTTCCGAC-3' 5'-GAGCAATGATCTTGATCTTCATGG-3'	145

Table 1. Forward (FW) and reverse (RV) primers used for RT-PCR of *BCR/ABL*, human (*h*) and mouse (*m*) *PTPRG* and human and mouse beta actin (*βACT*) genes.

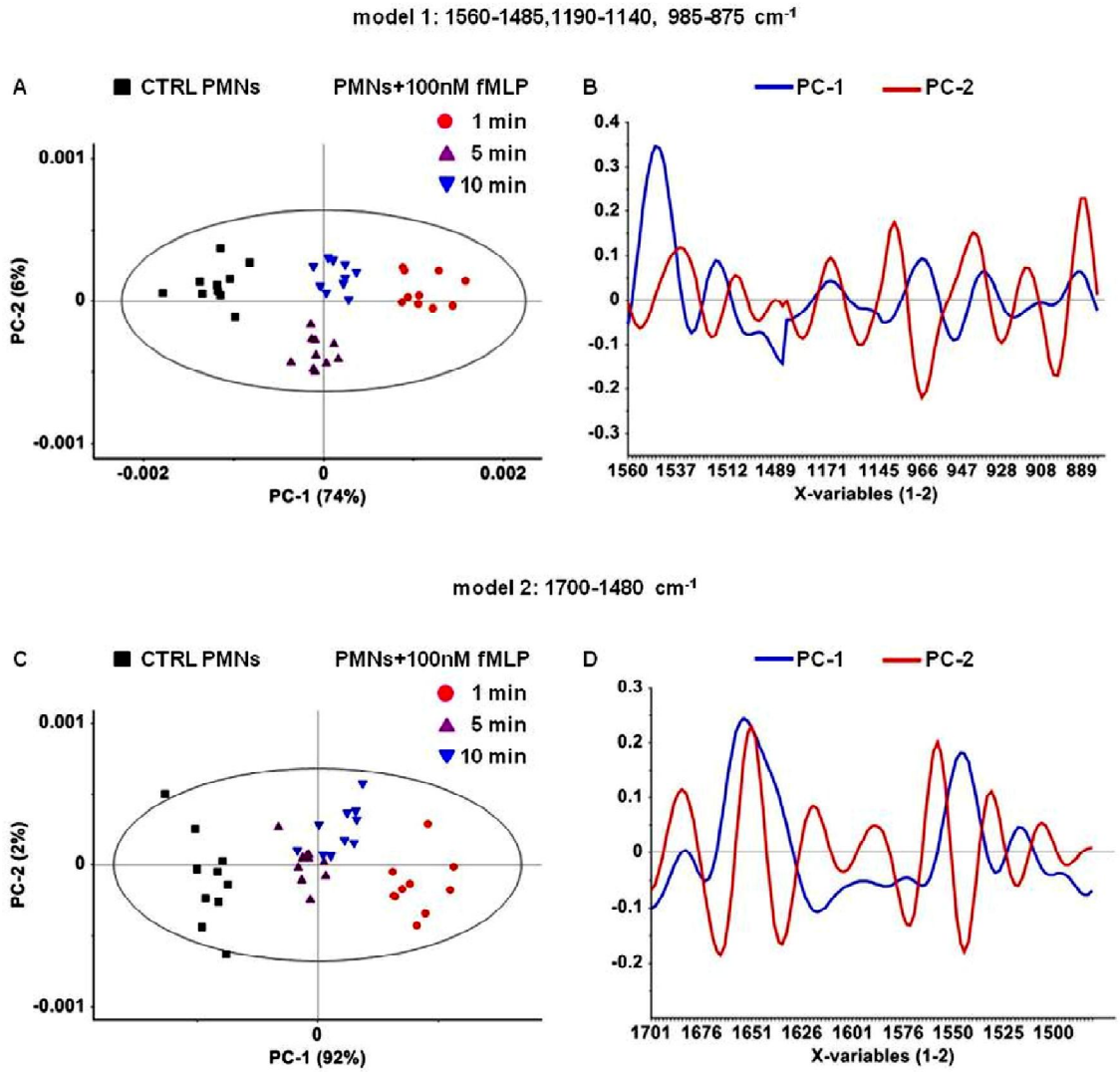


Figure S1. MicroFTIR performed with the conventional IR source (globar) and principal component analysis (PCA) with models 1 (A-B) and 2 (C-D), respectively. The dataset comprises the spectra of PMNs exposed to 100 nM fMLP for 1 min (red dot), 5 min (violet triangle) and 10 min (blue inverted triangle), and the spectra of non stimulated CTRL PMNs (black box). Each symbol represents the average spectrum mediating IR signals from 10-12 cells spread over an area of 30x30 μm^2 in sizes. Grey ellipse delimits 95% confidence interval. Statistics are available in supplementary material S5.

