

Supplementary file

# New insights into the Multivariate Analysis of SER spectra collected on blood samples for Prostate Cancer Detection: towards a better understanding of the role played by different biomolecules on cancer screening

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**Table S1.** The SERS peaks tentative assignments of major vibrational bands in plasma and serum samples from PCa patients and healthy donors.

Peak positions (cm <sup>-1</sup> )	Vibrational mode	Assignments
390	n/a	Uric acid [1]
480	Ring torsion vibration, (N-C-S) stretching [2]	DNA, Guanine, arginine, valine, glutamate, tyrosine, tryptophan, mannose, glucose, acetyl coenzyme A, acetoacetate, cholesterol [2–4]
498	Ring torsion vibration, (N-C-S) and S-S stretching [2,5–7] proteins	Protein, lipid or carbohydrate components, guanine, thymine, arginine, valine, glutamate, tyrosine, tryptophan, mannose, glucose, acetyl coenzyme A, acetoacetate, uric acid [1,2,5,7–12]
535	(S-S) stretching in proteins [2,13]	Uracil, alanine, phenylalanine, glutamate, tyrosine, tryptophan, cysteine, mannose, fructose, galactosamine, N-acetyl-D-glucosamine, phosphoenolpyruvate, acetyl coenzyme A, D-fructose-6-phosphate, riboflavin, phosphatidylserine, cholesterol ester [2,5,7]
596	(C-S) and 4(PO <sub>4</sub> <sup>3-</sup> ) stretching [2]	Amide VI, ascorbic acid, glutamate, tryptophan, methionine, tyrosine, cytosine, lactose, N-acetyl-D-glucosamine, pyruvate, acetyl coenzyme A, phosphatidylinositol [2,7,14]
642	Ring stretching of uric acid and hypoxanthine [10] (C-S) stretching [5,7,15] (C-C) twisting [8,10,16] Ring breathing modes [17] Skeletal ring deformation [18]	DNA bases, lipids and proteins, tyrosine [5–8,10,12,16,17,19,20]
690	In-phase ring stretching of the six-membered ring except C <sub>4</sub> C <sub>5</sub> [11,12,21–23]	Guanine, cytosine, glutathione, tyrosine [1,6,11,12,21–23]
728	Ring stretching in uric acid and hypoxanthine [10] (C-S), (C-C), (C-N), (CH <sub>2</sub> ), CN <sup>-</sup> (CH <sub>3</sub> ) <sub>3</sub> , N <sup>+</sup> (CH <sub>3</sub> ) <sub>3</sub> stretching [2,17] (C-H) and (N-H) bending [7,10,18]	DNA/RNA bases, glycine, tryptophan, histidine, proline, oleic acid, triolein, mannose, citric acid, coenzyme A, acetyl coenzyme A, glutathione, phospholipids, hypoxanthine, phenylalanine [2,4,21–23,7–13,17]

