

14 July, 2021

Dear ERIC Member,

Thank you for your successful participation in the ERIC project for Harmonization of IGHV Somatic Hypermutation (SHM) Testing in chronic lymphocytic leukemia. Completing the survey about your experience in IGHV SHM analysis, the applied technique and details about reporting qualified your center for this test. Therefore, we provided 5 genomic DNA samples from different patients, as depicted below, to each lab for mutation status assessment and reporting of the findings.

Sample result overview

Sample ID	IGHV gene and allele	IGHD gene and allele	IGHJ gene and allele	IGHV gene % identity to germline	SHM status	Comments
ERIC7-1	IGHV3-48*04	IGHD5-24*01	IGHJ1*01	97.92	borderline mutated	
ERIC7-2	IGHV4-4*	Not determined	IGHJ4*02	90.97	mutated	
ERIC7-3	IGHV1-69*01	IGHD3-9*01	IGHJ4*02	100.00	unmutated	
ERIC7-4	IGHV2-5*02	IGHD3-22*01	IGHJ4*03	96.56	mutated	
ERIC7-5	IGHV3-21*01	ND	IGHJ6*02	97,19	borderline mutated	stereotyped subset #2

Please see your results below together with the requirements necessary for the certificate.

Accreditation requirements and your result	Your result	Minimal requirements	Good laboratory practice requirements
Participating in ERIC IG survey	✓	✓	✓
Covering VH FR1 – VH CDR3 of all samples	✓	✓	✓
Identification of sample ERIC7-1 as IGHV-borderline mutated	✓	✓	✓
Raise caution about the borderline somatic hypermutation status of ERIC7-1	✓	✓	✓
Identification of sample ERIC7-2 as IGHV-mutated	✓	✓	✓
Identification of sample ERIC7-3 as IGHV-unmutated	✓	✓	✓
Identification of sample ERIC7-4 as IGHV-mutated	✓	✓	✓
Identification of sample ERIC7-5 as belonging to stereotyped subset #2	✓	✓	✓
Correct annotation	✓	✓	✓
Provided Lab specific report	✓	✓	✓
Correct interpretation	✓	✓	✓
Finished and submitted analysis before the deadline	✓	✓	✓