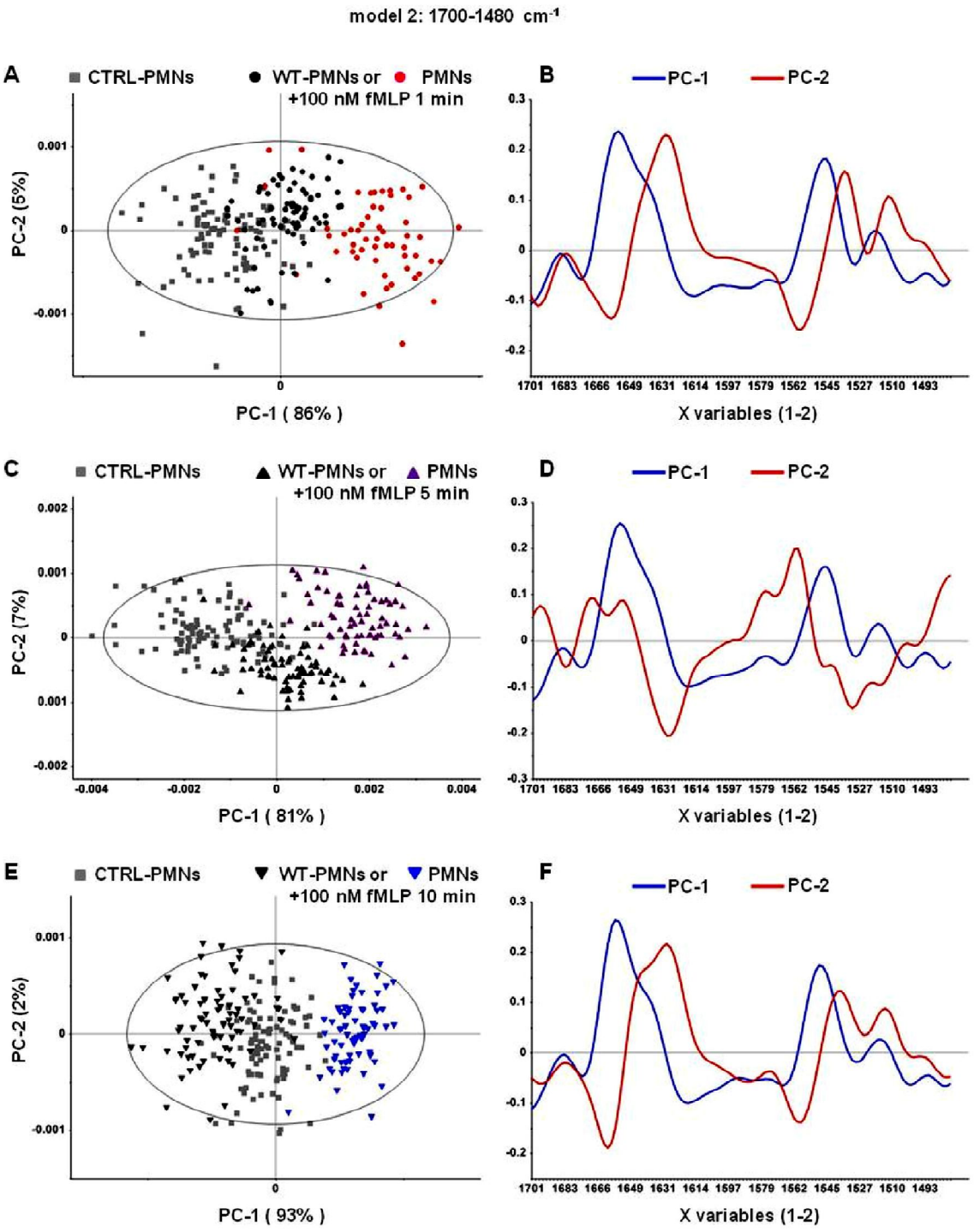


Figure S2. SR microFTIR and principal component analysis (PCA) with the model 2 (1700-1480 cm^{-1}). The dataset composes of spectra of neutrophil leukocytes pre-incubated with 100 nM wortmannin (WT-PMNs) the specific and irreversible inhibitor of phosphoinositol 3 phosphate kinase (PI3K) activity and stimulated with 100 nM fMLP (black symbols), the spectra of PMNs stimulated with fMLP without the inhibition of PI3K (red, violet, and blue symbols) and the spectra of non stimulated CTRL PMNs (grey box). fMLP stimulation for 1, 5, and 10 min is indicated by dot, triangle and inverted triangles, respectively. Grey ellipse delimits 95% confidence interval. Statistics are available in supplementary material S5.