Ring breathing modes of DNA/RNA bases and (O-P-O) stretching in DNA [16]		
769	Ring breathing and deformation [2,3]	Cytosine, thymine, uracil, glutamate, tyrosine, tryptophan, fumarate, proline, N-acetyl-D-glucosamine, phosphoenolpyruvate, acetoacetate, phospholipids, riboflavin, pyrimidine, phosphatidylserine [2,3,14]
815	(C-C-O) and (C-C) stretching [5,7,8] Ring vibration [18]	Collagen L-serine, glutathione, uric acid [5,7,8,10]
893	(C-C) stretching [8,19] (C-O-H) and (N-H) bending [2,5,7,8,18]	Deoxyribose phosphate backbone, D-galactosamine, tryptophan, uric acid [5,7,8,10,12,24]
915	(C-COO <sup>-</sup> ) stretching in carbohydrates [25]	Glucose, lactic acid [3]
969	Skeletal vibration [6,24]	Phosphodiester, saccharides, deoxyribose [16]
1010	Symmetric ring breathing mode of phenylalanine [8,15,26] (CO), (CC) and (OCH) bending [3] (C-C) skeletal in phenylalanine [6]	Aromatic aminoacids, carbohydrates, phenylalanine, proteins, lipids, thymine, deoxyribose phosphate backbone, 5-methylcytosine [3,8-10,12,16,23,27,28]
1075	(C-C), (C-N) and (C-O) stretching [2,3,7,8,17] Symmetric stretching of (PO <sub>2</sub> <sup>-</sup> ) [16] (C-S) stretching and (NH <sub>2</sub> ) rocking [29]	Nucleic acids, saccharides, adenine, glycine, serine, glutamate, tryptophan, histidine, fatty acids, mannose, glucose, lactose, galactosamine, N-acetyl-D-glucosamine, acetyl coenzyme A, D-fructose-6-phosphate, glutathione, phospholipids, collagen, proteins [2,3,7,8,16,17]
1099	(C-N), (C-C) and (PO <sub>2</sub> <sup>-</sup> ) stretching in carbohydrates and lipids [13,16,19,24]	DNA, phenylalanine, proteins, lipids, phospholipids and carbohydrates [12,16,20,22,24]
1136	(C-O), (C-N), (C-C) stretching mode [2,4,5,18,30-33] (C-H), (C-N) bending [4,29,31,32] (CH <sub>3</sub> ) rocking [4,31,32]	adenine, glycine, serine, glutamate, tryptophan, histidine, fatty acids, mannose, glucose, lactose, galactosamine, N-acetyl-D-glucosamine, acetyl coenzyme A, D-fructose-6-phosphate, glutathione, phospholipids, uric acid, tyrosine, ascorbic acid, D-mannose [2,5,7,8,10,14]
1209	(C-C <sub>6</sub> H <sub>5</sub> ) stretching [8,17] (N-C-C) stretching and bending [18] (C <sub>m</sub> H) bending [34]	proteins arising from aromatic amino acids such as tyrosine, phenylalanine, tryptophan, adenine, thymine, amide III, uric acid [6-8,10,15-17,19,20]
1256	Ring stretching in uric acid and hypoxanthine [10] (C-N) and (C-C) stretching [3,16] (CH) bending in lipids [13] Asymmetric (PO <sub>2</sub> <sup>-</sup> ) stretching [35]	Proteins, amide III, collagen, lipids, adenine, cytosine [1,3,6,16,17,20,27]
1336	(CH), (CH <sub>2</sub> ) and (CH <sub>3</sub> ) bending [2,6,10,19] (CH <sub>3</sub> CH <sub>2</sub> ) wagging in nucleic acids, (CH <sub>2</sub> ) deformation [16] Symmetric stretch of the (NO <sub>2</sub> ) group [36]	hydrocarbon chains of the fatty acids, with a possible small contribution from the CH <sub>2</sub> groups of cholesterol, triglycerides, collagen, nucleic acid bases, proteins, tryptophan, valine, serine, arginine, phenylalanine, tyrosine, tryptophan, histidine, proline, lactose, mannose, galactosamine, N-acetyl-D-glucosamine, acetyl coenzyme A, glutathione, phospholipids,

		(C-H) and (CH <sub>3</sub> ) stretching, (C <sub>3</sub> -C <sub>3</sub> ), (C <sub>5</sub> -O <sub>5</sub> ), (CH <sub>2</sub> ), (CH <sub>3</sub> CH <sub>2</sub> ), CH deformation, (C-NH <sub>2</sub> ) stretching in amide II [37]	hypoxanthine, amide III, amide linkages, [2,3,5,7,10,15,16,24,38]
1369		(C-H), (CH <sub>3</sub> ), (C <sub>3</sub> -C <sub>3</sub> ), (C <sub>5</sub> -O <sub>5</sub> ), (CH <sub>α</sub> ), (CH <sub>3</sub> CH <sub>2</sub> ) stretching [18] (CH <sub>3</sub> ) and (CH <sub>2</sub> ) bending, [18] Thymine: C-H + Methyl bend [12,14,28] (COO <sup>-</sup> ) small stretching [31] Symmetrical stretching of the half ring in pyridine [34]	adenine, thymine, guanine, valine, serine, arginine, phenylalanine, tyrosine, tryptophan, histidine, proline, fatty acids, lactose, mannose, galactosamine, N-acetyl-D-glucosamine, acetyl coenzyme A, glutathione, phospholipids, amid III [2,4,13,16]
1406		(CH <sub>2</sub> ) deformation [5] (CH <sub>3</sub> /CH <sub>2</sub> ) twisting and bending of lipids and collagen [16] IgG (COO <sup>-</sup> ) symmetrical stretching [6]	Collagen, lipids and phospholipids, citrate anions. Proteins, uracil [5,6,8,11,16,39]
1447		(CH <sub>2</sub> /CH <sub>3</sub> ) deformation [4,9,34,10,13,15–17,19,24,27]	hydrocarbon chains of the fatty acids, with a possible small contribution from the CH <sub>2</sub> groups of cholesterol, phospholipids, glutathione, deoxyribose [6,14,16,20,38]
1506		n/a	DNA/RNA bases, β-carotene, amide II, tryptophan, phenylalanine [16]
1577		(C=C) bending [5,7] DNA-RNA ring breathing modes of adenine and guanine [6] (C-C) stretching and (NH <sub>2</sub> ) bend [29,34]	Phenylalanine, DNA/RNA bases [5,6,24,7,8,10–12,16,21,22]
1617		(C=O), (NH <sub>2</sub> ) and (C=C) stretching [2,9,34]	Adenine, cytosine, thymine, tryptophan, tyrosine, fatty acids, galactosamine, phenylalanine, pyruvate, coenzyme A, acetoacetate, ascorbic acid, amide I, α helix, phospholipids [2,9,16,19,20,40]
1662		(C=O) stretching mode in β-sheets [41]	amide I α-helix conformation, lipids/ proteins [5,8,9,15,16,26,41,42]

