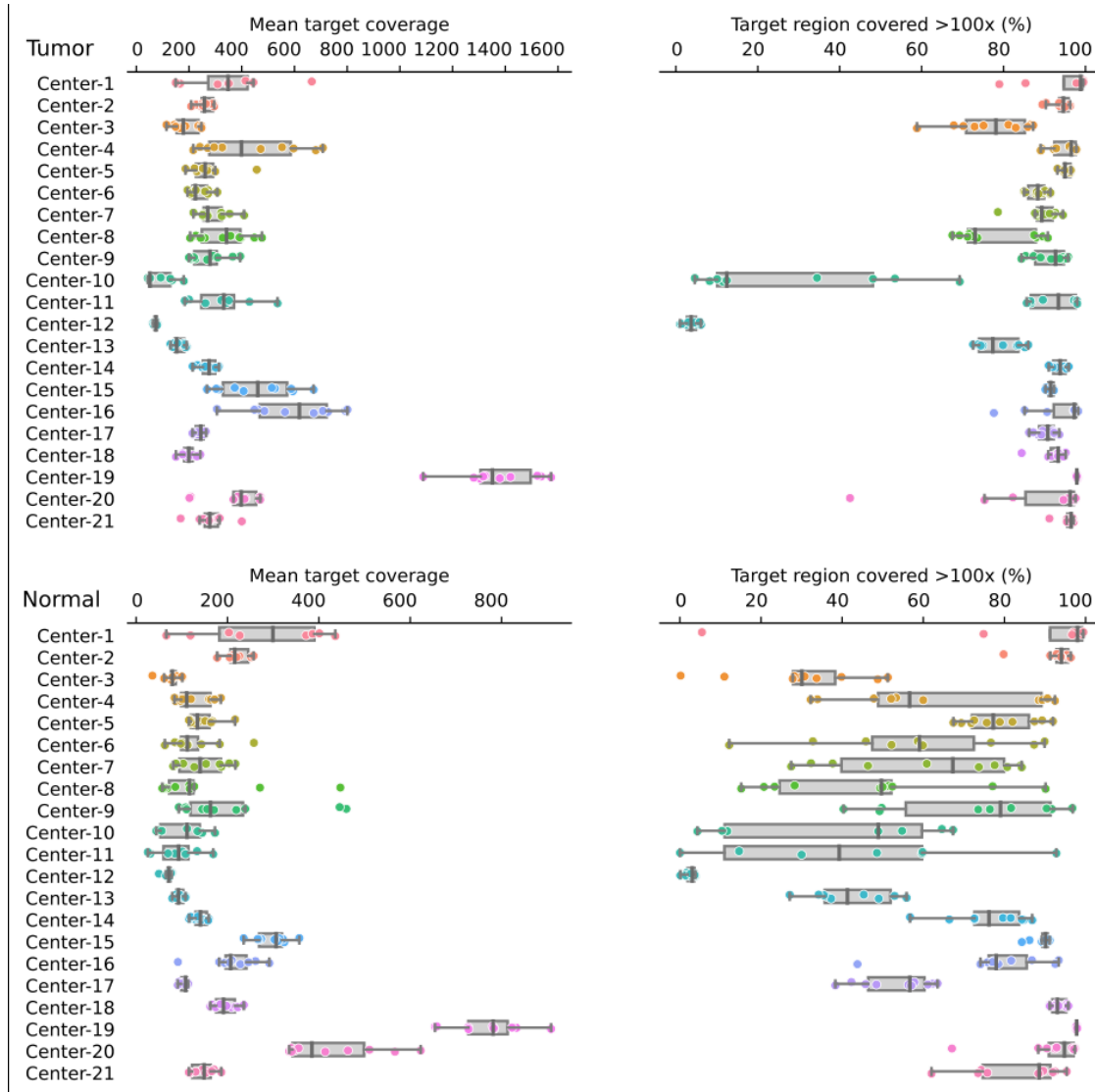
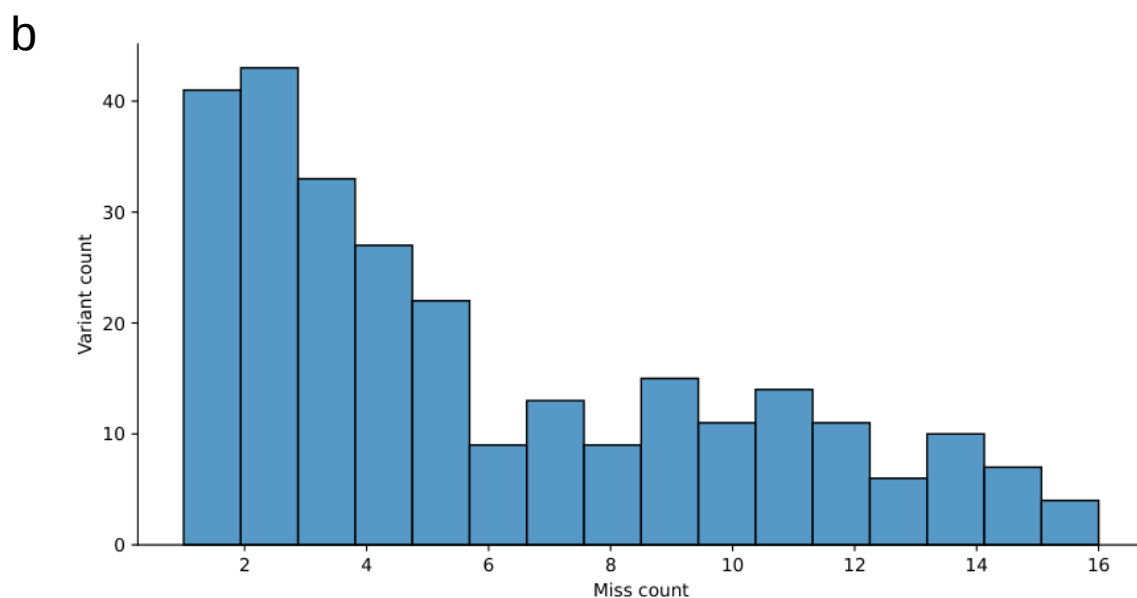
