Supplementary Figure S1: VJ gene usage. A. Peripheral blood mononuclear cells (MF5 PBMC) sample was used for whole exome capture and sequenced at a maximum depth of 400 million reads. Sequenced samples were analyzed for V and J gene combination and no preferential combination was identified as oppose to the high frequency VJ combination identified in **(B)** that can be associated with presence of dominant clone in a MF5_1T sample. **(C)** VJ gene usage of MF5_2P.

Supplementary Figure S2: Correlation of inverse Simpson index and dominant clone frequency against tumor enrichment. Microdissected island containing atypical lymphoma cells were subjected to WES/WTS. **(A)** Inverse Simpson index reflects the TCR repertoire richness. **(B)** Indicates the most frequent most clonotype for TCRα, -β and -ɣ. Proportion of tumor-derived DNA in the sample was calculated based on copy number aberration analysis from WES. Symbols represent values for individual samples.

Supplementary Figure S3: Shared T-cell clonotypes: Identified CDR3 sequences using whole exome sequencing (WES) were tested for overlap. Heatmaps representing the shared clonotypes in the 33 MF samples **(A)** TCRα **(B)** TCRβ and **(C)** TCRɣ clonotypes. The overlap represent the contamination from reactive T-cells along with the malignant clonotypes.

Supplementary Figure S4. VJ gene usage for top 10 high frequency clonotypes identified using WES in top 10 dominant clones. The samples correspond to those in Fig 3.

Supplementary Figure S5. VJ gene usage for top 10 high frequency clonotypes identified using WTS in top 10 dominant clones. The samples correspond to those in Fig 3.

Supplementary Table S1. Samples included in the study, with patient age, sex and diagnosis.

Supplementary Table S2. Number of clonotypes identified by WES (DNA) and WTS (RNA) in patients with MF. Samples are annotated as patient number (see Fig 1) with the suffix P (plaque), T (tumor) or PB (peripheral blood mononuclear cells). Normal Lymphocytes are pooled CD4+ cells from 4 healthy donors.

