

Supplemental Dataset S1: GLIPH Analysis

Post-vaccination graft dysfunction/aplastic anemia relapse with massive clonal expansion of autologous CD8+ lymphocytes

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TCR table of the patient's 78 uniquely paired TCR α and β CDR3 sequences

CDR3b	TRBV	TRBJ	CDR3a	TRAV	TRAJ	Patient
CASSIGGIGELFF	TRBV19	TRBJ2-2	CAASVTGDGNKLVF	TRAV29DV5	TRAJ47	578_1
CASSLGLAGAYAYEQYF	TRBV28	TRBJ2-7	CVVNPGSTLGRLYF	TRAV12-1	TRAJ18	578_1
CASSLERGGKSYEQFF	TRBV7-8	TRBJ2-1	CAVFFSGGYNKLIF	TRAV1-1	TRAJ4	578_1
CASSWTSGSSYEQYF	TRBV28	TRBJ2-7	CVVNRGSTLGRLYF	TRAV12-1	TRAJ18	578_1
CASSLGTGRDNEQFF	TRBV5-1	TRBJ2-1	CAENWETDKLIF	TRAV13-2	TRAJ34	578_1
CASSIGGIAGAYF	TRBV19	TRBJ2-5	CAGSGGLIDSYGNKLVF	TRAV35	TRAJ47	578_1
CASSPPLAGPGTVETQYF	TRBV14	TRBJ2-5	CAASYGNQFYF	TRAV29DV5	TRAJ49	578_1
CARTQENTGELFF	TRBV2	TRBJ2-2	CAVNRGNNDMRF	TRAV12-1	TRAJ43	578_1
CASSYGTGNSYEQYF	TRBV9	TRBJ2-7	CAVNDVNTDKLIF	TRAV8-1	TRAJ34	578_1
CASSLGTGRDNEQFF	TRBV5-1	TRBJ2-1	CALSQGGKLIF	TRAV9-2	TRAJ23	578_1
CSASPQSYEQYF	TRBV20-1	TRBJ2-7	CAVGASTDKLIF	TRAV8-3	TRAJ34	578_1
CARTQENTGELFF	TRBV2	TRBJ2-2	CALSGLSGNTGKLIF	TRAV19	TRAJ37	578_1
CASSTRAHNEQFF	TRBV19	TRBJ2-1	CAVQAGWNQGGKLIF	TRAV20	TRAJ23	578_1
CASSSVGGYGYTF	TRBV6-5	TRBJ1-2	CVGRDNYGQNFVF	TRAV12-1	TRAJ26	578_1
CASSESSTDTQYF	TRBV2	TRBJ2-3	CAVETPQTGANNLFF	TRAV2	TRAJ36	578_1
CASSLERGGKSYEQFF	TRBV7-8	TRBJ2-1	CAFFFSGGYNKLIF	TRAV1-1	TRAJ4	578_1
CASSQDPKGDMSGAEAFF	TRBV4-1	TRBJ1-1	CAMSAGAGKSTF	TRAV12-3	TRAJ27	578_1
CASSVEGTSGRAKFGEQFF	TRBV9	TRBJ2-1	CAEKSTNFGNEKLTf	TRAV13-2	TRAJ48	578_1
CSVEVGAANTEAFF	TRBV29-1	TRBJ1-1	CAMSALQGAQKLVF	TRAV14DV4	TRAJ54	578_1
CATSRTGRWETQYF	TRBV15	TRBJ2-5	CALSEGSGNTGNQFYF	TRAV19	TRAJ49	578_1
CASSLEQGVRSQFF	TRBV5-1	TRBJ2-1	CALSEAYTGRRALTF	TRAV19	TRAJ5	578_1
CASSLGGPSGNTIYF	TRBV7-9	TRBJ1-3	CAVSFSGNTPLVF	TRAV20	TRAJ29	578_1
CASSQGRWYEQYF	TRBV4-1	TRBJ2-7	CAVLNNNDMRF	TRAV22	TRAJ43	578_1
CASSLSMTGGGYEQYF	TRBV28	TRBJ2-7	CAATPYNNNDMRF	TRAV29DV5	TRAJ43	578_1
CASSETTG DNEQFF	TRBV7-3	TRBJ2-1	CAVRALYSAGSYQLTF	TRAV3	TRAJ28	578_1
CASSQGQGDYEQYF	TRBV4-2	TRBJ2-7	CAVSFYGGSQGNLIF	TRAV41	TRAJ42	578_1
CSADPGFGQETQYF	TRBV20-1	TRBJ2-5	CVVDYGQNFVF	TRAV12-1	TRAJ26	578_1
CASTDWSSGNTIYF	TRBV28	TRBJ1-3	CALSESNTDKLIF	TRAV16	TRAJ34	578_1
CSARPRGHYNEQFF	TRBV20-1	TRBJ2-1	CATDSSDNAGNMLTF	TRAV17	TRAJ39	578_1
CASSLNQGASAEAFF	TRBV5-1	TRBJ1-1	CALRPGGSYIPTF	TRAV19	TRAJ6	578_1
CASSLGNSGIQYF	TRBV12-4	TRBJ2-4	CAVLGNAGNMLTF	TRAV21	TRAJ39	578_1
CASGGESKSGYGYTF	TRBV9	TRBJ1-2	CAFEGYNNNDMRF	TRAV21	TRAJ43	578_1
CASSQDLGTGGANGYTF	TRBV4-1	TRBJ1-2	CAGCRDSSYKLIF	TRAV27	TRAJ12	578_1
CASSLLAGTGETQYF	TRBV7-2	TRBJ2-5	CAASGSTGANNLFF	TRAV29DV5	TRAJ36	578_1
CASSFTGSEDEQFF	TRBV7-3	TRBJ2-1	CAVRSLYSGAGSYQLTF	TRAV3	TRAJ28	578_1
CASSFGNEQFF	TRBV27	TRBJ2-1	CAVQNYGQNFVF	TRAV1-1	TRAJ26	578_1
CASSLGSGLETQYF	TRBV7-2	TRBJ2-5	CAAQTGFQKLVF	TRAV1-1	TRAJ8	578_1
CASSQGEDRTPGANVLTF	TRBV3-1	TRBJ2-6	CAAF TG GGNKLTf	TRAV1-2	TRAJ10	578_1
CASSPGGGETQYF	TRBV18	TRBJ2-5	CAVRDRHQAGTALIF	TRAV1-2	TRAJ15	578_1
CASSGHENYGYTF	TRBV16	TRBJ1-2	CAVRGDSGNTPLVF	TRAV1-2	TRAJ29	578_1
CASSISSNSYNEQFF	TRBV19	TRBJ2-1	CAVEFGNEKLTf	TRAV12-1	TRAJ48	578_1
CASSLEQGVRSQFF	TRBV5-1	TRBJ2-1	CADTNSGGSNYKLTf	TRAV13-2	TRAJ53	578_1