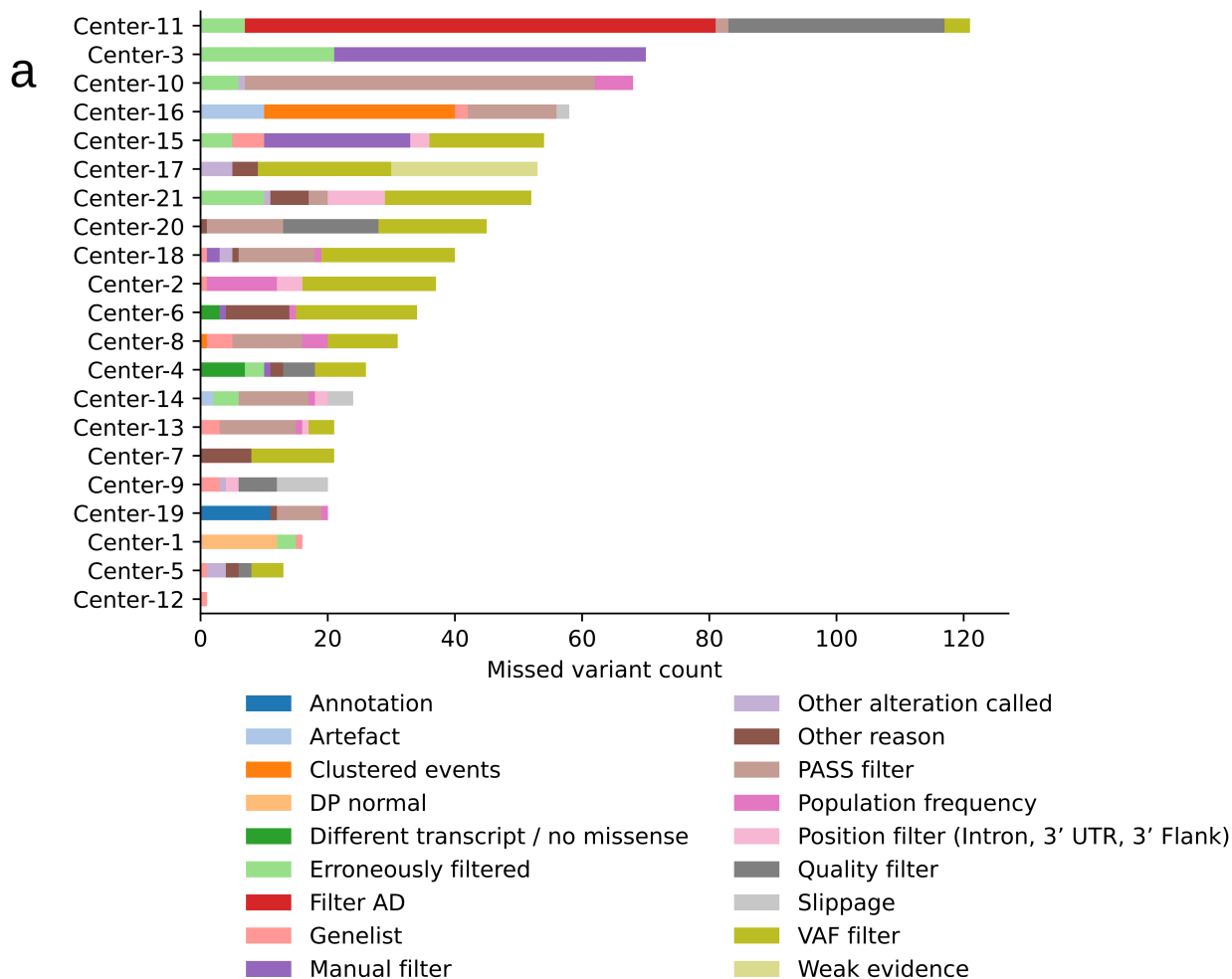