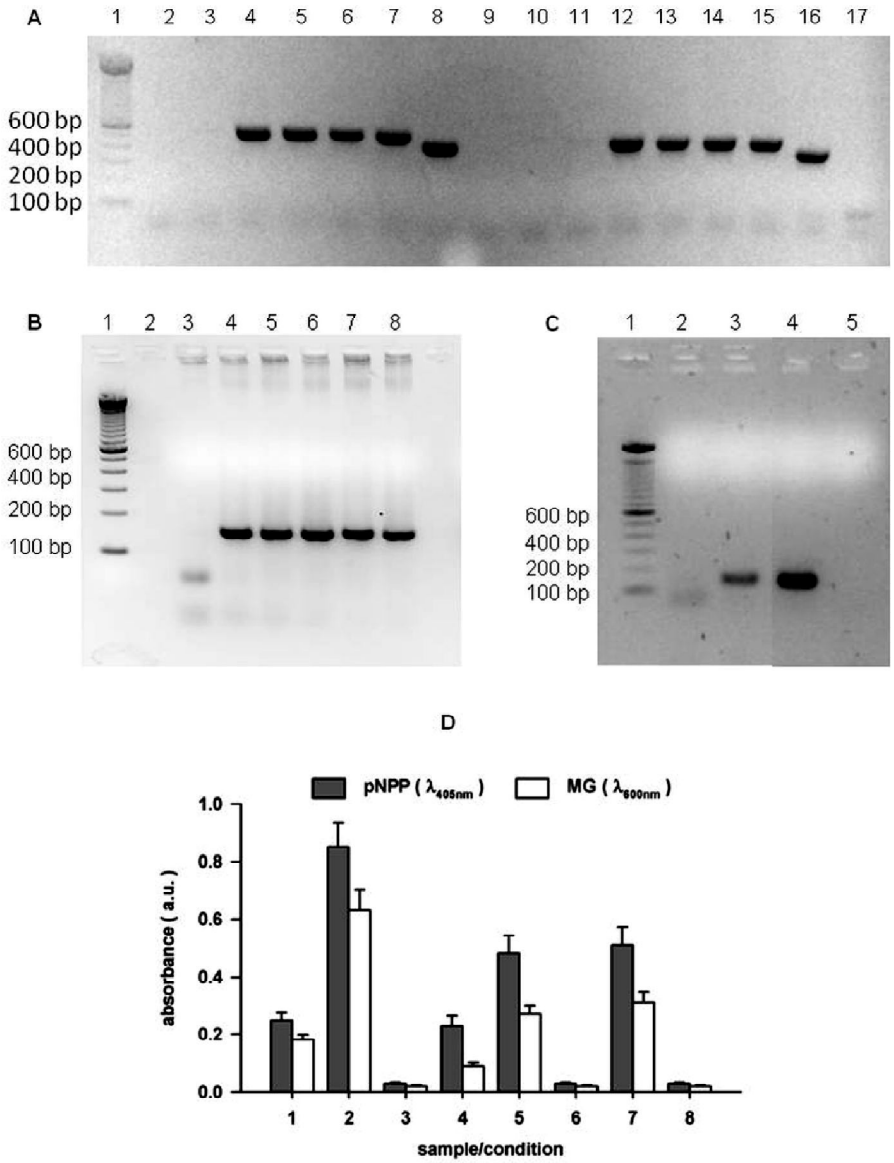


Figure S3. The presence of p210$^{BCR/ABL}$ (A) and of mouse (B) or human (C) *PTPRG* cDNAs checked in Ba/F3 and in K562 cells sub-clones by polymerase chain reaction (RT-PCR). A (p210$^{BCR/ABL}$) lanes: base pair (100bp) ladder (1); Ba/F3#PAR (2,3, 10, and 11); Ba/F3 transfected with p210$^{BCR/ABL}$ cDNA (Ba/F3#WT, 4 and 12); K562#MK (5,13), K562#G1 (6,14), K562#DA (7,15); BCR/ABL positive CTRL MEG-01 leukemia cell line (8 and 16); H_20 (9 and 17), respectively. B (*mPTPRG*) lanes: bp ladder (1); H_20 (2); H_2O PCR ms nest483 F/R (3); Ba/F3#PAR (4 and 5); Ba/F3#WT (6 and 7); CTRL mouse F317L cells (8). C (*hPTPRG*) lanes: bp ladder (1); K562#MK (2); K562#DA (3); K562#G1 (4); H2O (5), respectively. D: protein phosphatase activity (mean ± SD of 2 independent experiments) determined by p-Nitrophenyl Phosphate (pNPP, grey bars) and malachite green (MG) assays, respectively. Sample/condition: K562#MK (1), K562#G1 (2), K562#G1 + 0.2 mM Na_3VO_4 (3); K562#DA (4), Ba/F3#PAR (5), Ba/F3#PAR + 0.2 mM Na_3VO_4 (6); Ba/F3#WT (7), and Ba/F3#WT + 0.2 mM Na_3VO_4 cell lysates (50µL sample adjusted to 1 mg total protein/mL cell lysate + 150 µL 50 mM Tris buffer pH 7.4, containing 1 mM EDTA and 1 mM DTT), respectively. In the MG assay 150 µM ENDpYINASL phosphopeptide was used as a substrate for PTP activity.