CASSILITDTQYF	TRBV19	TRBJ2-3	CAMTSGNTPLVF	TRAV14DV4	TRAJ29	578_1
CATSDSGRFSGANVLTF	TRBV24-1	TRBJ2-6	CAMREVNNNARLMF	TRAV14DV4	TRAJ31	578_1
CATSDSLAGFYNEQFF	TRBV24-1	TRBJ2-1	CALDYGGATNKLIF	TRAV14DV4	TRAJ32	578_1
CASSKSGRPEMEAFF	TRBV5-6	TRBJ1-1	CAMREDNSGGGADGLTF	TRAV14DV4	TRAJ45	578_1
CASSQDPGGQGYEQYF	TRBV4-1	TRBJ2-7	CAMRGQSYGKLTf	TRAV14DV4	TRAJ52	578_1
CASSLVPGQINYGYTF	TRBV11-2	TRBJ1-2	CAMRGGSYIPTF	TRAV14DV4	TRAJ6	578_1
CASSSRRLGSYNEQFF	TRBV11-3	TRBJ2-1	CATVPASGAGSYQLTF	TRAV17	TRAJ28	578_1
CASSYQGAYNEQFF	TRBV6-6	TRBJ2-1	CALSEGGSYSGKLTf	TRAV19	TRAJ52	578_1
CASSETGSSTDTQYF	TRBV2	TRBJ2-3	CAVEDPPTGANNLFF	TRAV2	TRAJ36	578_1
CASSEGAGTEAFF	TRBV9	TRBJ1-1	CAVRHQTSGSRLTF	TRAV21	TRAJ58	578_1
CASSPAGTSTDTQYF	TRBV7-8	TRBJ2-3	CAPLKGNKLTf	TRAV24	TRAJ17	578_1
CASSKPPGGGETQYF	TRBV7-8	TRBJ2-5	CAFDNYGQNfVF	TRAV24	TRAJ26	578_1
CSVLESGSQPQHf	TRBV29-1	TRBJ1-5	CARNNNARLMF	TRAV24	TRAJ31	578_1
CASSNGYNEQFF	TRBV19	TRBJ2-1	CARAGTSYDKVIF	TRAV24	TRAJ50	578_1
CASSMGYNEQFF	TRBV19	TRBJ2-1	CALGETSYDKVIF	TRAV24	TRAJ50	578_1
CASRGESGTGELFF	TRBV28	TRBJ2-2	CASNSGGTSYGKLTf	TRAV24	TRAJ52	578_1
CASSLSGYEQYF	TRBV5-1	TRBJ2-7	CAGDESGSTLTf	TRAV25	TRAJ11	578_1
CASSPFQEAGNTIYF	TRBV19	TRBJ1-3	CAGDWYNNDMRF	TRAV25	TRAJ43	578_1
CASSLRDRVWTDQYF	TRBV5-8	TRBJ2-3	CAGRAVGNQFYF	TRAV25	TRAJ49	578_1
CASLPAGNTEAFF	TRBV7-9	TRBJ1-1	CAQGYGKLTf	TRAV25	TRAJ52	578_1
CASSLLSGRADEQYF	TRBV28	TRBJ2-7	CIVRGGIRGGGSEKLfVf	TRAV26-1	TRAJ57	578_1
CASSIQGHEQFF	TRBV6-5	TRBJ2-1	CAEIDSNYQLIW	TRAV27	TRAJ33	578_1
CASTPGTVQNSFF	TRBV28	TRBJ2-1	CAASAGDNNDMRF	TRAV29DV5	TRAJ43	578_1
CASSLLVFGTDTQYF	TRBV12-4	TRBJ2-3	CAASYNNDMRF	TRAV29DV5	TRAJ43	578_1
CASSMGYNEQFF	TRBV19	TRBJ2-1	CAASVTGDGNKLfVf	TRAV29DV5	TRAJ47	578_1
CASSLGSDLSGELFF	TRBV7-9	TRBJ2-2	CAVRDWSGGYQKVTF	TRAV3	TRAJ13	578_1
CASSEGGFDGNTIYF	TRBV19	TRBJ1-3	CAVRGGFISNFGNEKLTf	TRAV3	TRAJ48	578_1
CASSFQGFYNEQFF	TRBV27	TRBJ2-1	CAVRDAGTGNQFYF	TRAV3	TRAJ49	578_1
CASSYAESYEQYF	TRBV6-5	TRBJ2-7	CGTEMGNRDDKIIF	TRAV30	TRAJ30	578_1
CASSPSGLADSSYEQYF	TRBV9	TRBJ2-7	CAYRSADNFNKFYF	TRAV38-2DV8	TRAJ21	578_1
CASSYQGAYNEQFF	TRBV6-6	TRBJ2-1	CASIPHSGGGADGLTF	TRAV38-2DV8	TRAJ45	578_1
CASSSPGPNLYEQYF	TRBV7-2	TRBJ2-7	CLVGGNLFF	TRAV4	TRAJ36	578_1
CASSQGLGDYEQYF	TRBV4-2	TRBJ2-7	CAVSYYGGSQGNLIF	TRAV41	TRAJ42	578_1
CASSYTYRDEQFF	TRBV6-3	TRBJ2-1	CVVSAHQAGTALIF	TRAV8-2	TRAJ15	578_1
CASSLGTGRDNEQFF	TRBV5-1	TRBJ2-1	CAVGASTDKLIF	TRAV8-3	TRAJ34	578_1
CASSPSGGTYNEQFF	TRBV13	TRBJ2-1	CALRGSNdYKLSF	TRAV9-2	TRAJ20	578_1