# Supplement

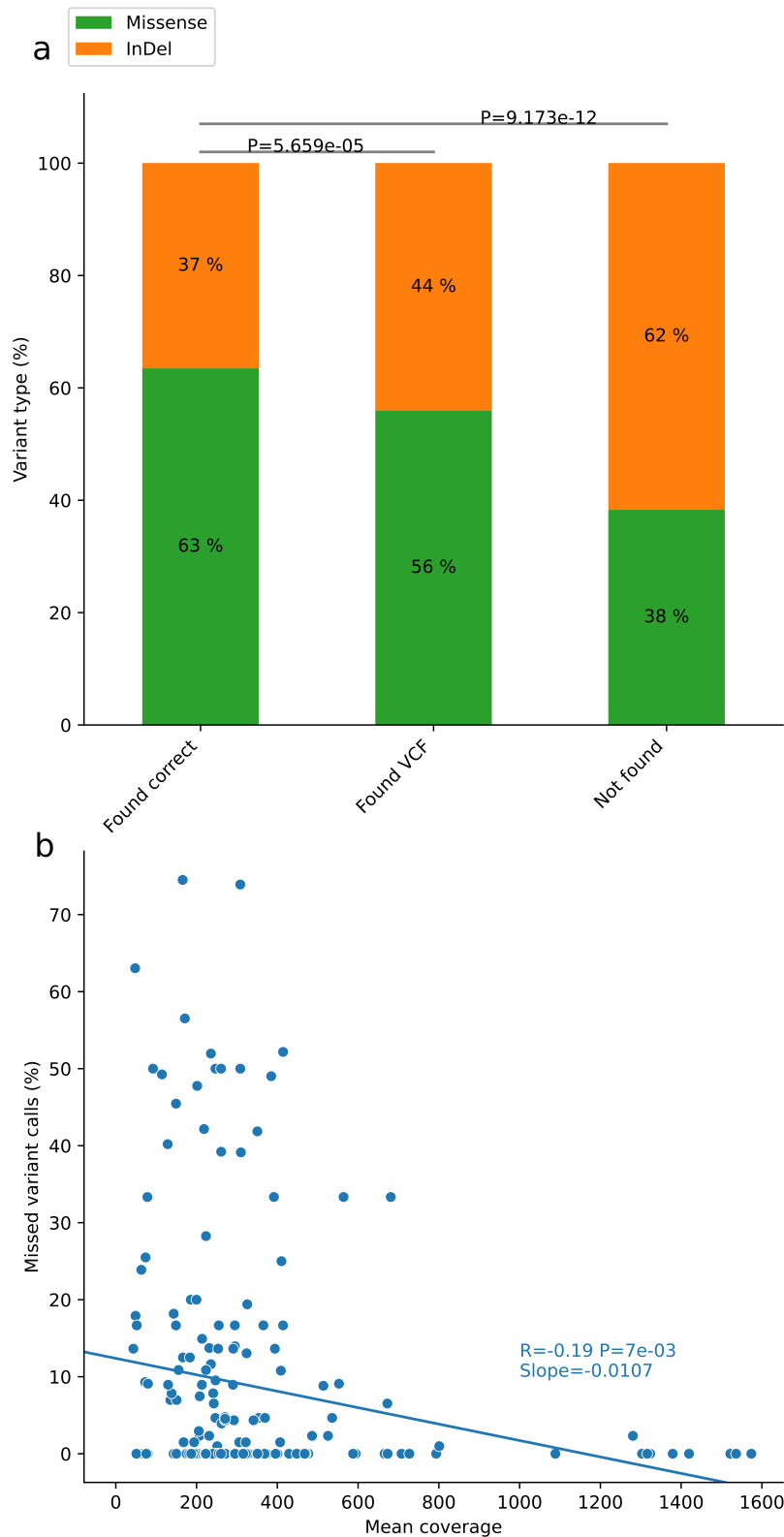
S



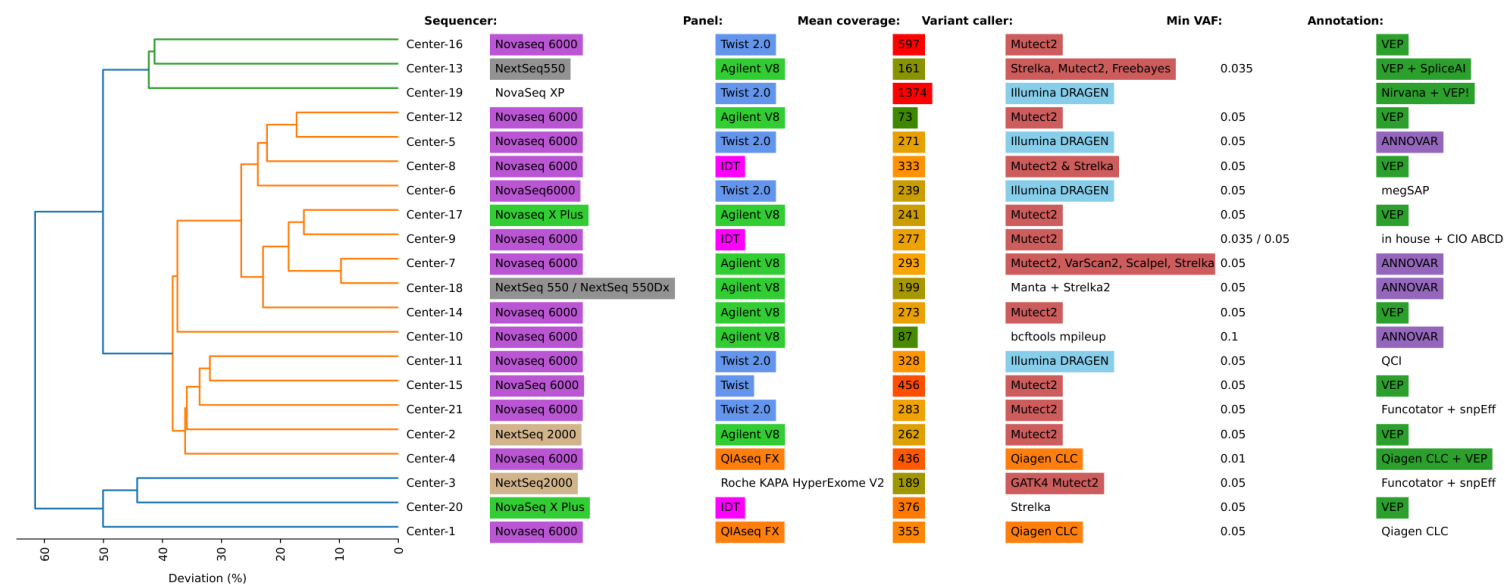
Supplementary Figure 1: Coverage analysis by center for both tumor and normal sequencing.



Supplementary Figure 2 a: Reasons for missed variant calls as reported by the centers. b: Histogram of missed variant by the count of centers that missed the variant.



Supplementary Figure 3: a: Fraction of missense variants and insertions and deletions in original data (left), unfiltered calls (middle), missed variants (right). b: Missed variants in relation to sequencing depth, each point corresponds to a sequenced sample.