Supplementary Table S3. Percentage of tumor DNA purity and dominant clone frequency for TCR-α, -β or -ɣ listed. Samples annotated as patient number followed by P for plaque and T for tumor (see figure 2B).
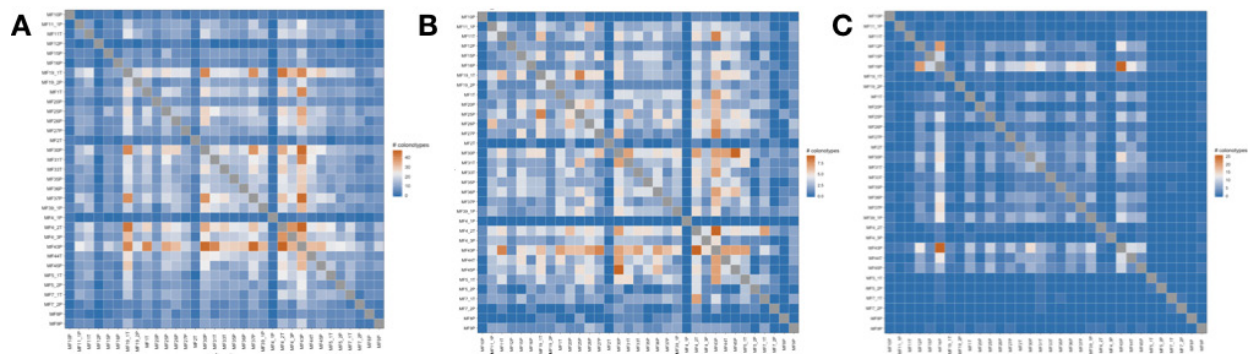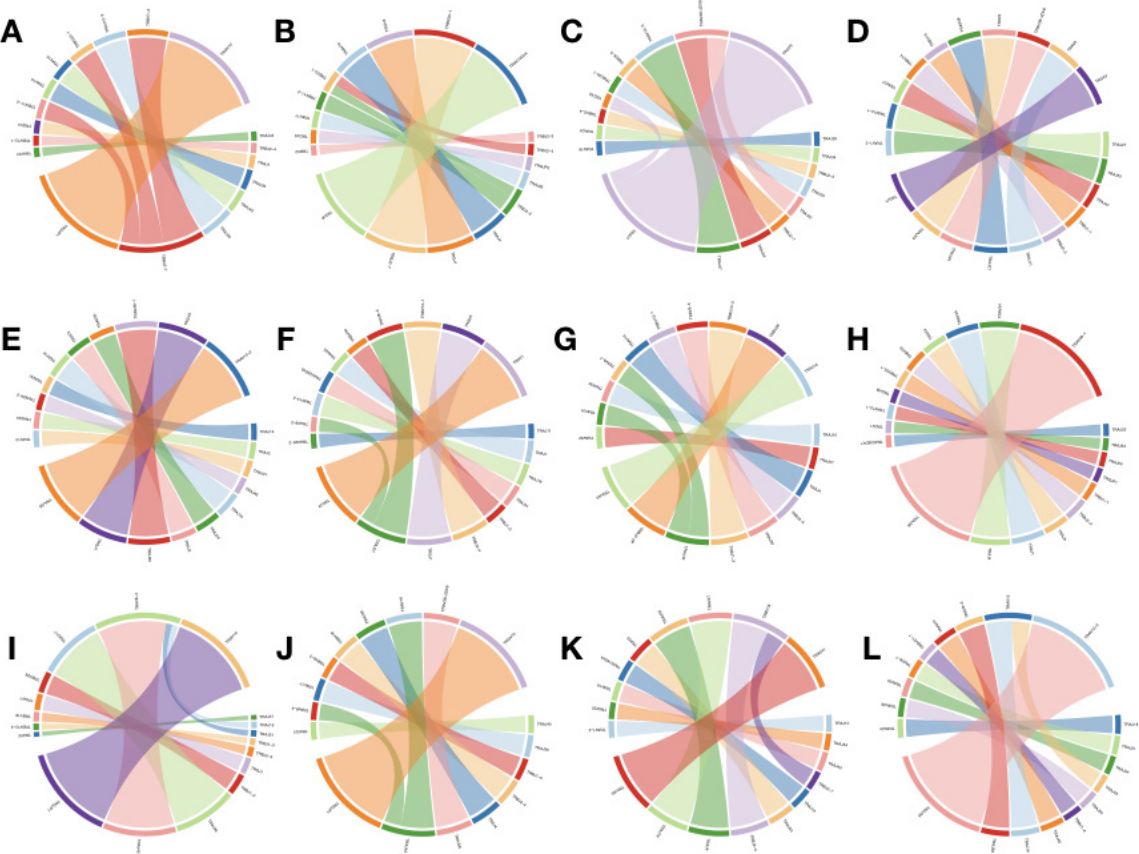
Supplementary Figure 1:
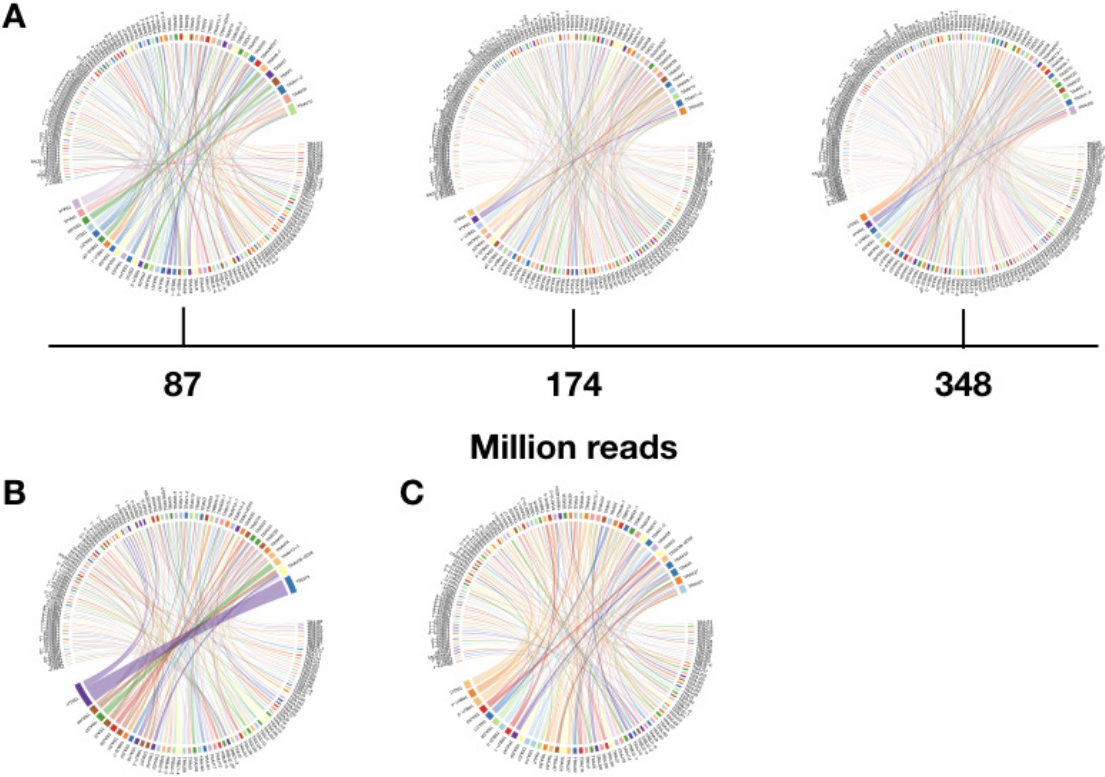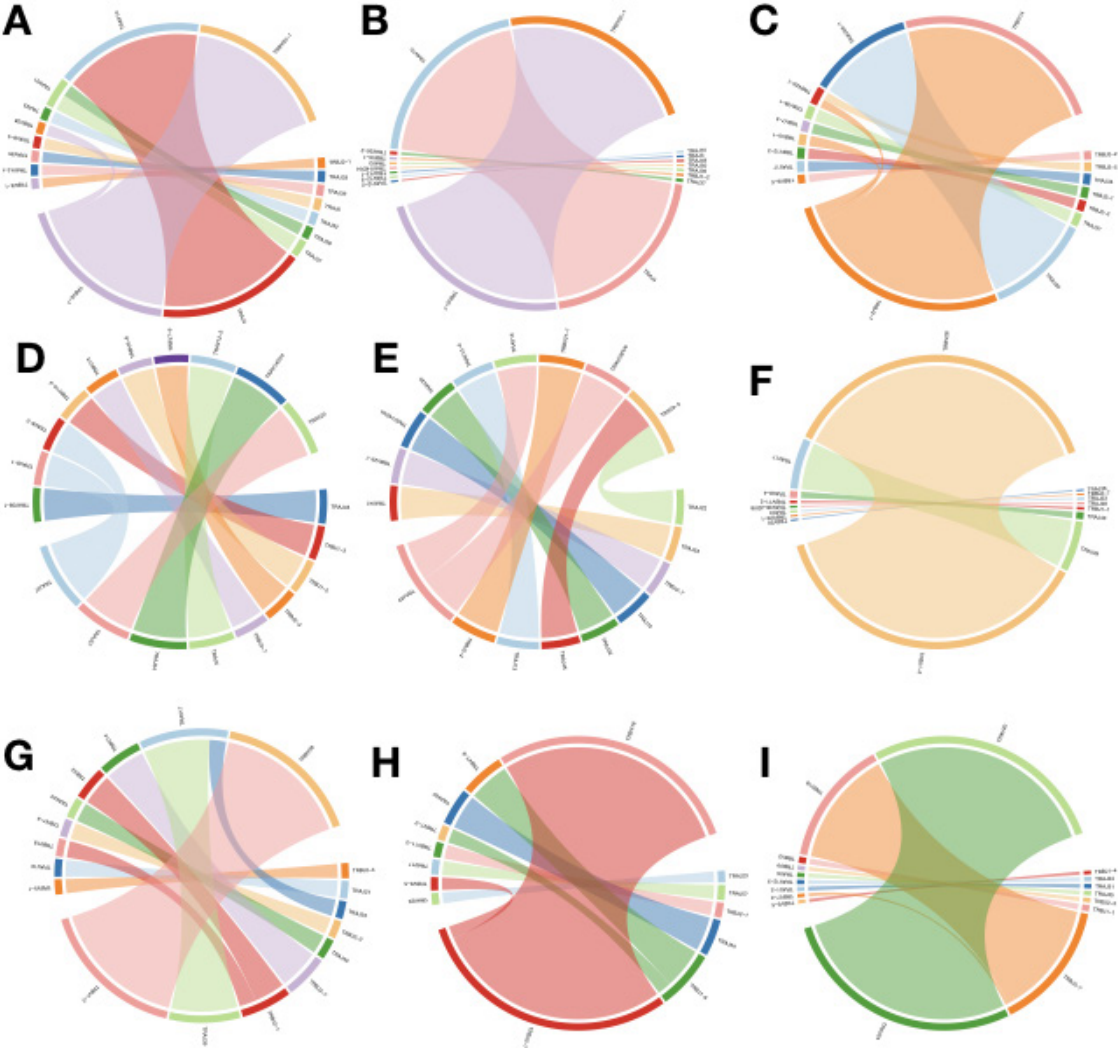
Supplementary Figure 2:
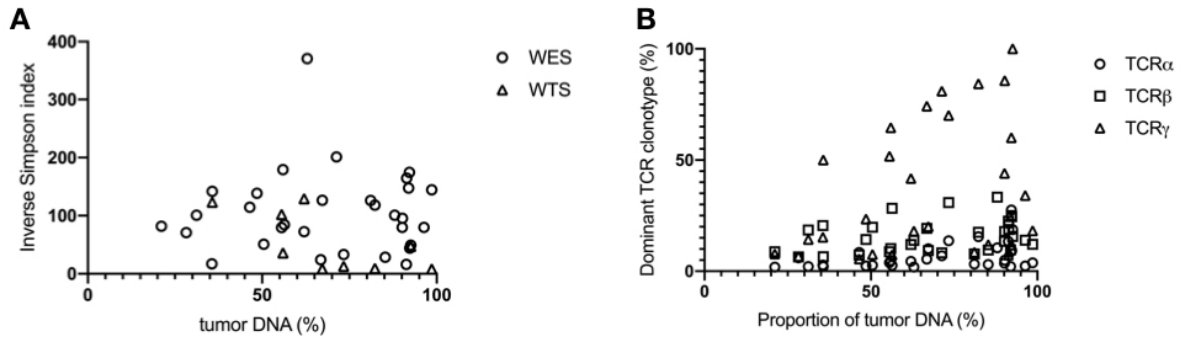
Supplementary Figure 3:

