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Table S1. Summary of the grouping of the calibration and prediction data set.

	a't	Time since Injury (TSI)							
	Site	0d	1d	2d	3d	4d	5d	6d	
Calibration group	Back	15	15	15	15	13	12	9	187
	Head	15	15	15	15	14	11	8	
Prediction group		0.5d	1.5d	2.5d	3.5d	4.5d	5.5d		90
	Neck	5	5	5	5	5	5		
	Right upper limb	5	5	5	5	5	5		
	Left lower limb	5	5	5	5	5	5		

As the table showed, there were 300 samples for the whole experiment. Thirteen of these samples were discarded because of local infection or almost complete absorption of the hematoma. Thus, a total of 277 samples were used for analysis.

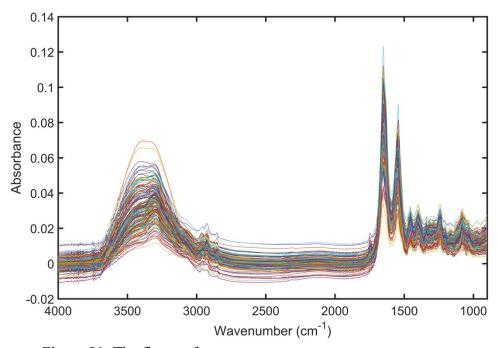


Figure S1. The figure of raw spectra.

Table S2. The number of correctly classified hematomas of different volumes obtained by the k-means clustering algorithm.

Site	Volumes									
Site	40μL	20μL	10 μL	5μL	2μL	1μL				
Back	10	10	10	10	10	6				
Head	10	10	10	10	10	4				