Supplementary Figure 4: Hierarchical clustering of somatic variant calls annotated by wet-lab and dry-lab tools.

a

Sample	Gene	Protein	cDNA	Center-2	Center-5	Center-6	Center-7	Center-9	Center-14	Center-15	Center-18	Center-19	Center-21
16	PMS2	p.E504X	c.1510G>T	Class 4	Class 4	Class 5	Class 4	Class 4	Class 4	Class 4	Class 5	uncalled / filtered	uncalled / filtered
19	BRCA1	p.Q1756Pfs*74	c.5266dup	Class 5	Class 5	Class 5	Class 5	Class 5	Class 5	Class 4	Class 5	Class 5	Class 5
3	RET	p.Y791F	c.2372A>T	Class 3	Class 1/2	Class 1/2	Class 1/2	Class 1/2	uncalled / filtered	Class 4	Class 1/2	Class 1/2	Class 1/2
20	TP53	p.R283C	c.847C>T	Class 1/2	Class 3	Class 1/2	Class 1/2	Class 1/2	uncalled / filtered	Class 4	Class 1/2	Class 1/2	Class 1/2

**Legend**

Class 5

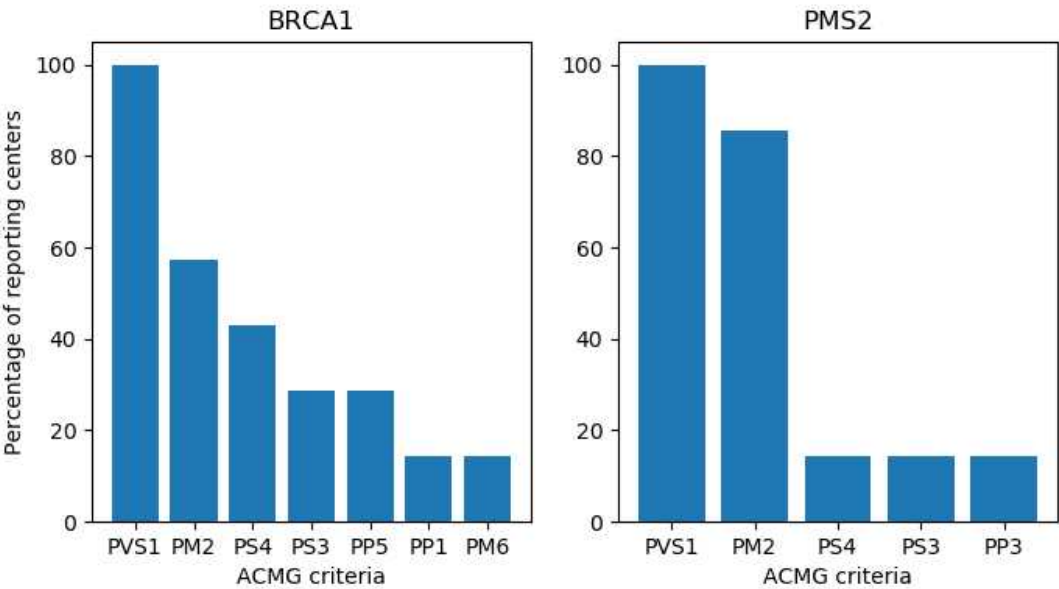
Class 4

Class 3

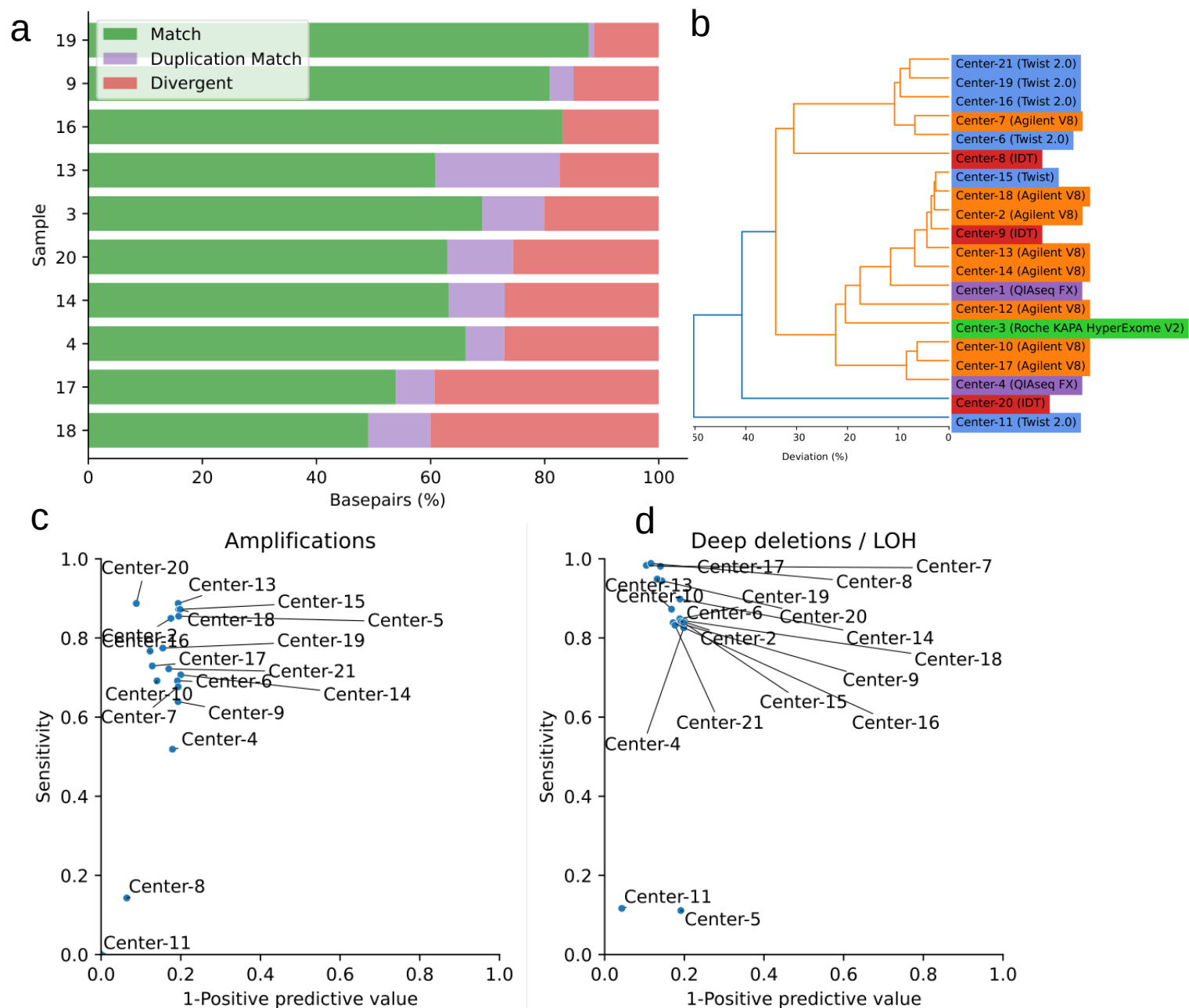
Class 1/2

uncalled / filtered

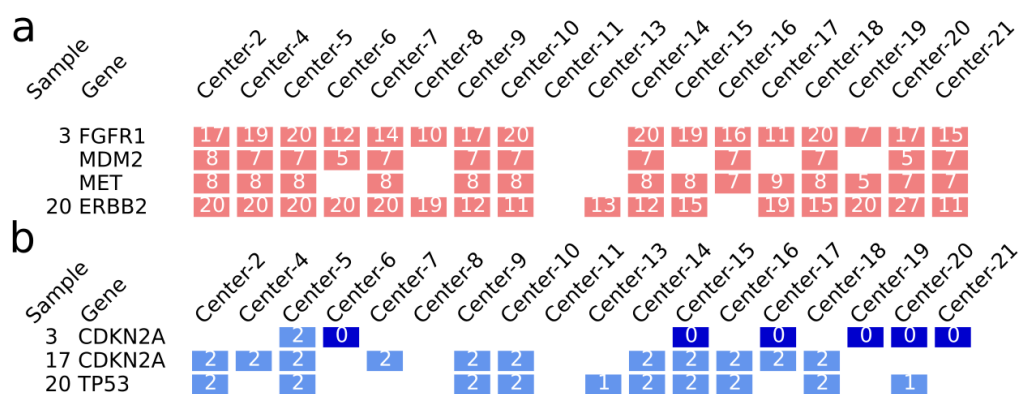
b



Supplementary Figure 5: Germline variant call comparisons. a: Variant calls and classifications. b: Classification criteria.



Supplementary Figure 6: CNV analysis a: Matching genomic region by the central bioinformatic pipeline b: Clustering with central CNV calling. c,d: Gene amplifications and deep or LOH deletions in relation to the five center consensus of the central bioinformatic pipeline.



Supplementary Figure 7: CNA of targetable genes. a: Amplifications with four copies more than the overall ploidy (red). b: Deletions with two copies or less (light blue) than the overall ploidy or zero copies (dark blue).

	HRD																				
	Center-1	Center-2	Center-3	Center-4	Center-5	Center-6	Center-7	Center-8	Center-9	Center-10	Center-11	Center-12	Center-13	Center-14	Center-15	Center-16	Center-17	Center-18	Center-19	Center-20	Center-21
Center-1	1.00	0.37	0.36	0.15	0.39	0.34	0.47	0.52	0.36	0.35	0.49	0.37	0.45	0.30	0.33	0.37	0.48	0.36	0.34	0.31	0.39
Center-2	0.37	1.00	1.00	0.90	1.00	0.98	0.93	0.95	1.00	1.00	0.79	0.99	0.98	0.99	0.97	1.00	0.94	0.98	0.91	0.99	0.93
Center-3	0.36	1.00	1.00	0.91	0.99	0.98	0.93	0.95	1.00	1.00	0.79	0.99	0.98	0.99	0.97	1.00	0.94	0.98	0.91	0.99	0.93
