									type	¹ type		
0.87	0.90	1.00	1.00	1.00	1.00	1.00	0.88	1.00	GLUE		Cell alignment	•
0.93	0.89	0.61	0.77	0.27		0.49	0.91	0.62	MaxFuse	8.0	Embedding ac	curacy
0.89	NA	0.55	NA	0.51	0.56	0.55	0.89	0.54	SIMBA	0.0	Ranking	
0.81	0.68	0.73	0.53	0.45	0.65	0.71	0.75	0.61	uniPort	0.6		
0.69	NA	0.67	NA	NA	NA	NA	0.69	0.67	unionCom	0.4		
0.74	0.74	0.60	0.60	0.32	0.61	0.70	0.74	0.57	Seurat v3 CCA	0		
0.72	0.71	0.61	0.56	0.43	0.60	0.65	0.71	0.57	Seurat v4 RPCA	0.2		
0.82	NA	0.50	NA	0.21	0.44	0.49	0.82	0.41	SCALEX			
0.61	NA	0.50	NA	0.27	0.43	0.46	0.61	0.42	bindSC	0		
0.80	0.52	0.23	0.20	0.12	0.39	0.35	0.66	0.26	LIGER INMF			
0.65	0.33	0.47	0.35	0.27	0.37	0.43	0.49	0.38	MultiMAP			
0.77	0.45	0.09	0.15	0.08	0.25	0.32	0.61	0.18	LIGER UINMF			
0.72	0.16	0.29		0.08	0.41	0.33	0.44	0.22	LIGER online iNMF			
0.11	NA	0.00	NA	0.01	0.00	0.00	0.11	0.00	Pamona			
BMMC Multiome p10 Embedding Acc	SHARE-seq skin Embedding Acc	BMMC Multiome p10 Cell Alignment Acc	SHARE-seq skin Cell Alignment Acc	HSPC Multiome p10 Cell Alignment Acc	10X PBMC Multiome Cell Alignment Acc	10X mouse brian Cell Alignment Acc	Embedding accuracy score	Cell alignment accuracy score				