

Table S2. Peak size distribution of the normalized dataset

	Min	1st Qu.	Median	Mean	3rd Qu.	Max
33,940 peaks at annotated transcripts						
A	2	5354	9678	10700	14730	386300
B	8	5203	9404	10450	14510	462000
A'	17	5798	9476	10410	13800	459900
B'	11	5553	9441	10340	13880	233600
11,070 genes						
A	1070	6141	10210	11240	14940	386300
B	1068	5957	9891	11050	14800	462000
A'	1091	6500	9852	10800	13980	459900
B'	1074	6298	9815	10780	14090	233600

33,940 peaks at annotated transcripts (ENSMUST, coverages > 0 in all four samples) were extracted from the database. Distribution of peak sizes at 11,070 genes with peak sizes larger than 1,068 in at least one of the datasets (see Methods).