Center-4	0.15	0.90	0.91	1.00	0.91	0.90	0.85	0.84	0.90	0.91	0.71	0.91	0.88	0.92	0.92	0.91	0.81	0.94	0.81	0.93	0.95
Center-5	0.39	1.00	0.99	0.91	1.00	0.97	0.95	0.96	1.00	1.00	0.80	0.99	0.98	0.99	0.98	0.99	0.93	0.99	0.92	0.98	0.94
Center-6	0.34	0.98	0.98	0.90	0.97	1.00	0.93	0.95	0.98	0.98	0.76	0.97	0.97	0.98	0.96	0.98	0.92	0.98	0.90	0.99	0.96
Center-7	0.47	0.93	0.93	0.85	0.95	0.93	1.00	0.97	0.94	0.94	0.76	0.92	0.95	0.94	0.96	0.93	0.84	0.96	0.88	0.93	0.92
Center-8	0.52	0.95	0.95	0.84	0.96	0.95	0.97	1.00	0.95	0.95	0.74	0.94	0.97	0.95	0.93	0.95	0.86	0.95	0.85	0.95	0.91
Center-9	0.36	1.00	1.00	0.90	1.00	0.98	0.94	0.95	1.00	1.00	0.80	0.99	0.98	1.00	0.98	1.00	0.94	0.99	0.92	0.98	0.93
Center-10	0.35	1.00	1.00	0.91	1.00	0.98	0.94	0.95	1.00	1.00	0.80	0.99	0.98	1.00	0.98	1.00	0.94	0.99	0.92	0.98	0.93
Center-11	0.49	0.79	0.79	0.71	0.80	0.75	0.75	0.74	0.80	0.80	1.00	0.82	0.84	0.76	0.79	0.80	0.69	0.78	0.66	0.77	0.70
Center-12	0.37	0.99	0.99	0.91	0.99	0.97	0.92	0.94	0.99	0.99	0.82	1.00	0.98	0.98	0.95	0.99	0.93	0.97	0.89	0.99	0.92
Center-13	0.45	0.98	0.98	0.88	0.98	0.97	0.95	0.97	0.98	0.98	0.84	0.98	1.00	0.96	0.95	0.98	0.88	0.97	0.86	0.98	0.92
Center-14	0.30	0.99	0.99	0.92	0.99	0.98	0.94	0.95	1.00	1.00	0.76	0.98	0.96	1.00	0.99	0.99	0.94	0.99	0.93	0.98	0.94
Center-15	0.33	0.97	0.97	0.92	0.98	0.96	0.96	0.93	0.98	0.98	0.79	0.95	0.95	0.99	1.00	0.97	0.91	0.99	0.94	0.96	0.95
Center-16	0.37	1.00	1.00	0.91	0.99	0.98	0.93	0.95	1.00	1.00	0.80	0.99	0.98	0.99	0.97	1.00	0.93	0.98	0.90	0.99	0.93
Center-17	0.48	0.94	0.94	0.81	0.93	0.92	0.84	0.86	0.94	0.94	0.69	0.93	0.88	0.94	0.91	0.93	1.00	0.92	0.97	0.93	0.88
Center-18	0.36	0.98	0.98	0.94	0.99	0.98	0.96	0.95	0.99	0.99	0.78	0.97	0.97	0.99	0.99	0.98	0.92	1.00	0.93	0.98	0.97
Center-19	0.34	0.91	0.91	0.81	0.92	0.90	0.88	0.85	0.92	0.92	0.66	0.89	0.86	0.93	0.94	0.90	0.97	0.93	1.00	0.89	0.94
Center-20	0.31	0.99	0.99	0.93	0.98	0.99	0.93	0.95	0.98	0.98	0.77	0.99	0.98	0.98	0.96	0.99	0.93	0.98	0.89	1.00	0.95
Center-21	0.39	0.93	0.93	0.95	0.94	0.96	0.92	0.91	0.93	0.93	0.70	0.92	0.92	0.94	0.95	0.93	0.88	0.97	0.91	0.95	1.00