Supplementary Figure 4:

Supplementary Figure 5:

Supplementary Table 1:

Patient ID (age [years], sex [M-male, F-female])	Sample ID	Lesion type	Diagnosis and stage
MF1 (78, F)	MF1T	Tumor	Mycosis Fungoides IIB
MF2 (83, M)	MF2T	Tumor	Mycosis Fungoides IIB
MF4 (69, M)	MF4_1P	Plaque	Mycosis Fungoides IIB
	MF4_2T	Tumor	
	MF4_3P	Plaque	
MF5 (44, F)	MF5_1T	Tumor	Folliculotropic Mycosis Fungoides IIB
	MF5_2P	Plaque	
MF7 (62, M)	MF7_1T	Tumor	Mycosis Fungoides IVA
	MF7_2P	Plaque	
MF8 (54, F)	MF8P	Plaque	Folliculotropic Mycosis Fungoides IIIB
MF9 (42, F)	MF9P	Plaque	Mycosis Fungoides IA
MF10 (56, M)	MF10P	Plaque	Mycosis Fungoides IB
MF11 (56, M)	MF11T	Tumor	Mycosis Fungoides IIB
	MF11_1P	Plaque	
MF12 (66, M)	MF12P	Plaque	Mycosis Fungoides IVA
MF15 (65, M)	MF15P	Plaque	Mycosis Fungoides IB
MF16 (68, M)	MF16P	Plaque	Mycosis Fungoides IB