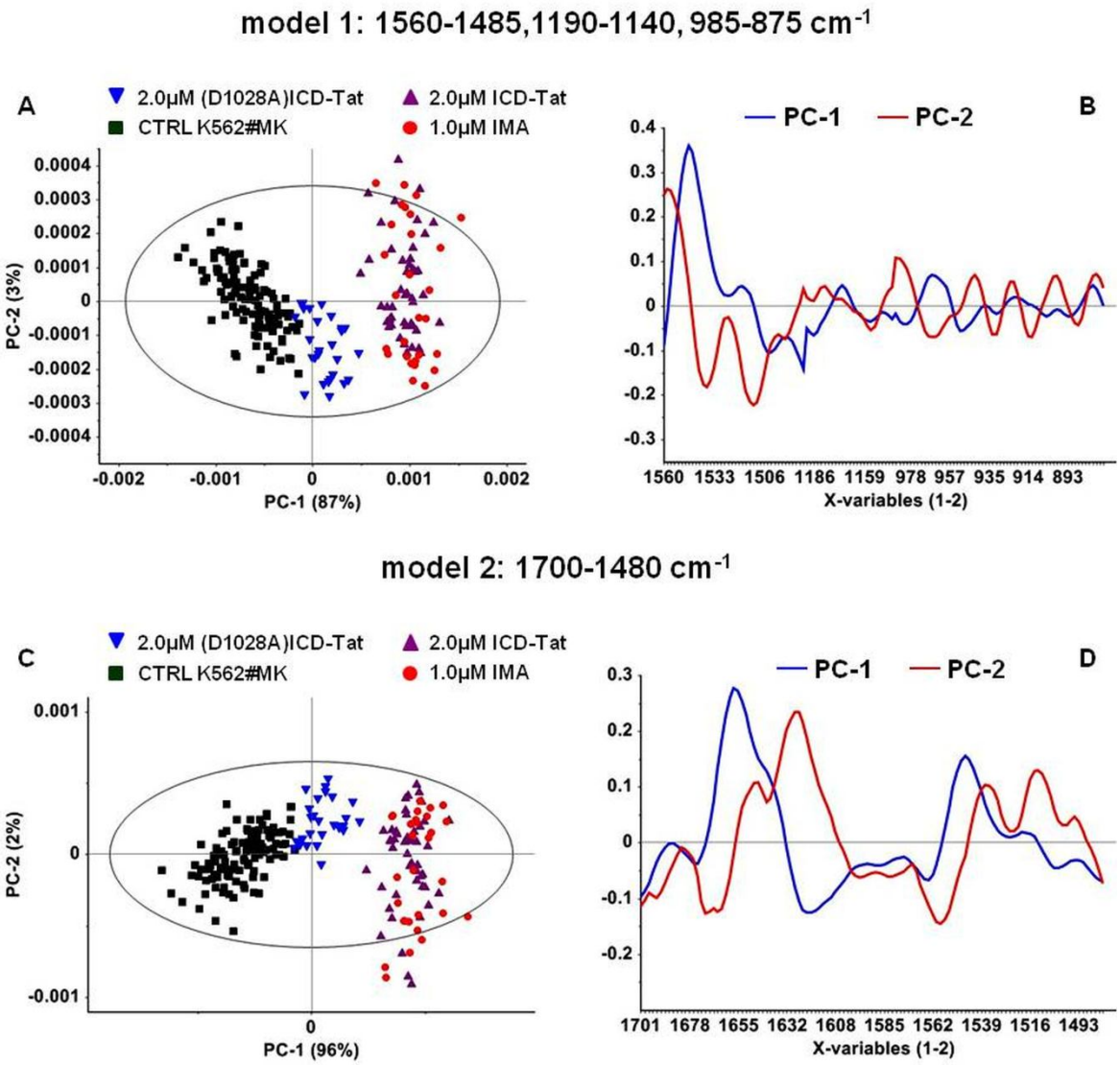


Figure S4. MicroFTIR performed with the conventional IR source (globar) and PCA with models 1 (A-B) and 2 (C-D) applied to explore K562#MK cells exposed to different experimental conditions. Each symbol average IR signals from 10-12 cells spread within 30x30 µm^2 spot areas. CTRL K562#MK (black box), and K562#MK samples exposed for 24 hours to 2.0 µM ICD-Tat (violet triangle) or to 2.0 µM (D1028A)ICD-Tat (blue inverted triangle) recombinant proteins, or to 1.0 µM imatinib mesylate (IMA) (red dot) are shown. Grey ellipse delimits 95% confidence interval. Statistics are available in supplementary material S5.

S5. Statistics performed on PCA data.

variables	type of test	result	comparison	significance level P<0.05
Figure 1 AB, model 1800-875 cm^{-1}				
PC-1	Kruskal-Wallis One Way ANOVA on Ranks	H = 171.568, (P=<0.001)		
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs. CTRL	YES
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	NO[a]
			1 min fMLP vs. 10 min fMLP	NO[b]
			5 min fMLP vs. 10 min fMLP	NO
PC-2	Kruskal-Wallis One Way ANOVA on Ranks	H = 221.591, (P=<0.001)		
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs CTRL	NO
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	YES
			5 min fMLP vs. 10 min fMLP	YES
Figure 1 CD, model 1 (1560-1485, 1190-1140, 985-875 cm^{-1})				
PC-1	Kruskal-Wallis One Way ANOVA on Ranks	H = 182.147, (P=<0.001)		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs. CTRL	YES
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	NO[c]
			5 min fMLP vs. 10 min fMLP	YES
PC-2	Kruskal-Wallis One Way ANOVA on Ranks	H = 234.088, (P=<0.001)		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs. CTRL	NO
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	YES
			5 min fMLP vs. 10 min fMLP	YES
Figure 1 EF, model 2 (1700-1480 cm^{-1})				
PC-1	Kruskal-Wallis One Way ANOVA on Ranks	H = 200.912, (P=<0.001)		