	TMB Missense																				
	Center-1	Center-2	Center-3	Center-4	Center-5	Center-6	Center-7	Center-8	Center-9	Center-10	Center-11	Center-12	Center-13	Center-14	Center-15	Center-16	Center-17	Center-18	Center-19	Center-20	Center-21
Center-1	1.00	0.89	0.97	0.97	0.95	0.95	0.99	0.96	0.99	0.97	0.54	0.96	0.95	0.99	0.97	0.94	0.99	0.96	0.92	0.29	0.93
Center-2	0.89	1.00	0.93	0.98	0.97	0.97	0.93	0.97	0.94	0.87	0.52	0.89	0.97	0.94	0.96	0.95	0.96	0.98	0.99	0.57	0.97
Center-3	0.97	0.93	1.00	0.95	0.94	0.95	0.99	0.95	0.99	0.99	0.78	0.93	0.94	0.99	0.95	0.94	0.98	0.96	0.97	0.57	0.94
Center-4	0.97	0.98	0.95	1.00	0.99	0.99	0.96	1.00	0.97	0.90	0.62	0.87	0.99	0.97	0.99	0.98	0.99	1.00	0.98	0.45	0.98
Center-5	0.95	0.97	0.94	0.99	1.00	1.00	0.94	1.00	0.95	0.88	0.62	0.84	1.00	0.95	1.00	1.00	0.98	1.00	0.97	0.40	1.00
Center-6	0.95	0.97	0.95	0.99	1.00	1.00	0.95	1.00	0.96	0.89	0.61	0.84	1.00	0.96	1.00	0.99	0.98	1.00	0.97	0.40	0.99
Center-7	0.99	0.93	0.99	0.96	0.94	0.95	1.00	0.96	1.00	0.98	0.75	0.92	0.95	1.00	0.96	0.94	0.99	0.96	0.97	0.54	0.93
Center-8	0.96	0.97	0.95	1.00	1.00	1.00	0.96	1.00	0.97	0.89	0.62	0.84	1.00	0.97	1.00	0.99	0.99	1.00	0.97	0.40	0.99
Center-9	0.99	0.94	0.99	0.97	0.95	0.96	1.00	0.97	1.00	0.97	0.72	0.92	0.95	1.00	0.97	0.95	0.99	0.97	0.97	0.53	0.94
Center-10	0.97	0.87	0.99	0.90	0.88	0.89	0.98	0.89	0.97	1.00	0.83	0.93	0.88	0.97	0.90	0.88	0.95	0.90	0.93	0.60	0.87
Center-11	0.54	0.52	0.78	0.62	0.62	0.61	0.75	0.62	0.72	0.83	1.00	0.70	0.62	0.73	0.65	0.68	0.70	0.63	0.63	0.47	0.62
Center-12	0.96	0.89	0.93	0.87	0.84	0.84	0.92	0.84	0.92	0.93	0.70	1.00	0.84	0.92	0.85	0.83	0.90	0.86	0.94	0.77	0.83
Center-13	0.95	0.97	0.94	0.99	1.00	1.00	0.95	1.00	0.95	0.88	0.62	0.84	1.00	0.96	1.00	0.99	0.98	1.00	0.97	0.41	1.00
Center-14	0.99	0.94	0.99	0.97	0.95	0.96	1.00	0.97	1.00	0.97	0.73	0.92	0.96	1.00	0.97	0.95	0.99	0.97	0.97	0.53	0.94
Center-15	0.97	0.96	0.95	0.99	1.00	1.00	0.96	1.00	0.97	0.90	0.65	0.85	1.00	0.97	1.00	0.99	0.99	1.00	0.96	0.40	0.99
Center-16	0.94	0.95	0.94	0.98	1.00	0.99	0.94	0.99	0.95	0.88	0.68	0.83	0.99	0.95	0.99	1.00	0.97	0.99	0.95	0.39	0.99
Center-17	0.99	0.96	0.98	0.99	0.98	0.98	0.99	0.99	0.99	0.95	0.70	0.90	0.98	0.99	0.99	0.97	1.00	0.99	0.98	0.49	0.97
Center-18	0.96	0.98	0.96	1.00	1.00	1.00	0.96	1.00	0.97	0.90	0.63	0.86	1.00	0.97	1.00	0.99	0.99	1.00	0.98	0.43	0.99
Center-19	0.92	0.99	0.97	0.98	0.97	0.97	0.97	0.97	0.97	0.93	0.63	0.94	0.97	0.97	0.96	0.95	0.98	0.98	1.00	0.59	0.96
Center-20	0.29	0.52	0.57	0.45	0.40	0.40	0.54	0.40	0.53	0.60	0.47	0.77	0.41	0.53	0.40	0.39	0.49	0.43	0.59	1.00	0.39
Center-21	0.93	0.97	0.94	0.98	1.00	0.99	0.93	0.99	0.94	0.87	0.62	0.83	1.00	0.94	0.99	0.99	0.97	0.99	0.96	0.39	1.00