**Table S2.** Different models (PCA-LDA and PLSDA) for both train and test samples.

		PCA-LDA 2	PCA-LDA 5	PCA-LDA 15 (99% EV)	PLSDA 2	PLSDA 5
Plasma	Train	90.1%	89.3%	97.6%	92.7%	100.0%
	Test	92.6%	85.4%	92.7%	90.2%	95.1%
Serum	Train	97.7%	100.0%	100.0%	99.8%	100.0%
	Test	97.7%	100.0%	100.0%	95.3%	100.0%

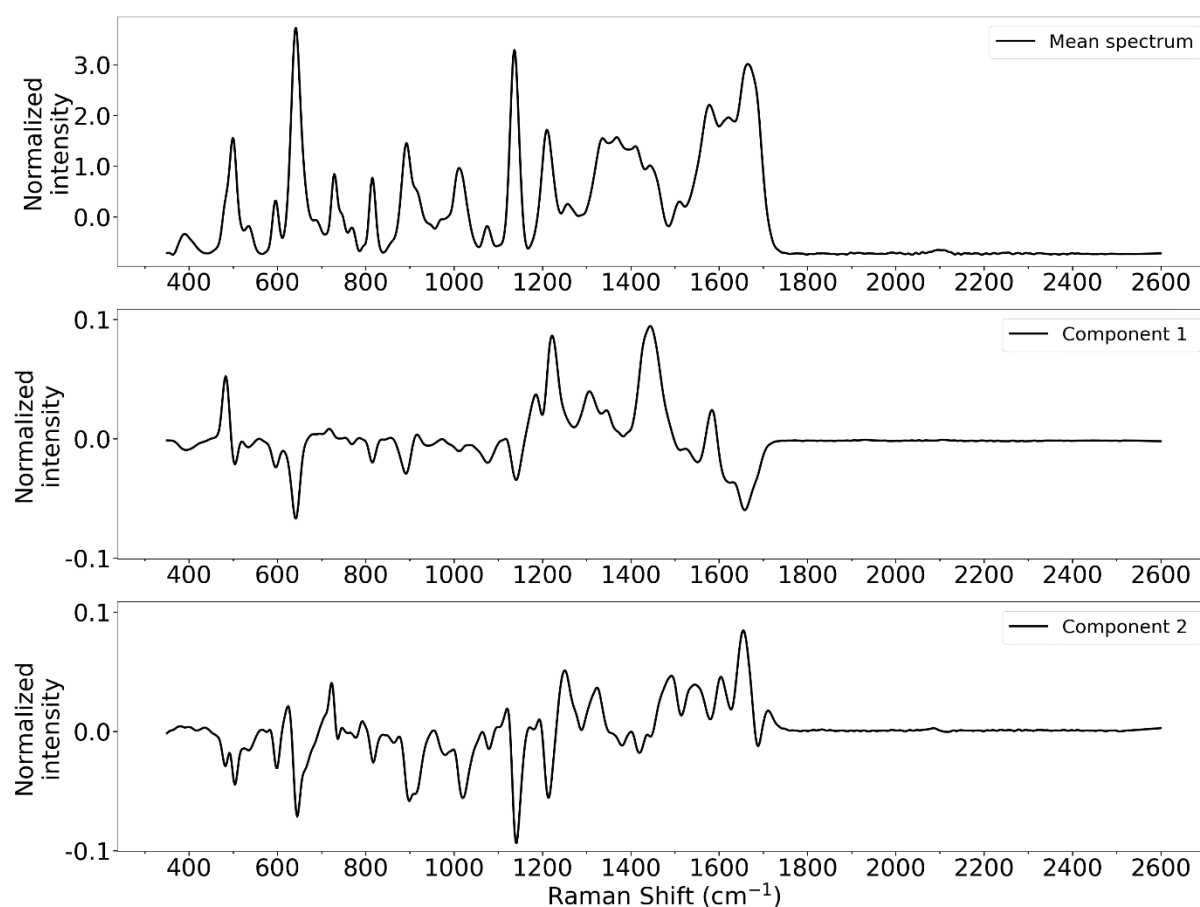
For both models employing SVMs, we used soft-margin SVMs where the trade-off constant C was selected through a grid search within a nested stratified k-fold cross-validation loop on the training data in each LOOCV fold.