MF19 (74, M)	MF19_1T	Tumor	Mycosis Fungoides IIB
	MF19_2P	Plaque	
MF20 (70, M)	MF20P	Plaque	Mycosis Fungoides IB
MF25 (48, F)	MF25P	Plaque	Mycosis Fungoides IB
MF26 (76, M)	MF26P	Plaque	Mycosis Fungoides IB
MF27 (71, M)	MF27P	Plaque	Mycosis Fungoides IA
MF30 (62, M)	MF30P	Plaque	Mycosis Fungoides IB
MF31 (67, M)	MF31T	Tumor	Folliculotropic Mycosis Fungoides IIB
MF33 (75, M)	MF33T	Tumor	Mycosis Fungoides IIB
MF35 (54, M)	MF35P	Plaque	Folliculotropic Mycosis Fungoides IIB
MF36 (64, M)	MF36P	Plaque	Mycosis Fungoides IA
MF37 (63, M)	MF37		Mycosis Fungoides IIB
MF39 (71, M)	MF39_1P	Plaque	Mycosis Fungoides IB
MF43 (60, M)	MF43P	Plaque	Folliculotropic Mycosis Fungoides IA
MF44 (85, M)	MF44T	Tumor	Mycosis Fungoides IIB
MF45 (77, M)	MF45P	Plaque	Mycosis Fungoides IIIA

Supplementary Table 2:

Samples (DNA)	Number of TCR clonotypes			Samples (RNA)	Number of TCR clonotypes	
	TCRα	TCRβ	TCRɣ		TCRα	TCRβ
MF1	165	40	19	MF4_2	48	24
MF2	85	20	25	MF4_3	86	47
MF4_1	37	5		MF5_1	98	148
MF4_2	394	95	15	MF7_1	21	10
MF4_3	279	65	7	MF7_2	29	21
MF5_1	160	41	8	MF11	12	4
MF5_2	143	32	6	MF11_1	179	131
MF7_1	172	25	4	MF19_1	6	10
MF7_2	89	19	6	MF19_2	134	84
MF8	127	25	1	Normal Lymphocytes	52	204
MF9	129	27	2			
MF10	70	21	2			
MF11	157	45	3			
MF11_1	146	45	8			
MF12	82	31	51			
MF15	197	67	25			

MF16	57	92	338		
MF19_1	375	82	15		
MF19_2	141	32	5		
MF20	132	40	8		
MF25	264	68	34		
MF26	175	46	23		
MF27	159	46	36		
MF30	285	81	85		
MF31	162	29	37		
MF33	158	29	31		
MF35	118	29	20		
MF36	121	45	42		
MF37	141	22	27		
MF39_1	141	42	56		
MF43	471	110	98		
MF44	145	37	36		
MF45	174	42	31		

Supplementary Table 3:

Samples	Tumor DNA Purity (%)	Alpha (%)	Beta (%)	Gamma (%)
MF2T	91.309	13.36406	22.5	7.317073
MF4_1P	87.97	10.52632	33.33333	
MF4_2T	66.79	5.447471	19.33086	74.19355
MF4_3P	73.37	13.68209	30.89888	70
MF5_1T	55.99	4.8	10.16949	64.58333
MF5_2P	35.67	2.16216	6.521739	50
MF7_1T	71.28	6.959707	8.333333	80.95238
MF7_2P	62.03	4.477612	12	41.66667
MF8P	92.58	18.70861	15.625	100
MF9P	90.17	4.966887	17.91045	85.71429
MF10P	92.18	27.57009	25	60
MF11T	82.29	15.51724	17.56757	84.28571
MF11_1P	55.58	3.902439	8.823529	51.72414
MF12P	91.39	21.42857	18.81188	8.695652
MF15P	91.96	2.089552	9.6	11.76471
MF16P	46.45	8.417508	7.274969	5.55767
MF19_1T	98.57	3.76506	12.12121	18.18182
MF19_2P	67.27	10.08772	9.302326	20
MF20P	90.16	3.606557	13.43284	44

MF25P	85.27	3.052065	9.52381	11.9403
MF26P	50.49	2.671756	19.82759	7.5
MF27P	92.312	9.247312	24.51613	11.76471
MF30P	62.89	1.912046	13.84615	18.01802
MF31T	81.08	3.184713	7.792208	8.510638
MF35P	31.22	2.12	18.52	14.29
MF36P	28.24	6.06	6.49	6.67
MF37P	48.53	2.41	14.29	23.44
MF39_1P	56.34	2.66	28.28	7.38
MF43P	21.14	1.89243	8.810573	7.792208
MF44T	35.59	2.766798	20.51282	15.27778
MF45P	96.36	2.372881	13.95349	34.06593