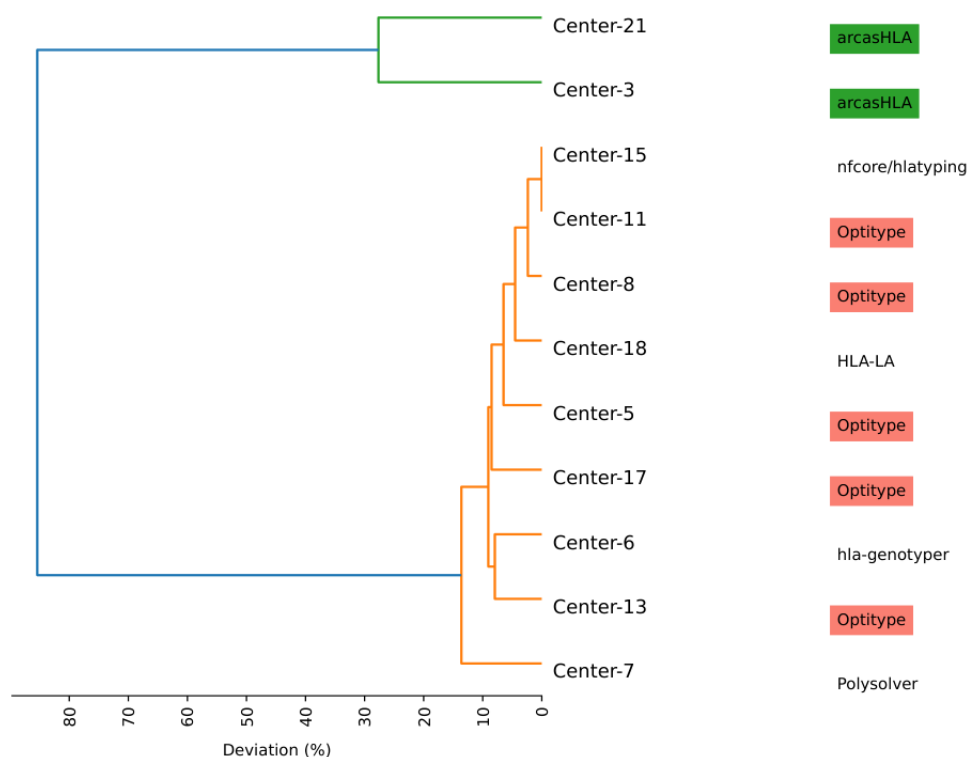
	MSI % Unstable																				
	Center-1	Center-2	Center-3	Center-4	Center-5	Center-6	Center-7	Center-8	Center-9	Center-10	Center-11	Center-12	Center-13	Center-14	Center-15	Center-16	Center-17	Center-18	Center-19	Center-20	Center-21
Center-1																					
Center-2	1.00																				
Center-3	0.96	1.00																			
Center-4	0.91	0.96	1.00																		
Center-5	0.95	0.99	0.98	1.00																	
Center-6	0.96	0.99	0.97	0.99	1.00																
Center-7	0.95	1.00	0.97	1.00	0.99	1.00															
Center-8	0.97	0.99	0.93	0.98	0.98	0.99	1.00														
Center-9	0.81	0.78	0.62	0.72	0.75	0.76	0.84	1.00													
Center-10	0.95	0.99	0.93	0.98	0.98	0.99	1.00	0.82	1.00												
Center-11	0.94	1.00	0.97	1.00	0.99	1.00	0.99	0.75	0.99	1.00											
Center-12	0.94	0.99	0.93	0.98	0.97	0.99	0.99	0.81	0.99	0.99	1.00										
Center-13	0.96	1.00	0.94	0.98	0.98	0.99	1.00	0.82	0.99	0.99	1.00	1.00									
Center-14	0.96	1.00	0.95	0.99	0.98	1.00	0.99	0.80	0.99	0.99	1.00	1.00	1.00								
Center-15	0.95	0.99	0.98	1.00	0.99	1.00	0.97	0.73	0.97	0.99	0.98	0.99	0.99	1.00							
Center-16	0.97	0.99	0.95	0.98	0.98	0.99	0.99	0.82	0.99	0.99	0.99	1.00	1.00	0.99	1.00						
Center-17	0.96	1.00	0.97	1.00	0.99	1.00	0.99	0.77	0.99	1.00	0.99	0.99	1.00	1.00	0.99	1.00					
Center-18	0.95	1.00	0.97	1.00	0.99	1.00	0.98	0.75	0.99	1.00	0.99	0.99	1.00	1.00	0.99	1.00	1.00				
Center-19	0.96	1.00	0.93	0.98	0.98	0.99	1.00	0.82	0.99	0.99	1.00	1.00	1.00	0.98	1.00	0.99	0.99	1.00			
Center-20	0.94	0.99	0.99	1.00	0.98	0.99	0.97	0.70	0.97	0.99	0.97	0.98	0.98	1.00	0.98	0.99	0.99	0.97	1.00	0.99	
Center-21	0.96	1.00	0.97	1.00	0.99	1.00	0.99	0.76	0.98	1.00	0.99	0.99	0.99	1.00	0.99	1.00	1.00	0.99	0.99	1.00	0.99