**Table S3.** The classification results of PCA-SVM, SVM and LDA analyses.

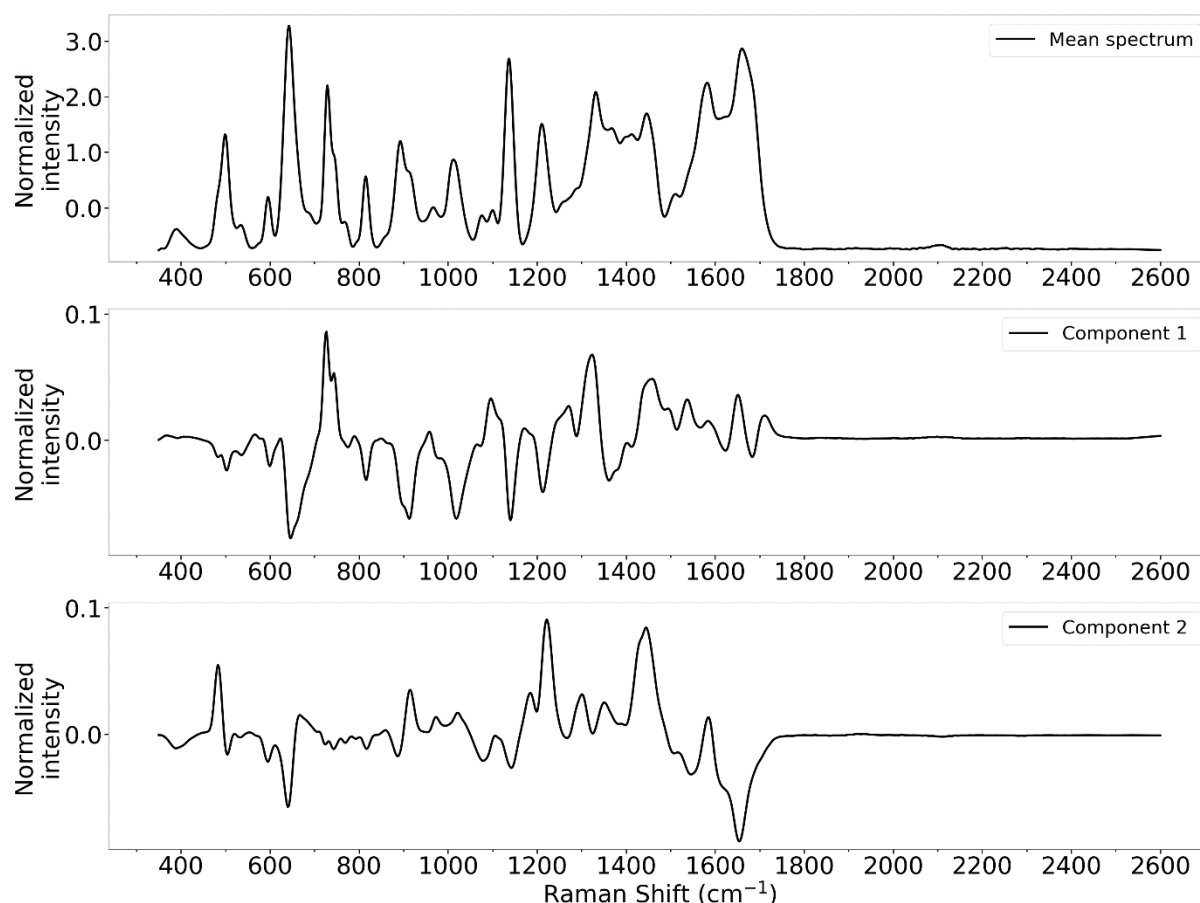
	Sample	AUC	Accuracy	Precision	Sensitivity	Specificity	True Pos.	True Neg.	False Pos.	False Neg.
PCA-SVM (2 PC, Linear)	Plasma	75.0%	82.9%	79.4%	100.0%	50.0%	27	7	7	0
	Serum	92.9%	95.3%	93.5%	100.0%	85.7%	29	13	2	0
SVM (Linear)	Plasma	91.0%	92.7%	92.9%	96.3%	85.7%	26	12	2	1
	Serum	89.3%	93.0%	90.6%	100.0%	78.6%	29	11	3	0
LDA	Plasma	93.9%	95.1%	96.3%	96.3%	92.9%	26	13	1	1
	Serum	100.0%	100.0%	100.0%	100.0%	100.0%	29	14	0	0

We note that the results do not deviate significantly from the ones obtained using the PCA-LDA approach, except for the PCA-SVM case, where performance seems to slightly drop.

*The first two principal components in the case of plasma and serum samples are presented in the figures below (Figures S1 and S2).*



**Figure S1.** Mean spectrum and first two principal components for plasma spectra.



**Figure S2.** Mean spectrum and first two principal components for serum spectra.

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