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs. CTRL	YES
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	YES
			5 min fMLP vs. 10 min fMLP	NO[d]
PC-3	Kruskal-Wallis One Way ANOVA on Ranks	H = 151.194, (P=<0.001)		
	All Pairwise Multiple Comparison (Dunn's Method)		1 min fMLP vs. CTRL	NO
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	YES
			5 min fMLP vs. 10 min fMLP	YES

[a] Mann-Whitney Rank Sum Test: T = 4853, P = 0.009
[b] Mann-Whitney Rank Sum Test: T = 4537, P = 0.042
[c] Mann-Whitney Rank Sum Test: T = 4471, P = 0.042
[d] t-test: t = 2.019, P = 0.045

Figure S5. Statistics performed on PCA data

Figure S1 AB, model 1 (1560-1485, 1190-1140, 985-874 cm^{-1})				
variables	Type of test	result	comparison	significance level P<0.05
PC-1	Kruskal-Wallis One Way ANOVA	F = 206.842, (P<0.001)		
	All Pairwise Multiple Comparison (Holm-Sidak method)		1 min fMLP vs. CTRL	YES
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	YES
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	YES
			5 min fMLP vs. 10 min fMLP	YES
PC-2	Kruskal-Wallis One Way ANOVA	F = 46.756, (P<0.001)		
	All Pairwise Multiple Comparison (Holm-Sidak method)		1 min fMLP vs. CTRL	NO
			5 min fMLP vs CTRL	YES
			10 min fMLP vs CTRL	NO
			1 min fMLP vs. 5 min fMLP	YES
			1 min fMLP vs. 10 min fMLP	NO
			5 min fMLP vs. 10 min fMLP	YES
Figure S1 CD, model 2 (1700-1480 cm^{-1})				
PC-1	Kruskal-Wallis One Way ANOVA			P=<0.001
	All Pairwise Multiple Comparison (Holm-Sidak method):		1 min fMLP vs. CTRL	P<0.05
			5 min fMLP vs CTRL	P<0.05
			10 min fMLP vs CTRL	P=0.970
			1 min fMLP vs. 5 min fMLP	P<0.05
			1 min fMLP vs. 10 min fMLP	P<0.05
			5 min fMLP vs. 10 min fMLP	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA on Ranks			P=0.243
	t-test on the means		1 min fMLP vs. CTRL	P = 0.710
			5 min fMLP vs CTRL	P = 0.352
			10 min fMLP vs CTRL	P=0.980
			1 min fMLP vs. 5 min fMLP	P=0.059
			1 min fMLP vs. 10 min fMLP	P=0.710
			5 min fMLP vs. 10 min fMLP	P=0.352