Convergence group annotation and CRG scores for the patient's 78 TCR α and β CDR3 pairs.

GLIPH - Grouping Lymphocyte Interfaces by Paratope Hotspots

An algorithm for statistical clustering of adaptive repertoire convergence

Evaluating CRG-CASSIGGIAGAYF (2 members: CASSIGGIGELFF CASSIGGIAGAYF)												
	1 subjects and 2 clones											
Motifs: Motifs:												
CASSIGGIGELFF	TRBV19	TRBJ2-2	CAASVTGDGNKLVF	TRAV29DV5	TRAJ47	578_1						
CASSIGGIAGAYF	TRBV19	TRBJ2-5	CAGSGGLIDSYGNKLVF	TRAV35	TRAJ47	578_1						
Final scores:												
	Vsegment_p	0.0725										
	cdr3len_p	0.1651										
	lowest_hla	1										
	expansion	1										
	cluster size	0.029106402										
	motifs	0.001										
	FINAL SCORE = 2.2297366741728e-05											
Name	CDR3s	Subjects	Clones	CRG_Score	Vb_p	CDR3_p	HLA_p	Expansion_p	Motif_p	Size_p	HLA	Motifs
CRG-CASSIGGIAGAYF	2	1	2	2.23E-05	0.0725	0.1651	1	1	0.001	0.029106402		