		HRD																					
		Center-2	Center-16	Center-20	Center-6	Center-19	Center-12	Center-1	Center-4	Center-5	Center-21	Center-13	Center-14	Center-8	Center-3	Center-11	Center-9	Center-15	Center-7	Center-18	Center-10	Center-17	Seracare
Sample	3	83	71	72	73	79	68	71	82	69	75	78	81	78	78	69	79	70	77	77	76	76	
	4	5	7	10	5	7	19	10	6	5	6	6	4	80	6	68	6	7	5	7	24	63	
	9	21	40	24	23	33	19	41	31	21	30	20	22	25	24	19	21	25	20	23	20	25	
	13	5	7	71	4	7	25	6	3	4	4	4	14	25	3	7	4	6	60	5	21	36	
	14	5	1	24	6	5	33	6	2	6	5	21	18	52	5	16	5	5	47	6	24	68	
	16	11	11	29	13	14	30	15	15	11	15	12	12	14	12	10	13	12	11	12	11	70	
	17	39	55	39	42	47	41	52	44	39	51	41	44	44	42	44	41	45	39	40	38	37	
18	9	1	42	0	1	29	2	2	0	4	12	7	64	0	1	2	7	0	2	22	41		
19	80	81	77	78	77	75	77	79	72	84	78	73	77	76	79	76	84	75	82	76	79	54	
20	30	26	30	25	39	29	29	29	31	29	32	31	26	32	25	33	30	26	31	26	24	31	

		TMB Missense																					
		Center-1	Center-2	Center-3	Center-4	Center-5	Center-6	Center-7	Center-8	Center-9	Center-10	Center-11	Center-12	Center-13	Center-14	Center-15	Center-16	Center-17	Center-18	Center-19	Center-20	Center-21	Seracare
Sample	3	0	2	5	4	2	2	2	4	3	1	2	2	2	2	2	7	2	2	3	103	2	
	4	28	25	28	26	17	25	26	32	23	22	23	24	20	16	26	31	24	26	28	27	26	
	9	2	2	3	2	1	1	1	7	4	2	5	1	1	1	2	6	1	1	2	6	2	
	13	49	58	57	59	42	59	58	56	61	52	50	56	46	42	61	72	54	60	65	94	62	
	14	37	34	33	36	24	35	33	37	35	31	41	32	29	27	35	55	31	35	37	63	36	
	16	29	48	37	55	37	53	52	56	50	44	10	46	39	29	53	60	48	51	57	120	53	
	17	9	8	9	9	6	9	8	11	8	7	7	9	8	7	9	9	8	9	9	7	9	7
18	16	16	18	16	12	16	15	18	15	13	16	16	15	13	16	17	16	16	16	16	16	13	
19	10	9	9	9	6	10	8	11	9	9	9	9	9	7	9	10	9	9	10	9	9		
20	8	10	9	10	7	10	9	12	10	9	10	9	9	7	10	11	10	10	10	11	10		

Sample	MSI % Unstable																				
	Center-13	Center-16	Center-5	Center-10	Center-14	Center-8	Center-19	Center-15	Center-7	Center-18	Center-4	Center-9	Center-2	Center-12	Center-3	Center-21	Center-20	Center-6	Center-17	Center-11	Center-1
3	1.6	5.6	2.4	1	1.6	4.2	4.6	3.2	1.3	1.9	2.2	3.4	2.6	1.8	3	2.3	5.5	2.6	2.1	0.2	0.8
4	29.6	37.4	26.9	26.4	22.8	29	40.4	33	26.8	28.9	31.1	31.4	30.6	27.6	24	29.3	37.6	31	26.2	0	29.2
9	0.4	5	0.6	0.3	0.6	3.2	1.9	1.2	0.5	0.5	1.9	1.1	0.8	0.5	0.8	0.7	1.8	0.7	0.8	0.8	1.2
13	28.7	34.4	23.9	22.4	21.5	36	34.7	28.1	26.3	28.6	25.1	27.3	28.4	26.4	22.8	23	34.1	22.3	25.5	24.6	32
14	9.3	15	8.8	6.2	5.6	17.8	12.8	10.3	8.5	13.4	2.8	6.1	12.8	6.9	4.1	2.6	18.4	12.5	5.7	6.9	5
16	32.7	34.2	26.7	26.8	23.4	30.3	40.3	33.1	30.9	31.8	29.4	32	32.1	29.5	22.4	27.7	40.1	29.8	26.4	23.9	20.1
17	1	4.8	1.1	0.5	0.8	3.1	2.4	1.9	0.9	1	2	1.2	1.4	0.9	1.3	1.6	4.6	1.1	1.1	4.4	1.8
18	0	0.1	0	0	0	0.2	0	0	0	0	0	0	0.1	0	0	0	0.1	0	0	0.2	0
19	1.8	4.3	1.9	1	1.6	4.1	4.1	3	1.6	1.7	3.5	2.8	2.6	1.6	1.8	2.2	4.4	1.9	1.9	4	2.2
20	0.5	1	0.4	0.2	0.2	1.4	0.8	0.6	0.4	0.4	0.6	0.7	0.7	0.4	0.2	0.5	1.2	0.3	0.4	0.9	0.4

Supplementary Figure 9: Complex biomarker results from the central bioinformatic pipeline based on the raw data from each center. Sorted by the original tool for comparability.



Supplementary Figure 10: Hierarchical clustering by HLA calls. Distance is defined as the number of overlapping HLA calls, while partial overlaps (match of the allele group, but mismatch of the specific HLA protein) are counted as  $\frac{1}{2}$  point. The bioinformatic tools utilized are annotated on the right.