Figure S5. Statistics performed on PCA data

variables	Type of test	Comparison	significance level
Figure 2 AB (1 min fMLP stimulation), model 1 (1560-1485, 1190-1140, 985-875 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 1 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison Procedures (Holm-Sidak method)	PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 1 min	P<0.05
Figure 2 CD (5 min fMLP stimulation), model 1 (1560-1485, 1190-1140, 985-875 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison Procedures (Holm-Sidak method)	PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 5 min vs. WT-PMNs +100 nM fMLP 5 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P=0.498
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 5 min	P<0.05
Figure 2 EF (10 min fMLP stimulation), model 1 (1560-1485, 1190-1140, 985-875 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 10 min vs. WT-PMNs +100 nM fMLP 10 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison Procedures (Holm-Sidak method)	PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 10 min vs. WT-PMNs +100 nM fMLP 10 min	P<0.05

Figure S5. Statistics performed on PCA data

Figure S2 AB (1 min fMLP stimulation), model 2 (1700-1480 cm^{-1})			
variables	**Type of test**	**comparison**	**significance level**
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 1 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P=0.860
		WT-PMNs +100 nM fMLP 1 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 1 min	P<0.05
Figure S2 CD (5 min fMLP stimulation), model 2 (1700-1480 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 5 min vs. WT-PMNs +100 nM fMLP 5 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 5 min vs. CTRL PMNs	P=0.498
		PMNs +100 nM fMLP 1 min vs. WT-PMNs +100 nM fMLP 5 min	P<0.05
Figure S2 EF (10 min fMLP stimulation), model 2 (1700-1480 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 10 min vs. WT-PMNs +100 nM fMLP 10 min	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison Procedures (Holm-Sidak method)	PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		WT-PMNs +100 nM fMLP 10 min vs. CTRL PMNs	P<0.05
		PMNs +100 nM fMLP 10 min vs. WT-PMNs +100 nM fMLP 10 min	P<0.05

Figure S5. Statistics performed on PCA data

Figure 4 AB, model 1 (1560-1485, 1190-1140, 985-874 cm-1)			
variables	**Type of test**	**comparison**	**significance level: P<0.05**
PC-1	t-test on tne means	Ba/F3 PAR vs. Ba/F3WT	P=<0.001
PC-2	Mann-Whitney Rank Sum Test		P=0.124
Figure 4 CD, model 2 (1560-1485, 1190-1140, 985-874 cm-1)			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	K562#MK vs. K562#DA	P<0.05
		K562#MK vs. K562#G1	P<0.05
		K562#G1 vs. K562#DA	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=0.238
	Mann-Whitney Rank Sum Test	K562#MK vs. K562#DA	P=0.538
		K562#MK vs. K562#G1	P=0.054
		K562#G1 vs. K562#DA	P=0.706
Figure 4 EF, model 1 (1700-1480 cm-1)			
PC-1	t-test on tne means	Ba/F3 PAR vs. Ba/F3WT	P=<0.001
PC-2	Mann-Whitney Rank Sum Test		P=0.329
Figure 4 GH, model 2 (1700-1480 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	K562#MK vs. K562#DA	P<0.05
		K562#MK vs. K562#G1	P<0.05
		K562#G1 vs. K562#DA	P<0.05
PC-2	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison (Holm-Sidak method)	K562#MK vs. K562#DA	P=0.724
		K562#MK vs. K562#G1	P<0.05
		K562#G1 vs. K562#DA	P<0.05