Evaluating CRG-CASSEGSSTDTQYF (2 members: CASSETGSSTDTQYF CASSEGSSTDTQYF)												
	1 subjects and 2 clones											
Motifs: Motifs:												
CASSETGSSTDTQYF	TRBV2	TRBJ2-3	CAVEDPPTGANNLFF	TRAV2	TRAJ36	578_1						
CASSEGSSTDTQYF	TRBV2	TRBJ2-3	CAVETPQTGANNLFF	TRAV2	TRAJ36	578_1						
Final scores:												
	Vsegment_p	0.0691										
	cdr3len_p	0.1706										
	lowest_hla	1										
	expansion	1										
	cluster size	0.029106402										
	motifs	0.001										
	FINAL SCORE = 2.19596579661389e-05											
Name	CDR3s	Subjects	Clones	CRG_Score	Vb_p	CDR3_p	HLA_p	Expansion_p	Motif_p	Size_p	HLA	Motifs
CRG-CASSEGSSTDTQYF	2	1	2	2.20E-05	0.0691	0.1706	1	1	0.001	0.029106402		

Evaluating CRG-CASSYQGAYNEQFF (2 members: CASSYQGAYNEQFF CASSFQGFYNEQFF)												
	1 subjects and 2 clones											
Motifs: Motifs:												
CASSYQGAYNEQFF	TRBV6-6	TRBJ2-1	CALSEGGGTSYGKLTf	TRAV19	TRAJ52	578_1						
CASSYQGAYNEQFF	TRBV6-6	TRBJ2-1	CASIPHSGGGADGLTF	TRAV38-2DV8	TRAJ45	578_1						
CASSFQGFYNEQFF	TRBV27	TRBJ2-1	CAVRDAGTGNQFYF	TRAV3	TRAJ49	578_1						
Final scores:												
	Vsegment_p	0.0695										
	cdr3len_p	0.1765										
	lowest_hla	1										
	expansion	1										
	cluster size	0.029106402										
	motifs	0.001										
	FINAL SCORE = 2.2850621230944e-05											
Name	CDR3s	Subjects	Clones	CRG_Score	Vb_p	CDR3_p	HLA_p	Expansion_p	Motif_p	Size_p	HLA	Motifs
CRG-CASSYQGAYNEQFF	2	1	2	2.29E-05	0.0695	0.1765	1	1	0.001	0.029106402		

Evaluating CRG-CASSNGYNEQFF (2 members: CASSNGYNEQFF CASSMGYNEQFF)												
	1 subjects and 2 clones											
Motifs: Motifs:												
CASSNGYNEQFF	TRBV19	TRBJ2-1	CARAGTSYDKVIF	TRAV24	TRAJ50	578_1						
CASSMGYNEQFF	TRBV19	TRBJ2-1	CAASVTGDGNKLVF	TRAV29DV5	TRAJ47	578_1						
CASSMGYNEQFF	TRBV19	TRBJ2-1	CALGETSYDKVIF	TRAV24	TRAJ50	578_1						
Final scores:												
	Vsegment_p	0.0742										
	cdr3len_p	0.168										
	lowest_hla	1										
	expansion	1										
	cluster size	0.029106402										
	motifs	0.001										
	FINAL SCORE = 2.32210409453568e-05											
Name	CDR3s	Subjects	Clones	CRG_Score	Vb_p	CDR3_p	HLA_p	Expansion_p	Motif_p	Size_p	HLA	Motifs
CRG-CASSNGYNEQFF	2	1	2	2.32E-05	0.0742	0.168	1	1	0.001	0.029106402		

Evaluating CRG-CASSQGQGDYEQYF (2 members: CASSQGQGDYEQYF CASSQGLGDYEQYF)												
	1 subjects and 2 clones											
Motifs: Motifs:												
CASSQGQGDYEQYF	TRBV4-2	TRBJ2-7	CAVSFYGGSQGNLIF	TRAV41	TRAJ42	578_1						
CASSQGLGDYEQYF	TRBV4-2	TRBJ2-7	CAVSYYGGSQGNLIF	TRAV41	TRAJ42	578_1						

Final scores:												
	Vsegment_p	0.0709										
	cdr3len_p	0.1639										
	lowest_hla	1										
	expansion	1										
	cluster size	0.029106402										
	motifs	0.001										
	FINAL SCORE = 2.16467990723213e-05											
Name	CDR3s	Subjects	Clones	CRG_Score	Vb_p	CDR3_p	HLA_p	Expansion_p	Motif_p	Size_p	HLA	Motifs
CRG-CASSQGGDYEQYF	2	1	2	2.16E-05	0.0709	0.1639	1	1	0.001	0.029106402		