Figure S5. Statistics performed on PCA data

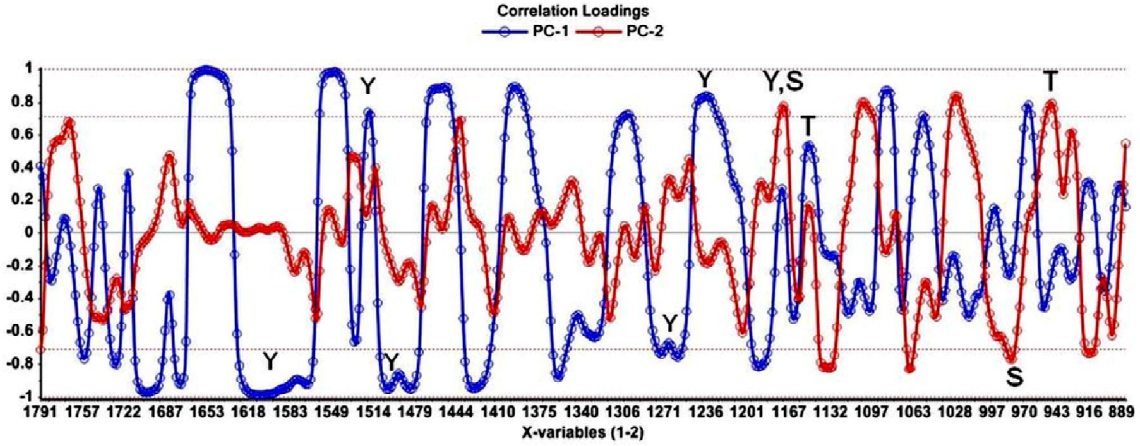
Figure 5 AB, model 1 (1560-1485, 1190-1140, 985-874 cm^{-1})			
variables	Type of test	comparison	significance level P<0.05
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#MK vs. 1.0 µM IMA	YES
		CTRL K562#MK vs. 2.0 µM ICD-Tat	YES
		CTRL K562#MK vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM ICD-Tat	NO
		2.0 µM ICD-Tat vs. 2.0 µM (D1028A)ICD-Tat	YES
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#MK vs. 1.0 µM IMA	NO
		CTRL K562#MK vs. 2.0 µM ICD-Tat	NO
		CTRL K562#MK vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM ICD-Tat	NO
		2.0 µM ICD-Tat vs. 2.0 µM (D1028A)ICD-Tat	YES
Figure 5 CD, model 2 (1700-1480 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#MK vs. 1.0 µM IMA	YES
		CTRL K562#MK vs. 2.0 µM ICD-Tat	YES
		CTRL K562#MK vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM ICD-Tat	NO
		2.0 µM ICD-Tat vs. 2.0 µM (D1028A)ICD-Tat	YES
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=0.243
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#MK vs. 1.0 µM IMA	NO
		CTRL K562#MK vs. 2.0 µM ICD-Tat	NO
		CTRL K562#MK vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM (D1028A)ICD-Tat	YES
		1.0 µM IMA vs. 2.0 µM ICD-Tat	NO
		2.0 µM ICD-Tat vs. 2.0 µM (D1028A)ICD-Tat	YES

Figure S5. Statistics performed on PCA data

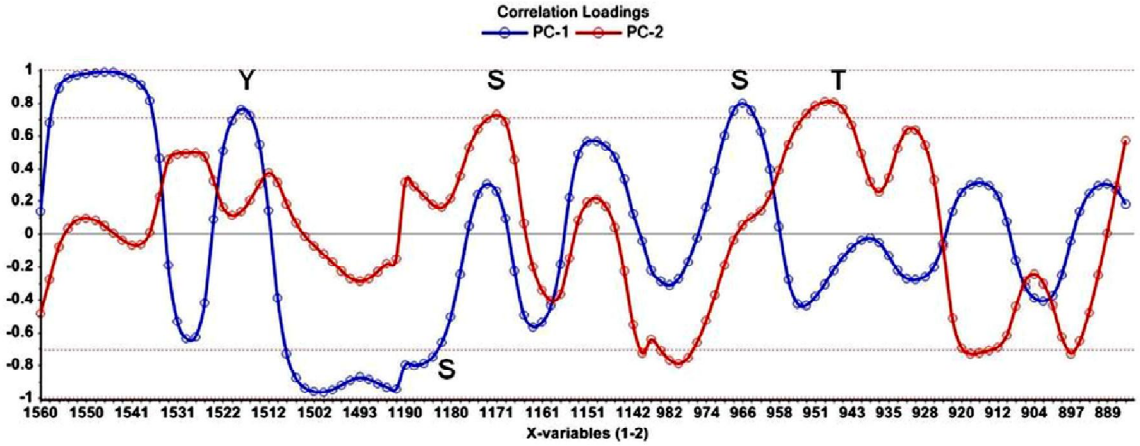
Figure 6 AB, model 1 (1560-1485, 1190-1140, 985-874 cm^{-1})			
variables	Type of test	comparison	significance level P<0.05
PC-1	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison (Holm-Sidak Method)	CTRL K562#G1 vs. CTRL K562#MK	YES
		CTRL K562#G1 vs. 0.5 µM IMA #G1	YES
		CTRL K562#G1 vs. 0.5 µM IMA #MK	YES
		CTRL K562#MK vs. 0.5 IMA µM #G1	YES
		CTRL K562#MK vs. 0.5 IMA µM #MK	YES
		0.5 µM IMA #G1 vs. 0.5 µM IMA #MK	YES
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=<0.001
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#G1 vs. CTRL K562#MK	YES
		CTRL K562#G1 vs. 0.5 µM IMA #G1	YES
		CTRL K562#G1 vs. 0.5 µM IMA #MK	YES
		CTRL K562#MK vs. 0.5 IMA µM #G1	YES
		CTRL K562#MK vs. 0.5 IMA µM #MK	YES
		0.5 µM IMA #G1 vs. 0.5 µM IMA #MK	YES
Figure 6 CD, model 2 (1700-1480 cm^{-1})			
PC-1	Kruskal-Wallis One Way ANOVA		P=<0.001
	All Pairwise Multiple Comparison (Holm-Sidak Method)	CTRL K562#G1 vs. CTRL K562#MK	YES
		CTRL K562#G1 vs. 0.5 µM IMA #G1	YES
		CTRL K562#G1 vs. 0.5 µM IMA #MK	YES
		CTRL K562#MK vs. 0.5 IMA µM #G1	YES
		CTRL K562#MK vs. 0.5 IMA µM #MK	YES
		0.5 µM IMA #G1 vs. 0.5 µM IMA #MK	YES
PC-2	Kruskal-Wallis One Way ANOVA on Ranks		P=0.243
	All Pairwise Multiple Comparison (Dunn's Method)	CTRL K562#G1 vs. CTRL K562#MK	YES
		CTRL K562#G1 vs. 0.5 µM IMA #G1	YES
		CTRL K562#G1 vs. 0.5 µM IMA #MK	YES
		CTRL K562#MK vs. 0.5 IMA µM #G1	YES
		CTRL K562#MK vs. 0.5 IMA µM #MK	YES
		0.5 µM IMA #G1 vs. 0.5 µM IMA #MK	YES

Figure S5. Statistics performed on PCA data

S6 Figure 1 AB: model 1800-875 cm^{-1}



S6 Figure 1 CD: model 1: 1560-1485, 1190-140, 985-875 cm^{-1}



S6 Figure 1 EF: model 2: 1700-1480 cm^{-1}

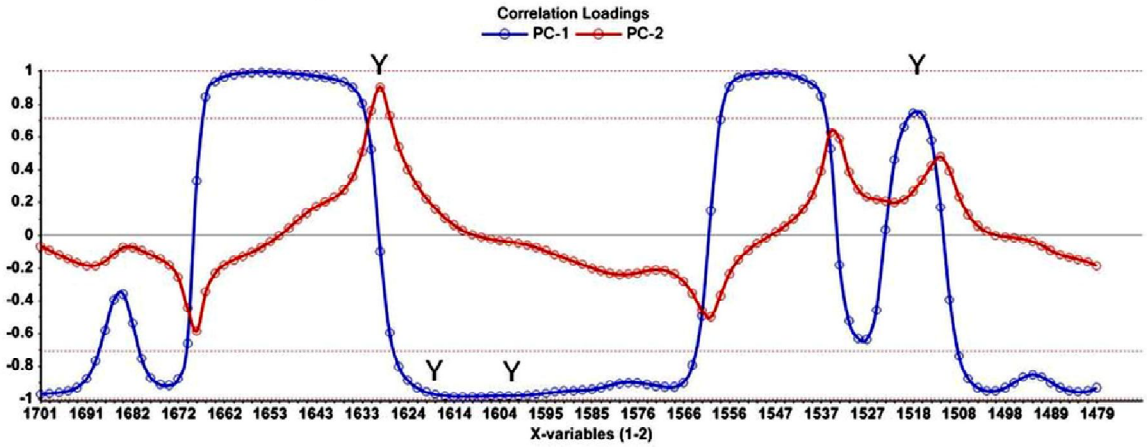


Figure S6. Correlation loadings of PCA in Figure 1 AB. The unsupervised identification of variables giving major contributions to the models. Values that lie within the upper and lower bounds of the plot are modelled by PCs. Those that lie between the two lower bounds are not. An attempt has been made to assign tyrosine (Y), serine (S), and threonine (T) according to the data available in the literature (Refs 43-48).